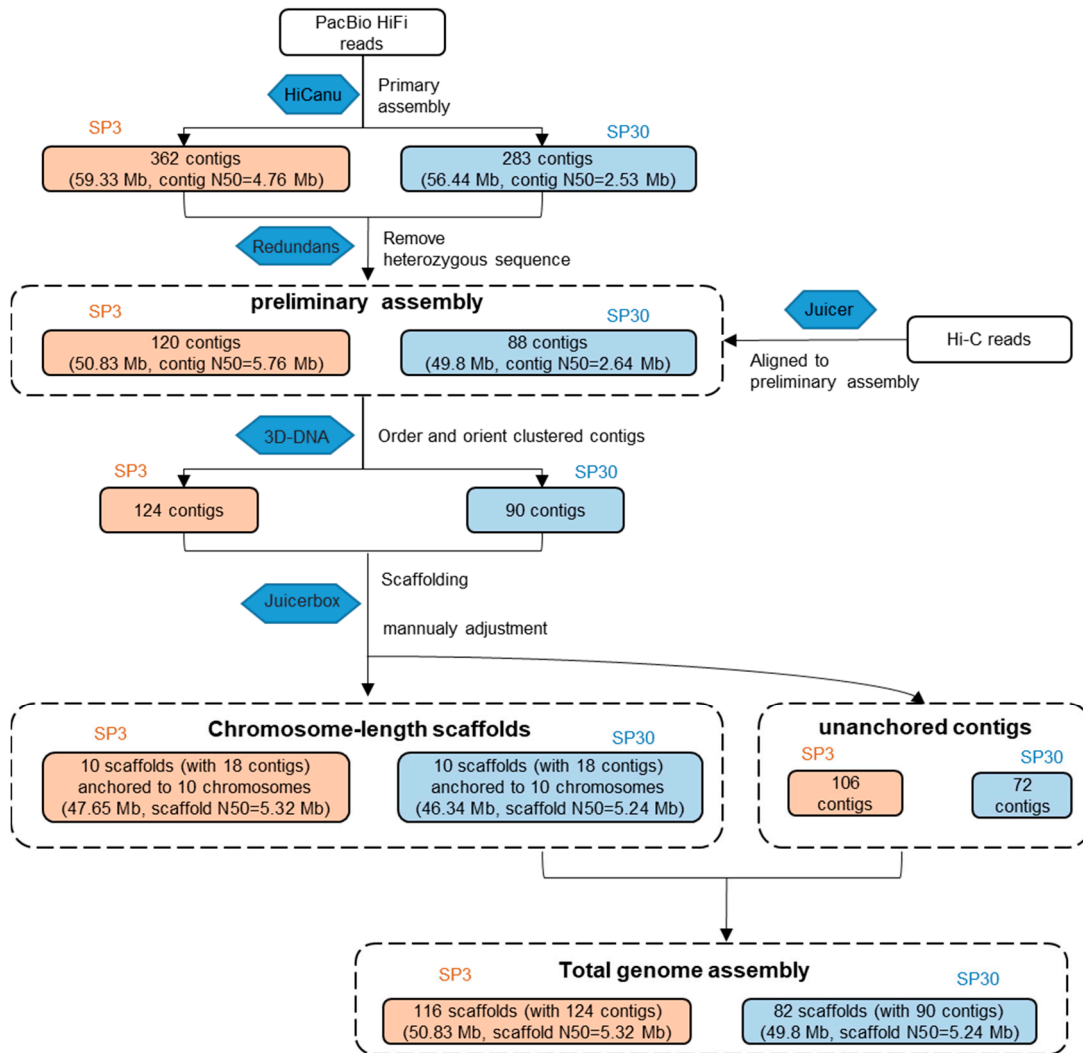
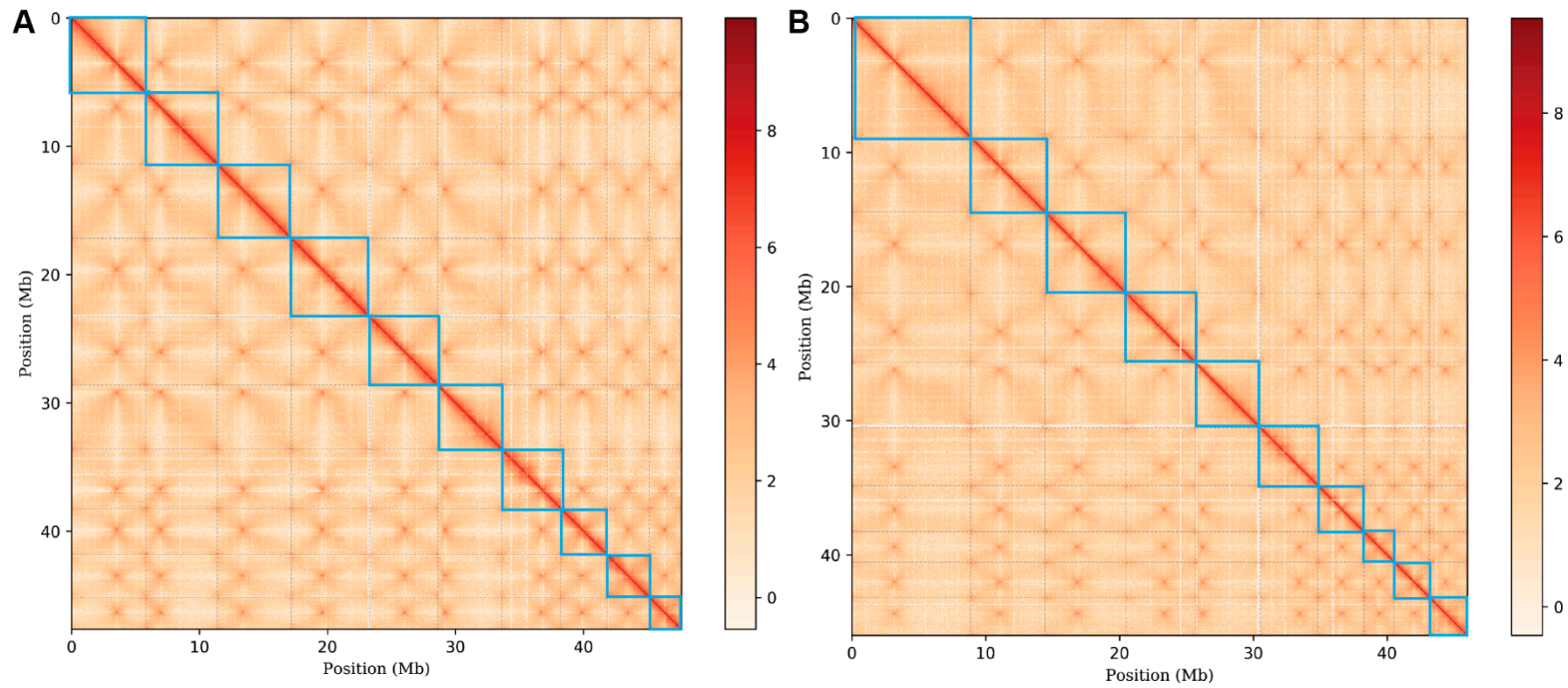


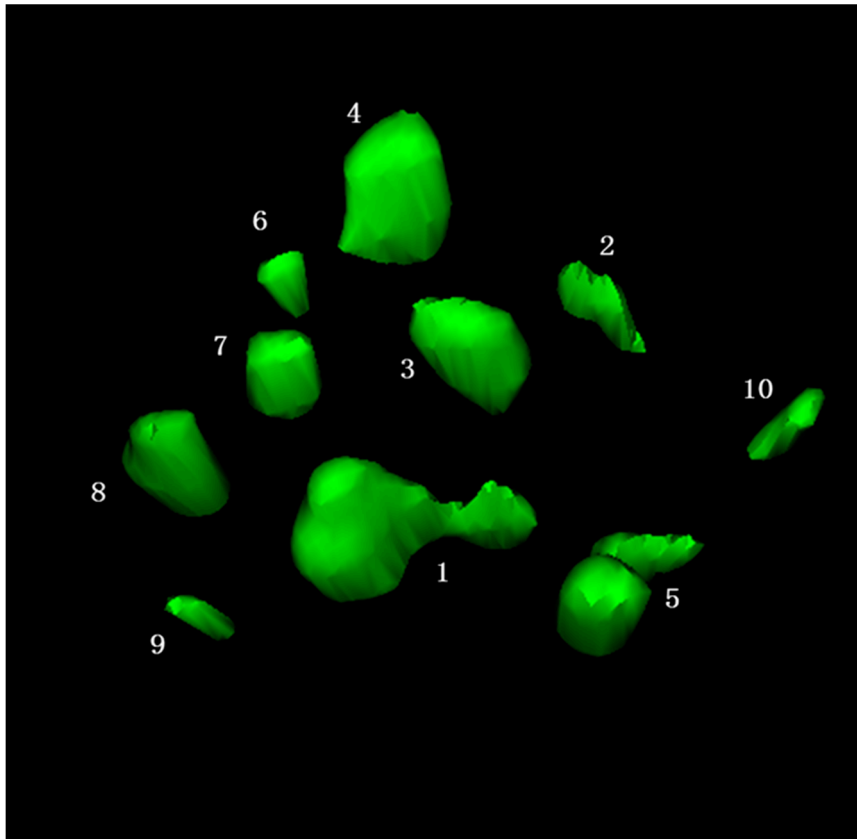
## Supplementary Materials



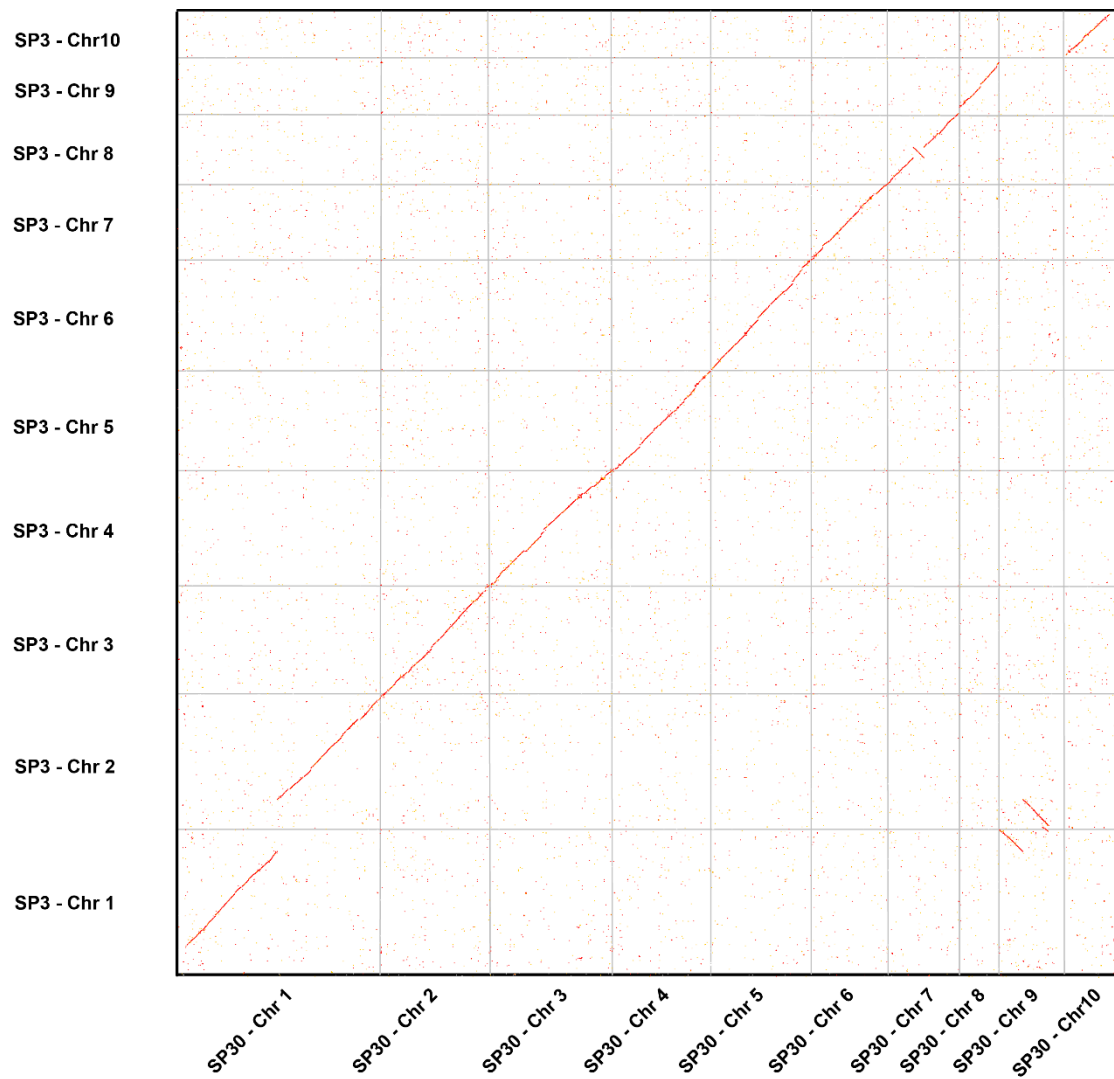
**Figure S1. Schematic diagram of the genome assembly process for strains SP3 and SP30.**



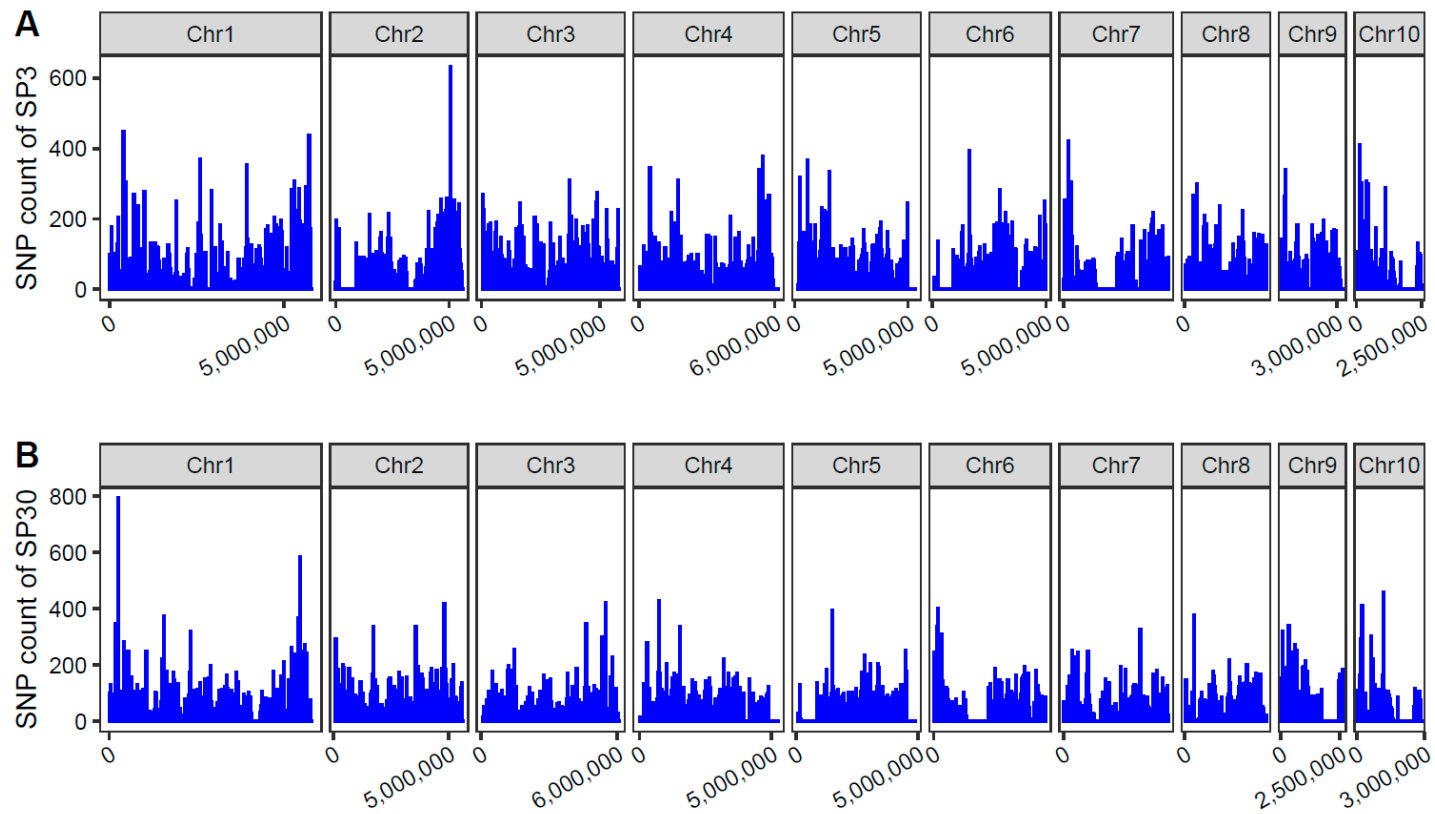
**Figure S2. Whole genome Hi-C interaction map at 50k resolution.** A: SP3. B: SP30. The color in the figure from lighter to darker indicates the increase in the intensity of the interaction, and the darker the stronger the interaction. The blue squares in the figure are the 10 chromosomes.



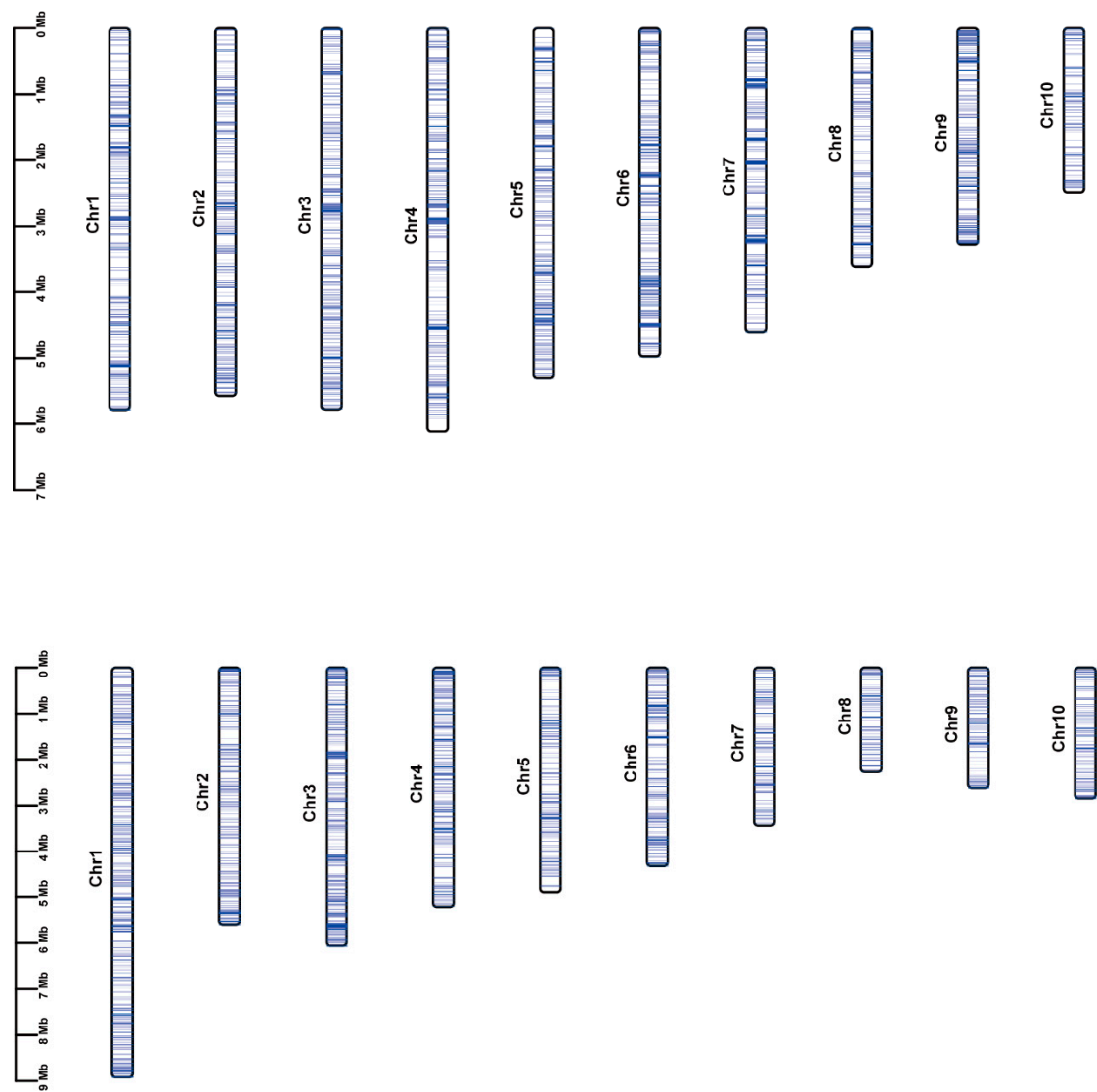
**Figure S3. 3D image of chromosome structure during cell fusion within the basidia of the dikaryon formed by mating strains SP3 and SP30.**



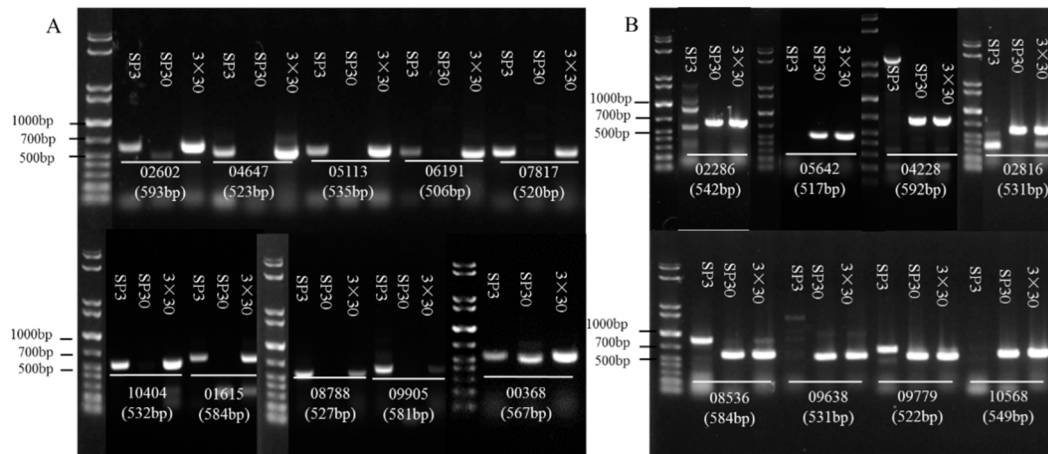
**Figure S4. Dot plot of collinearity between the genomes of strains SP3 and SP30.**



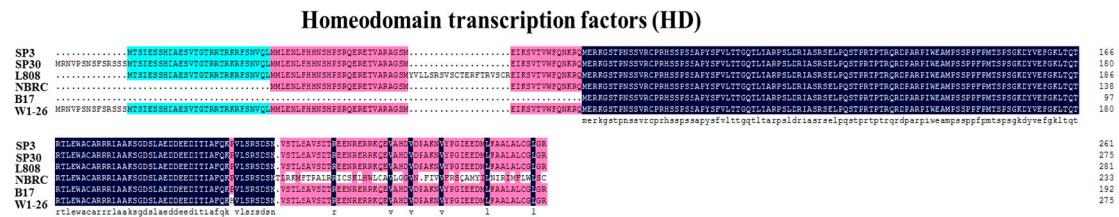
**Figure S5. The distribution of SNPs across the SP3 and SP30 chromosomes.** The X-axis represents chromosome length (bp), and the Y-axis represents the number of SNPs. Each bar represents the number of SNPs between homologous genes at 10kb sliding window.



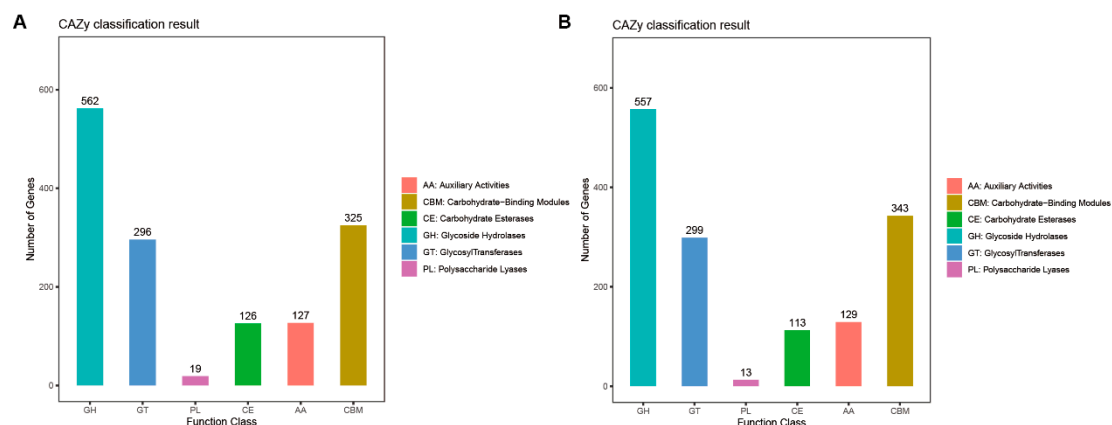
**Figure S6. Locations of the two monokaryons' rearranged genes on each chromosome.** A: Rearranged genes in the chromosomes of strain SP3. B: Rearranged genes in the chromosomes of strain SP30.



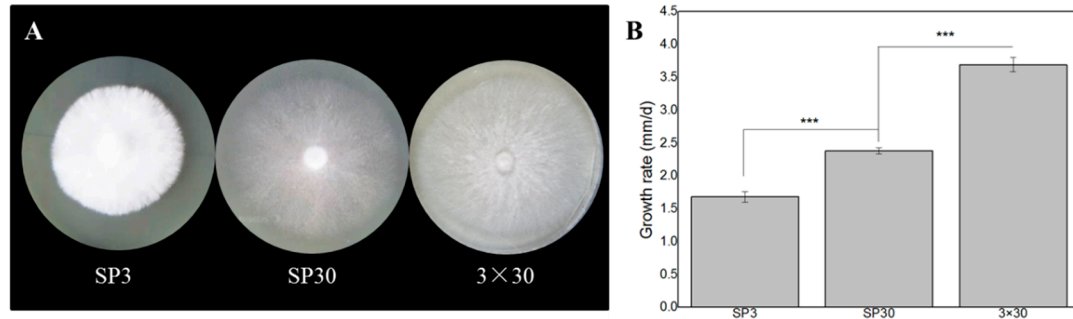
**Figure S7. PCR verification of selected unique genes.** A: Unique genes of SP3. B: Unique genes of SP30. Strain 3×30 is the dikaryon derived from mating between strains SP3 and SP30.



**Figure S8. Amino acid sequence alignment of the new homeodomain transcription factor (HD) among six monokaryotic strains of *Lentinula edodes*.**



**Figure S9. Distributions of CAZymes within the genomes of strains SP3 and SP30.** A: strain SP3. B: strain SP30.



**Figure S10. Colony morphology and growth differences between the two monokaryons and their mating product dikaryon 3x30. A: Colony morphology developed after 12 days of growth on PDA; B: Radial growth rate differences among the three strains on PDA.**



**Table S1. Contig numbers and length of (pseudo-)chromosomes within each of the two sequenced strains.**

<b>Chromosome name</b>	<b>Number of Contigs</b>	<b>Length of Super-scaffold (bp)</b>	<b>Chromosome name</b>	<b>Number of Contigs</b>	<b>Length of Super-scaffold (bp)</b>
SP3-Chr1	1	5,795,191	SP30-Chr1	1	8,935,014
SP3-Chr2	2	5,586,483	SP30-Chr2	2	5,610,796
SP3-Chr3	2	5,791,229	SP30-Chr3	1	6,077,720
SP3-Chr4	3	6,127,555	SP30-Chr4	3	5,235,283
SP3-Chr5	2	5,320,140	SP30-Chr5	1	4,901,421
SP3-Chr6	2	4,985,548	SP30-Chr6	3	4,334,663
SP3-Chr7	2	4,624,895	SP30-Chr7	2	3,460,111
SP3-Chr8	1	3,626,384	SP30-Chr8	1	2,291,016
SP3-Chr9	2	3,297,434	SP30-Chr9	1	2,637,355
SP3-Chr10	1	2,496,968	SP30-Chr10	3	2,862,145
<b>TOTAL</b>	<b>18</b>	<b>47,651,827</b>	<b>TOTAL</b>	<b>18</b>	<b>46,345,524</b>

Table S2. Statistics of repeat sequence types in each genome

	Type	RepeatMasker TEs		RepeatProteinMask TEs		De novo		Repeat Finder (TRF)		Combined TEs	
		Length (Bp)	% in genome	Length (Bp)	% in genome	Length (Bp)	% in genome	Length (Bp)	% in genome	Length (Bp)	% in genome
SP3	DNA	8,697	0.02	34,162	0.07	478,438	0.94	0	0	511,505	1.01
	LINE	7,136	0.01	79,425	0.16	331,080	0.65	0	0	380,201	0.75
	SINE	3,348	0.01	0	0	205,340	0.4	0	0	207,438	0.41
	LTR	1,077,132	2.12	4,389,225	8.63	12,833,588	25.25	0	0	13,004,473	25.58
	Tandem repeats	2,120	0	0	0	86,376	0.17	734,303	1.44	822,799	1.61
	Unknown	515	0	0	0	1,721,271	3.39	0	0	1,721,786	3.39
	Total TE	1,098,336	2.16	4,502,182	8.86	15,426,739	30.35	734,303	1.44	15,937,806	31.35
SP30	DNA	8,664	0.02	49,476	0.1	528,975	1.06	0	0	576,412	1.16
	LINE	9,787	0.02	97,664	0.2	420,114	0.84	0	0	455,977	0.92
	SINE	3,283	0.01	0	0	39,446	0.08	0	0	41,907	0.08
	LTR	975,268	1.96	4,115,631	8.26	12,341,153	24.78	0	0	12,448,254	24.99
	Tandem repeats	2,214	0.01	0	0	137,405	0.27	754,178	1.51	893,797	1.79
	Unknown	352	0	0	0	1,817,603	3.65	0	0	1,817,955	3.65
	Total TE	999,333	2.01	4,262,771	8.56	15,157,417	30.43	754,178	1.51	15,580,460	31.28

**Table S3. Summary statistics of functional gene annotations based on information from different databases**

	SP3		SP30	
	Number	Percent(%)	Number	Percent(%)
<b>Total</b>	11,455		11,245	
<b>InterPro</b>	6,953	60.7	6,901	61
<b>GO</b>	5,044	44.03	4,985	44
<b>KEGG_ALL</b>	9,839	85.89	9,673	86
<b>KEGG_KO</b>	3,590	31.34	3,523	31
<b>Swissprot</b>	5,744	50.14	5,739	51
<b>TrEMBL</b>	11,242	98.14	11,026	98
<b>NR</b>	11,258	98.28	11,035	98
<b>Annotated</b>	11,261	98.31	11,037	98
<b>Unannotated</b>	194	1.69	208	1.85

**Table S4. Annotation statistics for non-protein coding RNA within each of the two genomes.**

	Type	Copy	Average length(bp)	Total length(bp)	% of genome
<b>SP3</b>	<b>tRNA</b>	347	89	30,795	0.0606
	<b>rRNA</b>	140	2,122	297,094	0.5844
	<b>rRNA</b>	<b>18S</b>	44	1,836	0.1589
		<b>28S</b>	48	4,392	0.4147
	<b>5S</b>	48	115	5,524	0.0109
	<b>snRNA</b>	63	77	4,830	0.0095
	<b>snRNA</b>	<b>CD-box</b>	47	2,683	0.0053
		<b>splicing</b>	16	134	0.0042
<b>SP30</b>	<b>tRNA</b>	412	86	35,586	0.0715
	<b>rRNA</b>	169	2,157	364,515	0.7319
	<b>rRNA</b>	<b>18S</b>	58	1,874	0.2182
		<b>28S</b>	55	4,534	0.5007
	<b>5S</b>	56	115	6,442	0.0129
	<b>snRNA</b>	73	73	5,364	0.0108
	<b>snRNA</b>	<b>CD-box</b>	58	3,313	0.0067
		<b>splicing</b>	15	137	0.0041

**Table S5. Information of publicly available genomes of four monokaryotic strains used in collinearity analyses.**

Strain	Isolate	BioSample	Submission	Sequence method	Level	Size (Mb)	GC%	Scaffolds	Contig N50 (Mb)	GenBank FTP
L808	monokaryon	SAMN14591202	China	PacBio Sequel	Scaffold	45.8703	46.0791	25	2.16	<a href="ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/015/476/405/GCA_015476405.1_ASM1547640v1">ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/015/476/405/GCA_015476405.1_ASM1547640v1</a>
B17	monokaryon	SAMN04457462	Korea	PacBio; Illumina HiSeq	Scaffold	46.1067	45.9	31	0.85	<a href="ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/562/095/GCA_001562095.1_B17">ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/562/095/GCA_001562095.1_B17</a>
W1-26	monokaryon	SAMN03418238	China	Illumina HiSeq	Scaffold	41.8187	46.1	335	0.1	<a href="ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/700/625/GCA_001700625.1_ASM170062v1">ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/700/625/GCA_001700625.1_ASM170062v1</a>
NBRC 11120 2	monokaryon	SAMD00054105	Japan	Illumina Hiseq 2500	Scaffold	39.9229	44.7	1951	0.44	<a href="ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/003/045/GCA_002003045.1_Lene_d_assembly01">ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/002/003/045/GCA_002003045.1_Lene_d_assembly01</a>

**Table S6. Top 20 GO term analysis of synteny genes**

<b>Class</b>	<b>ID</b>	<b>Description</b>	<b>P value</b>	<b>Fg_num</b>	<b>Bg_num</b>	<b>Ratio</b>
Biological Process	GO:0009987	cellular process	5.75E-05	2548	4390	0.58
Molecular Function	GO:0043021	ribonucleoprotein complex binding	0.000549538	16	17	0.941
Molecular Function	GO:0043168	anion binding	0.000663945	997	1709	0.583
Molecular Function	GO:0003909	DNA ligase activity	0.000740123	12	12	1
Molecular Function	GO:0003910	DNA ligase (ATP) activity	0.000740123	12	12	1
Molecular Function	GO:0000988	transcription factor activity, protein binding	0.00083219	34	43	0.791
Molecular Function	GO:0016874	ligase activity	1.12E-05	106	147	0.721
Molecular Function	GO:0016740	transferase activity	0.000126033	716	1198	0.598
Cellular Component	GO:0098687	chromosomal region	0.000358785	27	31	0.871
Cellular Component	GO:0043233	organelle lumen	0.000367872	152	223	0.682
Cellular Component	GO:0070013	intracellular organelle lumen	0.000367872	152	223	0.682
Cellular Component	GO:0016592	mediator complex	0.000404134	24	27	0.889
Cellular Component	GO:0000775	chromosome, centromeric region	0.000846118	25	29	0.862
Cellular Component	GO:0005885	Arp2/3 protein complex	0.001237776	12	12	1
Cellular Component	GO:0008180	COP9 signalosome	0.001237776	12	12	1
Cellular Component	GO:0032991	macromolecular complex	0.0013853	664	1090	0.609
Cellular Component	GO:0000776	kinetochore	0.00195659	23	27	0.852
Cellular Component	GO:0031981	nuclear lumen	0.001991594	135	201	0.672
Cellular Component	GO:0043234	protein complex	0.002050707	512	832	0.615
Cellular Component	GO:0031974	membrane-enclosed lumen	0.002243533	152	229	0.664

**Table S7. Top 20 KEGG term analysis of synteny genes**

<b>Class</b>	<b>ID</b>	<b>Description</b>	<b>P value</b>	<b>Fg_num</b>	<b>Bg_num</b>	<b>Ratio</b>
Metabolism	ko00900	Terpenoid backbone biosynthesis	0.0005926	29	34	0.853
Metabolism	ko00670	One carbon pool by folate	0.007766	20	24	0.833
Metabolism	ko00640	Propanoate metabolism	0.0189288	28	37	0.757
Metabolism	ko00514	Other types of O-glycan biosynthesis	0.0318249	14	17	0.824
Metabolism	ko00780	Biotin metabolism	0.0318249	14	17	0.824
Metabolism	ko00515	Mannose type O-glycan biosynthesis	0.0376213	6	6	1
Metabolism	ko00100	Steroid biosynthesis	0.0577929	24	33	0.727
Metabolism	ko00280	Valine, leucine and isoleucine degradation	0.0594712	48	71	0.676
Metabolism	ko00062	Fatty acid elongation	0.0631628	10	12	0.833
Metabolism	ko00400	Phenylalanine, tyrosine and tryptophan biosynthesis	0.0933658	29	42	0.69
Metabolism	ko00520	Amino sugar and nucleotide sugar metabolism	0.0950497	66	102	0.647
Metabolism	ko00290	Valine, leucine and isoleucine biosynthesis	0.1020119	20	28	0.714
Metabolism	ko00562	Inositol phosphate metabolism	0.1043755	40	60	0.667
Metabolism	ko00332	Carbapenem biosynthesis	0.1123555	4	4	1
Genetic Information Processing	ko03010	Ribosome	0.0037207	130	193	0.674
Genetic Information Processing	ko04141	Protein processing in endoplasmic reticulum	0.0656539	106	166	0.639
Genetic Information Processing	ko03450	Non-homologous end-joining	0.0339706	16	20	0.8
Genetic Information Processing	ko00970	Aminoacyl-tRNA biosynthesis	0.007792	54	75	0.72
Genetic Information Processing	ko03060	Protein export	0.0314432	30	41	0.732
Cellular Processes	ko04145	Phagosome	0.0016994	60	81	0.741

**Table S8. CAZyme cluster genes that are not syntenic between strains SP3 and SP30**

CAZymes	SP3-special gene numbers	SP30-special gene numbers
GH	58	98
GT	20	36
PL	4	4
CE	7	18
AA	8	24
CBM	35	85
GH0	1	3
GH1	1	1
GH2	1	0
GH3	5	7
GH5	1	4
GH6	1	2
GH10	1	0
GH11	1	1
GH12	1	0
GH13	2	3
GH15	2	3
GH16	2	7
GH17	2	1
GH18	4	11
GH19	4	2
GH23	0	1
GH26	0	1
GH27	0	3
GH28	7	9
GH29	0	1
GH30	2	0
GH31	2	2
GH35	0	1
GH36	0	1
GH37	0	1
GH38	3	2
GH43	3	4
GH45	0	1
GH47	1	0
GH55	1	3
GH71	0	3
GH75	2	1
GH78	2	2
GH79	0	3



GH92	0	2
GH93	1	2
GH95	1	1
GH100	3	1
GH105	0	1
GH109	0	1
GH128	0	3
GH133	1	2
GH134	0	1
GT0	0	3
GT1	8	7
GT2	3	6
GT4	2	4
GT7	0	1
GT8	0	1
GT15	1	0
GT20	0	1
GT27	0	1
GT31	1	0
GT32	1	0
GT34	1	2
GT47	0	6
GT50	0	2
GT90	3	1
GT92	0	1
PL1	2	2
PL4_2	2	2
CE0	0	1
CE4	1	4
CE6	0	4
CE8	2	2
CE11	1	3
CE12	1	0
CE16	2	4
AA1	0	2
AA2	2	3
AA3	3	11
AA5	0	1
AA7	1	2
AA9	1	3
AA10	1	2
CBM1	7	12
CBM2	3	6
CBM5	0	1
CBM6	2	5
CBM13	4	16

CBM18	1	2
CBM19	0	1
CBM20	2	6
CBM21	2	1
CBM24	0	3
CBM32	1	6
CBM35	1	2
CBM43	2	0
CBM48	1	6
CBM50	4	7
CBM51	0	1
CBM57	4	9
CBM63	0	1
CBM67	1	0

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**Table S9. GO term analysis of rearranged genes between SP3 and SP30.**

The highlight lines were presented in the Figure 4.

Genome	GO_class	GO ID	Description	Fg_num	Bg_num	Pvalue	Gene percent (%)
SP3	Cellular component	GO:0000943	retrotransposon nucleocapsid	18	21	3.1E-13	85.71
	Cellular component	GO:0044428	nuclear part intracellular	42	188	0.00101	22.34
	Cellular component	GO:0030529	ribonucleoprotein complex	31	136	0.00363	22.79
	Cellular component	GO:1990904	ribonucleoprotein complex	31	137	0.0041	22.63
	Cellular component	GO:0005840	ribosome	21	97	0.02861	21.65
	Cellular component	GO:0043228	non-membrane-bounded organelle intracellular non-	41	225	0.04739	18.22
	Cellular component	GO:0043232	membrane-bounded organelle	41	225	0.04739	18.22
	Molecular function	GO:0004672	protein kinase activity	57	214	0.00012	26.64
	Molecular function	GO:0016301	kinase activity	63	251	0.00034	25.10

Molecular function	GO:0015926	glucosidase activity	9	16	0.00037	56.25
Molecular function	GO:0004674	protein serine/threonine kinase activity	15	39	0.00095	38.46
Molecular function	GO:0061134	peptidase regulator activity	6	9	0.00115	66.67
Molecular function	GO:0016773	phosphotransferase activity, alcohol group as acceptor	58	241	0.00175	24.07
Molecular function	GO:0020037	heme binding	39	148	0.00178	26.35
Molecular function	GO:0046906	tetrapyrrole binding	39	148	0.00178	26.35
Molecular function	GO:0004470	malic enzyme activity malate dehydrogenase	5	7	0.00204	71.43
Molecular function	GO:0004471	(decarboxylating) (NAD+) activity	5	7	0.00204	71.43
Molecular function	GO:0004573	mannosyl- oligosaccharide glucosidase activity	5	7	0.00204	71.43
Molecular function	GO:0016615	malate dehydrogenase activity	5	7	0.00204	71.43
Molecular function	GO:0004866	endopeptidase inhibitor activity	4	5	0.00339	80.00

Molecular function	GO:0004867	serine-type endopeptidase inhibitor activity	4	5	0.00339	80.00
Molecular function	GO:0030414	peptidase inhibitor activity	4	5	0.00339	80.00
Molecular function	GO:0061135	endopeptidase regulator activity	4	5	0.00339	80.00
Molecular function	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen transferase activity, transferring phosphorus-containing groups	38	151	0.00481	25.17
Molecular function	GO:0016772	DNA helicase activity	73	331	0.00555	22.05
Molecular function	GO:0003678	oxidoreductase activity	9	23	0.00874	39.13
Molecular function	GO:0016491	iron ion binding	119	593	0.01273	20.07
Molecular function	GO:0005506	ATP phosphoribosyltransferase activity	33	136	0.01449	24.26
Molecular function	GO:0003879	catalase activity	3	4	0.01641	75.00
Molecular function	GO:0004096		3	4	0.01641	75.00

Molecular function	GO:0004523	RNA-DNA hybrid ribonuclease activity	3	4	0.01641	75.00
Molecular function	GO:0004748	ribonucleoside- diphosphate reductase activity, thioredoxin disulfide as acceptor	3	4	0.01641	75.00
Molecular function	GO:0016725	oxidoreductase activity, acting on CH or CH2 groups	3	4	0.01641	75.00
Molecular function	GO:0016728	oxidoreductase activity, acting on CH or CH2 groups, disulfide as acceptor	3	4	0.01641	75.00
Molecular function	GO:0016872	intramolecular lyase activity	3	4	0.01641	75.00
Molecular function	GO:0061731	ribonucleoside- diphosphate reductase activity	3	4	0.01641	75.00
Molecular function	GO:0046914	transition metal ion binding	77	369	0.01796	20.87
Molecular function	GO:0005524	ATP binding adenyl	108	540	0.01931	20.00
Molecular function	GO:0032559	ribonucleotide binding	108	540	0.01931	20.00

Molecular function	GO:0030554	adenyl nucleotide binding	108	541	0.02034	19.96
Molecular function	GO:0004553	hydrolase activity, hydrolyzing O- glycosyl compounds	35	153	0.02872	22.88
Molecular function	GO:0004857	enzyme inhibitor activity	4	8	0.0311	50.00
Molecular function	GO:0004932	mating-type factor pheromone receptor activity	4	8	0.0311	50.00
Molecular function	GO:0016503	pheromone receptor activity	4	8	0.0311	50.00
Molecular function	GO:0004934	mating-type alpha- factor pheromone receptor activity	3	5	0.03593	60.00
Molecular function	GO:0036318	peptide pheromone receptor activity	3	5	0.03593	60.00
Molecular function	GO:0004601	peroxidase activity	8	24	0.03606	33.33
Molecular function	GO:0004497	monooxygenase activity	14	52	0.04271	26.92
Molecular function	GO:0016798	hydrolase activity, acting on glycosyl bonds	35	159	0.04801	22.01
Molecular function	GO:0001653	peptide receptor activity	4	9	0.0487	44.44

Molecular function	GO:0008528	G-protein coupled peptide receptor activity	4	9	0.0487	44.44
Biological process	GO:0015074	DNA integration	23	25	1.7E-16	92.00
Biological process	GO:0006259	DNA metabolic process	56	180	5.1E-07	31.11
Biological process	GO:0008152	metabolic process	435	2374	4.5E-06	18.32
Biological process	GO:0006468	protein phosphorylation	53	205	0.00033	25.85
Biological process	GO:0000723	telomere maintenance	8	15	0.00119	53.33
Biological process	GO:0032200	telomere organization	8	15	0.00119	53.33
Biological process	GO:0060249	anatomical structure homeostasis	8	15	0.00119	53.33
Biological process	GO:0009405	pathogenesis	4	5	0.00326	80.00
Biological process	GO:0055114	oxidation-reduction process	116	562	0.0033	20.64
Biological process	GO:0051276	chromosome organization	26	93	0.00363	27.96
Biological process	GO:0043170	macromolecule metabolic process	246	1311	0.00376	18.76
Biological process	GO:0044238	primary metabolic process	318	1745	0.00408	18.22



Biological process	GO:0016310	phosphorylation	54	233	0.00445	23.18
Biological process	GO:0009403	toxin biosynthetic process	5	8	0.00447	62.50
Biological process	GO:0009404	toxin metabolic process	5	8	0.00447	62.50
Biological process	GO:0043385	mycotoxin metabolic process	5	8	0.00447	62.50
Biological process	GO:0043386	mycotoxin biosynthetic process	5	8	0.00447	62.50
Biological process	GO:0044710	single-organism metabolic process	200	1060	0.00928	18.87
Biological process	GO:0071704	organic substance metabolic process	325	1816	0.01387	17.90
Biological process	GO:0019748	secondary metabolic process	5	10	0.01505	50.00
Biological process	GO:0044550	secondary metabolite biosynthetic process	5	10	0.01505	50.00
Biological process	GO:0051704	multi-organism process	5	10	0.01505	50.00
Biological process	GO:0043484	regulation of RNA splicing	3	4	0.01595	75.00
Biological process	GO:0046165	alcohol biosynthetic process	4	7	0.01727	57.14

Biological process	GO:0046700	heterocycle catabolic process cellular	11	34	0.01758	32.35
Biological process	GO:0044260	macromolecule metabolic process	217	1175	0.01793	18.47
Biological process	GO:0019538	protein metabolic process	133	689	0.01925	19.30
Biological process	GO:1901361	organic cyclic compound catabolic process	11	35	0.02192	31.43
Biological process	GO:1901606	alpha-amino acid catabolic process	5	11	0.0239	45.45
Biological process	GO:0006979	response to oxidative stress	7	19	0.02712	36.84
Biological process	GO:0000105	histidine biosynthetic process	4	8	0.03006	50.00
Biological process	GO:0006547	histidine metabolic process	4	8	0.03006	50.00
Biological process	GO:0052803	imidazole- containing compound metabolic process	4	8	0.03006	50.00
Biological process	GO:0009311	oligosaccharide metabolic process	5	12	0.0355	41.67
Biological process	GO:0044270	cellular nitrogen compound catabolic process	10	33	0.03619	30.30

	Biological process	GO:1901565	organonitrogen compound catabolic process	8	25	0.04316	32.00
SP30	Cellular component	GO:0000943	retrotransposon nucleocapsid	10	13	1.4E-07	76.92
	Cellular component	GO:0045263	proton-transporting ATP synthase complex, coupling factor F(o)	7	13	0.00036	53.85
	Cellular component	GO:0045259	proton-transporting ATP synthase complex	7	17	0.00264	41.18
	Cellular component	GO:0033177	proton-transporting two-sector ATPase complex, proton-transporting domain	7	19	0.0055	36.84
	Cellular component	GO:0005576	extracellular region	8	25	0.008	32.00
	Cellular component	GO:0005618	cell wall	5	13	0.01551	38.46
	Cellular component	GO:0009277	fungus-type cell wall	5	13	0.01551	38.46
	Cellular component	GO:0030312	external encapsulating structure	5	13	0.01551	38.46
	Cellular component	GO:0000118	histone deacetylase complex	3	5	0.01553	60.00
	Cellular component	GO:0070824	SHREC complex	3	5	0.01553	60.00

Cellular component	GO:0017053	transcriptional repressor complex	3	6	0.02825	50.00
Cellular component	GO:0090568	nuclear transcriptional repressor complex	3	6	0.02825	50.00
Cellular component	GO:0016469	proton-transporting two-sector ATPase complex	7	27	0.04089	25.93
Cellular component	GO:0005887	integral component of plasma membrane	2	3	0.04218	66.67
Cellular component	GO:0031226	intrinsic component of plasma membrane	2	3	0.04218	66.67
Cellular component	GO:0032592	integral component of mitochondrial membrane	2	3	0.04218	66.67
Cellular component	GO:0098573	intrinsic component of mitochondrial membrane	2	3	0.04218	66.67
Cellular component	GO:0032993	protein-DNA complex	5	17	0.04938	29.41
Molecular function	GO:0003678	DNA helicase activity	23	40	2.4E-09	57.50
Molecular function	GO:0004386	helicase activity	26	58	2E-07	44.83
Molecular function	GO:0004523	RNA-DNA hybrid ribonuclease activity	6	7	0.0001	85.71

Molecular function	GO:0017111	nucleoside-triphosphatase activity	57	236	0.00066	24.15
Molecular function	GO:0016462	pyrophosphatase activity	57	242	0.00128	23.55
Molecular function	GO:0003777	microtubule motor activity	9	19	0.0014	47.37
Molecular function	GO:0016818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	57	245	0.00174	23.27
Molecular function	GO:0016817	hydrolase activity, acting on acid anhydrides	57	248	0.00234	22.98
Molecular function	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	37	147	0.00273	25.17
Molecular function	GO:0004866	endopeptidase inhibitor activity serine-type	4	5	0.00292	80.00
Molecular function	GO:0004867	endopeptidase inhibitor activity	4	5	0.00292	80.00
Molecular function	GO:0030414	peptidase inhibitor activity	4	5	0.00292	80.00

Molecular function	GO:0061135	endopeptidase regulator activity	4	5	0.00292	80.00
Molecular function	GO:0020037	heme binding	36	143	0.00308	25.17
Molecular function	GO:0046906	tetrapyrrole binding	36	143	0.00308	25.17
Molecular function	GO:0016891	endoribonuclease activity, producing 5'-phosphomonoesters	7	15	0.00538	46.67
Molecular function	GO:0004672	protein kinase activity	46	200	0.00595	23.00
Molecular function	GO:0005506	iron ion binding	33	134	0.00648	24.63
Molecular function	GO:0046914	transition metal ion binding	76	363	0.00675	20.94
Molecular function	GO:0016893	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	7	16	0.00826	43.75
Molecular function	GO:0003774	motor activity	9	25	0.01248	36.00
Molecular function	GO:0061134	peptidase regulator activity	4	7	0.01559	57.14

Molecular function	GO:0030246	carbohydrate binding	10	31	0.01963	32.26
Molecular function	GO:0016301	kinase activity	50	236	0.02096	21.19
Molecular function	GO:0001871	pattern binding	8	23	0.02259	34.78
Molecular function	GO:0030247	polysaccharide binding	8	23	0.02259	34.78
Molecular function	GO:0004521	endoribonuclease activity	7	19	0.02345	36.84
Molecular function	GO:0016787	hydrolase activity	156	846	0.0237	18.44
Molecular function	GO:0008521	acetyl-CoA transporter activity	2	2	0.02596	100.00
Molecular function	GO:0022843	voltage-gated cation channel activity	2	2	0.02596	100.00
Molecular function	GO:0051184	cofactor transporter activity	2	2	0.02596	100.00
Molecular function	GO:0051185	coenzyme transporter activity	2	2	0.02596	100.00
Molecular function	GO:0016773	phosphotransferase activity, alcohol group as acceptor	48	228	0.02607	21.05
Molecular function	GO:0008017	microtubule binding	7	20	0.0312	35.00
Molecular function	GO:0015926	glucosidase activity	5	12	0.0317	41.67

Molecular function	GO:0016772	transferase activity, transferring phosphorus-containing groups	64	320	0.03215	20.00
Molecular function	GO:0004339	glucan 1,4-alpha-glucosidase activity	3	5	0.03234	60.00
Molecular function	GO:2001070	starch binding	3	5	0.03234	60.00
Molecular function	GO:0004857	enzyme inhibitor activity	4	9	0.04291	44.44
Molecular function	GO:0005488	binding	414	2442	0.04417	16.95
Molecular function	GO:0032559	adenyl ribonucleotide binding	99	527	0.04485	18.79
Molecular function	GO:0005199	structural constituent of cell wall	5	13	0.04485	38.46
Molecular function	GO:0030554	adenyl nucleotide binding	99	528	0.04687	18.75
Biological process	GO:0015074	DNA integration	24	25	8.1E-19	96.00
Biological process	GO:0000723	telomere maintenance	24	33	3.5E-13	72.73
Biological process	GO:0032200	telomere organization	24	33	3.5E-13	72.73



Biological process	GO:0060249	anatomical structure homeostasis	24	33	3.5E-13	72.73
Biological process	GO:0006259	DNA metabolic process	67	189	6.2E-12	35.45
Biological process	GO:0042592	homeostatic process	28	65	1.2E-07	43.08
Biological process	GO:0065008	regulation of biological quality	31	84	1.5E-06	36.90
Biological process	GO:0051276	chromosome organization	35	103	3E-06	33.98
Biological process	GO:0008152	metabolic process	403	2322	4.5E-05	17.36
Biological process	GO:0006281	DNA repair	35	120	0.00012	29.17
Biological process	GO:0006974	cellular response to DNA damage stimulus	35	125	0.0003	28.00
Biological process	GO:0043170	macromolecule metabolic process	236	1282	0.00065	18.41
Biological process	GO:0006950	response to stress	38	147	0.00093	25.85
Biological process	GO:0033554	cellular response to stress	35	133	0.00104	26.32
Biological process	GO:0006928	movement of cell or subcellular component	9	19	0.0012	47.37

Biological process	GO:0007018	microtubule-based movement	9	19	0.0012	47.37
Biological process	GO:1902589	single-organism organelle organization	33	126	0.00158	26.19
Biological process	GO:0006468	protein phosphorylation	47	198	0.00178	23.74
Biological process	GO:0071704	organic substance metabolic process	312	1787	0.00237	17.46
Biological process	GO:0044238	primary metabolic process	299	1710	0.0032	17.49
Biological process	GO:0044260	cellular macromolecule metabolic process	209	1154	0.00465	18.11
Biological process	GO:0015988	energy coupled proton transmembrane transport, against electrochemical gradient	7	16	0.00739	43.75
Biological process	GO:0015991	ATP hydrolysis coupled proton transport	7	16	0.00739	43.75
Biological process	GO:0090662	ATP hydrolysis coupled transmembrane transport	7	16	0.00739	43.75
Biological process	GO:0006754	ATP biosynthetic process	8	20	0.00802	40.00

		energy coupled proton transport, down				
Biological process	GO:0015985	electrochemical gradient	8	20	0.00802	40.00
Biological process	GO:0015986	ATP synthesis coupled proton transport	8	20	0.00802	40.00
Biological process	GO:0006996	organelle organization	42	188	0.0097	22.34
Biological process	GO:0009142	nucleoside triphosphate biosynthetic process	8	21	0.0112	38.10
Biological process	GO:0009145	purine nucleoside triphosphate biosynthetic process	8	21	0.0112	38.10
Biological process	GO:0009201	ribonucleoside triphosphate biosynthetic process	8	21	0.0112	38.10
Biological process	GO:0009206	purine ribonucleoside triphosphate biosynthetic process	8	21	0.0112	38.10
Biological process	GO:0016310	phosphorylation	48	223	0.01207	21.52
Biological process	GO:0007017	microtubule-based process	11	34	0.01241	32.35

Biological process	GO:0009163	nucleoside biosynthetic process	9	26	0.0145	34.62
Biological process	GO:0042451	purine nucleoside biosynthetic process	9	26	0.0145	34.62
Biological process	GO:0042455	ribonucleoside biosynthetic process	9	26	0.0145	34.62
Biological process	GO:0046129	purine ribonucleoside biosynthetic process	9	26	0.0145	34.62
Biological process	GO:1901659	glycosyl compound biosynthetic process	9	26	0.0145	34.62
Biological process	GO:0006793	phosphorus metabolic process	74	373	0.01605	19.84
Biological process	GO:0006796	phosphate-containing compound metabolic process	73	369	0.01788	19.78
Biological process	GO:0090304	nucleic acid metabolic process	120	645	0.01864	18.60
Biological process	GO:0050896	response to stimulus	56	276	0.02291	20.29
Biological process	GO:0006450	regulation of translational fidelity	2	2	0.02499	100.00

	Biological process	GO:0009127	purine nucleoside monophosphate biosynthetic process	8	24	0.02624	33.33
	Biological process	GO:0009156	ribonucleoside monophosphate biosynthetic process	8	24	0.02624	33.33
	Biological process	GO:0009168	purine ribonucleoside monophosphate biosynthetic process	8	24	0.02624	33.33
	Biological process	GO:0051716	cellular response to stimulus	53	262	0.02801	20.23
	Biological process	GO:0015672	monovalent inorganic cation transport	12	43	0.03029	27.91
	Biological process	GO:0006139	nucleobase-containing compound metabolic process	132	729	0.03206	18.11
	Biological process	GO:0009124	nucleoside monophosphate biosynthetic process	8	25	0.03342	32.00
	Biological process	GO:0065007	biological regulation	81	427	0.03449	18.97
	Biological process	GO:0006725	cellular aromatic compound metabolic process	138	770	0.03885	17.92

Biological process	GO:0006818	hydrogen transport	10	35	0.03958	28.57
Biological process	GO:0015992	proton transport	10	35	0.03958	28.57
Biological process	GO:1902600	hydrogen ion transmembrane transport	10	35	0.03958	28.57
Biological process	GO:1901360	organic cyclic compound metabolic process	140	783	0.0402	17.88
Biological process	GO:0034641	cellular nitrogen compound metabolic process	161	911	0.04022	17.67
Biological process	GO:0051704	multi-organism process	4	9	0.04026	44.44
Biological process	GO:0009152	purine ribonucleotide biosynthetic process	8	26	0.04183	30.77
Biological process	GO:0009260	purine ribonucleotide biosynthetic process	8	26	0.04183	30.77
Biological process	GO:0046390	ribose phosphate biosynthetic process	8	26	0.04183	30.77
Biological process	GO:0072522	purine-containing compound biosynthetic process	9	31	0.04519	29.03

Biological process	GO:0046483	heterocycle metabolic process	137	768	0.04553	17.84
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**Table S10. KEGG term analysis of rearranged genes between SP3 and SP30**

Genome	KEGG_A_class	KEGG_B_class	Pathway ID	Pathway	out (319)	All (2086)	P value	K_IDs
SP3	Organismal Systems	Aging	ko04213	Longevity regulating pathway - multiple species	15	34	4.94E-05	K04345+K03283+K03283+K03283+K03781+K03283+K06067+K04564+K03781+K03695+K03781+K12767+K07203+K07203+K07827
	Metabolism	Nucleotide metabolism	ko00240	Pyrimidine metabolism	15	40	0.0004433	K10808+K10807+K10807+K10808+K01591+K10807+K10808+K06966+K06966+K10808+K10807+K10807+K10808+K03783+K13800
	Metabolism	Metabolism of other amino acids	ko00480	Glutathione metabolism	16	46	0.0007621	K10808+K10807+K10807+K10808+K00799+K00799+K00799+K07160+K10807+K10808+K01469+K18592+K10808+K10807+K10807+K10808
	Genetic Information Processing	Transcription	ko03040	Spliceosome	25	103	0.009632	K12858+K03283+K03283+K12812+K12832+K11096+K12840+K03283+K12856+K12843+K12840+K03283+K12856+K12860+K12860+K12867+K12840+K12870+K12840+K12834+K12815+K12815+K12815+K12812+K12844
	Metabolism	Nucleotide metabolism	ko00230	Purine metabolism	16	62	0.0202741	K10808+K10807+K10807+K10808+K00365+K01477+K10807+K10808+K06966+K06966+K10808+K10807+K10807+K01487+K10808+K03783
	Genetic Information Processing	Folding, sorting and degradation	ko04141	Protein processing in endoplasmic reticulum	20	88	0.038509	K03283+K09490+K12670+K09490+K03283+K03283+K01230+K06689+K03283+K01230+K13993+K13993+K09518+K13993+K10575+K10088+K14005+K13993+K10661+K09503
	Metabolism	Metabolism of other amino acids	ko00460	Cyanoamino acid metabolism	7	23	0.0497053	K05349+K05349+K01188+K05349+K05349+K18592+K13051
	Metabolism	Carbohydrate metabolism	ko00053	Ascorbate and aldarate metabolism	5	15	0.0654789	K00012+K00128+K01053+K00128+K00128
	Environmental Information Processing	Signal transduction	ko04011	MAPK signaling pathway - yeast	18	85	0.086753	K07973+K11246+K11229+K19860+K04627+K04627+K04627+K19860+K03781+K11227+K03114+K03781+K02220+K03781+K04627+K04563+K04371+K10591
	Genetic Information Processing	Replication and repair	ko03430	Mismatch repair	8	33	0.1187127	K10756+K03657+K10756+K10756+K10858+K10756+K10756+K10755



SP30	Metabolism	Amino acid metabolism	ko00340	Histidine metabolism	7	29	0.142154 <sub>2</sub>	K00128+K00765+K00765+K01814+K00128+K00765+K00128
	Cellular Processes	Cell growth and death	ko04113	Meiosis - yeast	14	68	0.144515 <sub>2</sub>	K04345+K03351+K03348+K02540+K03114+K02220+K12767+K07203+K07203+K02216+K04563+K06269+K02178+K07827
	Metabolism	Carbohydrate metabolism	ko00040	Pentose and glucuronate interconversions	6	25	0.171225 <sub>3</sub>	K01213+K00012+K00963+K00008+K01213+K00008
	Metabolism	Global and overview maps	ko01200	Carbon metabolism	20	106	0.179580 <sub>9</sub>	K14454+K01624+K15634+K00027+K00122+K00237+K01053+K17066+K03781+K00237+K03781+K00234+K03781+K00029+K00029+K00234+K00029+K00029+K00927+K17066
	Metabolism	Metabolism of cofactors and vitamins	ko00790	Folate biosynthesis	4	15	0.185802 <sub>5</sub>	K03635+K20457+K20457+K01113
	Metabolism	Energy metabolism	ko00910	Nitrogen metabolism	4	15	0.185802 <sub>5</sub>	K00459+K15371+K00459+K00459
	Metabolism	Glycan biosynthesis and metabolism	ko00513	Various types of N-glycan biosynthesis	6	26	0.195838 <sub>8</sub>	K12670+K01230+K03847+K01230+K03847+K03847
	Genetic Information Processing	Folding, sorting and degradation	ko04120	Ubiquitin mediated proteolysis	13	66	0.198040 <sub>9</sub>	K03361+K03361+K10577+K10686+K03351+K06689+K03348+K03178+K03361+K10575+K10590+K10591+K10582
	Metabolism	Amino acid metabolism	ko00380	Tryptophan metabolism	9	43	0.200366 <sub>7</sub>	K00128+K01426+K03781+K03781+K03781+K00128+K00486+K01556+K00128
	Genetic Information Processing	Translation	ko03015	mRNA surveillance pathway	12	62	0.229051 <sub>5</sub>	K03265+K12812+K15542+K03267+K03267+K03267+K03267+K03267+K03267+K06269+K12812+K00565
SP30	Environmental Information Processing	Signal transduction	ko04011	MAPK signaling pathway - yeast	26	91	0.000174 <sub>1</sub>	K07973+K10591+K19860+K19860+K04371+K04627+K04627+K04627+K02677+K02677+K02677+K19704+K19704+K11227+K03114+K12412+K02220+K06630+K04371+K02516+K19860+K19806+K00889+K19838+K09265+K09051
	Genetic Information Processing	Transcription	ko03040	Spliceosome	24	102	0.005857 <sub>5</sub>	K12871+K12858+K12813+K12813+K12624+K12811+K12811+K12852+K12813+K12854+K12870+K12860+K12860+K12860+K12812+K12877+K12897+K12854+K12854+K12854+K12854+K12854+K12820+K12811

Metabolism	Carbohydrate metabolism	ko00500	Starch and sucrose metabolism	14	54	0.0141855	K01176+K05349+K05349+K01196+K01178+K01196+K01178+K01178+K00963+K05349+K05349+K01179+K01188+K01194
Metabolism	Lipid metabolism	ko01040	Biosynthesis of unsaturated fatty acids	7	21	0.0202875	K10256+K10256+K10256+K07513+K10256+K10256+K10256
Genetic Information Processing	Folding, sorting and degradation	ko04120	Ubiquitin mediated proteolysis	16	68	0.0228466	K03361+K03361+K10686+K10686+K10591+K10590+K03361+K10592+K10592+K04554+K03361+K03361+K10575+K03357+K10579+K03360
Environmental Information Processing	Signal transduction	ko04070	Phosphatidylinositol signaling system	8	27	0.0275011	K02677+K02677+K02677+K07756+K01099+K00889+K05857+K00915
Metabolism	Global and overview maps	ko01212	Fatty acid metabolism	10	39	0.0384956	K10256+K10256+K01897+K00249+K10256+K07513+K01897+K10256+K10256+K10256
Environmental Information Processing	Membrane transport	ko02010	ABC transporters	4	10	0.0402952	K05658+K05658+K05658+K05658
Genetic Information Processing	Replication and repair	ko03440	Homologous recombination	7	25	0.0510998	K10879+K10901+K10901+K10901+K10901+K10901+K10873
Genetic Information Processing	Translation	ko03013	RNA transport	23	117	0.0538224	K03257+K14288+K12160+K14290+K14290+K03260+K14315+K14288+K03259+K03259+K14325+K14309+K14288+K14298+K14298+K02516+K14326+K12812+K12877+K14303+K13126+K00784+K14288
Metabolism	Metabolism of other amino acids	ko00460	Cyanoamino acid metabolism	6	22	0.0771401	K05349+K05349+K05349+K05349+K18592+K01188
Cellular Processes	Cell growth and death	ko04111	Cell cycle - yeast	17	92	0.1390532	K03361+K03361+K02365+K06682+K04371+K06636+K02179+K03114+K12412+K02220+K03361+K04371+K03361+K03361+K02516+K03357+K03360
Metabolism	Biosynthesis of other secondary metabolites	ko00232	Caffeine metabolism	1	1	0.1407767	K00365
Metabolism	Lipid metabolism	ko00561	Glycerolipid metabolism	7	32	0.1527004	K00128+K00128+K15728+K15728+K07407+K07407+K13519

Metabolism	Energy metabolism	ko00190	Oxidative phosphorylation	14	75	0.159289	K03946+K02132+K02267+K03935+K02259+K02259+K02128+K02133+K02128+K02128+K02128+K02128+K02128+K02128
Metabolism	Lipid metabolism	ko00071	Fatty acid degradation	7	33	0.171921 6	K00128+K00128+K01897+K00249+K07513+K01897+K00121
Metabolism	Energy metabolism	ko00680	Methane metabolism	5	22	0.187628 4	K00122+K01624+K17066+K17066+K00121
Metabolism	Metabolism of cofactors and vitamins	ko00860	Porphyrin and chlorophyll metabolism	4	18	0.240716 9	K21480+K01719+K02259+K02259
Metabolism	Lipid metabolism	ko00600	Sphingolipid metabolism	5	25	0.269879 5	K12351+K07407+K07407+K04708+K04709
Metabolism	Glycan biosynthesis and metabolism	ko00603	Glycosphingolipid biosynthesis - globo and isoglobo series	2	8	0.313555	K07407+K07407

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**Table S11. Unique genes and primers for PCR analysis**

No	Gene name	Chromosome	Length (bp)	Function	Primer name	Primer sequence
1	gene-Led00368-sp3	Superscaffold1	1197	hypothetical protein	00368.1-F 00368.1-R	TACCTTCCTCTCCCACTCGG AATCTGCCTTTCTCAGCCC
2	gene-Led02602-sp3	Superscaffold2	2241	ribonucleoside-diphosphate reductase subunit M1	02602.1-F 02602.1-R	CATGGAGCGCTTGAAAGTCG CTTCGCGATCATCAGCTTGC
3	gene-Led04647-sp3	Superscaffold3	2546	ATP-dependent DNA helicase PIF1	04647.1-F 04647.1-R	CTCTCATGCCGACCGCTATT GTCCTCTGCGGTGACTTTCA
4	gene-Led05113-sp3	Superscaffold4	1414	hypothetical protein	05113.1-F 05113.1-R	CGGCGTGTTGGAACATGATC CACCAGGGCTGAAATGCAAC
5	gene-Led06191-sp3	Superscaffold5	688	alternative cyclin pcl1	06191.1-F 06191.1-R	AACATCGAGTGCAGCCTTCA AAAGCACCGCGTTACACATG
6	gene-Led08788-sp3	Superscaffold7	688	hypothetical protein	08788.1-F 08788.1-R	AAAGCACCGCGTTACACATG AATGCTTGGAGTAGCTGCGT
7	gene-Led09905-sp3	Superscaffold8	685	alternative cyclin pcl1	09905.1-F 09905.1-R	GTCCCGGTTGACACATTCTT AACATCGAGTGCAGCCTTGA
8	gene-Led07817-sp3	Superscaffold6	1992	Holliday junction resolvase	07817.1-F 07817.1-R	ACACAGACGTTTCGGCTCAT TGCCATCGACGTGAATGGAA
9	gene-Led10404-sp3	Superscaffold9	638	serine/threonine-protein kinase	10404.1-F 10404.1-R	CAGATAGGTGACGGTGGCTC CGGTGACATATGCCCTTGCT
10	gene-Led01615-sp3	Superscaffold10	2035	hypothetical protein	01615.1-F 01615.1-R	ATATTGCCAAACGCGCTGAC AGATGACCACCGCTGACAAG
11	gene-Led02286-sp30	Superscaffold1	5723	DNA helicase	02286.1-F 02286.1-R	GCAATCCGAAGCATTCCGTC CCGAATTCTTGGCCTCCTGT
12	gene-Led04228-sp30	Superscaffold3	2546	Glucose-methanol-choline oxidoreductase	04228.1-F 04228.1-R	AGTGAATTCCAGGTCCAGCG GGAGGTCAGTTCTCCTGTGC

13	gene-Led05642-sp30	Superscaffold4	2517	serine threonine protein kinase [ <i>Lentinula edodes</i> ]	05642.1-F 05642.1-R	GCCCGTTCCAAACAAAGCAT AGAGTCTTGACACGCATCGG
14	gene-Led08536-sp30	Superscaffold6	1524	8-amino-7-oxononanoate synthase	08536.1-F 08536.1-R	TCAAGGCCACTACACTGCTG ATCCCTCAGGCTGGAGATGT
15	gene-Led09638-sp30	Superscaffold7	4290	hypothetical protein	09638.1-F 09638.1-R	TCGCCCTTTGCCTTTCAGAT TCTGGCAAACTGCGAATGC
16	gene-Led09779-sp30	Superscaffold8	1964	ribosomal protein L32	09779.1-F 09779.1-R	CGAGTTCAACGACCCCAGAA TCCAGGAGCCCCGAGGATAAA
17	gene-Led10568-sp30	Superscaffold9	2547	hypothetical protein LENED_003051 [ <i>Lentinula edodes</i> ]	10568.1-F 10568.1-R	ACATAGCAGTCGGTCCTCCT GGCTCGGTGACATCCATAGG
18	gene-Led02816-sp30	Superscaffold10	1008	hypothetical protein	02816.1-F 02816.1-R	TCAGGCTGAGGCATCTACCT GTCGGACAAACATGGGTGC

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**Table S12. PCR and Sanger sequencing identity of the unique genes within each of two genomes**

No	Gene name	DNA temple	Identity of PCR product
1	gene-Led00368-sp3	SP3	98%
		SP30	63%
		3×30	98%
2	gene-Led02602-sp3	SP3	98%
		SP30	band with unexpected size
		3×30	98%
3	gene-Led04647-sp3	SP3	97%
		SP30	no band
		3×30	97%
4	gene-Led05113-sp3	SP3	98%
		SP30	no band
		3×30	98%
5	gene-Led06191-sp3	SP3	98%
		SP30	no band
		3×30	98%
6	gene-Led08788-sp3	SP3	98%
		SP30	no band
		3×30	98%
7	gene-Led09905-sp3	SP3	90%
		SP30	no band
		3×30	90%
8	gene-Led07817-sp3	SP3	98%
		SP30	no band
		3×30	98%
9	gene-Led10404-sp3	SP3	98%
		SP30	no band
		3×30	98%

10	gene-Led01615-sp3	SP3	97%
		SP30	band with unexpected size
		3×30	97%
11	gene-Led02286-sp30	SP3	15%
		SP30	97%
		3×30	97%
12	gene-Led04228-sp30	SP3	no band
		SP30	98%
		3×30	98%
13	gene-Led05642-sp30	SP3	no band
		SP30	99%
		3×30	99%
14	gene-Led08536-sp30	SP3	band with unexpected size
		SP30	99%
		3×30	99%
15	gene-Led09638-sp30	SP3	band with unexpected size
		SP30	99%
		3×30	99%
16	gene-Led09779-sp30	SP3	band with unexpected size
		SP30	99%
		3×30	99%
17	gene-Led10568-sp30	SP3	no band
		SP30	99%
		3×30	99%
18	gene-Led02816-sp30	SP3	band with unexpected size
		SP30	99%
		3×30	99%

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**Table S13. The numbers of retrotransposons belonging to various long terminal repeat (LTR) superfamilies in the two monokaryotic strains**

LTR superfamily	SP3	SP30
<b>Gypsy</b>	12681	11170
<b>Copia</b>	1526	1326
<b>Ngaro</b>	76	227
<b>Unknown</b>	1633	1303
<b>Total</b>	15916	14026