

Telomere-to-telomere genome assembly of Tibetan medicinal mushroom *Ganoderma leucocontextum* and the first *Copia* centromeric retrotransposon in macro-fungi Genome

Miao Wang^{1, 2}, Guoliang Meng^{1, 2}, Ying Yang^{1, 2}, Xiaofang Wang¹, Rong Xie³ and Caihong Dong^{1*}

¹ *State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing, 100101, China*

² *University of Chinese Academy of Sciences, Beijing, 100049, China*

³ *Institute of Vegetables and Ornamental Sciences, Tibet Academy of Agricultural and Animal Husbandry Sciences, Lhasa, 850000, China*

Miao Wang, email: mwan2136@gmail.com; Guoliang Meng, email:

18706387822@163.com; Ying Yang, email: yangy@im.ac.cn; Xiaofang Wang, email:

wang227529@163.com; Rong Xie, email: xr-20082004@163.com

* Corresponding author

Postal address: No.1 Beichen West Road, Chaoyang District Beijing, 100101, P.R. China

Telephone numbers: 86-10-64806193

E-mail addresses: dongch@im.ac.cn (CH Dong)

SUPPORTING INFORMATION

Figure S1

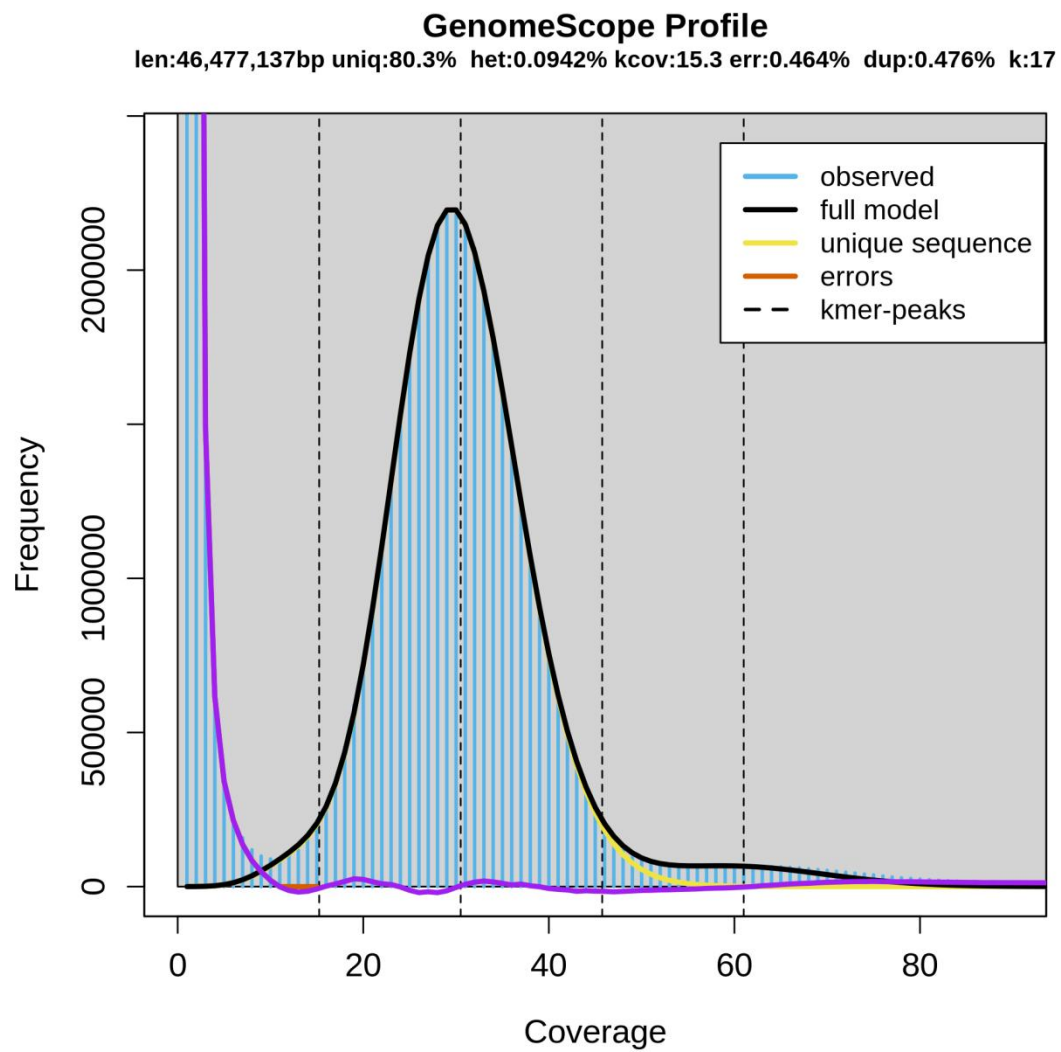


Figure S2

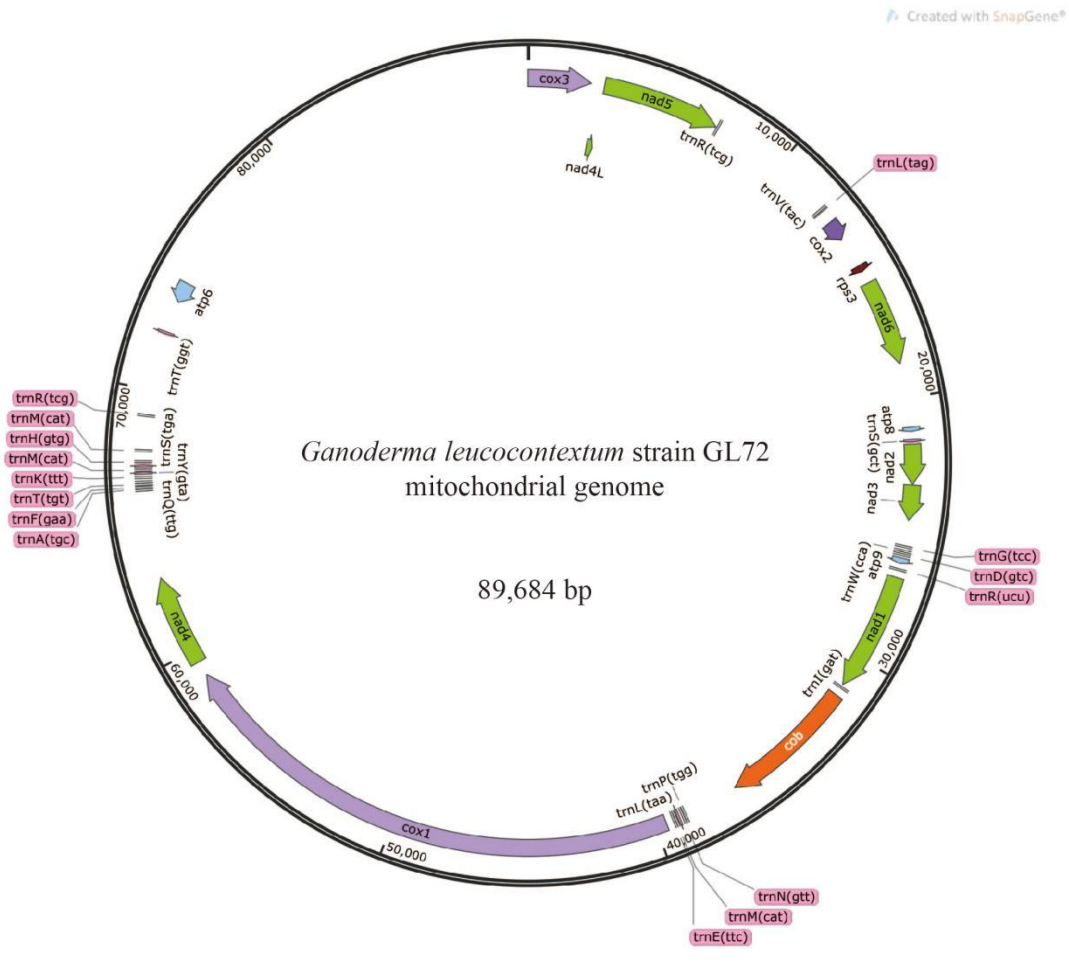


Figure S3

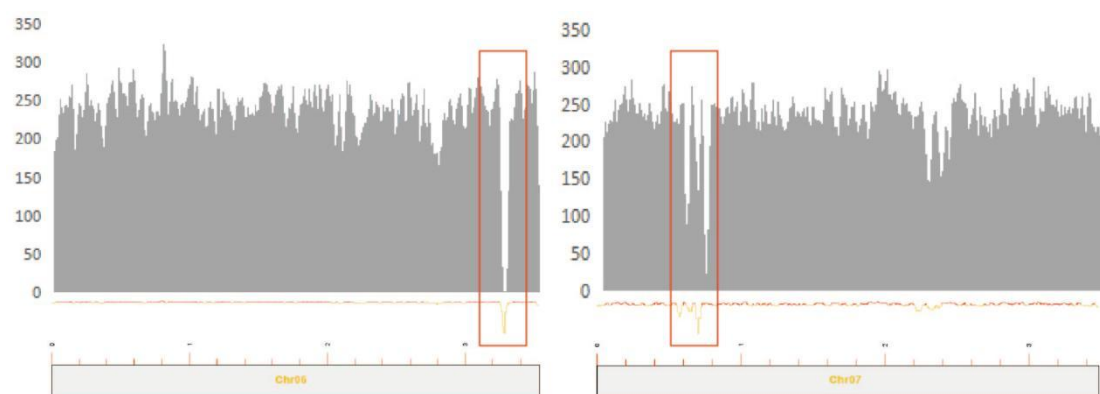
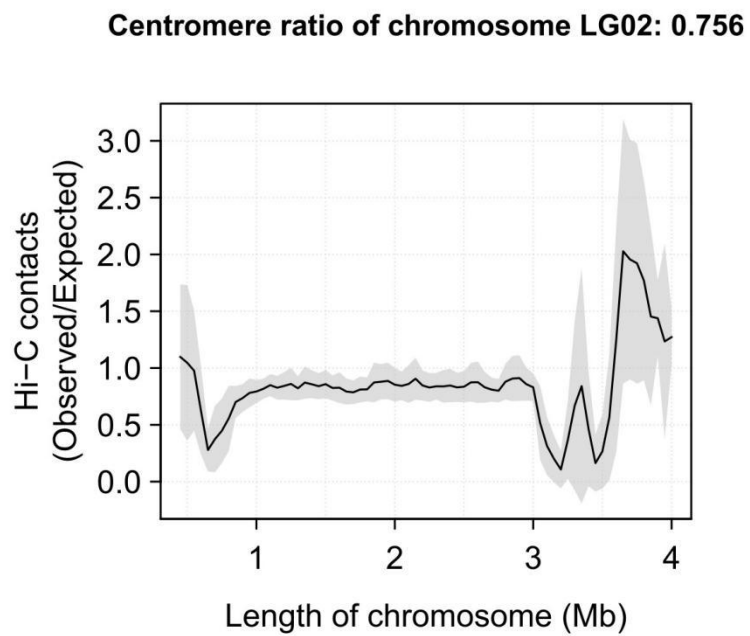
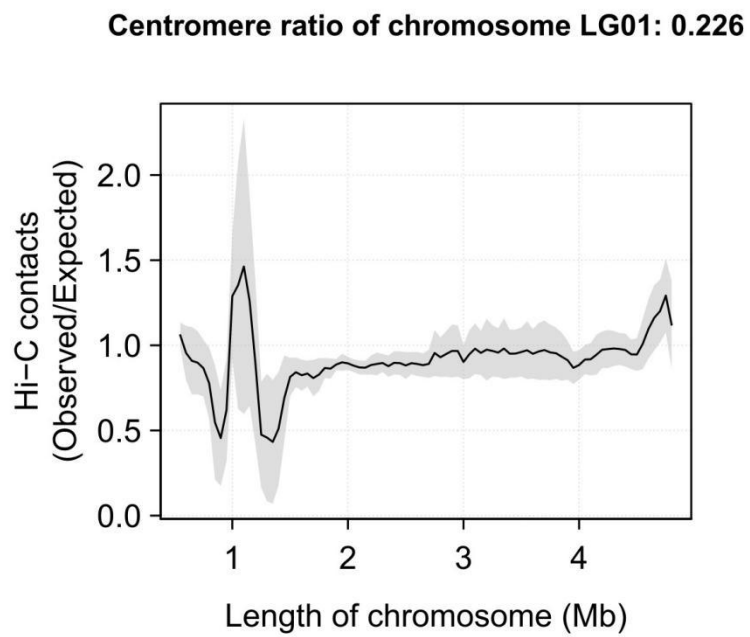
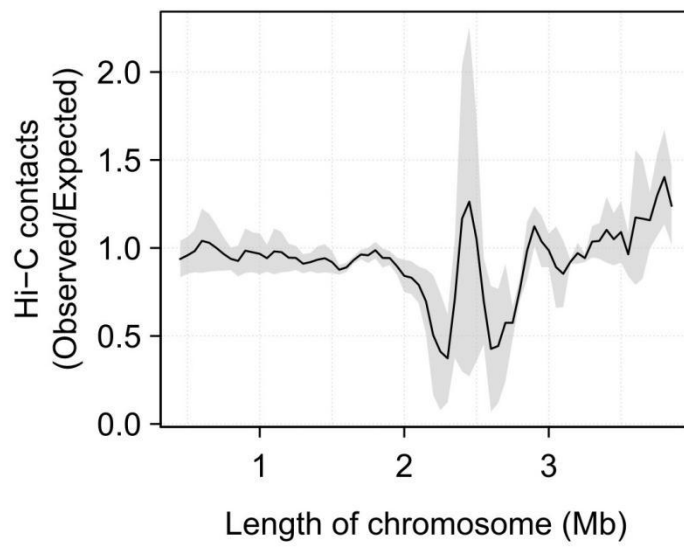


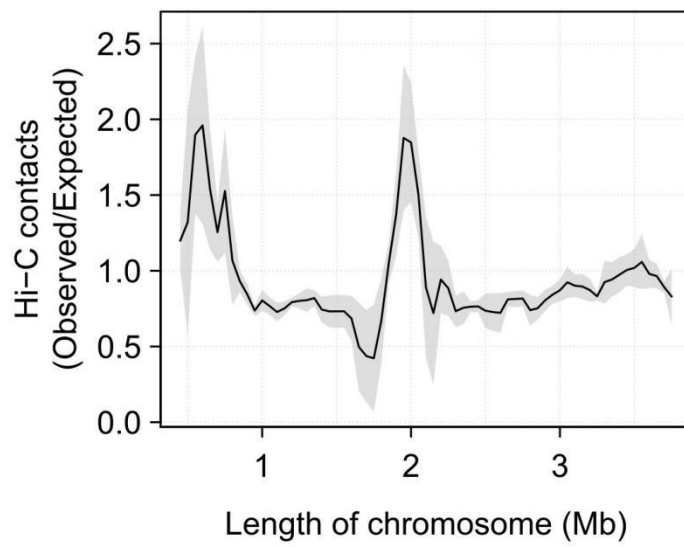
Figure S4



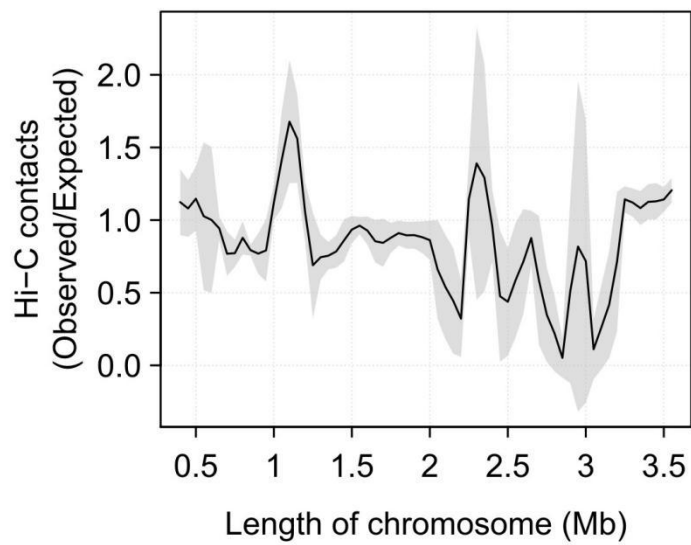
Centromere ratio of chromosome LG03: 0.576



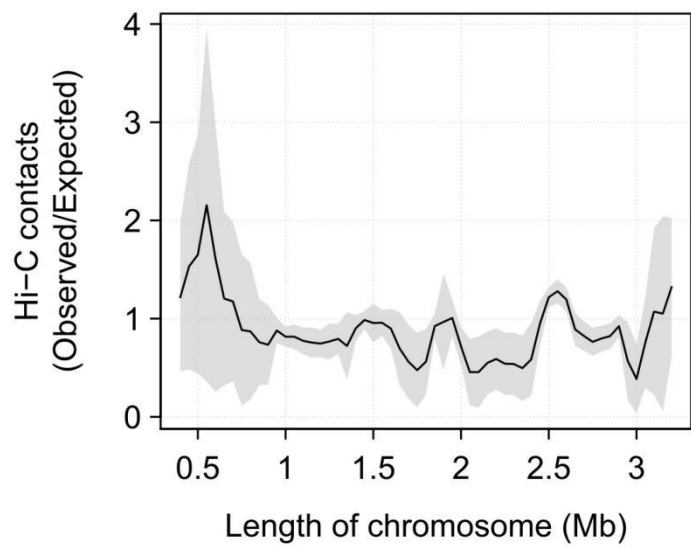
Centromere ratio of chromosome LG04: 0.416



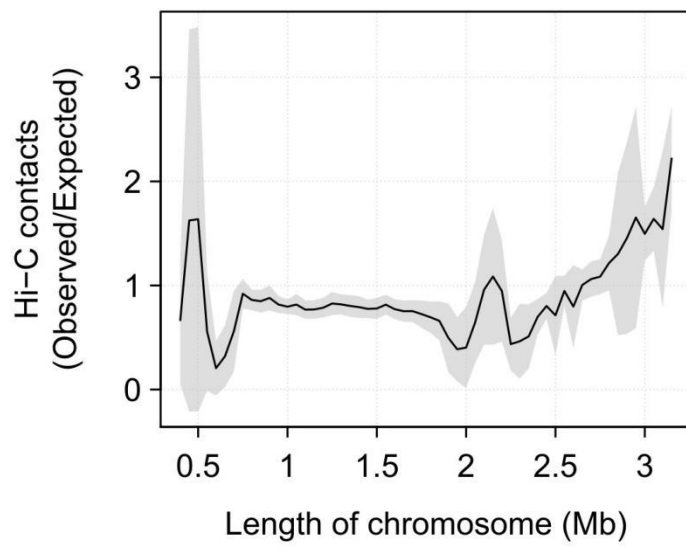
Centromere ratio of chromosome LG05: 0.756



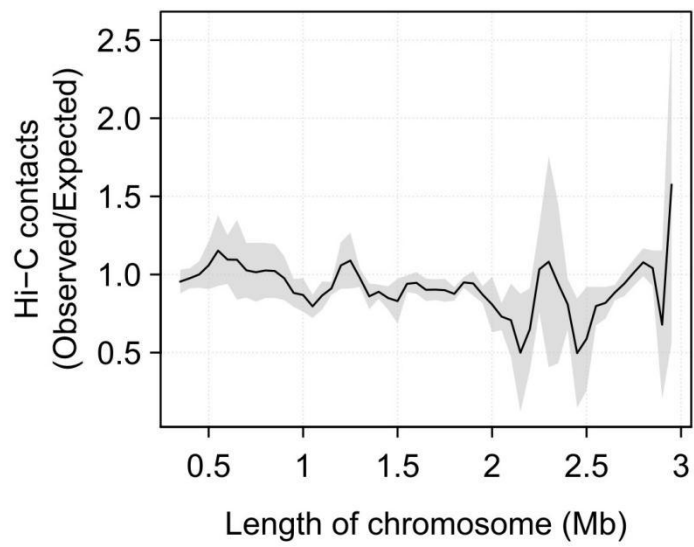
Centromere ratio of chromosome LG06: 0.627



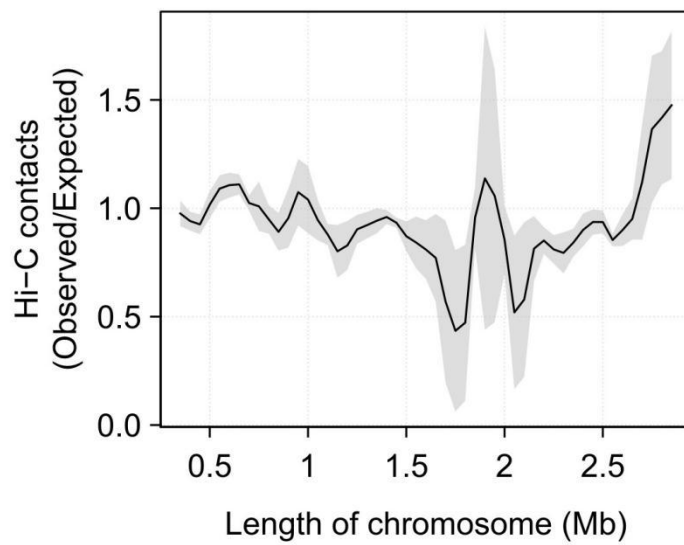
Centromere ratio of chromosome LG07: 0.371



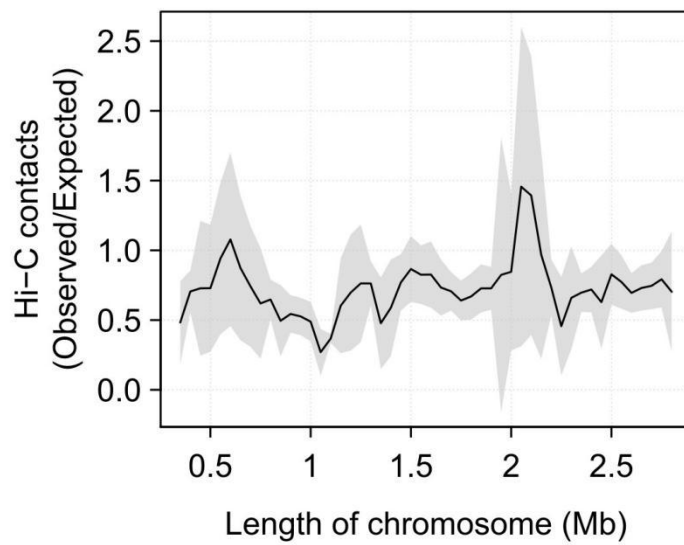
Centromere ratio of chromosome LG08: 0.715



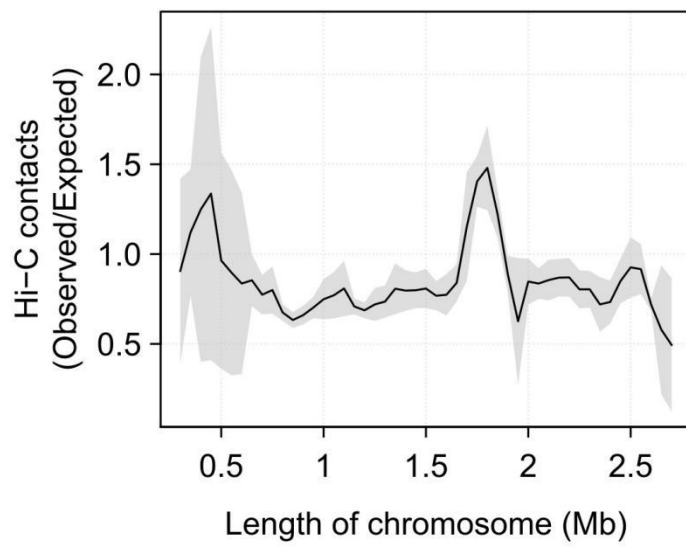
Centromere ratio of chromosome LG09: 0.579



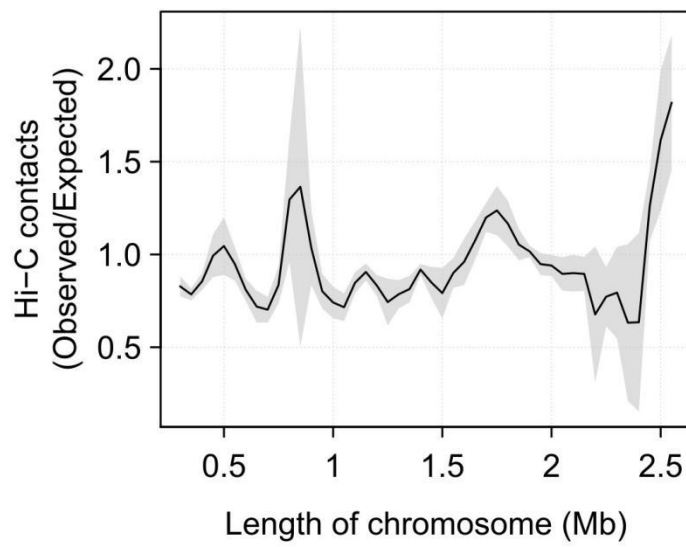
Centromere ratio of chromosome LG10: 0.464



Centromere ratio of chromosome LG11: 0.691



Centromere ratio of chromosome LG12: 0.683



Centromere ratio of chromosome LG13: 0.567

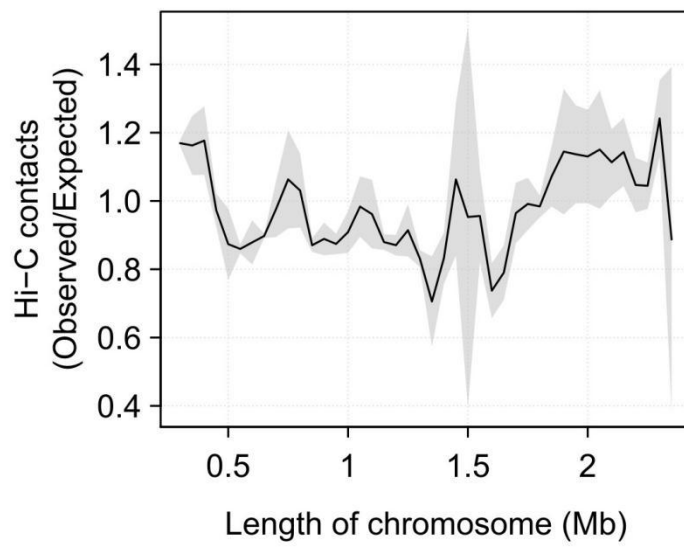


Figure S5

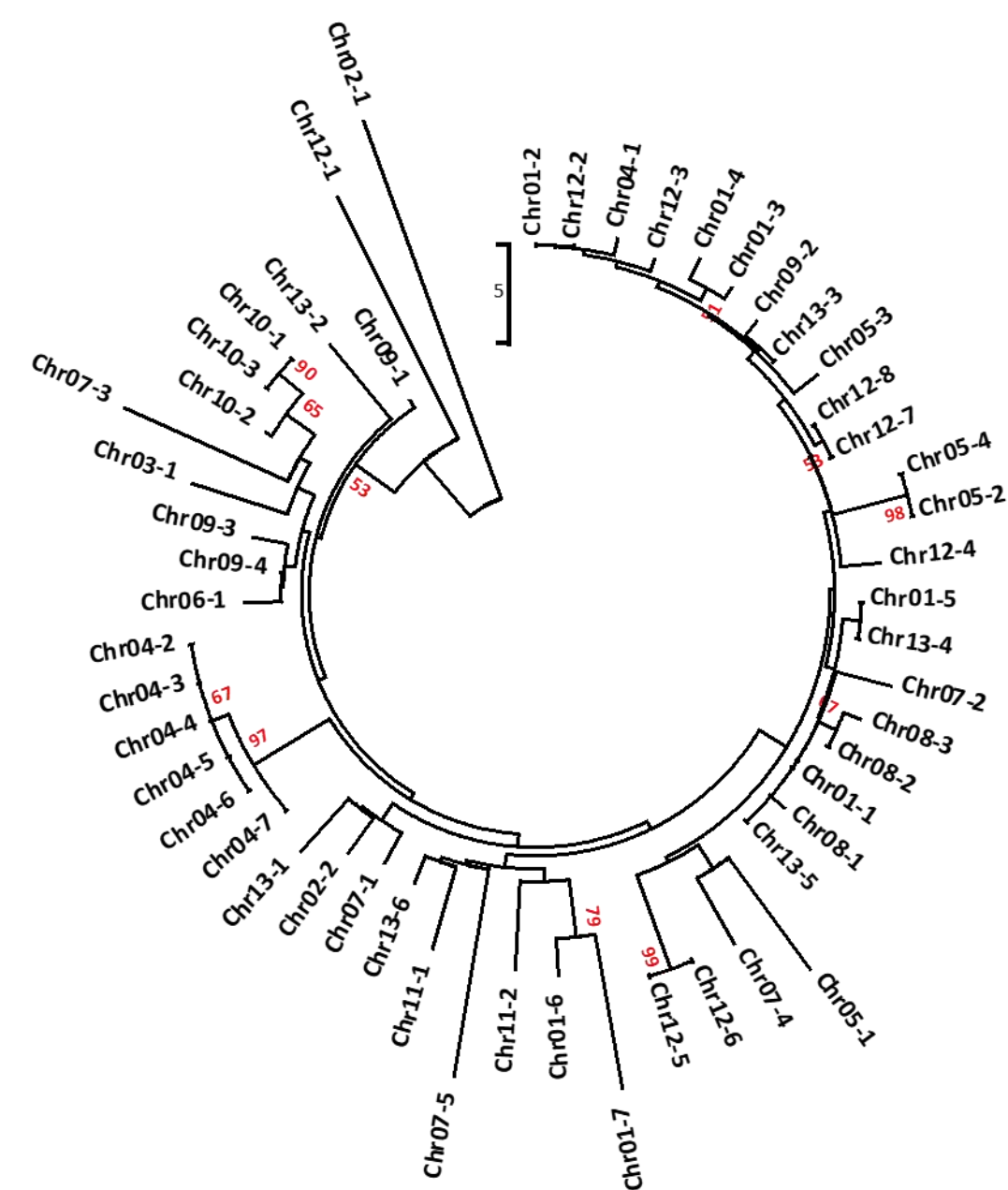


Figure S6

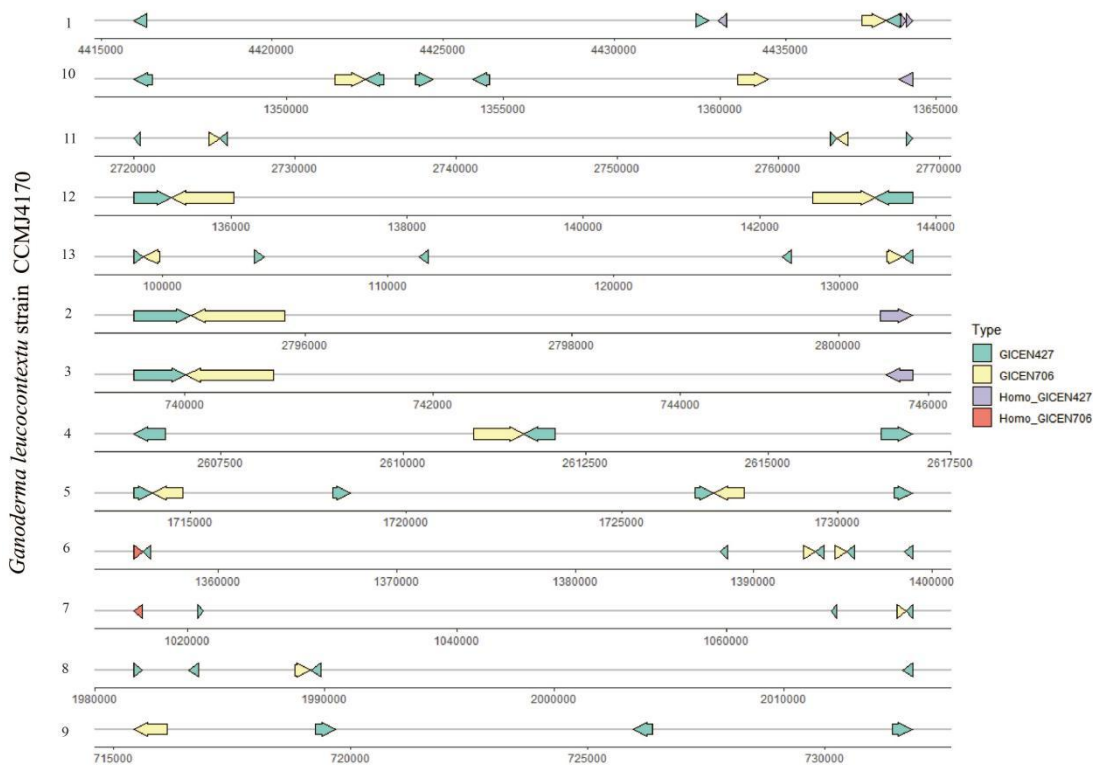


Figure S7

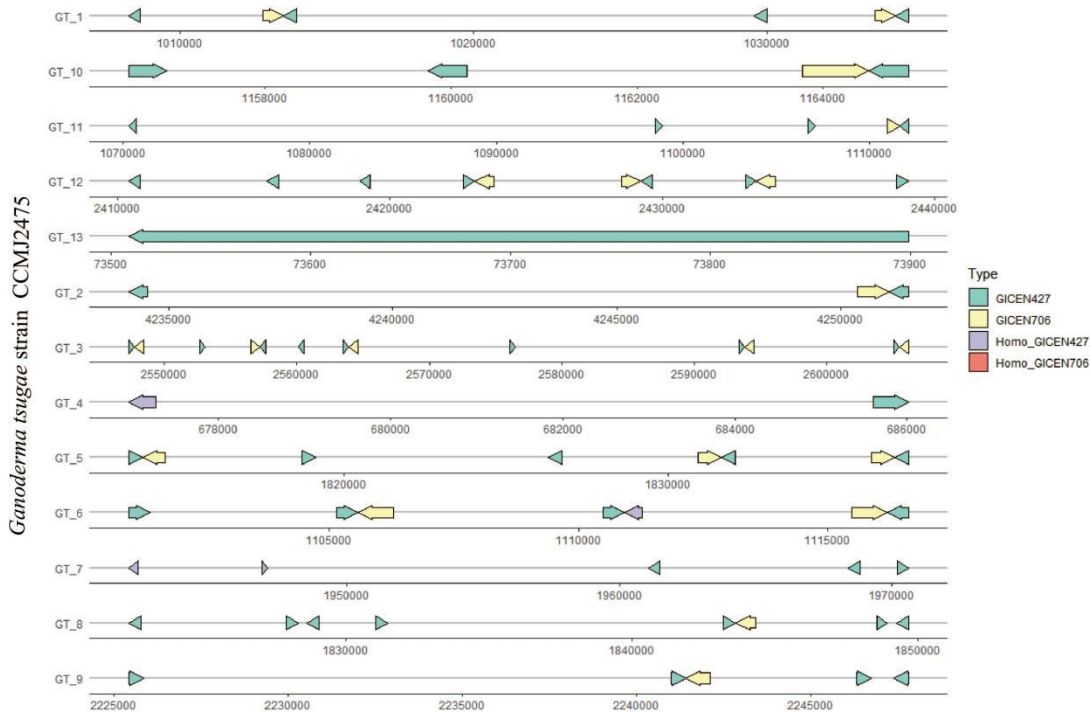


Figure S8

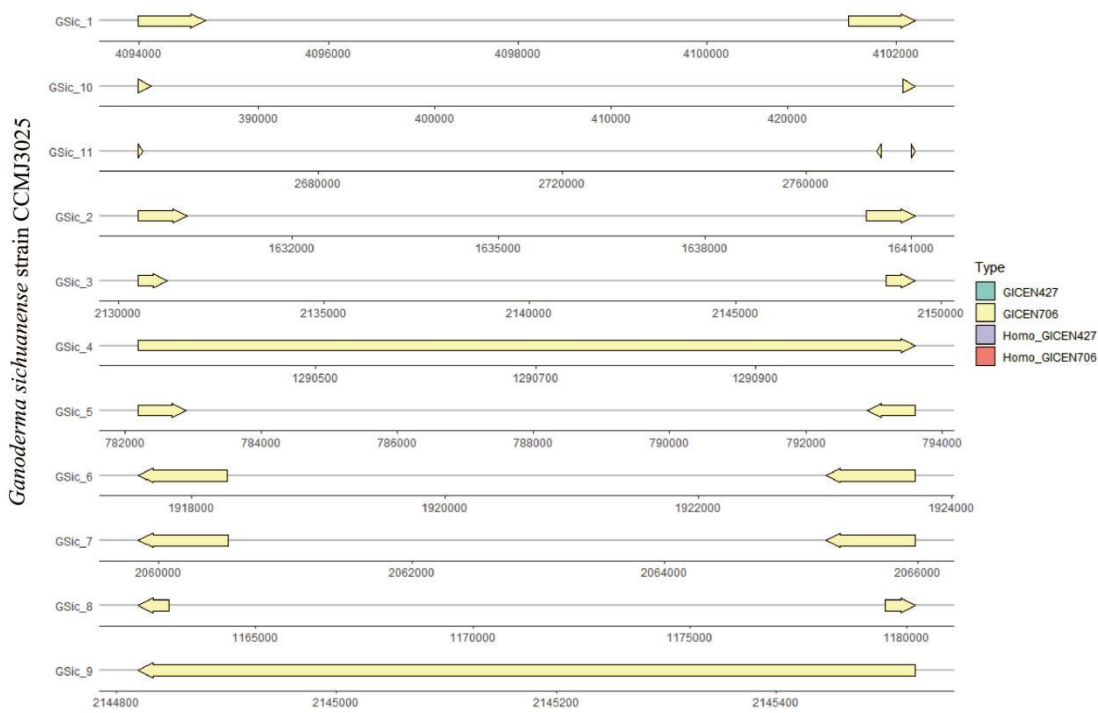


Figure S9



Figure S10

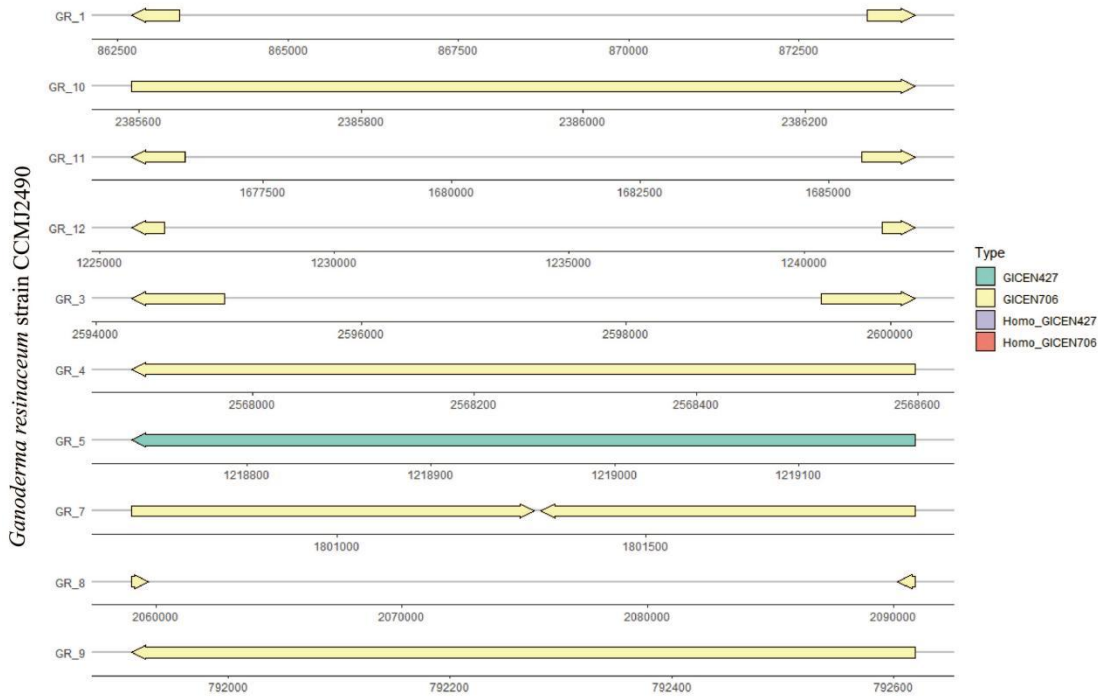


Figure S11

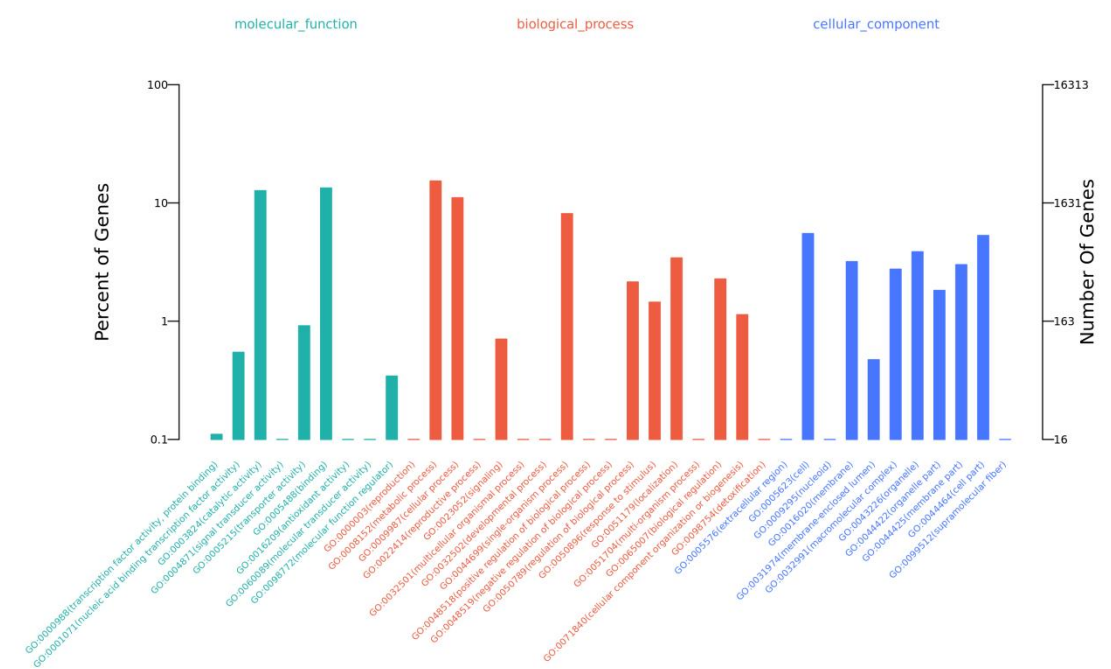


Figure S12

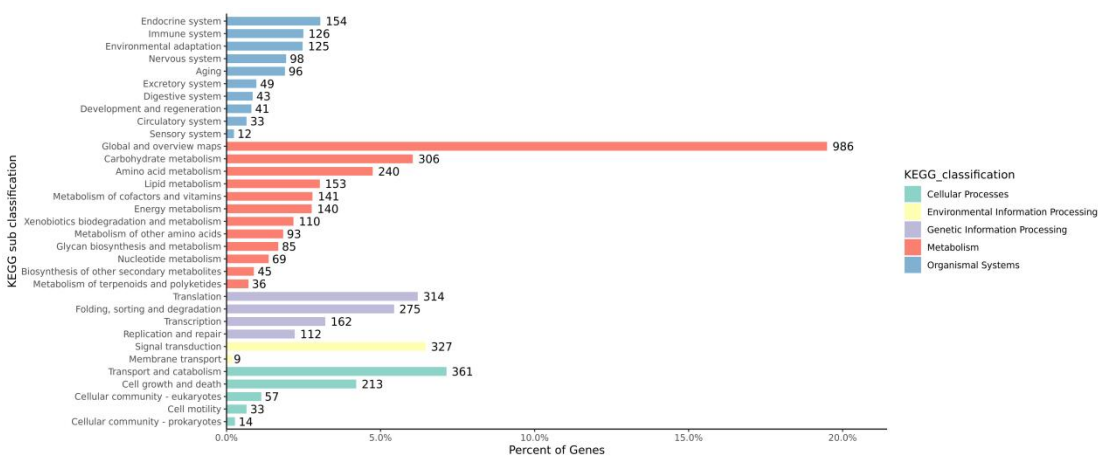


Figure S13

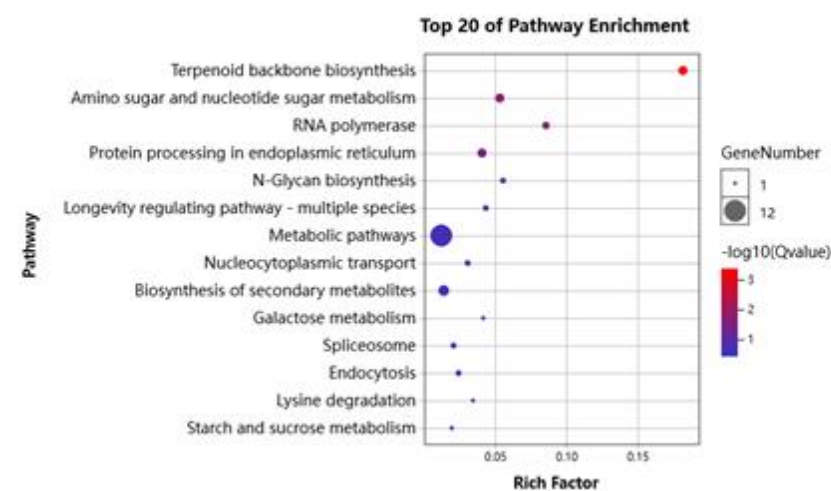


Figure S14

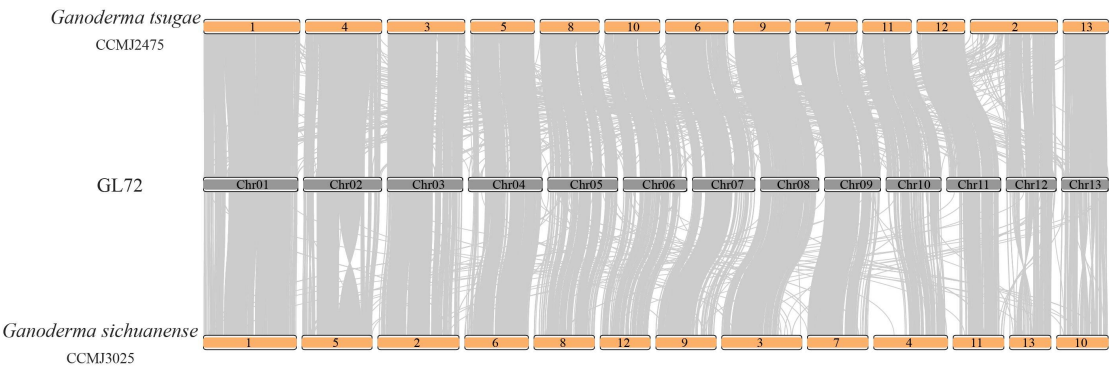


Figure S15

Copu9	0
Copu5	0
GS1c_4.1	0
GS1c_6.2	MLATCHSSGMRIVMTRAGAGRAVSCCEQETRMCLHIY	40
GS_1.3	0
GS_3.1	0
GL72_3.1	0
GL72_13.3	0
Consensus	0
Copu9	0
Copu5	0
GS1c_4.1	0
GS1c_6.2	ASHFICEDMRSFEPFEPVLTGSFSAQLGACIKHGRRY	80
GS_1.3	0
GS_3.1	0
GL72_3.1	0
GL72_13.3	0
Consensus	0
Copu9MSFIATF	7
Copu5MH	2
GS1c_4.1MSACF	5
GS1c_6.2	RLFSSEFVSHSFHFAFFVLSFVITLLSSVIRLLMRIA	120
GS_1.3MSACF	5
GS_3.1MAIA	4
GL72_3.1MAIT	4
GL72_13.3MEACF	6
Consensus	6
Copu9	TTTSEENATKFIPLDVSCTYPELLNMCNCFVARASE	47
Copu5	LFEPFH.....FLFDFSSHCSYFELRLNHCVAARASE	36
GS1c_4.1	MEAAFR...FSDLIFFDLITFCYFELRVNFQCLASAEK	42
GS1c_6.2	ASKEFFT.TEDHFVLEFVLVACNCFLAYHHEGEVAIESV	159
GS_1.3	MEAAFR...FCDLIFFLITFCYFELRVNFQCLASAEK	42
GS_3.1	ASKEFF.TEDHFVLEFVLVSCNCFLAYHHEGECLAEVS	42
GL72_3.1	ASKEFF.TEDHFVLEFVLVSCITFLAYHHEGEVAIESV	42
GL72_13.3	MEAAFR...FSDLIFFDLITFCYFELRVNFQCLASTEK	43
Consensus	43
Copu9	QWLIAGARLQEPFR...TFENGILLAGELTACYFHACAS	83
Copu5	QWLIAGARLQEPFR...TFENGILLAGELTACYFHACAS	76
GS1c_4.1	QWLIAGARLQEPFR...TFENGILLAGELTACYFHACAS	78
GS1c_6.2	RWLEGGCFELSFGR...RALYGLQAGELTAYCYFYCSTE	196
GS_1.3	QWLIAGARLQEPFR...TFENGILLAGELTACYFHACAS	78
GS_3.1	RWLEGGCFELSFGR...RALYGLQAGELTAYCYFYCSTE	79
GL72_3.1	RWLEGGCFELSFGR...RALYGLQAGELTAYCYFYCSTE	79
GL72_13.3	QWLIAGARLQEPFR...TFENGILLAGELTACYFHACAS	79
Consensus	79
Copu9	HLRVCSDFMNLFLHNCIDNLCDFEDCTGMRHCCLGAFRD	123
Copu5	ELRVVSDYNNLFTLDCNWCDFEAGVRLGCQVMGLYD	116
GS1c_4.1	ELRVCCDWINYLPHLNCIDNLCDFEDCTGMRHCCLGAFRD	118
GS1c_6.2	ELRVVSDYNNLPHLNCIDNLCDFEDCTGMRHCCLGAFRD	236
GS_1.3	ELRVCCDWINYLPHLNCIDNLCDFEDCTGMRHCCLGAFRD	118
GS_3.1	ELRVVSDYNNLPHLNCIDNLCDFEDCTGMRHCCLGAFRD	119
GL72_3.1	ELRVVSDYNNLPHLNCIDNLCDFEDCTGMRHCCLGAFRD	119
GL72_13.3	ELRVCCDWINYLPHLNCIDNLCDFEDCTGMRHCCLGAFRD	119
Consensus	119
Copu9	FVGFETIKLGG.....IMKSEFFSFRCDDGGPGC	152
Copu5	FT.VETIKRAG.....RLARFNLRIATAGFV	144
GS1c_4.1	FHNFEASSAVG.....RLTQSFNGRIATASGA	147
GS1c_6.2	FLRYMTACDGEKFADEVSAGELARDYWTICRDAEGP	276
GS_1.3	FHNFEASSAVG.....RLTQSFNGRIATASGA	147
GS_3.1	FLRYMTACDGEKFADEVSAGELARDYWTICRDAEGP	159
GL72_3.1	FLRYMTACDGEKFADEVSAGELARDYWTICRDAEGP	159
GL72_13.3	FHGFRASSAVG.....RLTQSFNGRIATASGA	148
Consensus	148
Copu9	TERFINTMLFFIAVAQAGERANGITFELESYIIVRUT	192
Copu5	QRRFIETELFFHVAVQAGERASGNIFELESYIAMRUT	184
GS1c_4.1	QRRFIETELFFHVAVQAGERASGNIFELESYIAMRUT	187
GS1c_6.2	QARRFENLELFFHVAVQAGERASGNIFELESYIAMRUT	316
GS_1.3	QRRFIETELFFHVAVQAGERASGNIFELESYIAMRUT	187
GS_3.1	QARRFENLELFFHVAVQAGERASGNIFELESYIAMRUT	199
GL72_3.1	QARRFENLELFFHVAVQAGERASGNIFELESYIAMRUT	199
GL72_13.3	QRRFIETELFFHVAVQAGERASGNIFELESYIAMRUT	188
Consensus	188
Copu9	SCCRFCFALIEYAAGIDLEFHVIVHETLAANEAHDLVT	232
Copu5	SCCRFVFLAEYAAGIDLEFVFEHETIQNTEAHDLVT	224
GS1c_4.1	SCCRFCWALIEYANNLIDLEFVFEHETIVLALGAANDLVT	227
GS1c_6.2	SCCRFVFLIEYANNLIDLEFVFEHETIVLALGAANDLVT	356
GS_1.3	SCCRFCWALIEYANNLIDLEFVFEHETIVLALGAANDLVT	227
GS_3.1	SCCRFVFLIEYANNLIDLEFVFEHETIVLALGAANDLVT	239
GL72_3.1	SCCRFVFLIEYANNLIDLEFVFEHETIVLALGAANDLVT	239
GL72_13.3	SCCRFCWALIEYANNLIDLEFVFEHETIVLALGAANDLVT	228
Consensus	228
Copu9	WSN.....DIFSNN	242
Copu5	WSN.....DIFSNN	234
GS1c_4.1	WSN.....DIFSNN	237
GS1c_6.2	WSN.....DIFSNN	366
GS_1.3	WSNVLLRNIP...RLGFAISSFFVLTFLRLQDIFSNN	265
GS_3.1	WSN.....DIFSNN	249
GL72_3.1	WSN.....DIFSNN	246
GL72_13.3	WSNVLLRNIPAPFFPFVTSLEFLVLRCLQDIFSNN	268
Consensus	268
Copu9	QVYEDTHNMIFVLMHREGLELQAGVFGVRLCGTIIEF	262
Copu5	QVYEDTHNMIFVLMHREGLELQAGVFGVRLCGTIIEF	274
GS1c_4.1	QVYEDTHNMIFVLMHREGLELQAGVFGVRLCGTIIEF	277
GS1c_6.2	QVYEDTHNMIFVLMHREGLELQAGVFGVRLCGTIIEF	406
GS_1.3	QVYEDTHNMIFVLMHREGLELQAGVFGVRLCGTIIEF	305
GS_3.1	QVYEDTHNMIFVLMHREGLELQAGVFGVRLCGTIIEF	289
GL72_3.1	QVYEDTHNMIFVLMHREGLELQAGVFGVRLCGTIIEF	286
GL72_13.3	QVYEDTHNMIFVLMHREGLELQAGVFGVRLCGTIIEF	308
Consensus	308
Copu9	ETERARLFSWGFEIDACQVGTIEGLQNMIVGSLHNSFET	322
Copu5	ESGRITLFSWGFEIDACQVGTIEGLQNMIVGSLHNSFET	314
GS1c_4.1	EALRALFSWGFEIDACQVGTIEGLQNMIVGSLHNSFET	317
GS1c_6.2	MENQNVFSFGFLERDVALYIQGLQNMIVGSLHNSFET	446
GS_1.3	EALRALFSWGFEIDACQVGTIEGLQNMIVGSLHNSFET	345
GS_3.1	MENQNVFSFGFLERDVALYIQGLQNMIVGSLHNSFET	329
GL72_3.1	MENQNVFSFGFLERDVALYIQGLQNMIVGSLHNSFET	326
GL72_13.3	EALRALFSWGFEIDACQVGTIEGLQNMIVGSLHNSFET	348
Consensus	348
Copu9	RYFGKGDHAKKHRIKLLFRVFOCA..	349
Copu5	RYFGKGRQVRCAGVVLSPHRAHRY..	341
GS1c_4.1	RYFGKGRQVRCAGVVLSPHRAHRY..	340
GS1c_6.2	RYFGKGRQVRCAGVVLSPHRAHRY..	475
GS_1.3	RYFGKGRQVRCAGVVLSPHRAHRY..	368
GS_3.1	RYFGKGRQVRCAGVVLSPHRAHRY..	358
GL72_3.1	RYFGKGRQVRCAGVVLSPHRAHRY..	347
GL72_13.3	RYFGKGRQVRCAGVVLSPHRAHRY..	371
Consensus	371

Table S1

Species	Strain	Numbler	Terpene	Clavariic acid	Source
<i>Ganoderma gibbosum</i>	CCMJ3046	45	26	no	[9]
<i>Ganoderma tsugae</i>	CCMJ2475	34	16	yes	[9]
<i>Ganoderma leucocontextum</i>	GL72	39	18	yes	This study
<i>Ganoderma resinaceum</i>	CCMJ2490	41	22	yes	[9]
<i>Ganoderma sinense</i>	CCMJ2497	37	17	yes	[9]
<i>Ganoderma applanatum</i>	CCMJ3043	40	23	yes	[9]
<i>Ganoderma multipileum</i>	CCMJ3051	42	22	yes	[9]
<i>Ganoderma australe</i>	CCMJ3053	43	22	yes	[9]
<i>Ganoderma sichuanense</i>	CCMJ3025	37	19	yes	[9]
<i>Ganoderma weberianum</i>	CCMJ3054	47	26	yes	[9]
<i>Ganoderma leucocontextum</i>	CCMJ2485	37	20	yes	[9]
<i>Amauroderma rugosum</i>	ACCC 51706	36	16	yes	NCBI: GCA_017499575.1
<i>Ganoderma lucidum</i>	Ling-Jian NO.2	33	17	yes	NCBI: GCA_019426095.1
<i>Ganoderma tsugae</i>	s90	26	9	no	[9]
<i>Ganoderma sinense</i>	ZZ0214-1	40	20	yes	[53]
<i>Ganoderma multipileum</i>	BCRC 37180	45	23	yes	NCBI: GCA_000338015.1
<i>Ganoderma boninense</i>	G3	57	24	no	NCBI: GCA_002900995.2

Table S2

Chr	Size(bp)
Chr01	5,257,413
Chr02	4,353,368
Chr03	4,221,714
Chr04	4,115,428
Chr05	3,900,741
Chr06	3,539,945
Chr07	3,483,796
Chr08	3,239,031
Chr09	3,131,638
Chr10	3,066,788
Chr11	3,007,772
Chr12	2,781,080
Chr13	2,587,874
Total	46,686,588

Table S3

Type	Number	Percent (%)
Complete BUSCOs (C)	1,758	99.7
Complete and single-copy BUSCOs (S)	1,742	98.8
Complete and duplicated BUSCOs (D)	16	0.9
Fragmented BUSCOs (F)	2	0.1
Missing BUSCOs (M)	4	0.2
Total BUSCO groups searched	1,764	100

Table S4

Chr numble	length	N counts
1	5,518,212	200
2	4,901,690	200
3	4,240,300	300
4	4,087,960	100
5	3,644,271	400
6	3,391,645	200
7	3,310,795	200
8	3,189,542	200
9	3,106,008	200
10	2,872,700	0
11	2,856,557	300
12	2,727,109	400
13	2,678,846	100
Total	46,525,635	2800

Table S5

	GICEN427	homo_ GICEN427	GICEN706	homo_ GICEN706
Chr01	7	2	4	0
Chr02	2	3	1	0
Chr03	1	1	0	1
Chr04	7	0	6	0
Chr05	4	2	2	0
Chr06	1	2	1	0
Chr07	5	0	1	0
Chr08	3	0	1	0
Chr09	4	0	0	0
Chr10	3	3	0	4
Chr11	2	0	1	0
Chr12	8	1	3	0
Chr13	6	0	2	0
Total	53	14	22	5

Table S6

Chr	source	start	end	Type	RT	RH	IN	Gag-protein	Transposase	Transcriptional reads
Chr 04	LTR_finder	2084675	2090288	Copia	RT_Tt o1	RNaseH_Vitico1-2	INT_SmCIN1_Repbased ccession_Polinton-1_SM	GAG_STcLV2PP1664	NA	0
Chr 01	LTR_finder	1219554	1226567	Copia	RT_marY1	RNaseH_marY1	INT_Amn-ichi	GAG_Amn-ni	TR_ApGINGER1c	0
Chr 01	LTR_havert	1257062	1262139	Copia	RT_Tt o1	RNaseH_CopiaSL_23	INT_Tricopia	GAG_V12	TR_NvGINGER2-2_Repbased eaccession_Ginger2-2_NV	2
Chr 01	LTR_havert	1308809	1315573	Copia	RT_Tt o1	RNaseH_CopiaSL_23	INT_Tricopia	NA	TR_NvGINGER2-2_Repbased eaccession_Ginger2-2_NV	15
Chr 02	LTR_havert	678987	682004	Copia	RT_marY1	RNaseH_marY1	INT_Amn-ichi	NA	TR_ApGINGER1c	0
Chr 04	LTR_havert	2074144	2079917	Copia	RT_Tt o1	RNaseH_Vitico1-2	INT_Tricopia	GAG_V12	NA	6

	t									
Chr 05	LTR_ havers t	2485 786	2499 251	Cop ia	RT_m arY1	RNaseH_C opiaSL_23	INT_Tricopia	NA	NA	38
Chr 06	LTR_ havers t	2057 204	2065 722	Cop ia	RT_X anthia s	RNaseH_V itico1-2	INT_Tricopia	GAG_HIV- 1	TR_NvGINGER2-2_Repbas eaccession_Ginger2-2_NV	0
Chr 07	LTR_ havers t	2251 481	2258 988	Cop ia	RT_Tt o1	RNaseH_V itico1-2	INT_Tricopia	GAG_V12	TR_NvGINGER2-2_Repbas eaccession_Ginger2-2_NV	0
Chr 08	LTR_ havers t	2428 819	2440 315	Cop ia	RT_B atata	RNaseH_V itico1-2	INT_Oryco1-1	GAG_Xant hias	NA	0
Chr 09	LTR_ havers t	2031 986	2035 087	Cop ia	NA	NA	NA	NA	NA	0
Chr 10	LTR_ havers t	1320 816	1325 469	Cop ia	RT_Tt o1	NA	INT_Tricopia	NA	TR_NvGINGER2-2_Repbas eaccession_Ginger2-2_NV	0

Chr 10	LTR_ havers t	1329 289	1333 141	Cop ia	NA	RNaseH_C opiaSL_23	INT_Tor1	NA	TR_NvGINGER2-2_Repbas eaccession_Ginger2-2_NV	0
Chr 11	LTR_ havers t	2915 460	2920 571	Cop ia	RT_Tt ol	RNaseH_C opiaSL_23	INT_Tricopia	GAG_Osva ldo	TR_NvGINGER2-2_Repbas eaccession_Ginger2-2_NV	0
Chr 12	LTR_ havers t	2614 314	2620 097	Cop ia	RT_Tt ol	RNaseH_C opiaSL_23	INT_Tricopia	GAG_V12	TR_NvGINGER2-2_Repbas eaccession_Ginger2-2_NV	9
Chr 12	LTR_ havers t	2678 831	2684 614	Cop ia	RT_Tt ol	RNaseH_C opiaSL_23	INT_Tricopia	GAG_V12	TR_NvGINGER2-2_Repbas eaccession_Ginger2-2_NV	41
Chr 13	LTR_ havers t	9851 6	1042 95	Cop ia	RT_Tt ol	RNaseH_C opiaSL_23	INT_Tricopia	GAG_V12	TR_NvGINGER2-2_Repbas eaccession_Ginger2-2_NV	87

Table S7

Gene set	Total number of genes	Average gene length(bp)	Average CDS length(bp)	Average exons number per gene	Average exon length(bp)	Average intron length(bp)
De novo	12,353	2,158.07	1,435.21	7.04	204	119.77
Homology	9,994	1,871.60	1,459.69	5.67	257.43	88.2
RNA-seq	8,456	1,910.20	1,489.91	5.82	256.02	87.21
Final set	12,493	2,125.25	1,433.83	6.6	217.23	123.46

Table S8

Term Name	Type	MainClass	Gene Hits In Selected Set	All Genes In Background	p-value	enrichFactor
Nicotinate and nicotinamide metabolism	Expanded	A09100 Metabolism	7	3651	1.3655 7E-14	109.2179487
Organismal Systems	Expanded	A09150 Organismal Systems	7	3651	6.6813 2E-13	66.03875969
Longevity regulating pathway - multiple species	Expanded	A09150 Organismal Systems	7	3651	6.6813 2E-13	66.03875969
Aging	Expanded	A09150 Organismal Systems	7	3651	6.6813 2E-13	66.03875969
DNA replication proteins	Expanded	A09180 Brite Hierarchies	7	3651	1.7740 7E-10	30.86594203
Metabolism of cofactors and vitamins	Expanded	A09100 Metabolism	7	3651	3.9272 6E-09	19.99765258
Chromosome and associated proteins	Expanded	A09180 Brite Hierarchies	7	3651	1.516E -06	8.527527528

Metabolism	Expanded	A09100 Metabolism	9	3651	7.1715 9E-06	3.717922607
Purine metabolism	Expanded	A09100 Metabolism	2	3651	0.0055 13403	17.26241135
Nucleotide metabolism	Expanded	A09100 Metabolism	2	3651	0.0116 32321	11.75845411
Biosynthesis of various plant secondary metabolites	Contracted	A09100 Metabolism	2	3651	0.0017 97277	30.68067227
Cyanoamino acid metabolism	Contracted	A09100 Metabolism	2	3651	0.0026 64057	25.26643599
Amino sugar and nucleotide sugar metabolism	Contracted	A09100 Metabolism	3	3651	0.0044 31714	8.706677266
Biosynthesis of other secondary metabolites	Contracted	A09100 Metabolism	2	3651	0.0082 23315	14.31764706
Carbohydrate metabolism	Contracted	A09100 Metabolism	5	3651	0.0105 16415	3.520732883
Starch and sucrose metabolism	Contracted	A09100 Metabolism	2	3651	0.0227 60378	8.422145329
Enzymes with EC numbers	Contracted	A09190 Not Included in Pathway or	3	3651	0.0267 32003	4.50555327

		Brite				
Unclassified: metabolism	Contracted	A09190 Not Included in Pathway or Brite	3	3651	0.0329 37575	4.156736243
Cytochrome P450	Contracted	A09180 Brite Hierarchies	1	3651	0.0411 78539	23.8627451

Table S9

Species	Strain	Numble	Terpene	Clavaric acid	Source
<i>Ganoderma gibbosum</i>	CCMJ3046	45	26	no	Jiang et al., 2022
<i>Ganoderma tsugae</i>	CCMJ2475	34	16	yes	Jiang et al., 2021
<i>Ganoderma leucocontextum</i>	GL72	39	18	yes	
<i>Ganoderma resinaceum</i>	CCMJ2490	41	22	yes	Jiang et al., 2022
<i>Ganoderma sinense</i>	CCMJ2497	37	17	yes	Jiang et al., 2022
<i>Ganoderma applanatum</i>	CCMJ3043	40	23	yes	Jiang et al., 2022
<i>Ganoderma multipileum</i>	CCMJ3051	42	22	yes	Jiang et al., 2022
<i>Ganoderma australe</i>	CCMJ3053	43	22	yes	Jiang et al., 2022
<i>Ganoderma sichuanense</i>	CCMJ3025	37	19	yes	Jiang et al., 2022
<i>Ganoderma weberianum</i>	CCMJ3054	47	26	yes	Jiang et al., 2022
<i>Ganoderma leucocontextum</i>	CCMJ2485	37	20	yes	Jiang et al., 2022
<i>Amauroderma rugosum</i>	ACCC 51706	36	16	yes	Lin et al.,2021
<i>Ganoderma lucidum</i>	Ling-Jian NO.2	33	17	yes	NCBI:GCA_019426095.1
<i>Ganoderma tsugae</i>	s90	26	9	no	Jiang et al., 2021
<i>Ganoderma sinense</i>	ZZ0214-1	40	20	yes	Zhu et al.,2015
<i>Ganoderma multipileum</i>	BCRC 37180	45	23	yes	NCBI:GCA_000338015.1
<i>Ganoderma boninense</i>	G3	57	24	no	NCBI:GCA_002900995.2

Table S10

Clust numble	Clust tpyle	Gene	Gene tpyle
Chr02.region005	terpene	LG02.1229	other gene
		LG02.1230	other gene
		LG02.1231	core biosynthetic genes
		LG02.1232	other gene
		LG02.1234	other gene

Table S11

Gene	Chromosome	Start	End	E-value	Rate
LG12.14	Chr12	71629	74031	1.30E-27	2.575582148
LG01.54	Chr01	236399	233967	0.0076	4.496489053
LG04.20	Chr04	195737	190760	1.40E-38	4.756176028
LG08.50	Chr08	158552	151394	6.10E-27	4.895044228
LG08.82	Chr08	263746	260316	2.40E-146	8.142743926
LG07.106	Chr07	367187	364660	3.90E-13	10.5395602
LG01.139	Chr01	647357	649641	3.80E-34	12.31322325
LG03.190	Chr03	572666	571115	2.50E-29	13.56477488
LG09.158	Chr09	524981	529871	5.80E-11	16.76378304
LG13.107	Chr13	541327	543315	1.10E-33	20.91782676
LG03.313	Chr03	942710	948717	6.60E-19	22.33002994
LG08.249	Chr08	860785	863221	3.30E-12	26.57538628
LG03.395	Chr03	1155819	1153370	9.10E-17	27.37795597
LG03.428	Chr03	1266514	1264899	9.00E-26	29.99999526
LG01.340	Chr01	1586772	1584643	2.20E-23	30.18161214
LG01.342	Chr01	1589311	1591493	2.70E-30	30.22990585
LG03.461	Chr03	1344330	1347177	2.10E-32	31.84322766
LG13.199	Chr13	846972	843901	3.30E-16	32.72848678
LG01.507	Chr01	2065900	2063949	2.30E-22	39.29499166
LG01.527	Chr01	2109930	2113800	5.50E-23	40.1324758
LG02.564	Chr02	1842557	1840147	2.60E-22	42.32486204
LG13.273	Chr13	1100314	1098656	4.40E-30	42.51806695
LG12.266	Chr12	1232736	1231210	1.30E-61	44.32580149
LG01.701	Chr01	2558809	2552004	8.20E-26	48.67049631
LG03.718	Chr03	2062791	2057848	2.30E-25	48.86145769
LG01.793	Chr01	2802334	2798533	2.40E-18	53.30252731
LG01.816	Chr01	2849239	2846309	1.50E-119	54.19469614
LG07.534	Chr07	1897708	1895051	2.90E-22	54.47090367
LG08.539	Chr08	1770691	1774453	8.00E-11	54.66730636
LG09.537	Chr09	1772850	1768809	2.50E-154	56.61094929
LG02.794	Chr02	2511794	2513437	4.00E-28	57.69771818
LG03.851	Chr03	2459180	2455125	9.10E-152	58.25074839
LG03.858	Chr03	2477620	2475371	1.80E-32	58.68753781
LG02.820	Chr02	2577268	2573624	4.90E-38	59.20170314
LG02.826	Chr02	2597124	2591163	1.90E-21	59.65780977
LG03.882	Chr03	2532323	2529419	1.20E-06	59.98329115
LG02.856	Chr02	2663603	2669595	1.30E-11	61.18488803
LG04.648	Chr04	2822270	2819946	4.80E-12	68.57780041
LG07.661	Chr07	2399006	2394465	3.40E-35	68.85992193
LG04.674	Chr04	2902143	2905325	2.20E-14	70.51861921
LG01.1156	Chr01	3771368	3776246	4.40E-11	71.73429213

LG05.686	Chr05	2804589	2806725	5.80E-28	71.89887767
LG03.1078	Chr03	3284942	3279870	5.30E-13	77.81062384
LG13.574	Chr13	2054157	2052052	9.00E-27	79.37623702
LG04.836	Chr04	3397889	3408414	2.00E-49	82.5646567
LG05.779	Chr05	3342965	3339167	8.80E-19	85.70076814
LG02.1152	Chr02	3771552	3769080	2.50E-20	86.63526722
LG03.1199	Chr03	3697429	3699820	5.90E-31	87.58122886
LG03.1202	Chr03	3710275	3707884	2.70E-31	87.88551285
LG06.766	Chr06	3141922	3144786	1.20E-66	89.81811238
LG06.798	Chr06	3426035	3421857	6.00E-19	97.94004964
