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Supplementary Table S1. BUSCO analysis results of the *L. tricolor* genome assembly with insecta database.

Complete BUSCOs(C)	Complete and single-copy BUSCOs(S)	Complete and duplicated BUSCOs(D)	Fragmented BUSCOs(F)	Missing BUSCOs(M)	Total Lineage BUSCOs
1350 (98.76%)	1327 (97.07%)	23 (1.68%)	5 (0.37%)	12 (0.88%)	1,367

Note: Complete BUSCOs: the complete BUSCO number; complete and single-copy BUSCOs: the number of single-copy BUSCOs in complete BUSCO; complete and duplicated BUSCOs: the number of multi-copy BUSCOs in a complete BUSCO; fragmented BUSCOs: predicted incomplete BUSCO number; missing BUSCOs: Number of BUSCOs not predicted.

Supplementary Table S2. Identification information of sex determination genes in *L. tricolor*.

Functional category	Gene	Gene ID	Length/ aa	Location	molecular weight/KDa	Isoelectric Point (pI)
Sex determination in the soma	da	Ltr0G114140.1	416	Chr_5	44.47	7.15
	dpn	comp85070_c0	591	-	67.19	8.70
	dsf	Ltr0G100300.1	424	Chr_1	47.72	8.87
	dsx	Ltr0G087190.1	273	Chr_6	30.29	9.29
	emc	Ltr0G111930.1	169	Chr_1	18.39	6.73
	fl(2)d	Ltr0G061030.1	429	Chr_2	48.23	4.89
	fru	Ltr0G056350.1	477	Chr_2	54.38	8.22
	gro	Ltr0G104800.1	734	Chr_1	79.06	6.65
	Imp	Ltr0G066660.1	620	Chr_2	66.82	8.99
	ix	transcript/2648 0	152	-	16.83	5.49
	PSI	Ltr0G071490.1	772	Chr_2	80.87	6.06
	run	Ltr0G059700.1	417	Chr_2	44.69	8.63
	snf	Ltr0G063930.1	242	Chr_2	27.52	9.57
	Sxl	Ltr0G093410.1	304	Chr_1	34.10	9.29
	tra	-				
	tra-2	Ltr0G115550.1	271	Chr_5	31.78	11.08
	vir	Ltr0G140060.1	1,996	Chr_1	227.75	5.66
	her	-				
	upd1	-				
	sisA	-				
Dosage compensation	mle	Ltr0G093440.1	1,248	Chr_1	139.18	7.10
	mof	Ltr0G100500.1	453	Chr_1	53.23	8.71
	msl-1	Ltr0G063100.1	416	Chr_2	47.67	6.60
	msl-2	Ltr0G001260.1	398	Chr_1	43.96	8.96
	msl-3	Ltr0G080750.1	556	Chr_3	63.49	5.80
Sex determination in the germline	otu	Ltr0G085180.1	686	Chr_3	78.00	5.83
	ovo	Ltr0G116900.1	1,110	Chr_5	121.31	6.66
	stat92E	Ltr0G087160.1	793	Chr_6	90.16	5.83
	hop	Ltr0G025740.1	1,106	Chr_8	127.58	6.86
	stil	-				

Note: “-” indicates that the corresponding gene has not been identified or identified in the transcriptome but unable to locate it on the chromosome.

Supplementary Table S3. The alignment of Illumina reads to *L. tricolor*.

Type	Total_reads	Mapped_reads	Mapped(%)	Properly_mapped_reads	Properly_mapped(%)
Illumina reads	271,094,914	269,036,915	99.24	262,767,632	97.58

Note: Total _ Reads: Clean Reads number; mapped reads: the number of Clean Reads mapped to the reference genome; mapped (%): the percentage of Clean Reads mapped to the reference genome to all Clean Reads; properly mapped: Double-ended sequencing sequences are located on the reference genome and the distance is consistent with the length distribution of the sequenced fragments.

Supplementary Table S4. BUSCO analysis results of the *L. tricolor* genome annotation.

Complete BUSCOs(C)	Complete and single-copy BUSCOs(S)	Complete and duplicated BUSCOs(D)	Fragmented BUSCOs(F)	Missing BUSCOs(M)	Total Lineage BUSCOs
1314 (96.12%)	1277 (93.42%)	37 (2.71%)	10 (0.73%)	43 (3.15%)	1,367

Note: Complete BUSCOs: the complete BUSCO number; complete and single-copy BUSCOs: the number of single-copy BUSCOs in complete BUSCO; complete and duplicated BUSCOs: the number of multi-copy BUSCOs in a complete BUSCO; fragmented BUSCOs: predicted incomplete BUSCO number; missing BUSCOs: Number of BUSCOs not predicted.