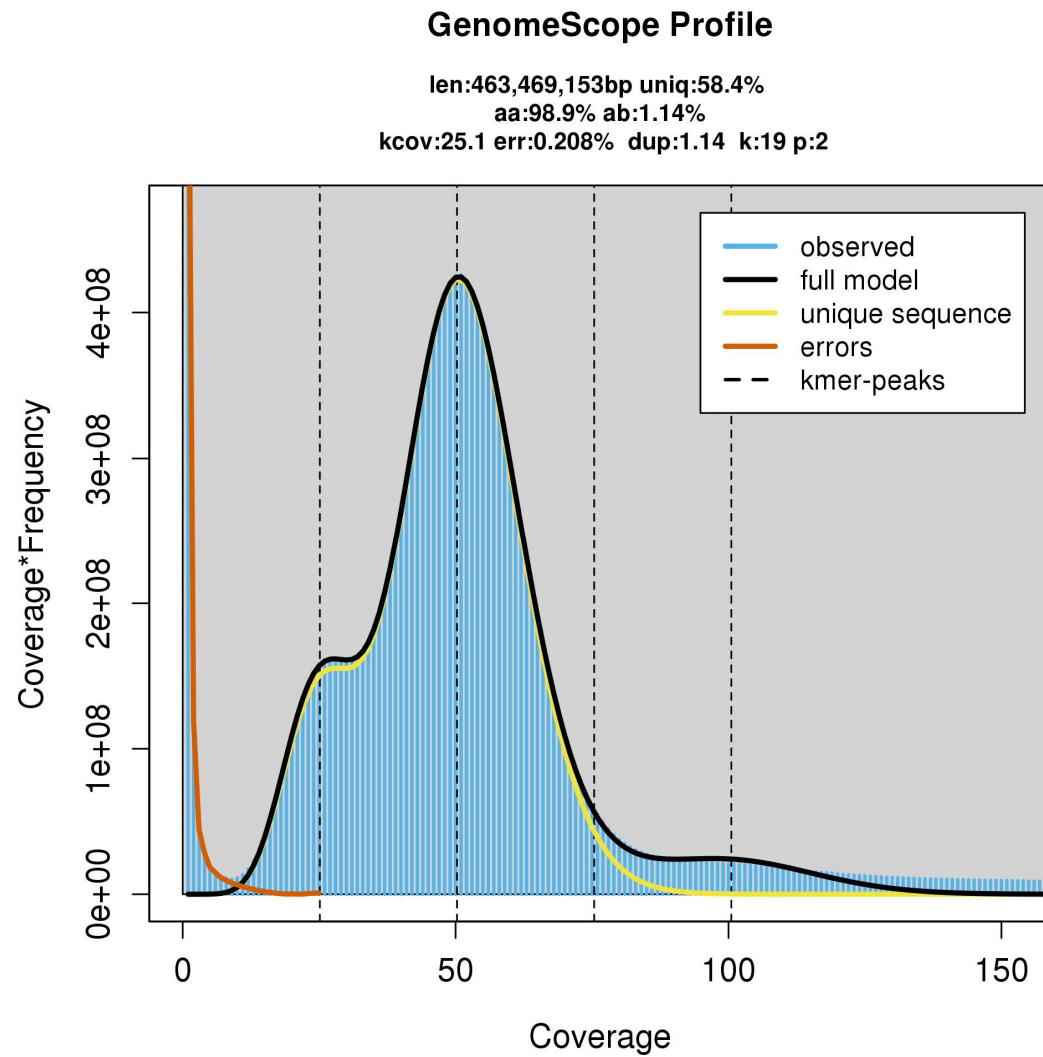
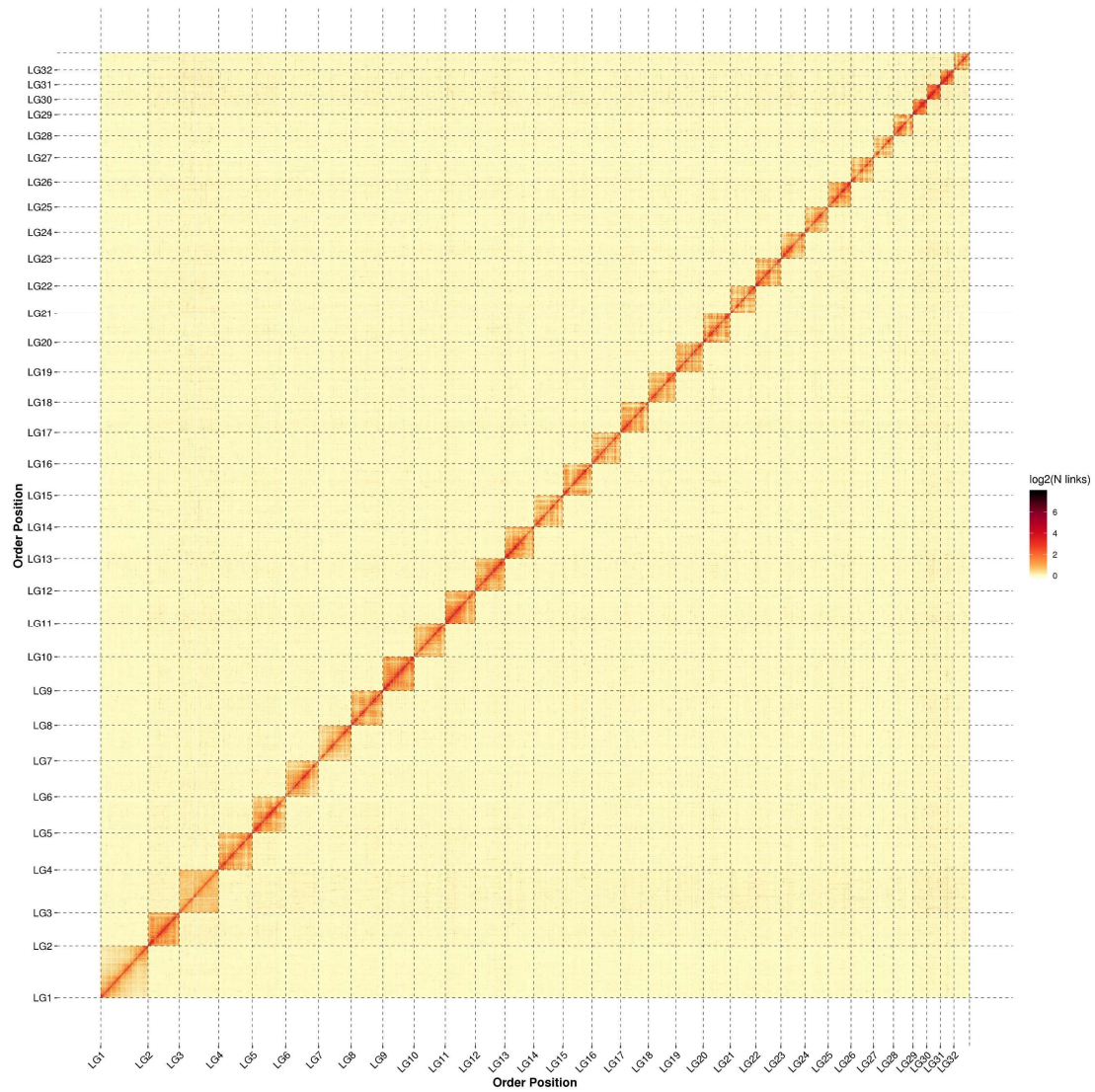
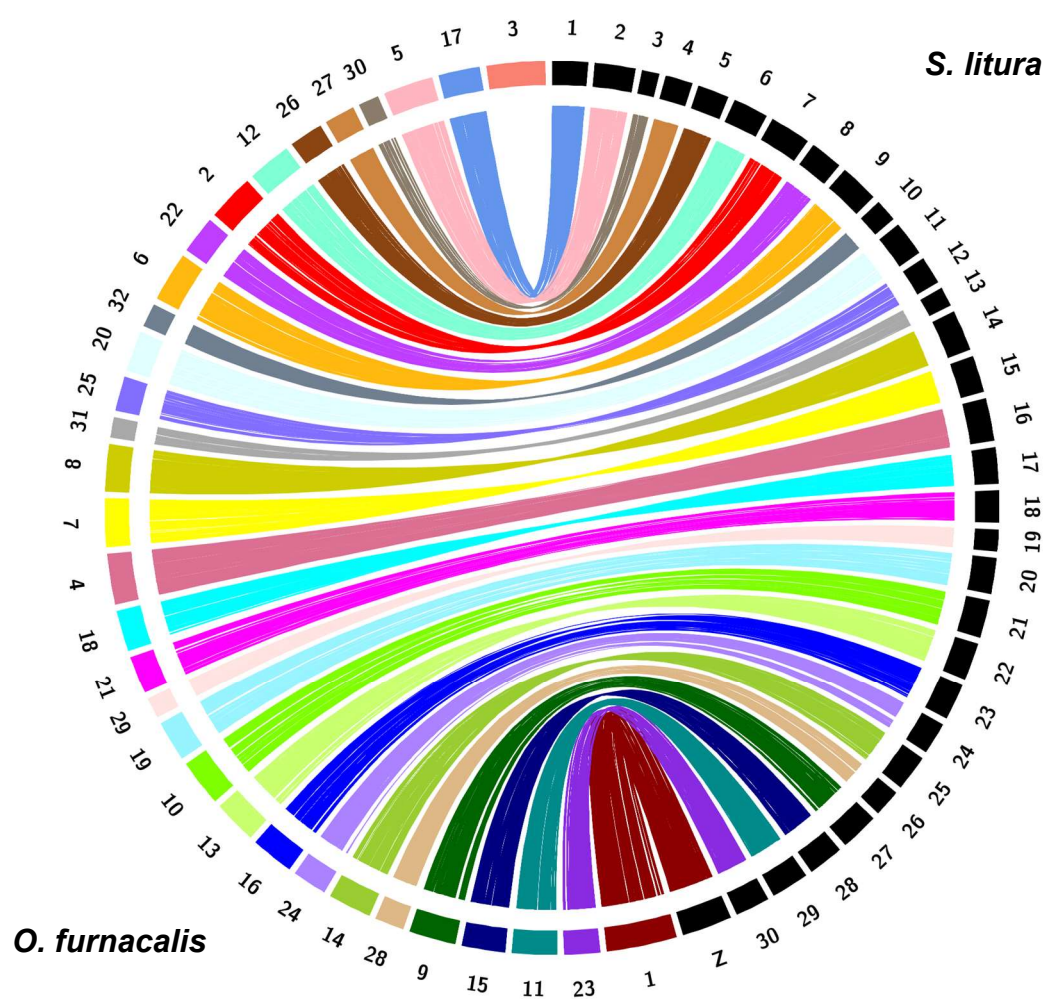




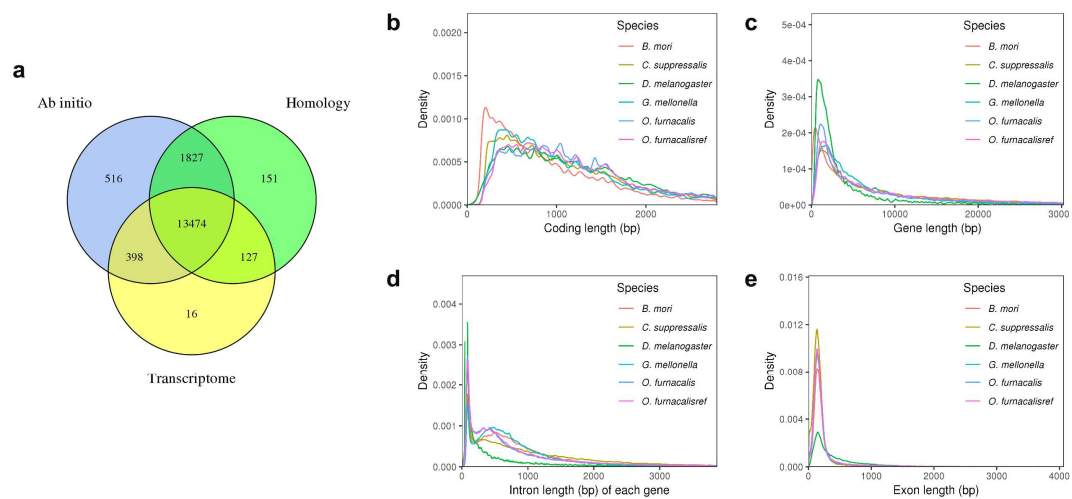
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2 **Supplementary Figure 1. Genome survey of *Ostrinia furnacalis* using K-mer**
3 **analysis.**



Supplementary Figure 2. The genome-wide Hi-C interaction maps of 32 chromosomes in *Ostrinia furnacalis*. The map indicates that intrachromosome interactions were strong while interchromosome interactions were weak. The shading gradient represents the chromosome interactions.



Supplementary Figure 3. Synteny analysis of between *Ostrinia furnacalis* and *Spodoptera litura* chromosomes.



Supplementary Figure 4. Annotation and evaluation of protein-coding genes. a. Genes annotated via Ab initio, Homology-based and RNA-seq methods. **b-e.** Comparison of *Ostrinia furnacalis* gene features with other lepidopteran gene.



Supplementary Figure 5. The number of repeat sequences in W chromosome (LG3).

45 **Table S1. Statistics of genomic sequencing data of *Ostrinia furnacalis* by PacBio**
46 **Sequel II**

Sequence Type	Reads Num	Total Bases (bp)	Reads N50 (bp)	Mean Length (bp)	Longest Read (bp)
Subreads	43,968,759	515,146,437,892	12,514	11,716	509,876
CCS	2,535,838	32,962,737,921	13,153	12,999	50,267

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Table S2. Statistics of genomic sequencing data of <i>Ostrinia furnacalis</i> by Hi-C						
Clean data by Hi-C						
ReadSum	BaseSum	GC(%)	N(%)	Q20(%)	Q30(%)	
177382279	53050949420	37.4	0	97.55	93.16	
Mapping rate of Hi-C clean data						
Total Read Pairs	Mapped Reads		Unique Mapped Read Pairs			
177,382,279	276,188,309		118,446,847			

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Table S3. Statistics of genomic resequencing data of female and male pupae

Sample	ReadSum (Mb)	BaseSum (Gb)	Q30(%)
female1	82.2	12.3	93
female2	94.0	14.1	94
female3	91.4	13.7	94
female4	92.3	13.8	93
female5	93.0	13.9	93
male1	93.8	14.0	93
male2	84.4	12.6	93
male3	95.0	14.2	93
male4	93.7	14.0	92
male5	87.7	13.1	93

Table S4 Chromosome-level assembled Lepidoptera genomes

	<i>O. furnacalis</i>	<i>C. medinalis</i>	<i>C. suppressalis</i>	<i>C. pomonella</i>	<i>T. ni</i>	<i>H. melpomene</i>	<i>B. mori</i>
Genome size (Mb)	493.1	528.3	824.4	772.9	368.2	269.0	460.3
Karyotype	2n=62	2n=62	2n=58	2n=56	2n=54	2n=42	2n=56
Number of contigs	57	4671	–	2221	26605	–	-
Number of scaffolds	43	3248	27144	1717	6181	3807	696
Number of assembled chromosomes	30A+Z+ W	29A+Z+ W	28A + Z	27A+Z+ W	26A+ Z+W	20A+Z	27A+ Z
Genome assembly quality							
Contig N50 (Mb)	15.7	0.5	0.3	0.9	0.6	0.1	12.2
Scaffold N50 (Mb)	16.5	16.1	1.8	8.9	14.2	0.3	16.8
Percentage of scaffolds in chromosomes (%)	86.8	89.1	92.5	97.5	90.6	82.7	87.3
BUSCO genes (%)	97.7	96.4	97.5	98.5	97.8	97.4	97.7
Genomic features							
Repeat (%)	41.5	39.5	46.4	42.9	20.5	24.9	46.8
G+C (%)	37.6	38.5	36.9	37.4	35.6	–	38.2
Gene annotation							
Number of genes	16509	15045	15653	17184	14043	12669	14623

58 **Table S5. Assessments of assembled genome**

CEGMA					
Number of 458 CEG* present in assembly	%of 458 CEGs present in assemblies		Number of 248 highly conserved CEGs present	% of 248 highly conserved CEGs present	
440	96.07%		196	79.03%	
BUSCOs					
Complete BUSCOs(C)	Complete and single-copy BUSCOs(S)	Complete and duplicated BUSCOs(D)	Fragmented BUSCOs(F)	Missing BUSCOs(M)	Total Lineage BUSCOs
932(97.69%)	926(97.06%)	6(0.63%)	6(0.63%)	16(1.68%)	954
DNA-seq data mapping					
Total_reads	Mapped reads	Mapped (%)	Properly mapped (%)	Properly mapped (%)	
183,973,226	182,267,035	99.07%	175,334,598	95.30%	

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Table S6. Genomic annotation of *Ostrinia furnacalis*.

	Annotated Number	Annotated Ratio
tRNA	7,710	—
rRNA	73	—
miRNA	39	—
pseudogenes	171	—
Annotation of protein-coding genes		
GO_Annotation	12013	72.77
KEGG_Annotation	12033	72.89
KOG_Annotation	9314	56.42
Swissprot_Annotation	10864	65.81
TrEMBL_Annotation	15901	96.32
eggNOG_Annotation	11746	71.15
nr_Annotation	16201	98.13
All_Annotated	16213	98.21