

Supplementary Table 1 Estimation of genome size

K-mer	Depth	n_K-mer	Genome size(Mb)	Revise Genome size(Mb)	Heteozygous rate(%)	Repeat rate(%)
19	51	157,918,766,016	3094.45	3,048	1.34	71

Supplementary Table 2 Sequencing libraries and statistics of the data used for the genome assembly

Pair-end libraries	Insert size	Total data (G)	Read length (bp)	Sequence coverage (X)
Illumina reads	350bp	191	150.00	63.67
Nanopore	--	440.60	--	146.87
Total	--	631.60	--	210.54

Supplementary Table 3 Characteristics of *Pse. libanotica* assembly containing 7 chromosome.

Chromosome name	Chromosome length (bp)	number of genes
chr1	343,212,279	5419
chr2	464,035,102	7220
chr3	408,139,130	6307
chr4	327,295,031	4534
chr5	398,549,212	6504
chr6	362,840,832	5344
chr7	449,314,708	6898
un	236,383,112	4143
total	2,989,769,406	46369

Supplementary Table 4 QV value in the *Pse. libanotica* genome

Chr	ue kmer in ge in genome and	QV	error rate
Chr1	35510771 343145998	22.8496	0.005188
Chr2	42946485 463956002	23.3585	0.004615
Chr3	37787741 408066087	23.3567	0.004617
Chr4	33167603 327239628	22.9448	0.005076
Chr5	38520265 398484011	23.161	0.004829
Chr6	33859959 362777071	23.3208	0.004655
Chr7	42003744 449230808	23.3127	0.004664

Supplementary Table 5 Evaluation of Benchmarking Universal Single-Copy Orthologs (BUSCO) and gene space coverage using core eukaryotic gene mapping approach (CEGMA) in *Pse. libanotica* genome

Species	Size (Mb)	BUSCO	CEGMA			
			Complete		Complete + partial	
<i>Pse. libanotica</i>	2.99Gb	C:95.2%[S:90.1%,D:5.1%],F:1.2%,M:3.6%,n:1440	Prots 228	Completeness (%) 91.94	Prots 239	Completeness (%) 96.37

Note:
Size: genome size.
BUSCO notation: C:Complete BUSCOs;S: Complete and single-copy BUSCOs;D: Complete and duplicated BUSCOs; F: Fragmented BUSCOs;M: Missing BUSCOs;n:Total BUSCO groups searched.
CEGMA notation: Complete: Over 70% assembled core genes.
CEGMA notation: Complete + partial: Partial assembled core gene; Prots: the number of assembled genes; %completeness: the proportion of assembled core gene to core gene from the database.

Supplementary Table 6 Statistics of short high-quality reads mapping

		Percentage
Reads	Mapping rate (%)	98.95
Genome	Average sequencing depth	58.95

Supplementary Table 7 Assessment of *Pse. libanotica* genome using full length EST sequences

	Dataset	Number	with >90% sequence in one scaffold		with >50% sequence in one scaffold	
			Number	Percent (%)	Number	Percent (%)
Version	>200bp	151,872	132,240	87.073	145,315	95.683
	>500bp	54,907	47,838	87.126	53,048	96.614
	>1000bp	25,517	22,361	87.632	24,824	97.284
	>2000bp	9,212	7,952	86.322	8,958	97.243

Supplementary Table 8 Prediction of protein-coding genes in *Pse. libanotica*

Gene set		Number	Average gene length (bp)	Average CDS length (bp)	Average exon length (bp)	Average intron length (bp)	Average exons per gene
De novo	Augustus	110,674	1809.41	819.70	304.51	584.98	2.69
	GlimmerH	464,723	5372.95	498.87	246.18	4748.53	2.03
	MM	260,231	3468.79	530.63	215.50	2009.27	2.46
	SNAP	207,833	6326.56	558.07	190.11	2980.25	2.94
	Genscan	352,062	2482.82	523.46	213.69	1351.61	2.45
	Geneid	45,820	2739.85	1013.98	295.85	711.00	3.43
Homolog	<i>Zea mays</i>	83,117	1580.19	713.71	294.24	607.80	2.43
	<i>Secale cereale</i>	83,198	2234.77	847.11	284.41	701.37	2.98
	<i>Triticum aestivum</i>	82,752	1922.42	799.69	286.07	625.34	2.80
	<i>Aegilops tauschii</i>	47,656	2656.60	1011.62	293.41	672.04	3.45
	<i>Sorghum bicolor</i>	71,014	2101.95	815.51	273.96	650.79	2.98
	<i>Triticum dicoccoide s</i>	58,702	2428.98	950.70	296.40	669.67	3.21
	<i>Brachypod ium</i>	71,014	2101.95	815.51	273.96	650.79	2.98
	<i>distachyon Triticum urartu</i>	74,755	2308.66	851.23	3.04	279.58	712.79
	<i>Triticum durum</i>	56,132	2256.06	906.08	305.03	685.11	2.97
	<i>Oryza sativa</i>	87,149	1627.20	718.52	279.53	578.60	2.57
	<i>Hordeum vulgare</i>	57,435	6023.16	1828.92	346.18	979.24	5.28
	Transcripts	109,908	3011.48	953.43	227.31	644.28	4.19
	PASA	163,236	2106.65	721.50	286.36	911.55	2.52
	EVM	162,902	2133.02	722.61	287.29	930.80	2.52
	PASA-update	102,333	2676.51	845.90	284.13	925.87	2.98
	Final set						