

Figure S1. Analysis of chromosomal breakpoints between *wAlbB-Uju* and *wAlbB-Hou*. Alignment boxes display long reads from both variants (SRA accessions: SRR21023725 and SRR7784287) aligned to the *wAlbB-Uju* genome at chromosomal breakpoints (A-G) and a large indel comprising horizontally-transferred *SecA* genes (H). Dashed red lines indicate chromosomal breakpoints. Tr: transposase ; RT: reverse transcriptase.

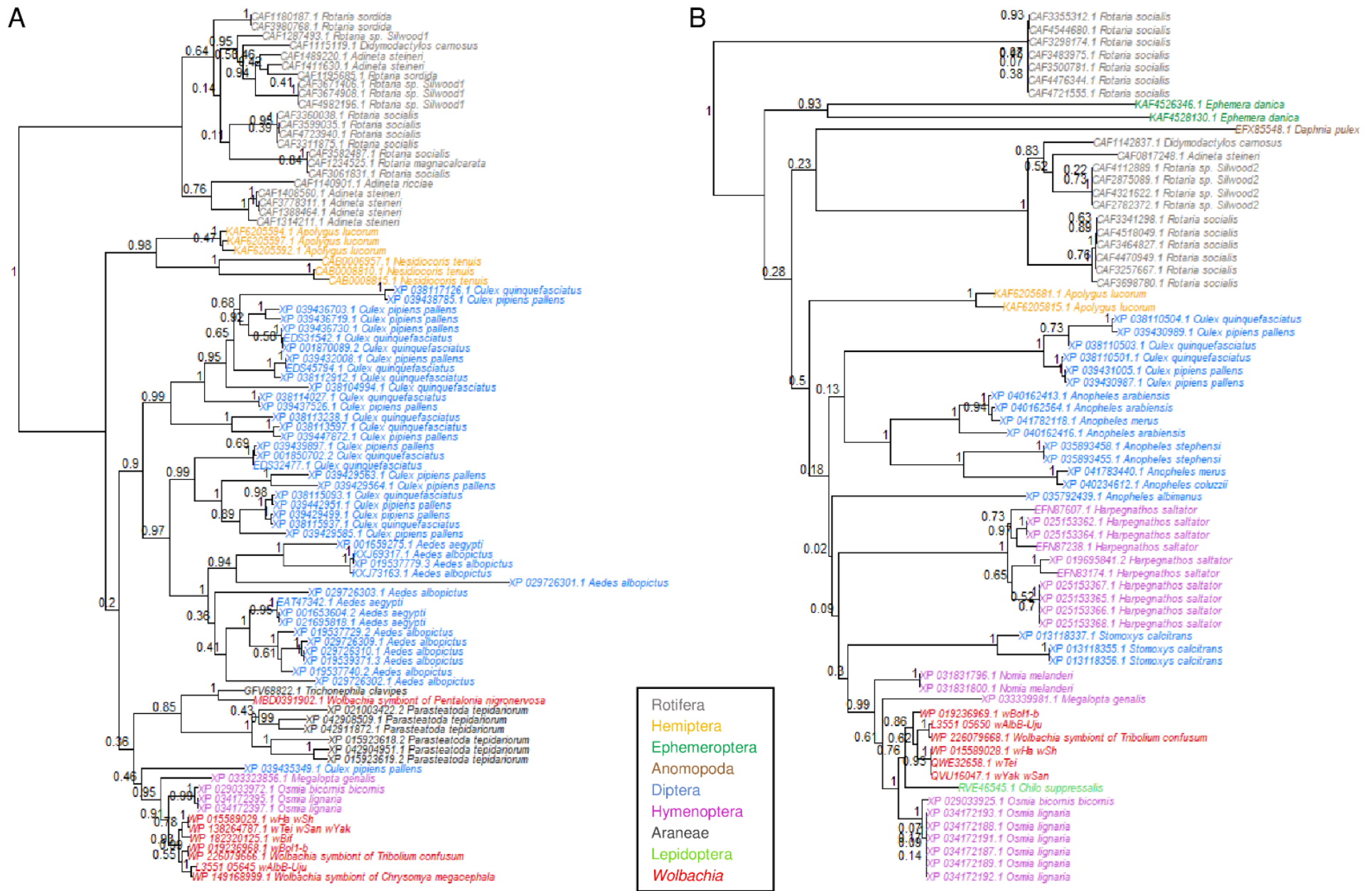


Figure S2. Maximum likelihood phylogenies of horizontally-transferred translocase subunit SecA genes. (A) L3551_05645 and (B) L3551_05650 amino acids were aligned with their homologues and conserved sites (Gblocks) were used to build the phylogenies with PhyML. Node labels are bootstrap supports calculated from 100 replicates.

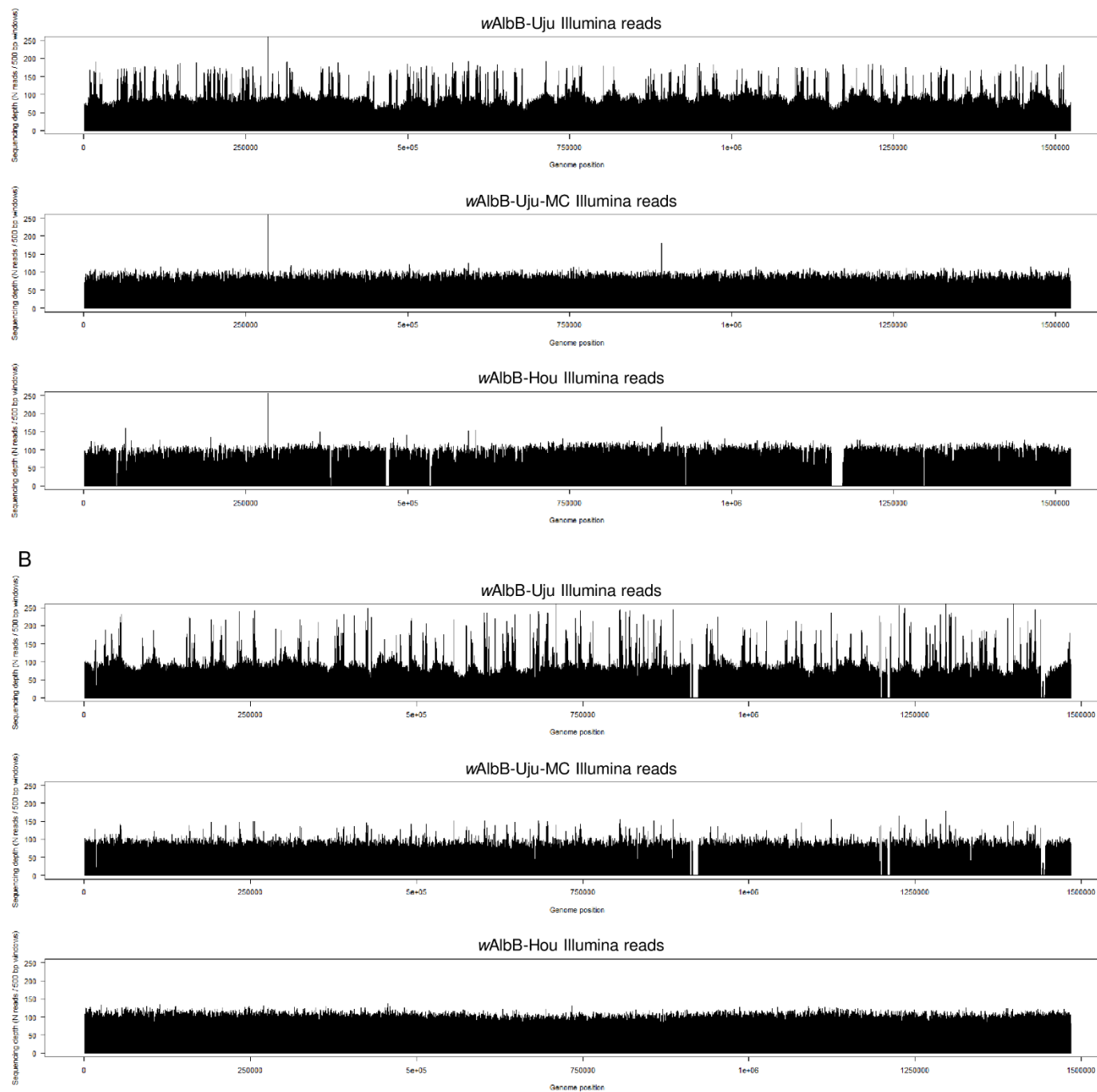


Figure S3. Sequencing depth plots. Mean sequencing depth per 500 bp window of Illumina reads mapped onto (A) *wAlbB-Uju* and (B) *wAlbB-Hou* genomes.

Trait	Factor	Type III Sum of Squares	df	Mean Square	F	P
Female <i>Wolbachia</i> density	wAlbB variant	2.863	1	2.863	11.068	0.001
	Nuclear background	0.637	1	0.637	2.464	0.119
	Error	39.57	153	0.259		
Male <i>Wolbachia</i> density	wAlbB variant	4.764	1	4.764	24.111	< 0.0001
	Nuclear background	0.216	1	0.216	1.093	0.298
	wAlbB variant by nuclear background	1.688	1	1.688	8.541	0.004
	Error	29.442	149	0.198		

Table S3. Statistical analysis of differences in density between wAlbB variants.

Sex	Factor	Type III Sum of Squares	df	Mean Square	F	P
Female	wAlbB variant	64.79	1	64.79	71.089	< 0.0001
	Nuclear background	4.738	1	4.738	5.199	0.024
	Temperature	41.206	1	41.206	45.211	< 0.0001
	wAlbB variant by Nuclear background	13.486	1	13.486	14.797	< 0.0001
	wAlbB variant by Temperature	28.611	1	28.611	31.393	< 0.0001
	Error	103.899	114	0.911		
Male	wAlbB variant	55.897	1	55.897	95.736	< 0.0001
	Nuclear background	1.162	1	1.162	1.991	0.161
	Temperature	30.633	1	30.633	52.467	< 0.0001
	wAlbB variant by Nuclear background	3.478	1	3.478	5.957	0.016
	wAlbB variant by Temperature	28.237	1	28.237	48.362	< 0.0001
	Error	66.56	114	0.584		

Table S4. Statistical analysis of wAlbB variant densities under heat stress.

Population comparison	Factor		Type III Sum of Squares	df	Mean Square	F	P
wAlbB-infected populations	Egg storage duration ²	Hypothesis	14.518	1	14.518	78.446	< 0.0001
		Error	41.27	223	0.185		
	Egg storage duration	Hypothesis	2.067	1	2.067	11.17	0.001
		Error	41.27	223	0.185		
wAlbB variant		Hypothesis	7.815	1	7.815	12.236	0.072
		Error	1.284	2.01	0.639		
Nuclear background		Hypothesis	1.754	1	1.754	9.475	0.002
		Error	41.27	223	0.185		
Replicate population within wAlbB variant		Hypothesis	1.285	2	0.643	3.472	0.033
		Error	41.27	223	0.185		
wAlbB variant by Nuclear background		Hypothesis	0.694	1	0.694	3.75	0.054
		Error	41.27	223	0.185		

Table S5. Statistical of quiescent egg viability.