**SUPPORTING INFORMATION AVAILABLE**

**Supplementary Figure 1**

The average numbers of offspring in each selection. In the first time select, the population was collected in rice fields. The following procedure was used to select the high-fecundity population (HFP) and low-fecundity population (LFP). "*" means statistically significant difference in the average numbers of offspring between HFP and LFP (t-test, $p < 0.05$), "**" means statistically highly significant difference in the average numbers of offspring between HFP and LFP (t-test, $p < 0.01$)

**Supplementary Figure 2**

The isolated protein spots, which have dynamic change regulation, were subjected to in-gel digestion and MALDI-TOF/TOF analysis. The obtained protein PMF and MS/MS data spectra were submitted to the *N.lugens* EST, NCBInr and the EST_others database for identification, for example, spot b41 was identified as glutamine synthetase 2. (A) PMF spectrum; (B) MS/MS spectrum

**Supplementary Figure 3**

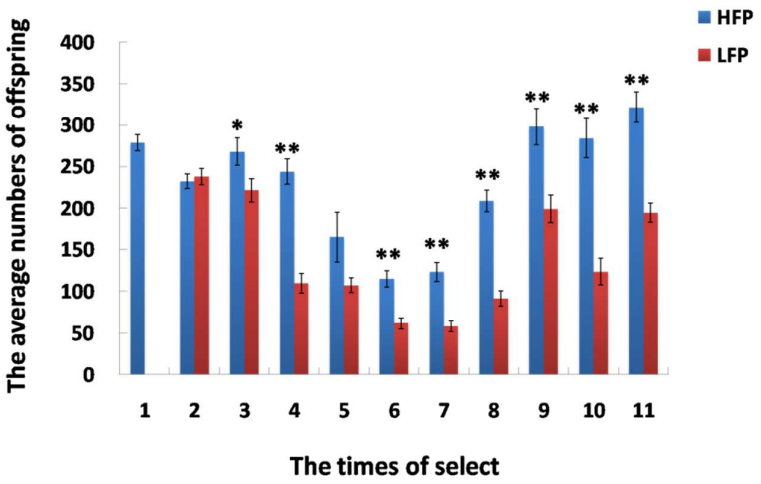
Validation of de novo gene expression levels using assemblies of BPH transcriptomics. The log10 (RPKM) values from the HFP were regressed against those from the LFP. (A) Expression level for 2$^{nd}$ day 5$^{th}$ instar nymph in the BPH transcriptome. (B) Expression level for 2$^{nd}$ day brachypterous female in the BPH transcriptome. RPKM number is for reads per kilobase of node per million reads.

**Supplementary Figure 4**

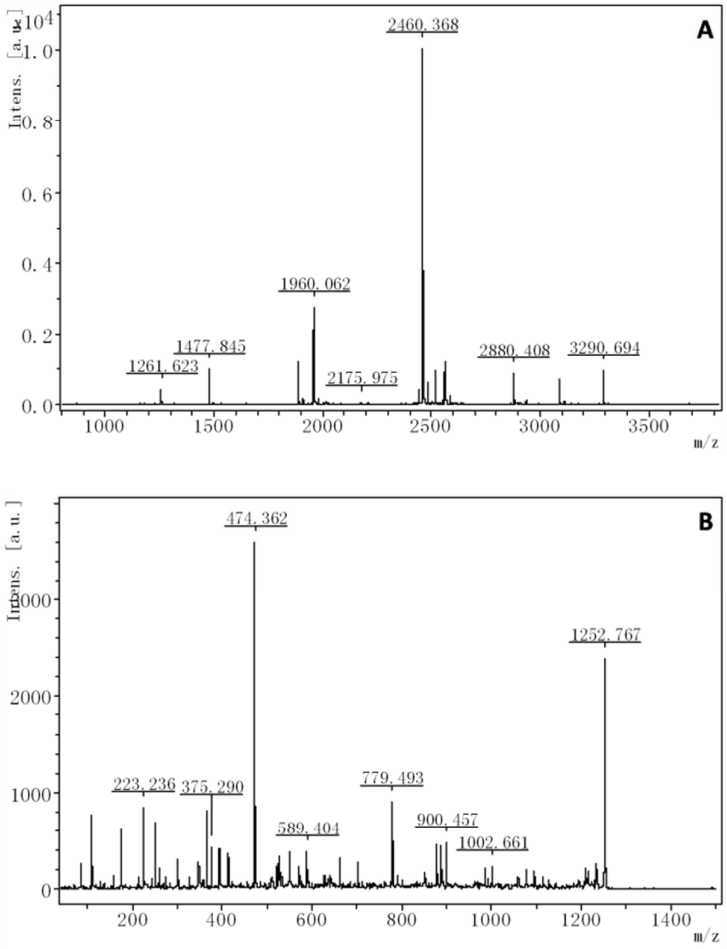
Detection of the specific *wsp* gene of *Wolbachia* in the two populations. In the high

fertility population, only one *wsp* gene was detected in BPH. By contrast, there were no *wsp* genes detected in the low fertility population.

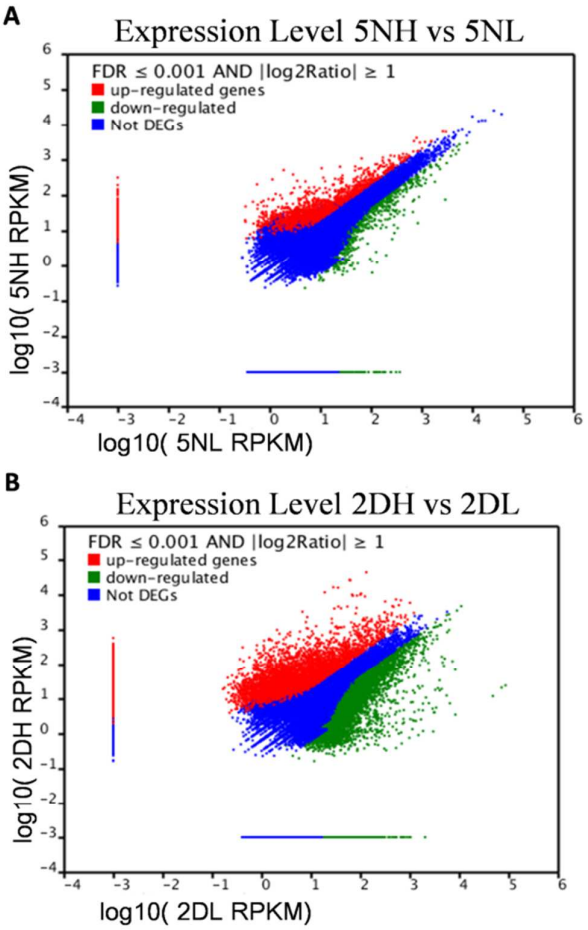
**Supplementary Fig.1**



**Supplementary Fig.2**



**Supplementary Fig.3**



**Supplementary Fig.4**