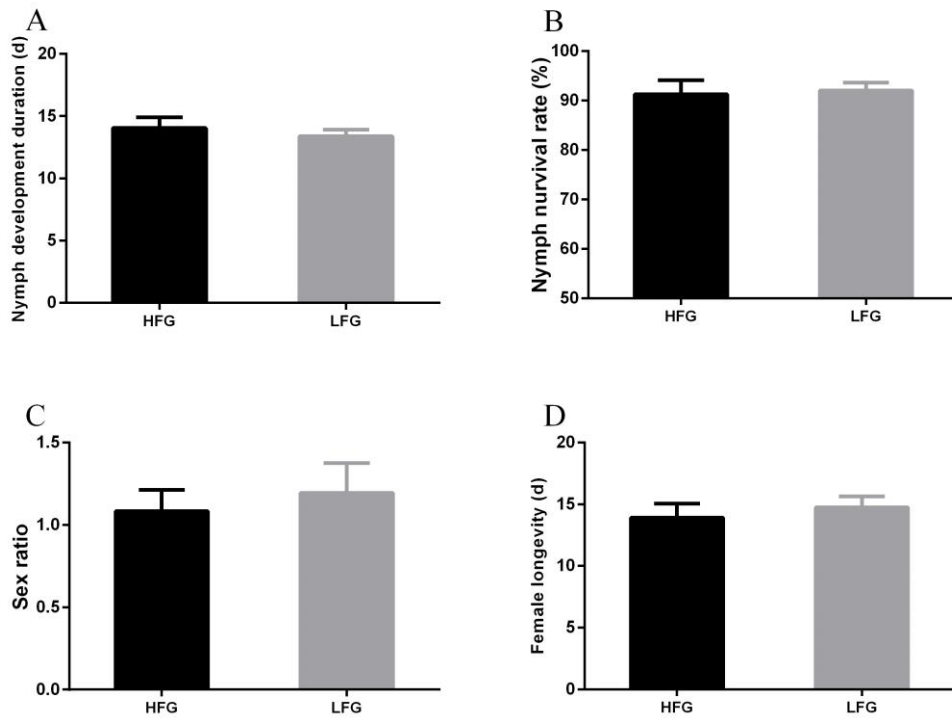


1 **Appendix A** qRT-PCR primers of each differentially expressed genes (DEGs) and  $\beta$ -actin

Gene	Primer sequence (5'-3')
<i>MGAM</i>	F: TTCGTCCCCAACCATTCCAG R: AGAACTCTCCCCGTTGCTTG
<i>FAS</i>	F: AGATGAGAGATGAAGAAGCAGCA R: TATTTTGGTTGCCCCTCGCT
<i>E20MO</i>	F: CTCTCAGTTCAGGGAGCGTC R: AACTGAATGTGGCCAGCGAA
<i>PNLIP</i>	F: CTCGGTCACGCTGACTTCTT R: GTGGTAGTTGTTGCACGCTG
<i>GAPDH</i>	F: CAAGGTCATCTCCAACGCCT R: CAGCTTTCCAGAAGGTCCGT
<i>STRAD</i>	F: GCTTCTAGACCGCACCCTT R: CGGGCGTAGGTCTTTCTTGA
<i>ACLY</i>	F: CGCGTACGCTCTCTTAGCTT R: TCAGCAGTGATGGTTGCGAA
<i>Vg</i>	F: GGCTCCGAGTCAAGTGACAA R: GTTGGCACCATCGTGGTAGA
$\beta$ -actin	F: CCCTCGCTCCCTCAACAATG R: TGGATGGACCAGACTCGTCGT

2



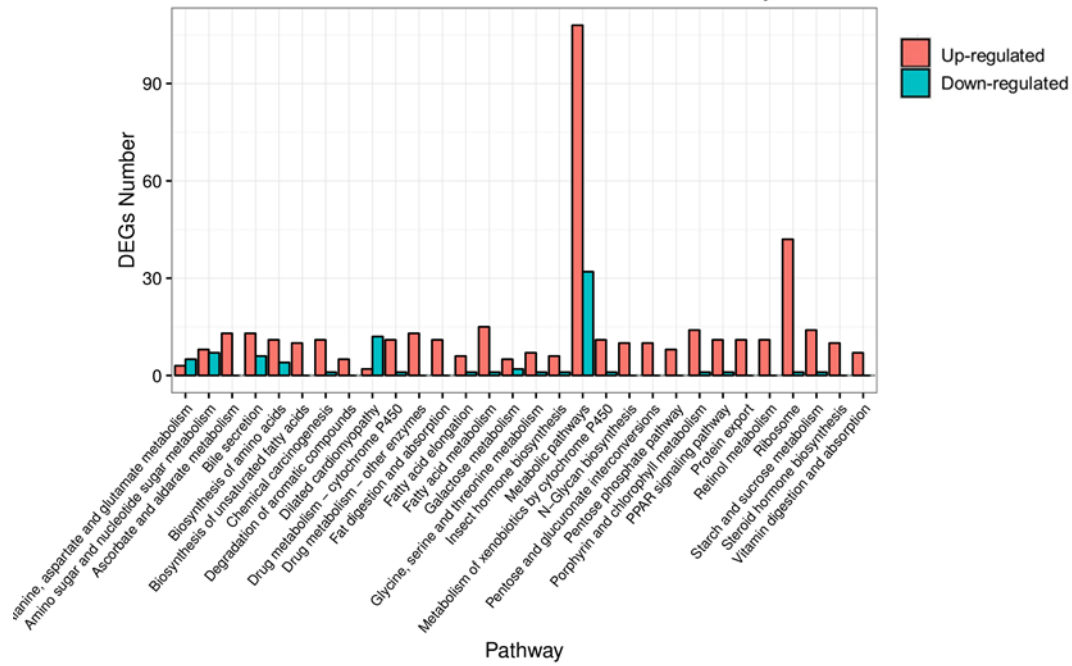
3

4 **Appendix B** The ecological fitness of the two genotypes of the brown planthopper  
 5 *Nilaparvata lugens*. A, Nymph development duration; B, Survival rate; C, Sex ratio;  
 6 D, Female longevity. HFG, high-fecundity genotype BPH; LFG, low-fecundity  
 7 genotype BPH. Data represent the mean  $\pm$  SE (n=15).

8 **Appendix C** Summary for the transcriptomes of the two genotypes of the brown planthopper  
 9 *Nilaparvata lugens*

Type	HFG	LFG
Read Length	150	150
Total Raw Reads	37,486,347	37,898,464
Total Raw Bases	5,622,952,050	5,684,769,600
Total Clean Reads	37,205,337	37,590,301
Total Clean Reads Ratio (%)	99.2	99.2
Total Clean Bases	5,580,800,550	5,638,545,150
Total Clean Bases Ratio (%)	99.2	99.2
Total Adatper Reads	277,911	302,423
Total Adatper Reads Ratio (%)	0.8	0.8
Total Low Quality Reads	3,099	5,740
Total Low Quality Reads Ratio (%)	0.01	0.02
Clean Reads GC (%)	44.1	46.0
Clean Reads Q20 (%)	96.3	95.6
Clean Reads Q30 (%)	91.1	89.8

10 HFG, high-fecundity genotype BPH; LFG, low-fecundity genotype BPH



11

12 **Appendix D** The differentially expressed genes (DEGs) in the most enriched  
 13 pathways. The bar represents the number of DEGs within a specific pathway.  
 14 Up-regulated, the numbers of up-regulated genes of HFG compared with LFG;  
 15 Down-regulated, the numbers of down-regulated genes of HFG compared with LFG.