

NOISeq MB-down biological process GO term	Fold enrichment
Oviposition	7.40
Nicotinamide nucleotide metabolic process	4.98
Cytoplasmic translation	4.04
Monocarboxylic acid biosynthetic process	3.35
Fatty acid metabolic process	2.95
Carbohydrate metabolic process	2.54
Generation of precursor metabolites and energy	2.50
Purine ribonucleotide metabolic process	2.41
Oxidation-reduction process	2.06
Cellular catbolic process	1.82

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NOISeq WH-down biological process GO term	Fold enrichment
Muscle contraction	12.87
Sarcomere organization	7.51
Muscle organ development	4.05
Actin filament organization	3.91
Axogenesis	2.56
Behaviour	2.08
Movement of cell or subcellular component	2.02
Locomotion	1.90
Sexual reproduction	1.65
Multicellular organismal reproductive process	1.64

Figure S2: Comparison of DE results between DESeq2 and NOISeq

(A-D) Venn diagrams showing overlap of differentially expressed (DE) genes between DESeq2 and NOISeq. (A) Upregulated MB 1h-AR (MB-up), (B) Upregulated WH 1h-AR (WH-up), (C) Downregulated MB 1h-AR (MB-down), (D) Downregulated WH 1h-AR (WH-down). (E-H) GO enrichment analysis for biological processes from NOISeq DE genes using PANTHER (p < 0.05, Binomial test with Bonferroni correction, minimum 5 genes, sorted by hierarchical view). The top GO terms, heading each GO hierarchical cluster are displayed, sorted by fold enrichment, for (E) MB-up, (F) WH-up, (G) MB-down, (H) WH-down.

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