**S2 Data**

**Transcriptomic analysis of *NlInR2*E4 and *NlInR1*RNAi female adults**

**Overview of transcriptomes.** Because *Nl*InR2 resembled *Nl*InR1 on fecundity, but differed from *Nl*InR1 on lifespan and starvation tolerance at the adult stage, we used RNA-seq to examine genome-wide gene expression in *Wt*SW, *NlInR2*E4, and *NlInR1*RNAi females. For this purpose, fourth-instar nymphs were microinjected with ds*NlInR1* to generate *NlInR1*RNAi females. At 12h after adult eclosion, females (*n* = 8) were pooled for RNA extraction, and a total of nine cDNA libraries were constructed from *Wt*SW, *NlInR2*E4, and *NlInR1*RNAi females with three biological replicates each. Then, cDNA libraries were further used for Illumina sequencing via Illumina Hiseq platform. More than 20.9 million raw reads were generated from each cDNA library with Q20 and Q30 values each exceeding 92.77% and 97.32% (S16 Table), respectively. Following the removal of adaptors, poly-N and low-quality reads, more than 20.1 million clean reads were retained for each sample. The mapping rate of clean reads against *N. lugens* reference genome ranged from 64.12% to 66.87%. The transcriptomic data was deposited into GenBank under the accession number PRJNA724037.

**Differentially expressed genes (DEGs) in *NlInR1*RNAi and *NlInR2*E4 females.** Using the fold change ≥ 2 and FDR< 0.05 as criteria, we identified 884 DEGs in *NlInR1*RNAi and 417 DEGs in *NlInR2*E4 compared to*Wt*SW females (S5 Fig), which only accounted for 4.8% and 2.2% of BPH encoding genes (18,534 genes), respectively. Among all the DEGs identified, 101 genes (S17 Table) were commonly regulated by *NlInR1*RNAi and *NlInR2*E4, of which six genes were up-regulated in *NlInR1*RNAi but down-regulated in *NlInR2*E4, 51 genes were up-regulated in both *NlInR1*RNAi and *NlInR2*E4, and 44 genes were down-regulated in both *NlInR1*RNAi and *NlInR2*E4 (S5 Fig). Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis showed that the 101 commonly-regulated DEGs were significantly involved into metabolic pathways (S5 Fig). In addition, 783 (S5 Fig and S18 Table) and 316 (S5 Fig and S19 Table) genes were specifically regulated by *NlInR1*RNAi and *NlInR2*E4, respectively. KEGG pathways enriched by genes of *NlInR1*RNAi-specific were visibly different from that enriched by genes of *NlInR2*E4-specific (S5 Fig). These observations indicate that *Nl*InR1 and *Nl*InR2 may have different sets of target genes.