

### **Description of Additional Supplementary Files**

File Name: Supplementary Data 1

Description: Expression abundances and heritabilities of 25,849 transcripts in 207 wild *C. elegans* strains

File Name: Supplementary Data 2

Description: GWA mapping results of 5,291 transcript expression traits, eQTL classification, and distant eQTL hotspots

File Name: Supplementary Data 3

Description: : Enrichment of genes with eQTL, distant eQTL in hotspots

File Name: Supplementary Data 4

Description: Fine mappings for distant eQTL in hotspots