These dataset from:https://www.cengen.org/downloads/

https://www.dropbox.com/sh/ewq7cu7sbjixfb4/AABO5Vv5rR-mK02Jble77TCka

The **single-cell sequencing data** is available under several formats:

• The raw reads are available on GEO (GSE 136049).

• Full dataset (100,955 cells) as a Seurat (500 MB) or Monocle (300 MB) object. Also available on Dropbox.

• Only the cells annotated as neurons (70,296 cells) as Seurat (4 GB) or Monocle (300 MB) object. Also available on Dropbox.

• For binary expression patterns, csv files are available for thresholds 1 (most permissive), 2 (medium), 3 (more conservative), and 4 (most stringent), here or on Dropbox. In these matrices, a gene determined not expressed in a cell has a value of 0, a gene above the threshold has a value >0 (the average TPM per gene per neuron type, as calculated by the monocle3 package).

In addition,

• The gene models used for alignment were based on the Wormbase WS273 GTF with extended 3’UTRs. These updated gene models are included with the single-cell GEO dataset.

• For comparison of scRNA-Seq and bulk RNA-Seq, 29 samples corresponding to 8 neuron classes were also described in the paper. The raw reads are uploaded on GEO (GSE169137), and the count matrix can be downloaded here.

Older Datasets are also available on https://www.dropbox.com/sh/ewq7cu7sbjixfb4/AABO5Vv5rR-mK02Jble77TCka