

**Figure S1. Synapse distribution, degree distribution, and other center subgraphs. Related to Figure 1.**

**A-B.** Distribution of the numbers of post and presynaptic sites, respectively. Data for # of postsynaptic sites  $\geq 1000$  and # of presynaptic sites  $\geq 500$  are not shown. Dashed lines illustrate thresholds for center subgraphs. More synaptic sites indicate less truncated neuropils.

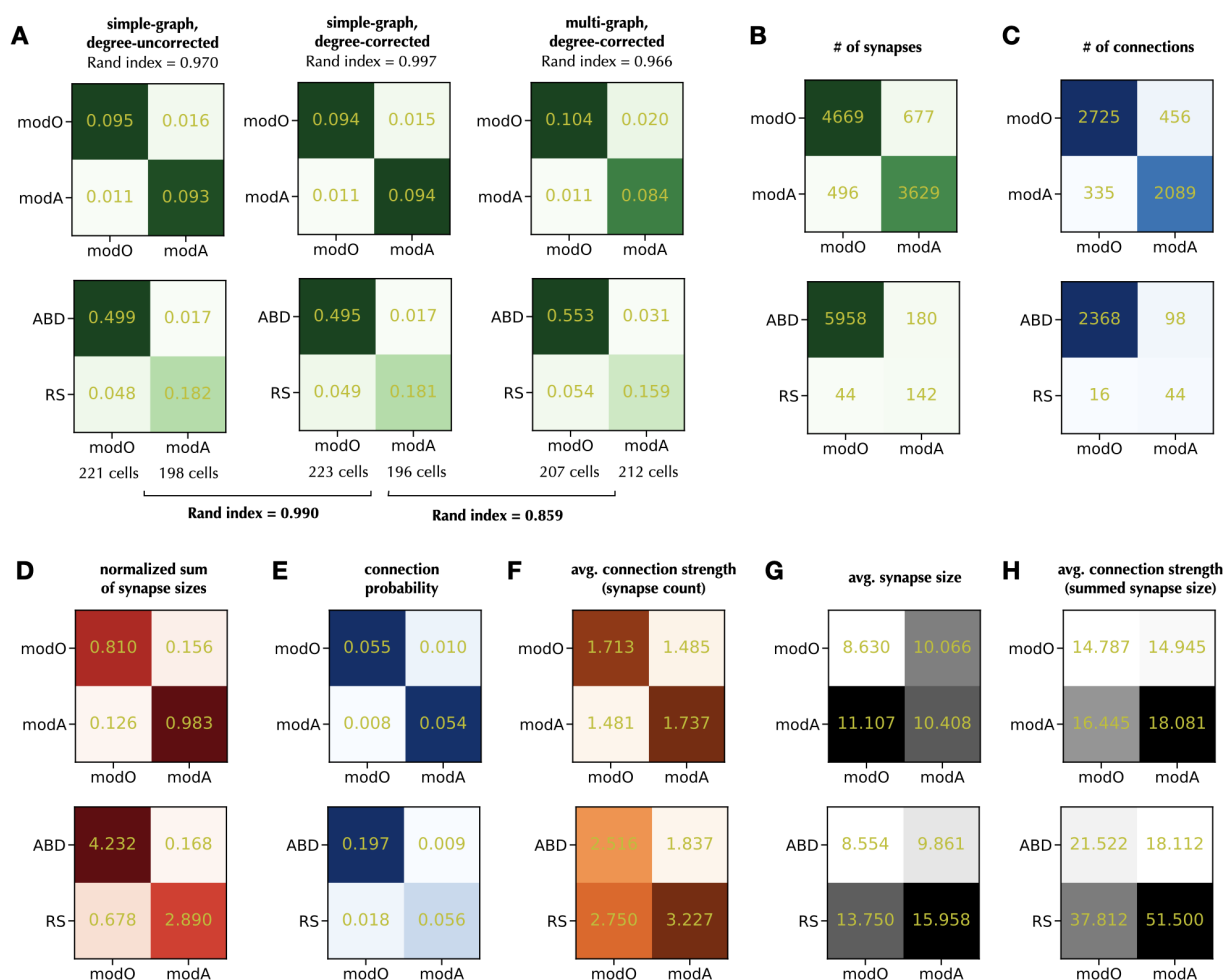
**C-D.** Distribution of in-degree and out-degree of the center subgraph in the main figure, respectively.

**E-F.** Distribution of weighted in-degree and out-degree of the center subgraph in the main figure, respectively.

**G.** Modular structure remains similar when the center subgraph is defined more restrictively than in the main figures (334 neurons with at least 100 presynapses. and 100 postsynapses).

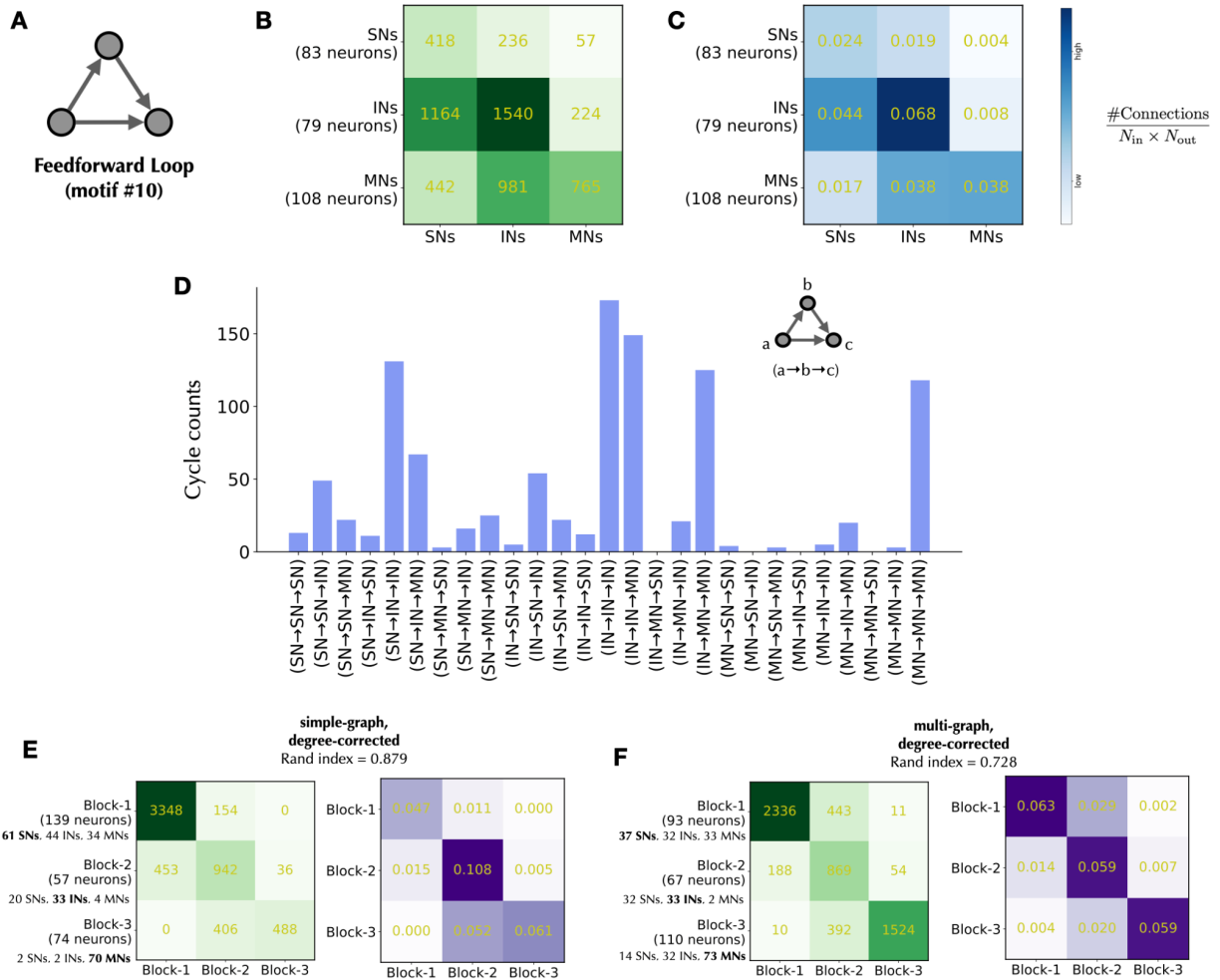
Numbers in blocks are synapse counts normalized by the numbers of input and output neurons.

Blocks in columns send connections to blocks in rows.



**Figure S2. Modularity under different metrics. Related to Figure 1.**

- A.** Similar modular structures discovered by a non-degree-corrected SBM model, a degree-corrected SBM model (shown in the main result), and a multi-graph degree-corrected SBM model. Numbers in blocks are synapse counts normalized by the numbers of input and output neurons. Blocks in columns send connections to blocks in rows. Rand indices on the top are averages of the inferred block membership from 10 runs, indicating the stability of the discovered structure. Rand indices at the bottom measure the agreement of block membership found by different variants of the algorithm.
- B.** Total numbers of synapses within and between modO and modA, ABD neurons, and large RS neurons.
- C.** Total numbers of connections within and between modO and modA, ABD neurons, and large RS neurons.
- D.** The summed synapse sizes normalized by the numbers of input and output neurons.
- E.** Total numbers of connections normalized by the numbers of input and output neurons.
- F.** Average numbers of synapses per connection among different groups of neurons.
- G.** Average synapse size among different groups of neurons.
- H.** Average summed synapse sizes per connection among different groups of neurons.



**Figure S3. Feedforward loop and block structure in *C. elegans*. Related to Figure 3.**

**A.** Cartoon of feedforward loop motif.

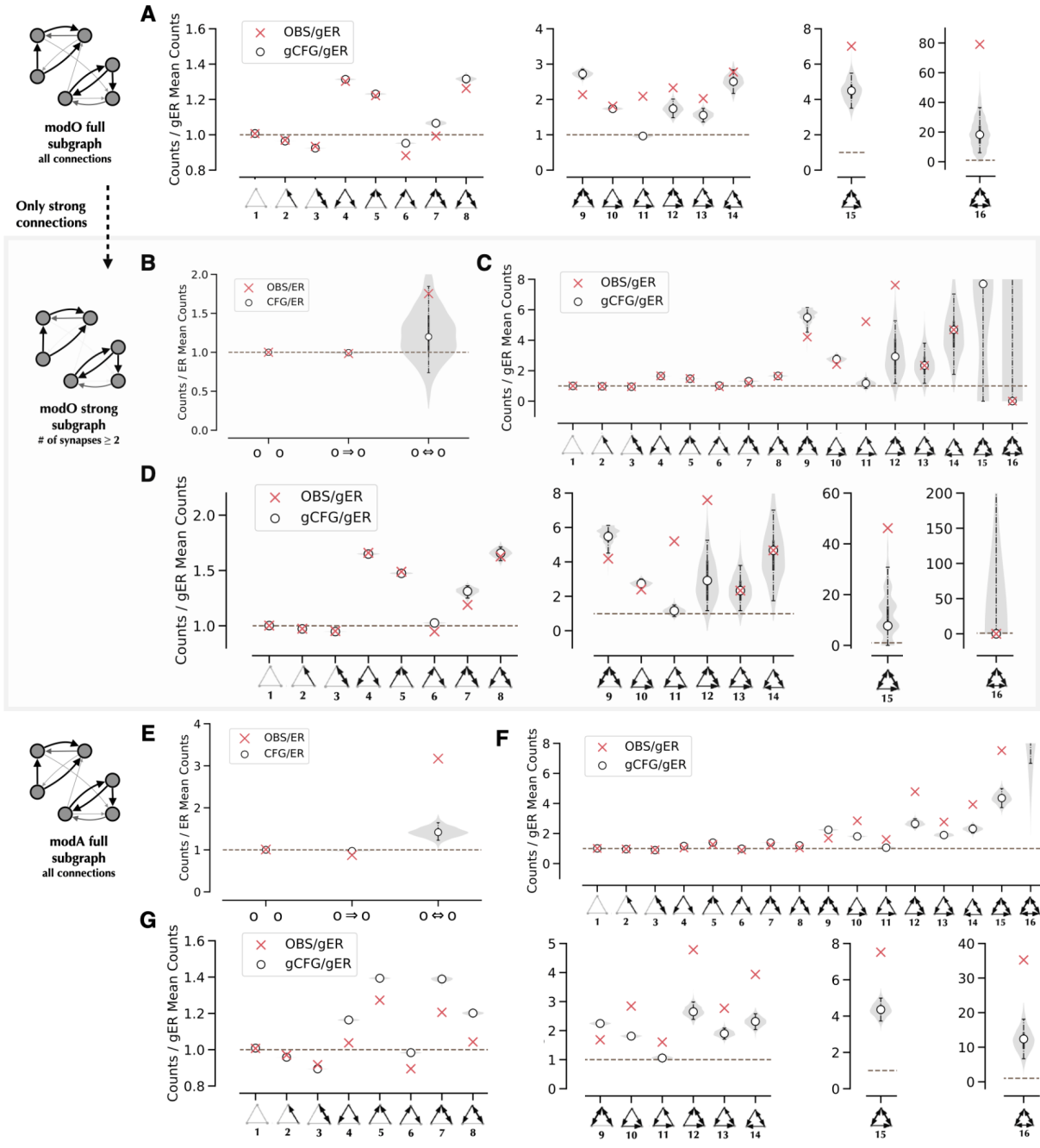
**B.** Matrix of synapse counts of *C. elegans* between blocks defined by neuron categories (SNs: sensory neurons; INs: interneurons; MNs: motor neurons). Blocks in columns send connections to blocks in rows.

**C.** Matrix of connection probabilities of *C. elegans* between blocks defined by neuron categories (SNs: sensory neurons; INs: interneurons; MNs: motor neurons). Blocks in columns send connections to blocks in rows.

**D.** Counts of feedforward loops from different blocks.

**E.** Matrices of synapse counts (left) and connection probability (right) of *C. elegans* between blocks found by a degree-corrected SBM fitted to the simple graph of the wiring diagram. Rand index on the top is an average of the inferred block membership from 10 runs, indicating the stability of the discovered structure.

**F.** Matrices of synapse counts (left) and connection probability (right) of *C. elegans* between blocks found by a degree-corrected SBM fitted to the multi-graph of the wiring diagram. Rand index on the top is an average of the inferred block membership from 10 runs, indicating the stability of the discovered structure.



**Figure S4. ModO and ModA motif distributions. Related to Figure 2.**

**A.** 3-cell motif frequencies in modO. Same plot as Figure 2E, with a different y-axis scale. The violin plot shows the smoothed distribution of the motif counts sampled from the generalized configuration model (gCFG). White points indicate medians, solid vertical lines indicate quartiles and dashed lines indicate the 95% confidence interval for 1,000 samples.

**B.** 2-cell motif frequencies in the strong subgraph of modO and a configuration model relative to the ER model. The shaded region shows the smoothed distribution of motif counts sampled from the configuration model. White points indicate medians, solid vertical lines indicate quartiles and dashed lines indicate the 95% confidence interval for 1,000 samples.

**C.** 3-cell motif frequencies in the strong subgraph of modO and the configuration model relative to a generalized ER model (gER). The violin plot shows the smoothed distribution of the motif counts sampled from the generalized configuration model (gCFG). White points indicate medians, solid vertical lines indicate quartiles and dashed lines indicate the 95% confidence interval for 1,000 samples.

**D.** 3-cell motif frequencies in the strong subgraph of modO. Same plot as Figure S4C, with a different y-axis scale.

**E.** 2-cell motif frequencies in modA and a configuration model relative to the ER model. The shaded region shows the smoothed distribution of motif counts sampled from the configuration model. White points indicate medians, solid vertical lines indicate quartiles and dashed lines indicate the 95% confidence interval for 1,000 samples.

**F.** 3-cell motif frequencies in modA and the configuration model relative to a generalized ER model (gER). The violin plot shows the smoothed distribution of the motif counts sampled from the generalized configuration model (gCFG). White points indicate medians, solid vertical lines indicate quartiles and dashed lines indicate the 95% confidence interval for 1,000 samples.

**G.** 3-cell motif frequencies in the strong subgraph of modA. Same plot as Figure S4F, with a different y-axis scale.