



Supplementary Figure S1. Shared pathways of *L. marina* and *C. elegans* Under CeMM Conditions. (A) Drug metabolism-cytochrome P450 related genes in *L. marina*. (B) Glutathione metabolism-related genes in *L. marina*. (C) Retinol metabolism genes in *L. marina*. (D) Carbon metabolism genes in *L. marina*. (E) Glyoxylate and dicarboxylate metabolism-related genes in *L. marina*. (F) Arachidonic acid metabolism-related genes in *L. marina*. (G) Tryptophan metabolism-related genes in *L. marina*. (H) Fatty acid degradation-related genes in *L. marina*. Log₂FC: Log₂(Fold Change). All data shown here are mean \pm SEM.

Supplementary Table S1. Sequencing data statistics

Samples	Clean reads	Clean bases	GC Content	%≥Q30
HQ-CeMM1	22,709,671	6,792,965,608	48.58%	93.98%
HQ-CeMM2	20,506,472	6,135,123,172	48.55%	94.00%
HQ-CeMM3	21,905,540	6,548,731,716	48.39%	93.72%
HQ-OP501	25,126,485	7,511,336,736	48.29%	93.86%
HQ-OP502	21,293,371	6,371,918,226	47.88%	93.54%
HQ-OP503	21,630,897	6,469,266,624	48.16%	93.65%
N2-CeMM1	21,697,850	6,495,321,086	46.12%	93.16%
N2-CeMM2	23,040,034	6,892,867,926	46.30%	93.60%
N2-CeMM3	22,586,570	6,755,922,018	46.50%	93.81%
N2-OP501	18,867,488	5,640,668,092	47.06%	93.84%
N2-OP502	21,592,609	6,448,173,608	47.26%	94.17%
N2-OP503	22,608,827	6,755,104,724	47.17%	93.97%

Note: (1)Samples: Sample name; 'HQ' and 'N2' represent *L. marina* and *C. elegans*, respectively.

(2)Clean reads: Counts of clean PE reads;

(3)Clean bases: total base number of Clean Data;

(4)GC content: Percentage of G,C in clean data.

(5)≥Q30%: Percentage of bases with Q-score no less than Q30.