

**Supplementary Table 5A. Expression of helicase-like genes at different developmental stages.**

	Whole genome	Helicase	Subfamily										
			DEAD-box	DEAH-box	SKI2	UPF1	SWI2/SNF2	MCM	PIF1	MPH1	RAD3	RECQ	Others
Total genes	18,010	134	37	11	8	10	28	6	10	4	5	4	11
Total genes from the categories below (%)	4705 (26.1)	66 (49.3)	19 (51.4)	7 (63.6)	5 (62.5)	3 (30.0)	13 (46.4)	5 (83.3)	1 (10.0)	2 (50.0)	3 (60.0)	4 (100.0)	4 (36.4)
<b>Gene expression categories in hermaphrodites (%)</b>													
Intrinsic	1250 (6.9)	29 (21.6)	9 (24.3)	4 (36.4)	2 (25.0)	2 (20.0)	4 (14.3)	0	1 (10.0)	2 (50.0)	2 (40.0)	2 (50.0)	1 (9.1)
Oogenesis-enriched	1030 (5.7)	29 (21.6)	9 (24.3)	3 (27.3)	1 (12.5)	1 (10.0)	4 (14.3)	5 (83.3)	0	0	1 (20.0)	2 (50.0)	3 (27.3)
Mixed oogenesis/somatic	622 (3.5)	3 (2.2)	1 (2.3)	0	1 (12.5)	0	1 (3.6)	0	0	0	0	0	0
Spermatogenesis enriched	864 (4.8)	1 (0.8)	0	0	1 (12.5)	0	0	0	0	0	0	0	0
Mixed spermatogenesis/somatic	479 (2.7)	1 (0.8)	0	1 (9.1)	0	0	0	0	0	0	0	0	0
Soma enriched	460 (2.6)	4 (3.0)	0	0	0	0	4 (14.3)	0	0	0	0	0	0

Gene numbers in the columns for "Helicase" and for each "Subfamily" representing the total *C. elegans* helicase-like genes and the members in each subfamily are derived from Supplementary Table 2. The number in the "Whole genome" column represents all identified *C. elegans* genes and the indicated expression categories in hermaphrodites are from Reinke et al<sup>3</sup>. The percentage of the total gene number for each column is indicated in parentheses. "Others" contains the orphan genes.

**Supplementary Table 5B. Expression of helicase-like genes in the embryonic stages.**

	Whole genome	Helicase	Subfamily										
			DEAD-box	DEAH-box	SKI2	UPF1	SWI2/SNF2	MCM	PIF1	MPH1	RAD3	RECQ	Others
Total gene number	18,791	134	37	11	8	10	28	6	10	4	5	4	11
Genes expressed at embryonic stages (%)	8890 (47.3)	84 (62.7)	28 (75.7)	9 (81.8)	4 (50.0)	4 (40.0)	15 (53.6)	6 (100.0)	2 (20.0)	3 (75.0)	3 (60.0)	4 (100.0)	6 (54.5)

Gene numbers in the "Helicase" and "Subfamily" columns are derived from Supplementary Table 2 and the gene number in the "Whole genome" column is from Baugh et al<sup>2</sup>.

"Others" contains the orphan genes.

**Supplementary Table 5C. Development- and sex-regulated expression of helicase-like genes.**

	Whole genome	Helicase	Subfamily										
			DEAD-box	DEAH-box	SKI2	UPF1	SWI2/SNF2	MCM	PIF1	MPH1	RAD3	RECQ	Others
Total genes	17,871	134	37	11	8	10	28	6	10	4	5	4	11
Genes described in the database (%)		85 (63.4)	24 (64.9)	7 (63.6)	6 (75.0)	5 (50.0)	21 (75.0)	6 (100.0)	3 (30.0)	2 (50.0)	3 (60.0)	1 (25.0)	7 (63.6)
<b>Genes in “Male dominant groups”</b>													
#10-11	944	5	1	0	0	0	2	0	1	0	0	1	0
#13-20	3446	10	0	0	2	0	2	0	4	1	0	0	1
#24-25	535	4	0	0	2	1	1	0	0	0	0	0	0
Total number of genes in all groups (%)	4925 (27.6)	17 (12.7)	1 (2.7)	0 (0.0)	3 <sup>*1</sup> (37.5)	1 (10.0)	5 (17.9)	0 (0.0)	3 <sup>*1</sup> (30.0)	1 (25.0)	0 (0.0)	1 (25.0)	1 (9.1)
<b>Genes in “Hermaphrodite dominant groups”</b>													
#2	1513	21	6	0	0	0	4	6	0	1	2	0	2
#4-7	1630	20	8	1	1	2	4	0	1	0	1	0	2
#9	1272	4	1	1	0	0	1	0	0	0	0	0	1
Total number of genes in all groups (%)	4415 (24.7)	43 (32.1)	14 <sup>*1</sup> (37.8)	2 (18.2)	1 (12.5)	2 (20.0)	9 (32.1)	6 (100.0)	1 <sup>*2</sup> (10.0)	1 (25.0)	3 (60.0)	0 (0.0)	4 <sup>*1</sup> (36.4)
<b>Genes in “Developmentally regulated groups” (without sex bias)</b>													
#1	427	8	3	2	1	0	2	0	0	0	0	0	0
#3	765	10	6	1	0	0	2	0	0	0	0	0	1
#22	256	3	0	1	0	1	1	0	0	0	0	0	0
Total number of genes in all groups (%)	1448 (8.1)	21 (15.7)	9 (24.3)	4 (36.4)	1 (12.5)	1 (10.0)	5 (17.9)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (9.1)

The indicated groups, group numbers, and gene numbers in the “Whole genome” column are derived from Jiang et al<sup>4</sup> and the gene numbers in the “Helicase” and each of the “Subfamily” columns are from Supplementary Table 2.

<sup>\*1</sup>A gene with multiple group numbers in the categorized group (e.g., Male dominant groups) was scored as one gene.

<sup>\*2</sup>A gene with multiple group numbers in two categorized groups such as *pif-1* was scored independently in each group.

“Others” contains orphan genes.