

Table S2. *lin-3* requires *let-23* and the core PCD pathway to increase numbers of embryonic cell corpses.

Genotype	Number of embryonic cell corpses ^a				
	Comma	1.5-fold	2-fold	3-fold	4-fold
Wild-type	10.0 ± 1.6	11.4 ± 1.5	10.0 ± 1.9	2.1 ± 1.7	0.5 ± 0.7
<i>syls1</i>	12.4 ± 2.4**	13.2 ± 2.2**	13.1 ± 2.1**	2.5 ± 1.8	0.5 ± 0.6
<i>let-23(n1045); syls1</i>	9.9 ± 2.4 ^{††}	10.8 ± 1.9 ^{††}	9.3 ± 2.6 ^{††}	2.2 ± 1.5	0.6 ± 0.6
<i>egl-1(n1084n3082)</i>	0.1 ± 0.3	0.1 ± 0.3	0.1 ± 0.3	0.0 ± 0.0	0.0 ± 0.2
<i>egl-1(n1084n3082); syls1</i>	0.1 ± 0.3	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.2
<i>ced-9(n1950)</i>	0.1 ± 0.3	0.4 ± 0.5	1.2 ± 1.1	0.5 ± 0.6	0.4 ± 0.6
<i>ced-9(n1950); syls1</i>	0.3 ± 0.5	0.4 ± 0.6	0.8 ± 0.8	0.7 ± 0.7	0.7 ± 0.7
<i>ced-4(n1162)</i>	0.1 ± 0.3	0.1 ± 0.3	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0
<i>ced-4(n1162); syls1</i>	0.1 ± 0.3	0.1 ± 0.3	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0
<i>ced-3(n717)</i>	0.1 ± 0.3	0.1 ± 0.3	0.1 ± 0.3	0.0 ± 0.0	0.0 ± 0.0
<i>ced-3(n717); syls1</i>	0.1 ± 0.3	0.1 ± 0.3	0.1 ± 0.3	0.0 ± 0.0	0.0 ± 0.0

^aCell corpses scored at the indicated developmental stages are presented as the mean ± SD. (n≥30). *syls1* is a chromosomal integrant of a repetitive *lin-3* transgene. *syls1* was compared to wild-type (**P*<0.05 and ***P*<0.001, two-tailed *t* test) and *let-23(n1045); syls1[lin-3(+)]* were compared to *syls1[lin-3(+)]* ([†]*P*<0.05 and ^{††}*P*<0.001, two-tailed *t* test).