

Supplementary File 1. Percentage of Pin Animals

Genotype	# Pin	N	% Pin	95% CI
N2	0	>500	0	ND
<i>sym-3(mn618)</i>	3	114	2.6	0.6–7.8
<i>sym-4 (mn619)</i>	76	539	14.1	11.4–17.3
<i>mec-8(u74)</i>	5	126	4.0	1.5–9.2
<i>mec-8; sym-3^a</i>	131	132	99	95.4–100
<i>mec-8; sym-4</i>	267	280	95.3	92.1–97.3
N2 control(<i>RNAi</i>)	0	42	0	ND
N2 <i>fbn-1(RNAi)</i>	0	113	0	ND
<i>sym-3; control(RNAi)</i>	2	123	1.6	0.1–6.1
<i>sym-3; fbn-1(RNAi)</i>	80	135	59.2	50.8–67.2 (± 8.2)
<i>sym-4; control(RNAi)</i>	4	86	4.7	1.5–11.4(± 5.1)
<i>sym-4; fbn-1(RNAi)</i>	44	135	32.6	25.2–40.9(± 7.9)
<i>mec-8; control(RNAi)</i>	10	132	7.6	4.2–13.4(± 4.6)
<i>mec-8; fbn-1(RNAi)</i>	50	196	25.5	19.9–32.0(± 6.1)
<i>lin-35; control(RNAi)</i>	0	86	0	ND
<i>lin-35; fbn-1(RNAi)</i>	23	68	33.8	23.7–45.7(± 11.0)
<i>lin-35; sym-3; control(RNAi)</i>	6	73	8.2	3.5–17.1(± 6.8)
<i>lin-35; sym-3; fbn-1(RNAi)</i>	66	75	88	78.5–93.8(± 7.7)
<i>lin-35; sym-4; control(RNAi)</i>	14	116	12.1	7.2–19.4(± 6.1)
<i>lin-35; sym-4; fbn-1(RNAi)</i>	113	120	94.2	88.2–97.4(± 4.6)
<i>mec-8; rrf-3; control(RNAi)</i>	5	94	5.3	2.0–12.2(± 5.1)
<i>mec-8; rrf-3; fbn-1(RNAi)</i>	35	42	83.3	69.1–92.0(± 11.5)
N2	0	>500	0	ND

<i>sym-3</i>	3	114	2.6	0.6–7.8
<i>sym-4</i>	76	539	14.1	11.4–17.3
<i>fbn-1(ns67)</i>	54	124	43.5	35.1–52.3
<i>fbn-1(ns283)</i>	66	154	42.9	35.3–50.8
<i>fbn-1(tm290)</i>	949	187	19.7	17.3–22.4
<i>fbn-1(ns67); sym-3</i>	89	90	98.9	93.4–100
<i>fbn-1(ns67); sym-4</i>	86	86	100	95–100
<i>mec-8; fbn-1(n67)</i>	58	60	96.7	88–99.7
<i>fbn-1(tm290); sym-3</i>	96	96	100	95.4–100
<i>fbn-1(tm290); sym-4</i>	71	71	100	93.9–100
<i>mec-8; fbn-1(tm290)</i>	155	155	100	97.1–100
N2	0	>500	0	ND
<i>mec-8; sym-4</i>	267	280	95.3	92.1–97.3
<i>mec-8; sym-4; fdEx251</i>	42	104	40.1	31.5–50.0
<i>mec-8; sym-4; fdEx254</i>	63	103	61.1	51.5–70.0
N2; control(RNAi)	0	42	0	0–10
N2; <i>fbn-1</i> (RNAi)	0	113	0	0–3.9
<i>mec-8</i> ; control(RNAi)	10	132	7.6	4.2–13.4(±4.6)
<i>mec-8; fbn-1</i> (RNAi)	50	196	25.5	19.9–32.0(±6.1)
<i>rde-1</i> ; control(RNAi-Hyp) ^b	0	58	0	ND
<i>rde-1; fbn-1</i> (RNAi-Hyp) ^b	0	93	0	ND
<i>mec-8; rde-1</i> ; control(RNAi-Hyp) ^b	14	177	7.9	4.7–12.9
<i>mec-8; rde-1; fbn-1</i> (RNAi-Hyp) ^b	31	159	19.5	14–26.4

^aBecause this strain (WY893) gives rise to a high frequency of viable *mnEx169*(–) progeny in the first generation following loss of the array (F1 escapers), next-generation progeny (F2) from *mnEx169*(–) F1

parents were scored. ^bStrains were derived from NR222. CI, confidence interval; ND, not determined. CIs were calculated using the Agresti-Coull method.