

Table S2. Raw data of genotype tested for axotomy.

strain	genotype	n	regenerated	%	p-value	v.s.
KU501	wild type	62	48	77	-	-
KU1270	<i>sqv-3(n2842)</i>	53	21	40	<0.0001	KU501
KU1271	<i>sqv-3(n2842) + P_{sqv-3}::sqv-3</i>	17	13	76	0.012	KU1270
KU1272	<i>sqv-3(n2842) + P_{unc-25}::sqv-3</i>	20	14	70	0.03	KU1270
KU1273	<i>svh-11(gk819558)</i>	84	32	38	<0.0001	KU501
KU1274	<i>svh-11(gk819558) + P_{unc-25}::svh-11</i>	51	36	71	0.0003	KU1273
KU86	<i>svh-11(km86)</i>	53	19	36	<0.0001	KU501
KU1285	<i>svh-11(km86) + P_{unc-25}::svh-11</i>	51	34	67	0.0019	KU86
KU1285*	<i>svh-11(km86)</i> (-array)	50	17	34	0.0014	KU1285
KU1275	<i>sqv-1(n2819)</i>	54	45	83	0.49	KU501
KU1276	<i>sqv-5(n3611)</i>	54	43	80	0.82	KU501
KU504	<i>mlk-1(km19)</i>	50	18	36	<0.0001	KU501
KU1277	<i>svh-11(gk819558) mlk-1(km19)</i>	47	18	38	0.84	KU504
					1	KU1273
KU1286	<i>svh-11(km86) mlk-1(km19)</i>	55	23	42	0.56	KU504
					0.72	KU86
KU1290	<i>svh-11(km86); ddr-2(ok574)</i>	58	22	38	0.85	KU86
					0.32	KU1201
KU1278	<i>svh-11(gk819558) + P_{mlk-1}::mlk-1</i>	59	35	59	0.017	KU1273
KU1287	<i>svh-11(km86) + P_{mlk-1}::mlk-1</i>	50	29	58	0.03	KU86
KU1287*	<i>svh-11(km86)</i> (-array)	51	17	33	0.017	KU1287
KU1279	<i>svh-11(gk819558) + P_{unc-25}::svh-2</i>	50	32	64	0.0044	KU1273
KU1288	<i>svh-11(km86) + P_{unc-25}::svh-2</i>	52	32	62	0.011	KU86
KU1288*	<i>svh-11(km86)</i> (-array)	52	21	40	0.049	KU1288
KU1280	<i>svh-11(gk819558) + P_{unc-25}::ddr-2</i>	67	33	49	0.19	KU1273
KU1289	<i>svh-11(km86) + P_{unc-25}::ddr-2</i>	54	26	48	0.24	KU86
KU1201	<i>ddr-2(ok574)</i>	56	16	29	<0.0001	KU501
KU1203	<i>ddr-2(ok574) + P_{unc-25}::ddr-2</i>	55	33	60	0.0011	KU1201
KU1281	<i>ddr-2(ok574) + P_{unc-25}::ddr-2(N141A)</i>	51	20	39	0.31	KU1201
KU1282	<i>ddr-2(ok574) + P_{unc-25}::ddr-2(N167A)</i>	53	26	49	0.032	KU1201
KU1283	<i>ddr-2(ok574) + P_{unc-25}::ddr-2(N264A)</i>	51	32	63	0.0005	KU1201
KU1284	<i>ddr-2(ok574) + P_{unc-25}::ddr-2(N353A)</i>	52	34	65	0.0002	KU1201

Asterisks indicate the non-transgenic sibling controls.