Hammarlund *et al.*, Supplemental Table 1

	Genotype	Strain	# animals	# axons	# regeneration	P vs. control
wild type	*oxIs12*	EG1285	50	105	73 (70%)	
MAPKKK	*dlk-1(ju476); oxIs12*	MJB1014	24	69	0	<.0001
DLK-1 rescue	*dlk-1(ju476) basEx2*	MJB1032	21	53	43 (81%)	0.1314
RPM-1 OE	*basEx3; oxIs268*	MJB1034	22	43	3 (7%)	<.0001
E3 ligase	*rpm-1(ju41); oxIs12*	MJB1027	24	51	44 (86%)	0.0296
F-Box	*fsn-1(gk429); oxIs12*	MJB1025	24	65	56 (86%)	0.0163
Rab GTPase	*glo-1(zu391); oxIs268*	MJB1017	24	65	33 (51%)	0.0155
Rab GEF	*glo-4(ok623); oxIs12*	MJB1024	25	59	39 (66%)	0.7272
wt L1/2 DD	*oxIs12*	EG1285	16	17	15 (88%)	0.1484
wt L1/2 VD	*oxIs12*	EG1285	14	14	13 (93%)	0.1087
wt 2 day adult	*oxIs12*	EG1285	19	47	17 (36%)	<.0001
wt 5 day adult	*oxIs12*	EG1285	16	32	4 (13%)	<.0001
dlk-1 L1/2 DD	*dlk-1(ju476); oxIs12*	MJB1014	18	18	0	<.0001
dlk-1 2 day adult	*dlk-1(ju476); oxIs12*	MJB1014	20	38	0	<.0001
HS 0	*oxIs12*	EG1285	25	58	53 (91%)	0.0015
HS 0	*dlk-1(ju476); oxIs12*	MJB1014	20	57	0	<.0001
no HS	*dlk-1(ju476); oxIs12 oxEx1268*	EG5203	22	55	0	<.0001
HS-11	*dlk-1(ju476); oxIs12 oxEx1268*	EG5203	3	9	0	<.0001
HS -8	"	"	15	37	2 (5%)	<.0001
HS -4	"	"	10	23	8 (35%)	0.0034
HS -2	"	"	7	17	7 (41%)	0.0292
HS 0	"	"	13	25	21 (84%)	0.2135
HS +2	"	"	10	24	10 (42%)	0.0169
HS +4	"	"	17	46	23 (50%)	0.0276
HS +8	"	"	14	34	13 (38%)	0.002
HS +24	"	"	22	60	8 (13%)	<.0001
HS +48	"	"	35	96	1 (1%)	<.0001
HS +48 L2	"	"	16	16	0	<.0001
MAPKK	*mkk-4(ju91); oxIs268*	MJB1015	31	76	0	<.0001
MAPK	*pmk-3(ok169); oxIs12*	MJB1013	22	69	0	<.0001
MAPKKK	*nsy-1(ok593); oxIs12*	MJB1026	21	48	34 (71%)	1
MAPKK	*sek-1(km4); oxIs268*	MJB1022	23	51	28 (56%)	0.0777
MAPKK	*jkk-1(km2); oxIs268*	MJB1021	24	46	27 (59%)	0.2618
MAPKKK	*mlk-1(ok2471); oxIs12*	MJB1029	24	52	12 (23%)	<.0001
MAPKK	*mek-1(ks54); oxIs268*	MJB1020	21	46	22 (48%)	0.0168
MAPK	*jnk-1(gk7); oxIs12*	MJB1023	27	68	65 (96%)	<.0001
DLK-1 OE L4	*basEx1; oxIs268*	MJB1011	22	43	42 (98%)	<.0001
DLK-1 OE 5 day adult	*basEx1; oxIs268*	MJB1011	27	53	38 (72%)	0.8548
DLK-1 OE, *mkk-4*	*mkk-4(ju91); basEx1; oxIs268*	MJB1038	24	50	14 (28%)	<.0001
DLK-1 OE, *pmk-3*	*pmk-3(ok169); basEx1; oxIs268*	MJB1039	25	46	3 (7%)	<.0001

Transgenes	Allele	Contents
GFP	*oxIs12 X*	P*unc-47*:GFP, *lin-15*(+)
GFP	*oxIs268 III*	P*unc-47*:GFP
DLK-1 rescue	*basEx2*	P*unc-47*:DLK-1 cDNA-GFP; P*unc-47*:mCherry; P*myo-2*:mCherry
DLK-1 HS	*oxEx1268*	P*hsp-16.2*:DLK-1 cDNA, P*myo-2*:GFP
DLK-1 OE	*basEx1*	P*unc-47*:DLK-1 minigene, P*myo-2*:mCherry
RPM-1 OE	*basEx3*	P*unc-25*:RPM-1 genomic (pCZ480—gift of Yishi Jin), P*myo-2*:mCherry

All P values are two-tailed and are calculated against the L4 wild type (EG1285 *oxIs12*, top row of this table) using Fisher's exact test (http://www.graphpad.com/quickcalcs/contingency1.cfm).