Table S1. Genetic interactions between _kuz, slit and robo_

A. Fas II axon guidance defects

Genotype	Number of segments scored (embryos)[1]	+	++	+++	FasII axon circling	% of FasII crossing defects[2]	% of FasII circling defects[3]	Statistics (unpaired _t_-test)
_w_^{1118}	110 (10)	0	0	0	0	0	0	–
kuz^{H143}/+	66 (6)	0	0	0	0	0	0	–
slit^{1}, _robo_^{5}/+	132 (12)	9	19	2	0	22.7	0	–
slit^{1}, _robo_^{5}/+, _kuz_^{H143}	143 (13)	27	39	8	ND	51.7	ND	$P<0.0001$
slit^{1}, _robo_^{5}/+, _kuz_^{112}	143 (13)	23	42	18	ND	58	ND	$P<0.0001$
slit^{1}, _robo_^{5}/+, _kuz_^{e29}	154 (14)	21	50	36	ND	69.5	ND	$P<0.0001$
kuz^{H143}	110 (10)	ND	ND	ND	4	50	3.6	–
kuz^{e29}	77 (7)	ND	ND	ND	2	76.6	2.6	–
slit^{1}, _robo_^{5}, _kuz_^{H143}/+, +, _kuz_^{H143}	110 (10)	ND	ND	ND	31	100	28.2	$P<0.0011$
slit^{1}, _robo_^{5}, _kuz_^{H143}/+, +, _kuz_^{e29}	110 (10)	ND	ND	ND	43	100	48.9	$P<0.0001$

B. Apterous axon crossing defects[4]

Genotype	Number of segments scored (embryos)[1]	Ap crossing defects	% of Ap crossing defects	Statistics (unpaired _t_-test)
_w_^{1118}	96 (12)	0	0	–
kuz^{H143}/+	104 (13)	20	19.2	–
slit^{2}/+	120 (15)	20	16.7	–
slit^{2}, +/ _kuz_^{H143}, +	288 (36)	117	40.6	$P<0.0001$
slit^{2}, +/ _kuz_^{2583}, +	224 (28)	92	41.1	$P<0.0001$
slit^{2}, +/ _kuz_^{112}, +	360 (45)	112	31.3	$P<0.0001$
UASKuzDN	96 (12)	13	13.5	–
slit^{2}/+;_UASKuzDN_	112 (14)	65	58	$P<0.0001$
robo/+	112 (14)	22	19.6	–
robo/+;UASKuzDN*	192 (24)	61	31.8	$P<0.05$

Stage 16-17 embryos stained with anti-FasII MAb were scored as follows: +, thinner than normal fascicle ectopically crossing the midline; ++, normal fascicle ectopically crossing the midline; +++, thicker than normal fascicle ectopically crossing the midline.

[1] Eight abdominal and three thoracic segments were scored in each animal for a total of eleven segments.

[2] Percentage of FasII crossing defects is defined as total number of defects divided by segments scored.

[3] Percentage of FasII circling defects is defined as total number of defects divided by segments scored.

[4] Eight abdominal segments were scored in each embryo.

ND, not determined.