

		+/+	<i>pyd</i> ^{[C5]/+}	<i>pyd</i> ^{[kam]/+}	<i>pyd</i> ^{[1]/+}	<i>pyd</i> ^{[LL]/+}	<i>Sema-1a</i> ^{[k]/+}	<i>trio</i> ^{[1]/+}	<i>Rac1</i> ^{[J11]/+}
	<i>n</i>	26	24	20	24	20	30	50	61
	Wild type	31	33	40	50	60	40	78	2
	Abnormal α/β morphology	35	67	60	50	40	53	20	10
	α/β misguidance (+ abnormal morphology)	35	0	0	0	0	6	2	2
	α/β axon stalling	0	0	0	0	0	0	0	87

		+/+	<i>Sema-1a</i> ^{[k]/+}	<i>trio</i> ^{[1]/+}	<i>Rac1</i> ^{[J11]/+}
	<i>n</i>	26	26	26	18
α	Wild type	100	94	100	0
	Misguidance	0	0	0	0
	Thin or absent	0	4	0	100
β	Wild type	100	73	100	0
	Misguidance	0	12	0	0
	Overextension	0	15	0	0
	Thin or absent	0	0	0	100
	<i>n</i>	26	20	22	26
α	Wild type	100	100	100	62
	Misguidance	0	0	0	8
	Thin or absent	0	0	0	31
β	Wild type	100	100	100	35
	Misguidance	0	0	0	35
	Overextension	0	0	0	0
	Thin or absent	0	0	0	31

MB α and β lobe phenotypes were scored in flies with (A) a mutation in *Nrg* and an additional mutation in either *pyd*, *Sema-1a*, *trio* and *Rac1*; (B) a mutation in *pyd*, *Sema-1a*, *trio* and *Rac1* in an OK107-driven NRG-180 overexpression background; and (C) a mutation in *pyd* and an additional mutation in *Sema-1a*, *trio* and *Rac1*. *n* is the number of brain hemispheres analyzed. The other numbers are percentages of analyzed hemispheres with the specified phenotype. The *Nrg*^{GFP/+};*Rac1*^{J11/+} genotype is lethal.