HSNI axon outgrowth HSNr axon outgrowth HSNI axon guidance HSNr axon guidance Genotype[†] defects‡ defects* defects defects§ negative control 2.0 + 1.24.0 + 1.20.0 + 0.01.3 + 1.3

Table S2. Genetic interactions of unc-40 and members of the WAVE complex in directing HSN axon outgrowth, but not guidance to

the midline

10

11 12 negative control(RNAi)

*gex-3(zu196)

mean, followed by a *P*-value relative to the data in the indicated row. *P*-values were calculated using a *t*-test. §The percentage of HSN axons that fail to ever extend ventrally. The annotation is the same as indicated above

	3 ,	, ,	(/ /		,
3	*negative control	1.3±1.3	1.3±0.7	1.3±1.3	1.3±0.7
4	*unc-40(n324)	59±9.4 (<0.01, 3)	66.0±1.2 (<0.001, 3)	50.7±7.8 (0.0017, 3)	56.0±3.1 (<0.001, 3)
5	unc-40(n324)	76.7±3.3 (<0.001. 1)	74.7±4.7 (<0.001. 1)	70.7±4.1 (<0.001. 1)	63.3±3.5 (<0.001, 1)

4.0+1.2(0.1.1)

unc-40(n324)	/0./±3.3 (<0.001, 1)	/4./±4./ (<0.001, 1)	/U./±4.1 (<u.uu1, 1)<="" th=""><th>65.5±5.5 (<0.001, 1)</th></u.uu1,>	65.5±5.5 (<0.001, 1)
unc-40(n324); negative control(RNAi)	77.6±3.9 (<0.001, 2)	77.9±1.2 (<0.001, 2)	63.3±3.3 (<0.001, 2)	67.7±2.3 (<0.001, 2)
gex-2(ok1603)	18.9±2.8 (<0.01, 1)	18.9±1.1 (<0.001, 1)	6.6±3.3 (0.06, 1)	1.1±1.1 (0.45, 1)
gex-2(ok1603); Ex[unc-86p::GEX-2::YFP] line 1	7.8±1.1 (0.01, 7)	6.7±1.9 (<0.01, 7)	_	_

3.3+0.7(0.3.1)

ine i	7.8±1.1 (0.01, 7)	6./±1.9 (<0.01, /)	_	_
ine 2	4.8±1.0 (<0.01, 7)	3.7±0.3 (<0.001, 7)	-	_
	11.7±0.5 (<0.01, 3)	11.7±0.5 (<0.001, 3)	0.0±0.0 (0.25, 1)	0.0±0.0 (0.11, 1)
	11.1±4.0 (0.08, 2)	12.2±2.9 (0.02, 2)	0.0±0	0.0±0.0 (0.2, 2)
	42.7.2.2 (0.02.2)	43.0.4.6.(0.06.3)	0.0.0	0.0.0.0.0.10.3

0.0 + 0.0

0.7±0.7 (0.3, 1)

11.7±0.5 (<0.01, 3)	11.7±0.5 (<0.001, 3)	0.0±0.0 (0.25, 1)	0.0±0.0 (0.11
11.1±4.0 (0.08, 2)	12.2±2.9 (0.02, 2)	0.0±0	0.0±0.0 (0.2)
12.7±3.3 (0.03, 2)	12.9±4.6 (0.06, 2)	0.0±0	0.0±0.0 (0.18
65.7±5.7 (0.09, 5)	70.0±5.1 (0.3, 5)	56.7±5.3 (0.05, 5)	63.4±7.0 (0.4

gex-3(RNAi)	11.1±4.0 (0.08, 2)	12.2±2.9 (0.02, 2)	0.0±0	0.0±0.0 (0.2, 2
wve-1(RNAi)	12.7±3.3 (0.03, 2)	12.9±4.6 (0.06, 2)	0.0±0	0.0±0.0 (0.18, 2
)(n324); gex-2(ok1603)	65.7±5.7 (0.09, 5)	70.0±5.1 (0.3, 5)	56.7±5.3 (0.05, 5)	63.4±7.0 (0.49,
10(n224): gay 2(PNAi)	747+22(026)	72 0+2 1 (0 1 6)	647+47 (0.41.6)	62 7+ 6 9 (0 26

12	VVVC-1 (MVAI)	12.7±3.3 (0.03, 2)	12.3±4.0 (0.00, 2)	0.0±0	0.0±0.0 (0.10, 2)
13	unc-40(n324); gex-2(ok1603)	65.7±5.7 (0.09, 5)	70.0±5.1 (0.3, 5)	56.7±5.3 (0.05, 5)	63.4±7.0 (0.49, 5)
14	unc-40(n324); gex-3(RNAi)	74.7±2.3 (0.3, 6)	73.0±3.1 (0.1, 6)	64.7±4.7 (0.41, 6)	62.7± 6.8 (0.26, 6)

13	unc-40(11324), gex-2(0k1003)	03.7±3.7 (0.03, 3)	70.0±3.1 (0.3, 3)	30.7±3.3 (0.03, 3)	03.4±7.0 (0.43, 3)
14	unc-40(n324); gex-3(RNAi)	74.7±2.3 (0.3, 6)	73.0±3.1 (0.1, 6)	64.7±4.7 (0.41, 6)	62.7± 6.8 (0.26, 6)
15	*unc-40(n324); gex-3(zu196)	90 (<i>n</i> =1×10)	80 (<i>n</i> =1×10)	80 (<i>n</i> =1×10)	60 (<i>n</i> =1×10)

14	unc-40(n324); gex-3(KNAI)	/4./±2.3 (0.3, 6)	/3.0±3.1 (0.1, 6)	64./±4./ (0.41, 6)	62.7± 6.8 (0.26, 6)
15	*unc-40(n324); gex-3(zu196)	90 (<i>n</i> =1×10)	80 (<i>n</i> =1×10)	80 (<i>n</i> =1×10)	60 (<i>n</i> =1×10)
16	unc-10(n321): wwo-1(RNAi)	71 1+2 9 (0 12 6)	73 3+0 (~0 01 6)	70 2+8 6 (0 25 6)	71 1+4 8 (0 28 6)

16 unc-40(n324); wve-1(RNAI) /U.2±8.6 (U.25, 6) / I. I±2.9 (U. I2, b) /3.3±U (<U.U1, b)

71.1±4.8 (0.28, 6)

The HSN cell bodies and axons of young adults were visualized with zdls13[tph-1::GFP] IV (a gift from Oliver Hobert), except for those genotypes marked with an asterisk that were

visualized with mgls42[tph-1::GFP + pRF4(rol-6(su1006))]. Unless otherwise indicated, 30 animals were counted in three separate trials. All counts made at 20°C.

*The percentage of HSNs extending an axon in a direction other than ventral for more than two cell diameters away from the cell body. Standard error of the mean follows the