

H. sapiens Gene	Variant	Ensemble Gene	C. elegans Locus ID	C. elegans Gene	Animals Defective (% ± SD) [*]	n	RNAi Phenotype
HSP90AA1	SYN-NET ^{LGD}	ENSG00000080824	C47E8.5	daf-21	72.0 ± 24.4	25	hyperbranching of dendrites in hypodermal region [†] hyperbranching of quaternary dendrites
INTS5	RVIS-SCZ	ENSG00000185085	Y51A2D.7	Y51A2D.7	52.5 ± 30.3	40	hyperbranching of quaternary dendrites
MLL2	RVIS-SCZ	ENSG00000167548	T12D8.1	set-16	33.3 ± 8.5	60	hypobranching of quaternary dendrites reduced quaternary dendrite extension
HSPA8	rdNS-SCZ SYN-NET ^{LGD}	ENSG00000109971	F26D10.3	hsp-1	28.8 ± 14.2	66	hyperbranching of dendrites in hypodermal region hyperbranching of quaternary dendrites
TRAPPC9	RVIS-SCZ	ENSG00000167632	C35C5.6	trpp-9	8.3 ± 2.4	60	none
MYH9	rdNS-SCZ SYN-NET ^{LGD}	ENSG00000100345	F52B10.1	nmy-1	7.1 ± 3.4	56	none
SEC31A	RVIS-SCZ	ENSG00000138674	T01G1.3	sec-31	5.8 ± 3.0	69	none
AP3D1	rdNS-SCZ	ENSG00000065000	W09G10.4	apd-3	5.5 ± 3.3	73	none
CHD8	RVIS-SCZ rLGD-ASD	ENSG00000100888	T04D1.4	chd-7	5.0 ± 3.5	80	none
PITPNM1	RVIS-SCZ rdNS-SCZ	ENSG00000110697	M01F1.7	pitp-1	5.0 ± 4.1	60	none
LPHN2	rdNS-SCZ	ENSG00000117114	B0286.2	lat-2	4.3 ± 6.8	70	none
XPNPEP1	RVIS-SCZ	ENSG00000108039	W03G9.4	app-1	3.8 ± 4.1	80	none
TAF13	rLGD-SCZ	ENSG00000197780	C14A4.10	taf-13	3.3 ± 4.7	60	none
KIAA1109	rdNS-SCZ	ENSG00000138688	Y47G6A.23	lpd-3	3.2 ± 5.8	63	none
PIK3C2B	rdNS-SCZ	ENSG00000133056	F39B1.1	piki-1	2.7 ± 2.9	75	none
VPS13D	RVIS-SCZ	ENSG00000048707	C25H3.8	C25H3.8	2.5 ± 2.6	79	none
HUWE1	RVIS-SCZ rdNS-SCZ	ENSG00000086758	Y67D8C.5	eel-1	2.5 ± 2.5	80	none
PLEKHH2	RVIS-SCZ	ENSG00000152527	C34B4.1	max-1	2.5 ± 2.5	80	none
LAMA2	rdNS-SCZ	ENSG00000196569	T22A3.8	lam-3	1.9 ± 3.1	54	none
DLG2	SYN-NET ^{LGD}	ENSG00000150672	C25F6.2	dlg-1	1.7 ± 2.4	60	none
DPYD	rdNS-SCZ	ENSG00000188641	C25F6.3	dpyd-1	1.7 ± 2.4	60	none
NUP98	RVIS-SCZ	ENSG00000110713	ZK328.5	npp-10	1.7 ± 2.4	60	none
RYR3	rdNS-SCZ	ENSG00000198838	K11C4.5	unc-68	0.0 ± 0.0	60	none
SLC4A8	rdNS-SCZ	ENSG00000050438	F52B5.1	abts-1	0.0 ± 0.0	60	none
AUTS2	RVIS-SCZ	ENSG00000158321	no ortholog	-			
CACNA1I	rdNS-SCZ	ENSG00000100346	no ortholog	-			
CD14	rdNS-SCZ	ENSG00000170458	no ortholog	-			
CRYBG3	rdNS-SCZ	ENSG00000080200	no ortholog	-			
KIF18A	rdNS-SCZ	ENSG00000121621	no ortholog	-			
LRP5	RVIS-SCZ	ENSG00000162337	no ortholog	-			
MECP2	RVIS-SCZ	ENSG00000169057	no ortholog	-			
MKI67	rLGD-SCZ	ENSG00000148773	no ortholog	-			
MKL2	RVIS-SCZ	ENSG00000186260	no ortholog	-			
NCKIPSD	SYN-NET ^{LGD}	ENSG00000213672	no ortholog	-			
NEB	rdNS-SCZ	ENSG00000183091	no ortholog	-			
NIPAL3	rdNS-SCZ	ENSG00000001461	no ortholog	-			
NLRC5	rdNS-SCZ	ENSG00000140853	no ortholog	-			
RBP3	RVIS-SCZ	ENSG00000265203	no ortholog	-			
RGS12	rdNS-SCZ	ENSG00000159788	no ortholog	-			
STAC2	rdNS-SCZ	ENSG00000141750	no ortholog	-			
pPD129.36 empty vector					7.9 ± 6.7	101	none

(1) * = % and standard deviation (SD) denote the weighted % and weighted standard deviation, respectively. (2) † = "hyperbranching in hypodermal region" may include an increase in secondary and/or ectopic tertiary dendrites as well as a misguidance of quaternary dendrites into the hypodermal region.