

<i>H. sapiens</i> Gene	Variant	Ensemble Gene	<i>C. elegans</i> Locus ID	<i>C. elegans</i> Gene	Animals Defective (% ± SD) ⁽¹⁾	n	RNAi Phenotype
ARID1B	rLGD-ASD	ENSG00000049618	C01G8.9	let-526	40.4 ± 20.1	47	hyperbranching of dendrites in hypodermal region ⁽²⁾ hypobranched of quaternary dendrites disorganization of arborization pattern
ANK2 ⁽³⁾	rLGD-ASD	ENSG00000145362	B0350.2	unc-44	20.0 ± 12.0	115	hypobranched of quaternary dendrites
TCF7L2	rLGD-ASD	ENSG00000148737	W10C8.2	pop-1	13.0 ± 9.2	54	multiple PVD-like cell bodies
TBR1	rLGD-ASD	ENSG00000136535	F40H6.4	tbx-11	10.0 ± 4.1	60	none
WDFY3	rLGD-ASD	ENSG00000163625	C26H9A.2	wdfy-3	9.9 ± 5.7	91	none
NCKAP1	rLGD-ASD	ENSG00000061676	F28D1.10	gex-3	9.0 ± 4.3	78	none
RIMS1	rLGD-ASD	ENSG00000079841	T10A3.1	unc-10	8.8 ± 12.4	80	none
CHD2	rLGD-ASD	ENSG00000173575	H06O01.2	chd-1	7.5 ± 7.5	80	none
GIGYF1	rLGD-ASD	ENSG00000146830	C18H9.3	C18H9.3	7.3 ± 3.7	55	none
DSCAM	rLGD-ASD	ENSG00000171587	F39H12.4	igcm-1	6.3 ± 2.2	80	none
CHD8	rLGD-ASD RVIS-SCZ	ENSG00000100888	T04D1.4	chd-7	5.0 ± 3.5	80	none
KDM5B	rLGD-ASD	ENSG00000117139	ZK593.4	rbr-2	5.0 ± 3.5	80	none
DIP2A	rLGD-ASD	ENSG00000160305	F28B3.4	dip-2	4.9 ± 3.5	81	none
PHF2	rLGD-ASD	ENSG00000197724	F29B9.2	jmjd-1.2	4.8 ± 4.1	63	none
KMT2E	rLGD-ASD	ENSG00000005483	Y51H4A.12	set-26	3.8 ± 2.2	53	none
KDM6B	rLGD-ASD	ENSG00000132510	D2021.1	utx-1	3.3 ± 2.4	60	none
MED13L	rLGD-ASD	ENSG00000123066	K08F8.6	let-19	2.6 ± 2.5	76	none
PHF2	rLGD-ASD	ENSG00000197724	F43G6.6	jmjd-1.1	1.7 ± 2.4	58	none
DYRK1A	rLGD-ASD	ENSG00000157540	T04C10.1	mbk-1	1.3 ± 2.5	76	none
KMT2E	rLGD-ASD	ENSG00000005483	F15E6.1	set-9	0.0 ± 0.0	58	none
ADNP	rLGD-ASD	ENSG00000101126	no ortholog	-			
ANKRD11	rLGD-ASD	ENSG00000167522	no ortholog	-			
FOXP1	rLGD-ASD	ENSG00000114861	no ortholog	-			
GRIN2B	rLGD-ASD	ENSG00000273079	no ortholog	-			
KATNAL2	rLGD-ASD	ENSG00000167216	no ortholog	-			
POGZ	rLGD-ASD	ENSG00000143442	no ortholog	-			
SCN2A	rLGD-ASD	ENSG00000136531	no ortholog	-			
TNRC6B	rLGD-ASD	ENSG00000100354	no ortholog	-			
WAC	rLGD-ASD	ENSG00000095787	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. (3) ‡ = ANK2 RNAi data as previously reported in Aguirre-Chen et al., 2011.