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Supplemental information

The branching code: A model of actin-driven dendrite arborization

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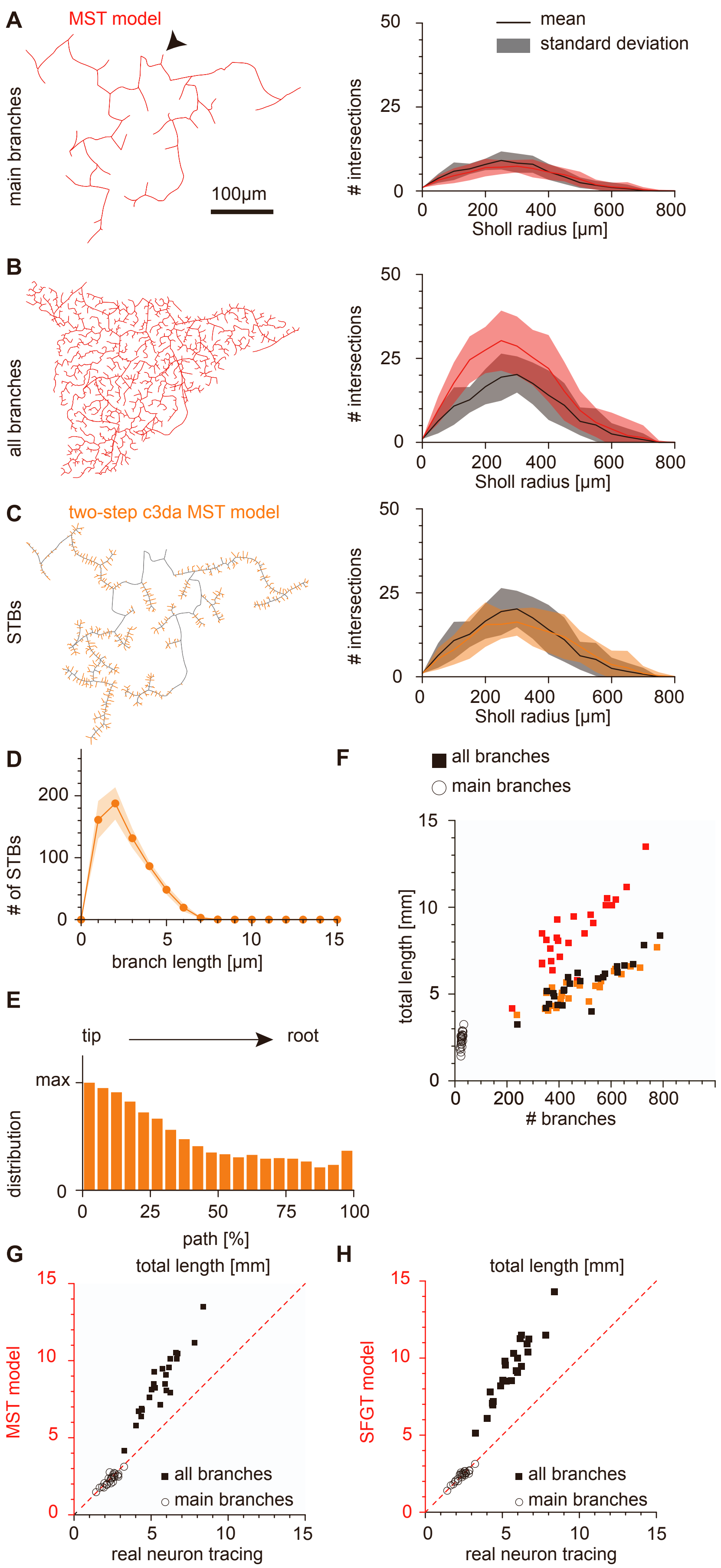

Fig S1. MST tree, Related to Figure 1

A,B,C, Synthetic dendritic trees (red or orange) focusing on the MBs (A), all branches (B) or the STBs (C) as seen in Figure 1 but now using the MST algorithm instead of the SFGT model. The arrowhead points to the root. Right hand Sholl analysis panels show the number of intersections of the dendritic trees with increasing Sholl radii around the soma in µm. Shaded area shows standard deviation. Solid lines show the mean Sholl intersections. The black line and grey shaded area show the data from tracings of a wild type c3da neuron as in Figure 1. A, B, The synthetic dendritic trees in red were generated with the MST algorithm (Cuntz et al., 2007), but the growth was interrupted either when the number of MBs (A) was reached or interrupted when the total number of branches (B) was reached. C, A second modelling step of the synthetic dendritic tree in orange allows STBs with a defined total length to develop in a close range to the MB with a given distribution along the MBs. D, The number of STBs in the synthetic trees obtained with the two-step model plotted against their length in µm. E, The number of STBs at positions along the MBs, from tip to root (depicted as a percentile of the path length). F, Number of branches vs. total length for MBs (empty dots) and complete trees (squares) are shown for real trees (black) compared to synthetic dendritic trees modelled with the MST (red) or the two-step model using the MST for the main branches (orange). G,H, Direct comparison of total length in mm between real neuron reconstructions and the MST model (G) or the SFGT model (H). See Materials and Methods for details.

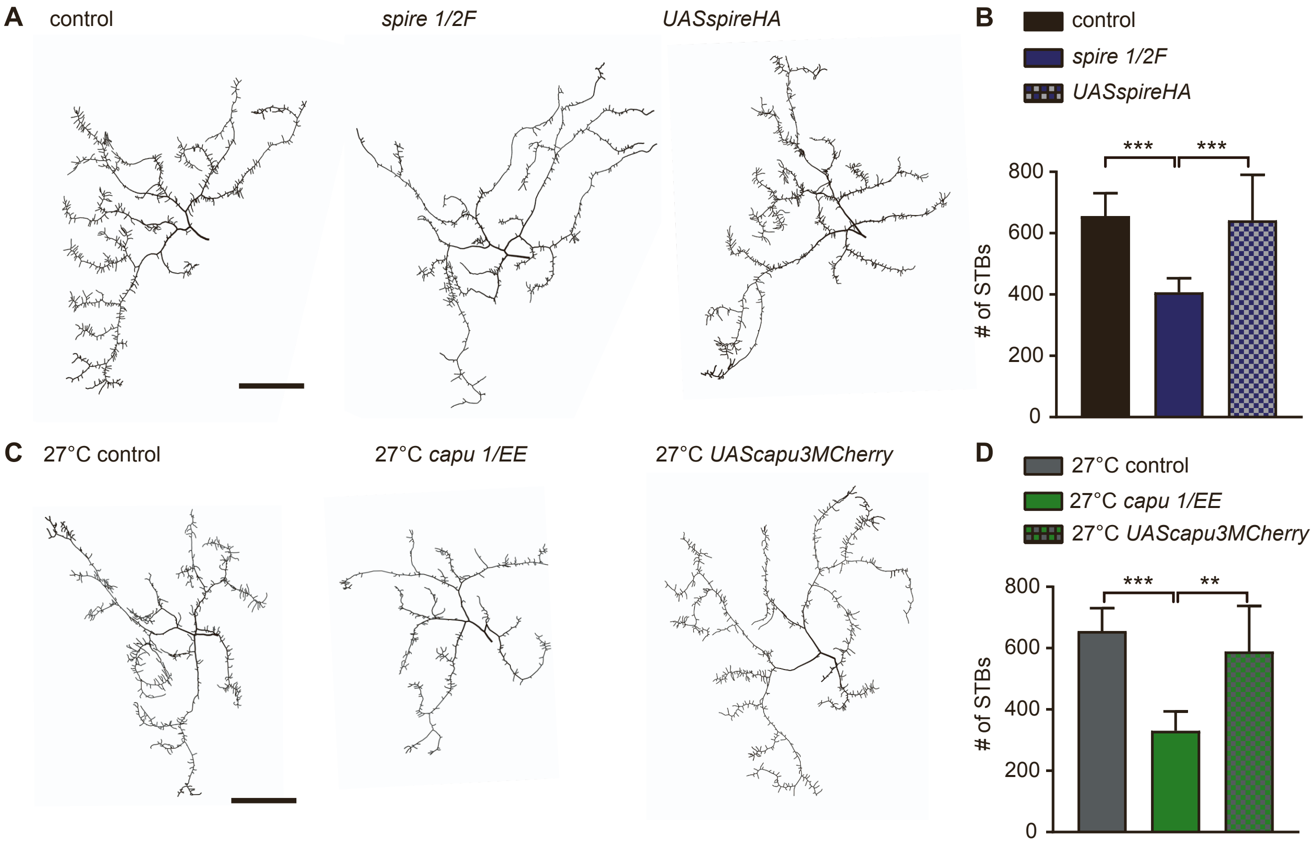

Fig S2. Spire and Capu Rescue, Related to Figure 3

A, Representative tracings of control, spire$^{1/2F}$ mutant and UASspirHA rescue. B, Quantification of STB number. C, Representative tracings of control, capu$^{1/EE}$ mutant and UAScapu3MCherry rescue. D, Quantification of branch number. (* is $p < 0.05$, ** is $p < 0.01$ and *** is $p < 0.001$). Mean with standard deviation. Scale bar is 100μm. n = 5 larva per genotype (see Table 1 for genotypes).

Fig S3. Morphological Analysis, Related to Figure 4

Thirteen morphological measurements for the c3da neurons. A-G, The thirteen measurements for each AMP mutant (and the capu^{1}/spire^{2F} heterozygous mutant) compared to corresponding controls. (Corrected p values * is $p < 0.05$, ** is $p < 0.01$ and *** is $p < 0.001$). Mean with standard deviation. The background is highlighted in blue for a significant decrease and in red for a significant increase. For a full list of corrected p values see Supplemental Table ST1, for full list of features and descriptions see Table 2 in Material and Methods. n = 8 for all apart from the heterozygous mutant capu^{1}/spire^{2F} which has a n = 5.

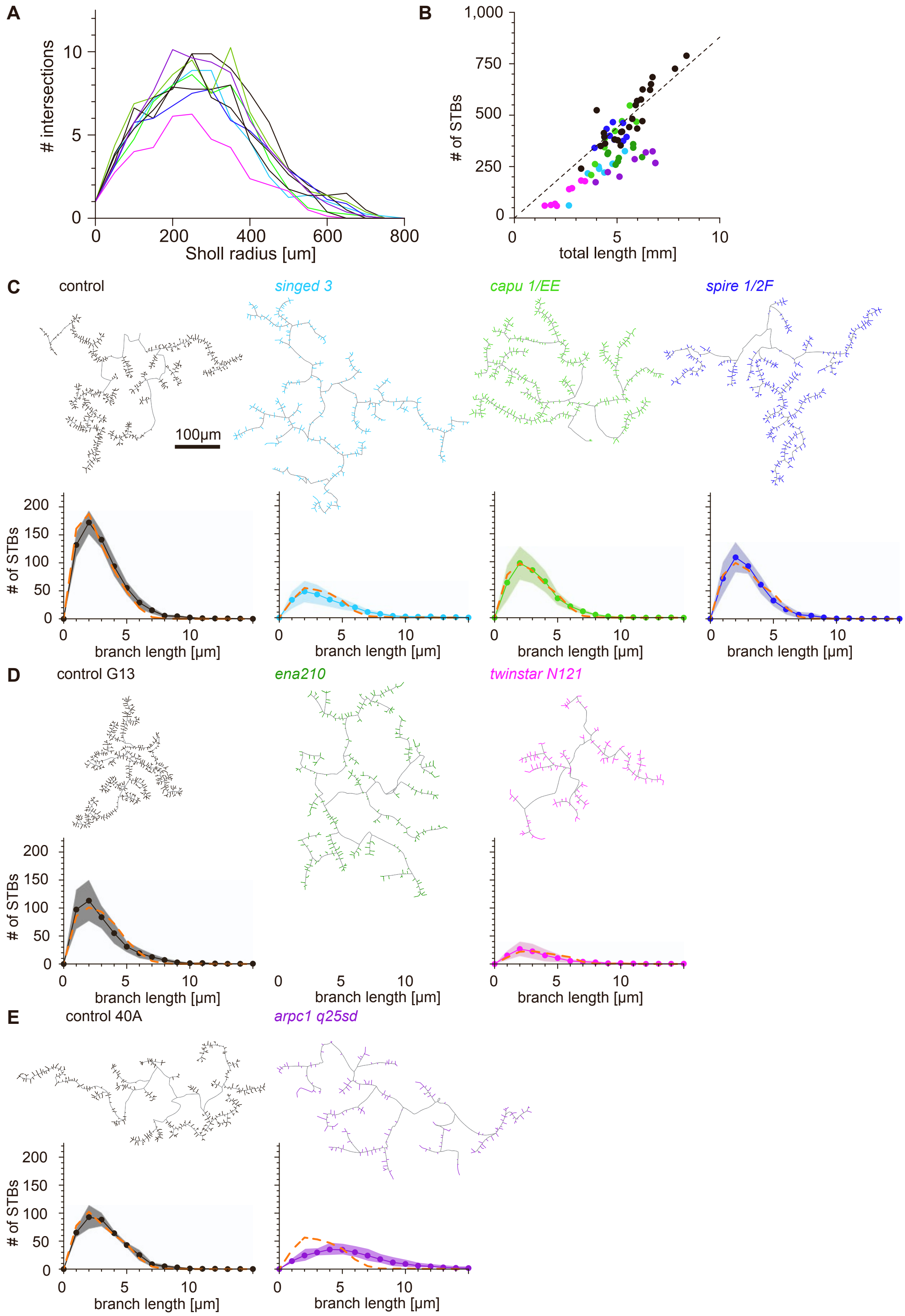

Fig S4. Further quantification of c3da neuron mutants and MST-based modelling version, Related to Figure 5

A, Sholl analysis of the MBs of control and mutant morphologies. B, The number of STBs against the total length for all controls and mutant tracings. C, D, E, The same representation as in Figure 5 but using the MST model for the main branches. Same colours as in Figure 5. For details see Material and Methods.

Table S1. Corrected p values for the 30 features, Related to Figure 4

Corrected p values for all six AMP mutants and all 30 dendrite features. The features shown in Figure 4 are in bold text. A note on the side gives the reason why the other feature were not used in the Figure 4, it states all, none or the number of the feature it correlates with. The background colour is red if there is a significant increase and blue if there was a significant decrease for the specific mutant condition. All trees, features and values are available in Zenodo (10.5281/zenodo.6347438).

#	Name	spire	capu	singed	twinstar	ena	arp	note
1	Number of STBs	<,001	<,001	<,001	<,001	0.03	<,001	all
2	**Number of MBs**	0.006	<,001	0.018	<,001	0.945	0.072	
3	**Total length of STBs**	<,001	0.001	<,001	<,001	0.644	0.072	
4	**Total length of MBs**	0.022	0.003	0.018	0.002	0.075	0.147	
5	**Mean length of STBs**	0.565	0.069	0.027	<,001	0.02	<,001	
6	**Mean length of MBs**	0.084	0.729	0.321	0.004	0.03	0.436	
7	**Mean branch order of MBs**	0.616	0.192	0.004	<,001	0.945	0.287	
8	**Mean tortuosity of STBs**	0.324	0.151	<,001	0.003	0.07	0.004	
9	**Mean branching angle**	0.223	0.657	0.011	0.024	0.093	0.191	
10	**Mean distance to nearest neighbour**	0.7	0.016	0.005	0.014	0.554	0.004	
11	**Skewness of STBs along MBs**	0.104	0.052	0.028	0.287	0.32	0.002	
12	**Mean van Pelt asymmetry**	0.113	0.057	0.024	<,001	0.004	<,001	
13	**Mean Euclidean distance to the root**	0.066	0.029	0.089	0.315	0.31	0.287	
14	**Surface**	0.003	0.002	0.004	0.006	0.115	0.001	
15	Mean branch order of STBs	0.05	0.016	<,001	<,001	0.036	<,001	all
16	Mean tortuosity of MBs	0.7	0.249	0.089	0.109	0.945	0.094	none
17	Number of branching points	<,001	<,001	<,001	<,001	0.03	<,001	all
18	Maximal branch length of STBs	0.223	0.656	0.011	0.012	0.03	0.001	see 5
19	Fraction of lengths of STBs / total length	0.012	0.021	<,001	<,001	0.036	0.272	see 3,4
20	Number of STBs / total length of MBs	<,001	0.007	<,001	<,001	0.03	<,001	all
21	Minimal branch length of MBs	0.7	0.46	0.335	0.315	0.516	0.486	none
22	Maximal branch length of MBs	0.134	0.617	0.081	0.127	0.144	0.508	none
23	Maximal branch order of MBs	0.026	0.029	0.018	<,001	0.91	0.484	see 7
24	Maximal branch order of STBs	0.134	0.021	<,001	<,001	0.093	0.003	see 15
25	Maximal Euclidean distance to the root	0.516	0.153	0.072	0.378	0.219	0.376	none
26	Mean Euclidean compactness	0.134	0.18	0.002	0.005	0.03	0.001	see 13,7
27	Maximal path distance to the root	0.789	0.228	0.08	0.228	0.219	0.147	none
28	Mean path distance to the root	0.516	0.037	0.072	0.399	0.093	0.376	see 13
29	Mean path compactness	0.104	0.258	0.002	0.006	0.03	0.003	see 13,7
30	Density	0.739	0.619	0.005	0.002	0.144	0.003	see 3,4,14