Figure S1

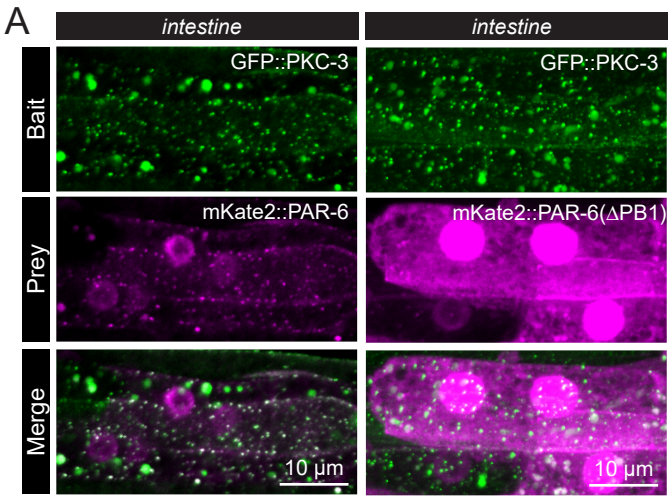

Figure S1. Intestinal interaction of PKC-3 with PAR-6 and a highly overexpressed interaction defective PAR-6 variant. Intestinal images from CeLINC interaction experiment of Figure 3C- D taken with same microscopy settings and displayed with same image processing settings.

Figure S2 (part 1 of 2)

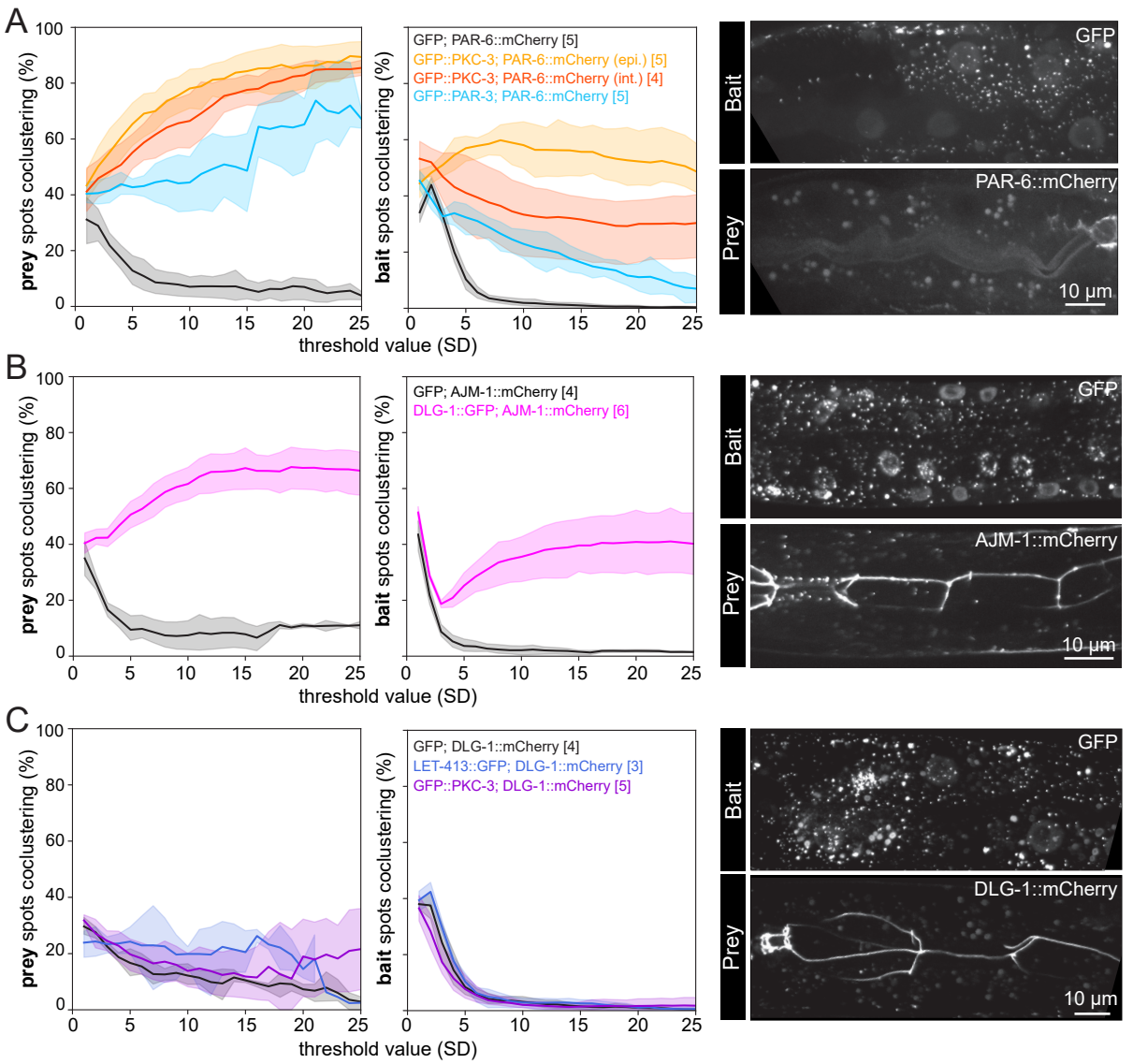

Figure S2 (part 2 of 2)

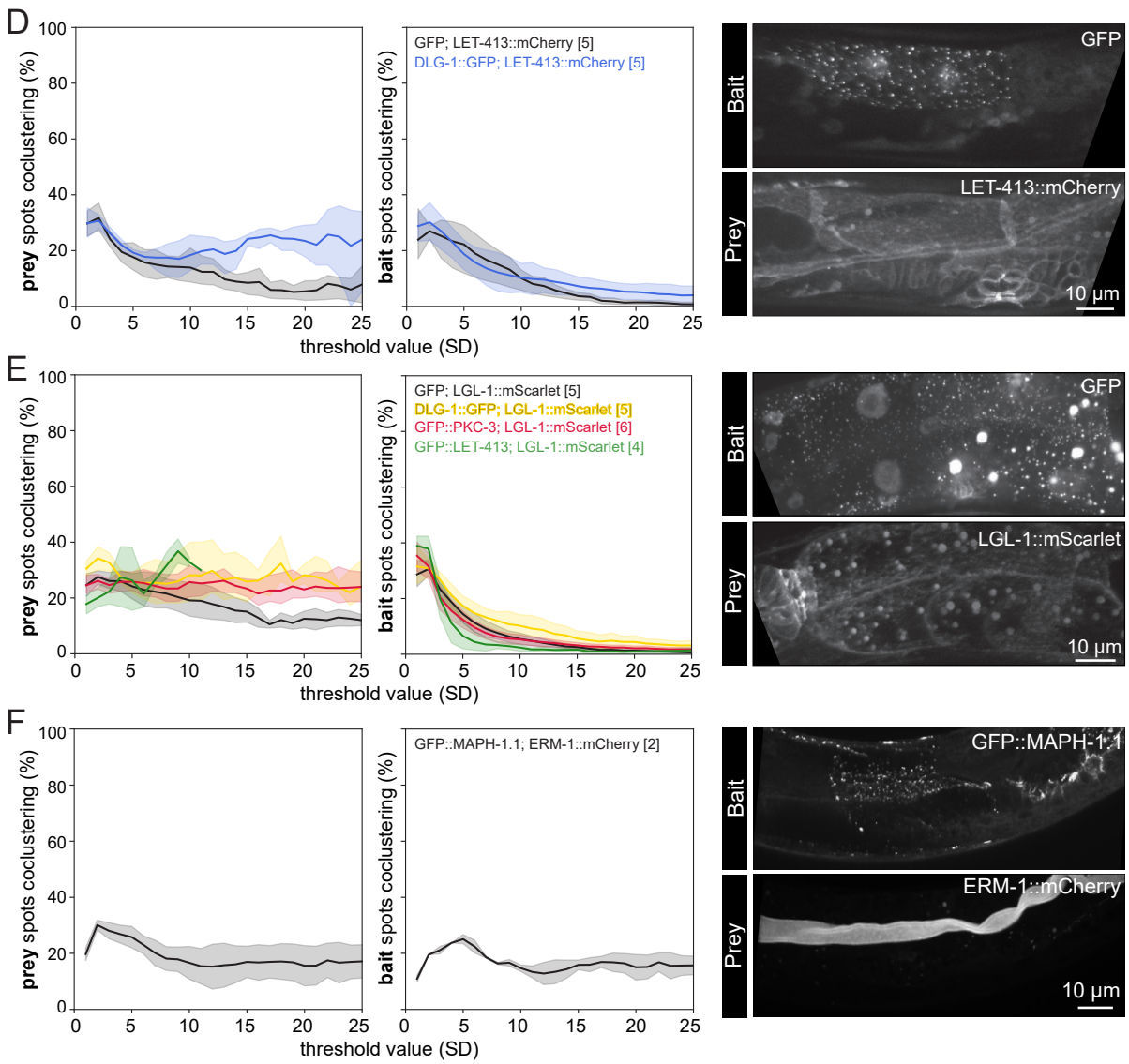

Figure S2. Image quantifications and negative controls for various CeLINC experiments. (**A–F**) The percentage of prey and bait spots colocalizing are graphed for indicated protein combinations. Dark line indicates the mean value, while shaded areas indicate the 95% confidence interval. Threshold value is the ComDet intensity threshold value used to detect an interaction. Negative controls use GFP protein alone expressed as bait. All CeLINC plasmids are expressed from the *rps-0* promoter. Representative images of the clustered GFP bait and prey are also shown. Intestinal cells were used for quantifications. The number of animals quantified in each genotype are shown in brackets on the graphs.

Figure S3

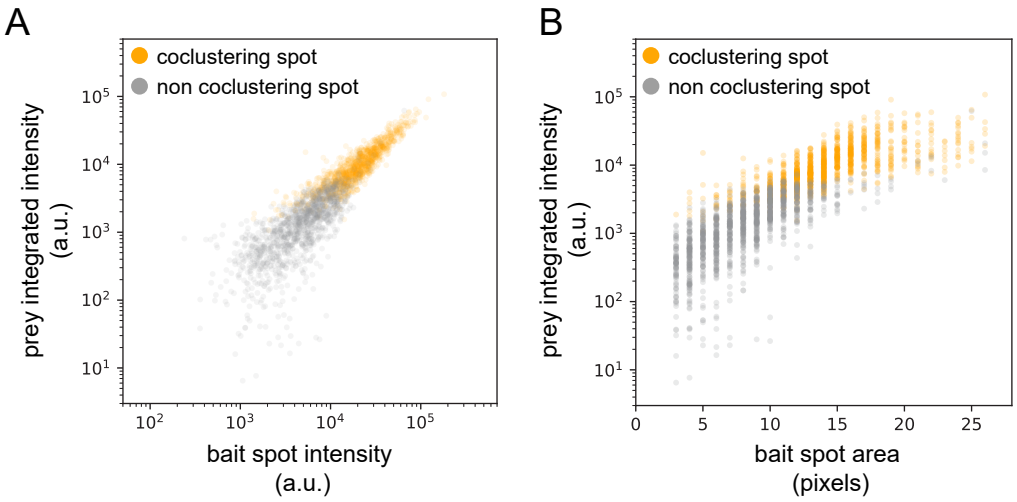

Figure S3. Correlation between bait cluster size and intensity with prey cluster intensity. (**A**) Correlation between the sum of pixel intensity in the bait and prey spots in endogenously tagged GFP::PKC-3; PAR-6::mCherry CeLINC protein expressing animals. For every bait spot detected, the sum of the pixel intensity in the bait spot and the corresponding area in the prey image is plotted. Images were analyzed at intensity threshold level of 25 and the sum of pixel intensities within each identified cluster were corrected for spot-specific background intensity by subtracting the average intensity of the surrounding pixels using the ComDet plugin. (**B**) The correlation between the size of the bait cluster in pixels and the sum of pixel intensity in the prey spot, as calculated in (A). (A–B) n = 1093 bait spots coclustering spots and 1352 bait spots that were found to be non coclustering, from the analysis of 5 animals.