Expanded View Figures

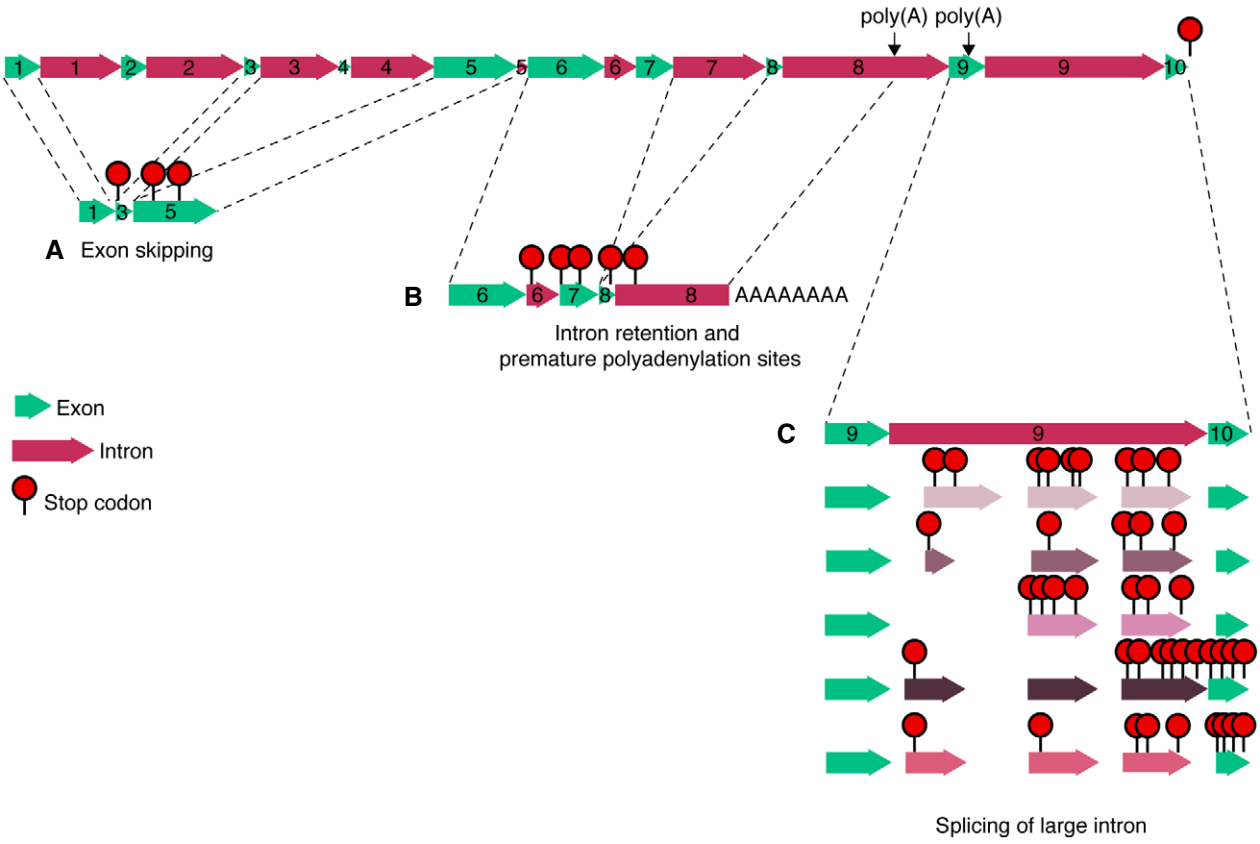

Figure EV1. *CYCB1;5* is a pseudogene.

A–C The predicted gene structure of *CYCB1;5*, including the observed cDNAs with exon skipping (A), intron retention and premature polyadenylation sites (B), and alternative splicing of a large intron (C).

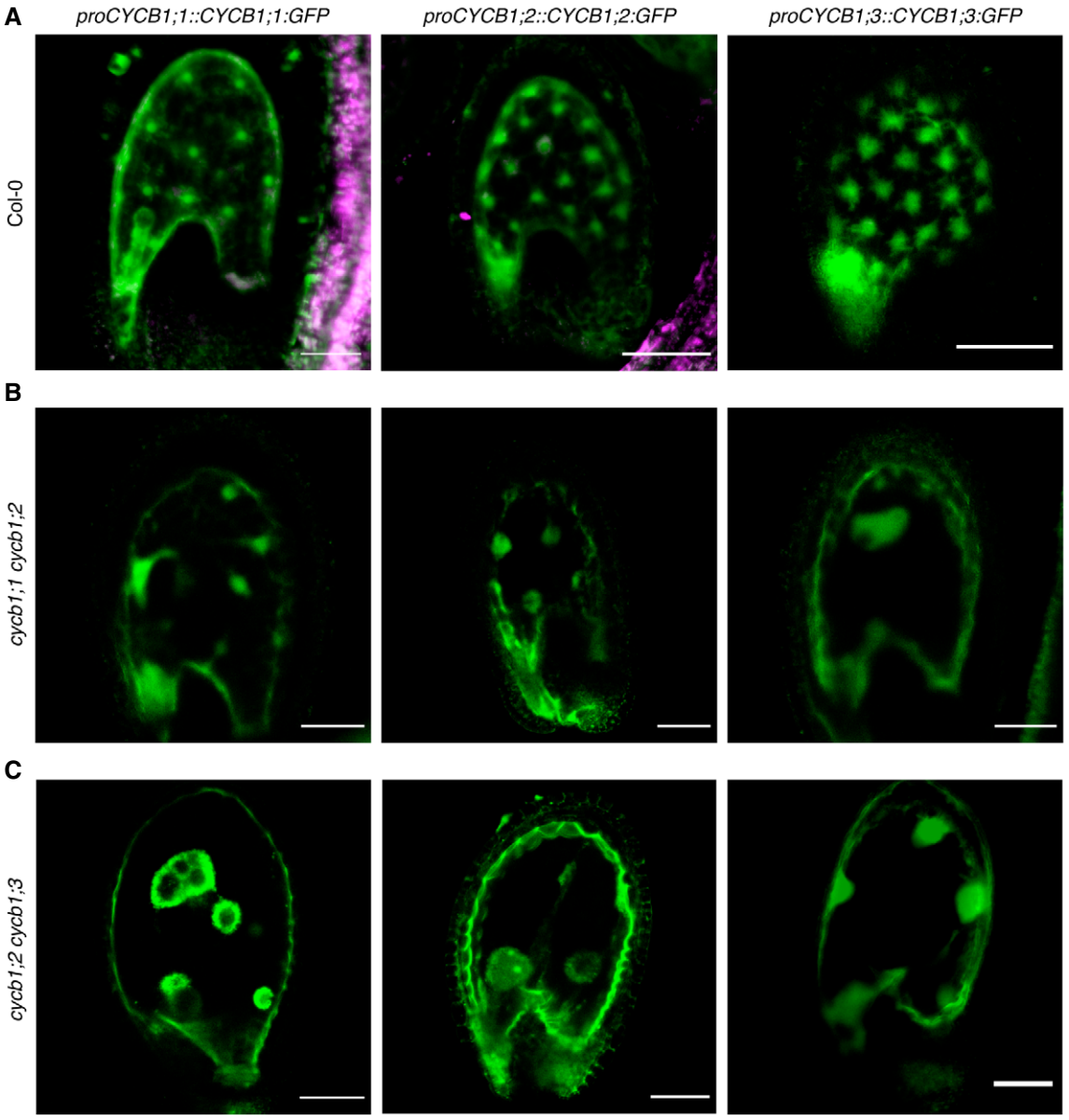

Figure EV2. *CYCB1;1*, *CYCB1;2*, and *CYCB1;3* but not *CYCB1;4* are expressed during seed development.

A–C Confocal microscope pictures of seeds expressing either *proCYCB1;1:GFP*, *proCYCB1;2:GFP* or *proCYCB1;3:GFP* in Col-0 (A), *cycb1;1 cycb1;2* (B), or *cycb1;2 cycb1;3* (C). Scale bars: 30 μm.

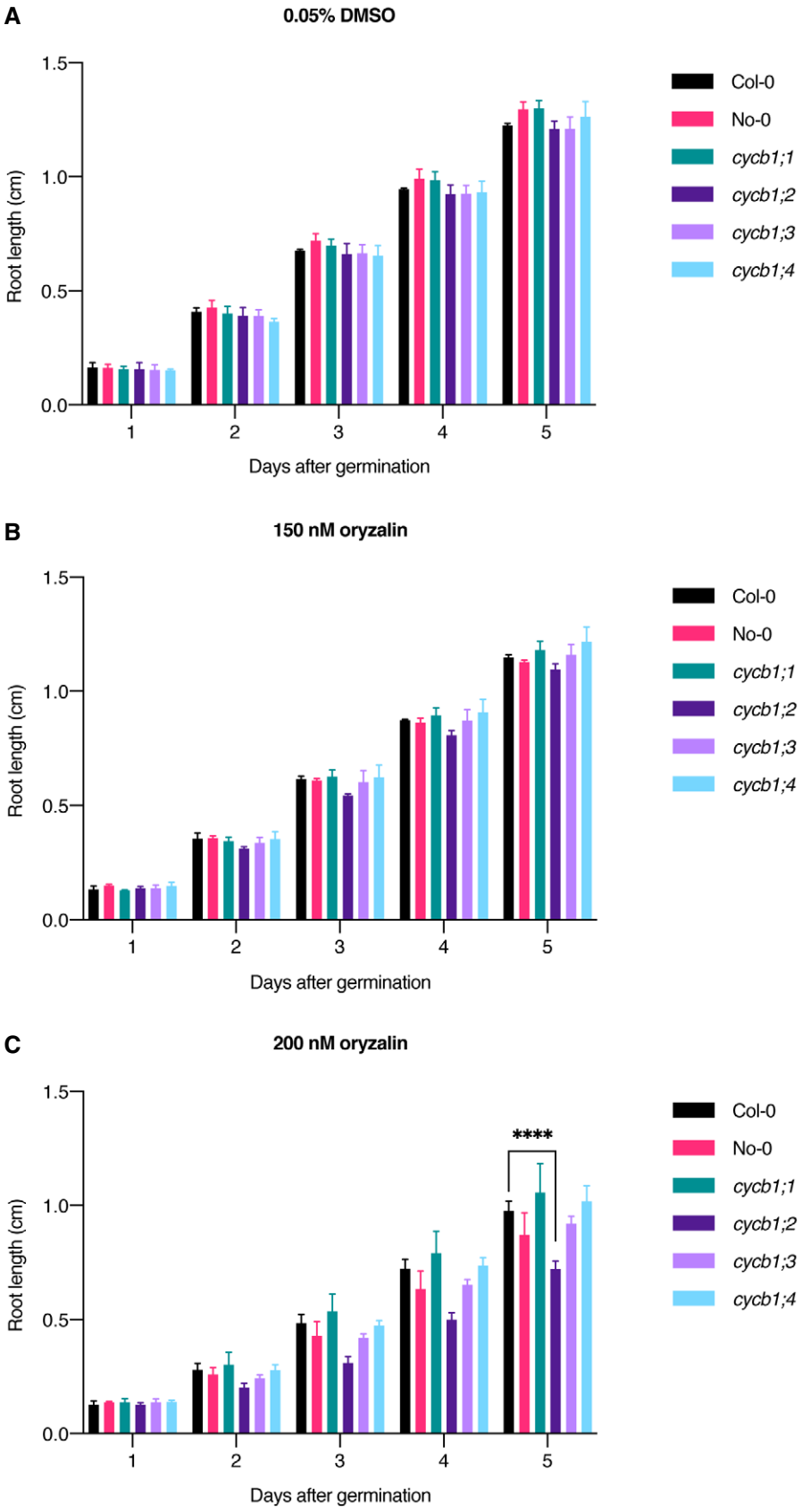

Figure EV3. Oryzalin root growth assays across time in *cycb1* single mutants.

A–C Quantification of root length in a control condition (A), 150 nM oryzalin (B) and 200 nM oryzalin (C). Graphs show mean ± SD of three biological replicates with at least 10 plants per genotype per replicate. Asterisks indicate a significant difference in root length in a two-way ANOVA followed by Tukey's multiple comparisons test (****$P < 0.0001$).

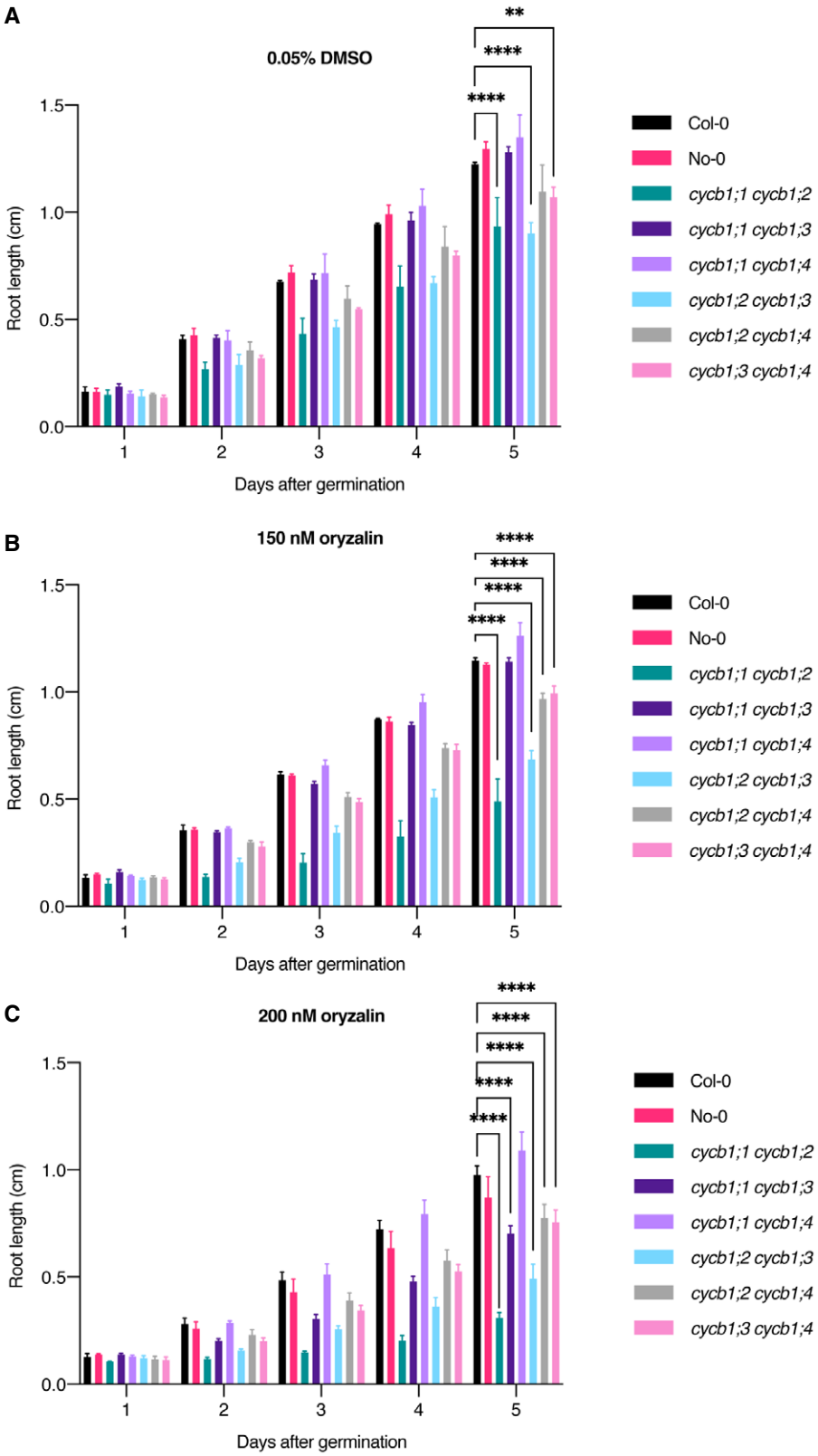

Figure EV4. Oryzalin root growth assays across time in *cycb1* double mutants.

A–C Quantification of root length in a control condition (A), 150 nM oryzalin (B), and 200 nM oryzalin (C). Graphs show mean ± SD of three biological replicates with at least 10 plants per genotype per replicate. Asterisks indicate a significant difference in root length in a two-way ANOVA followed by Tukey's multiple comparisons test (**$P < 0.01$ and ****$P < 0.0001$).

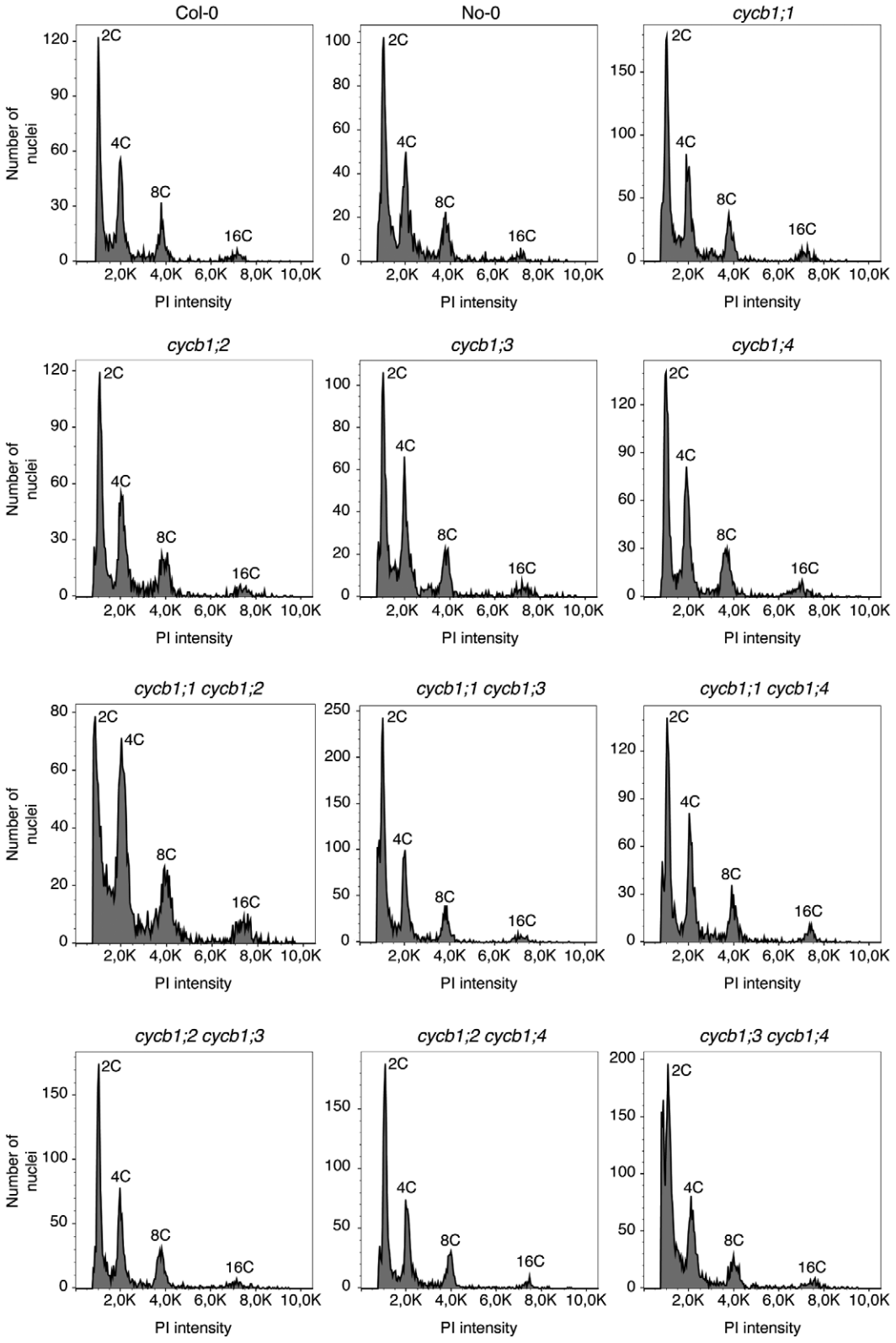

Figure EV5. Ploidy analysis of young seedlings of the single and double mutants.

Flow cytometrical quantification of the different nuclear ploidies, as indicated by propidium iodide (PI) intensity. Single (top rows) and double (bottom rows) mutants have been analyzed. The individual genotypes are indicated on the top of each graph. Each peak has been labeled according to the expected nuclear content (2C, 4C, 8C or 16C).