Figure S2  Gene ontology (GO) terms enriched in the set of suppressors identified in the WEE-1.3 RNAi suppressor screen. The top scoring GO: Biological Process and GO: Cellular Component categories with $P$ values of <0.05 are shown. Reported terms are subontologies that belong to either biological process (BP; tissue morphogenesis, meiosis/mitosis, phosphorylation, translation, nuclear migration, RNA processing, and proteolysis) or cellular component (CC; intracellular organelle/nucleus and proteasome complex) categories. Enrichment and $P$-values are as follows: intracellular organelle/nucleus ($E = 6.92$, $P$-value = 9.3e-10), tissue morphogenesis ($E = 3.25$, $P$-value = 4.4e-4), proteasome complex ($E = 2.68$, $P$-value = 1.6e-4), meiosis/mitosis ($E = 2.62$, $P$-value = 1.0e-3), nuclear migration ($E = 1.38$, $P$-value = 4.3e-2), and RNA processing ($E = 0.85$, $P$-value = 1.8e-2).