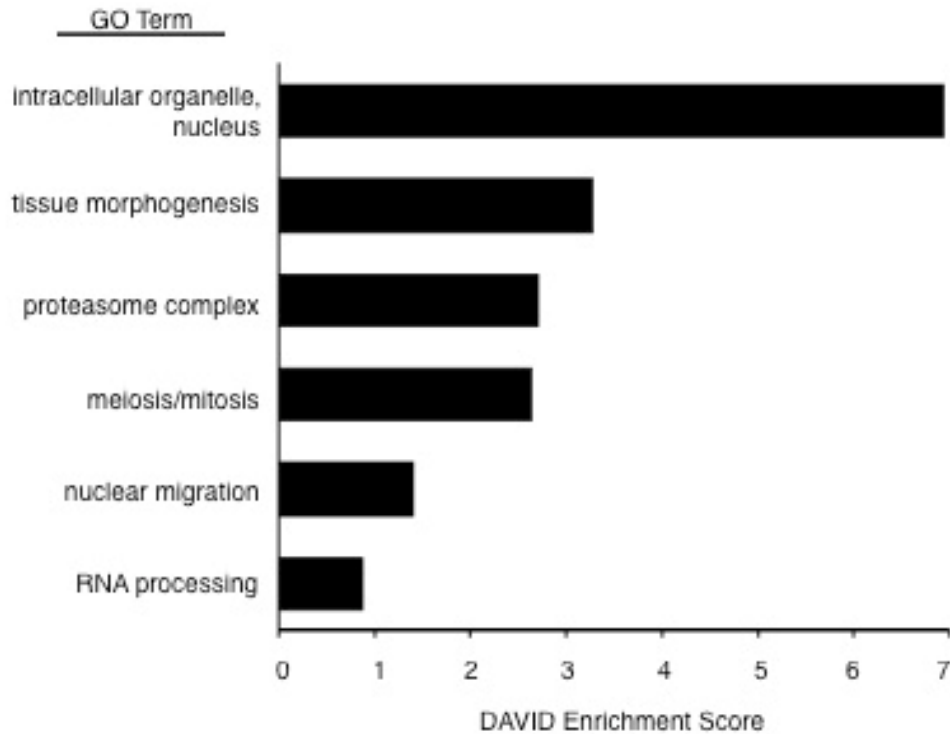


**Figure S2**



**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 =  $1.8e-2$ ).