



Figure S2. RNAi screen data analysed in terms of gene classification and gene ontology.

- (A) Data analysis according to distribution through kinase and kinase-related families.
- (B) Data analysis according to gene ontology and molecular function.
- (C) Gene ontology enrichment analysis of 3 RNAi screens showing only significantly enriched kinases ( $p \le 0.05$ ).

Spheres on Pass 3 pie plots denote the 5 kinases identified in the RNAi screen.