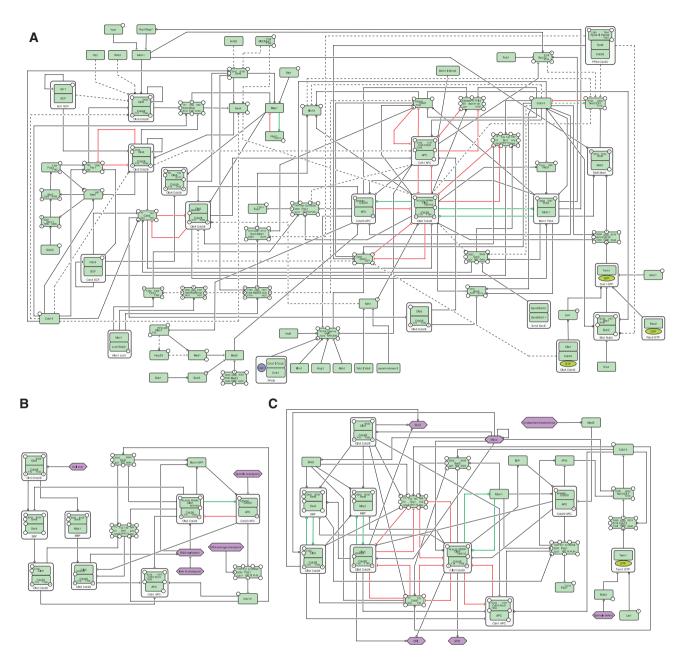**Figure 3** Directed graph views of abstracted interaction models used for comparative motif analyses. Each node represents the active state of species and edges between nodes indicate regulations (e.g. phosphorylation, degradation, transcriptional regulation). The bold colored lines indicate mutual regulations (green for activation and red for inhibition). (**A**) Interaction of core cycle entities in this study. The edge with dotted line represents the regulation with only genetic, but no direct evidence for the interaction. See annotations in the original network (Supplementary information S1) for details of each interaction. (**B**) Interaction of core cycle entities in Li *et al* (2004). (**C**) Interaction of core cycle entities in Chen *et al* (2004). See Supplementary information S12 for the further explanation.