Figure S1: Maximum likelihood tree phylogram showing relationships among LSD genes of metazoa. Numbers on the nodes correspond to support from the Shimodaira-Hasegawa approximate likelihood-ratio test, approximate Bayes test, and ultrafast bootstrap values. The scale denotes substitutions per site and colors represent gene lineages. Monoamine-oxidases (MAO-A and MAO-B) sequences from human (Homo sapiens), chicken (Gallus gallus), spotted gar (Lepisosteus oculatus), and coelacanth (Latimeria chalumnae) were used as outgroup (not shown).
Figure S2: Comparison of the molecular details of the LSD1-RCOR1 and LSD1-RCOR3 interaction. A) (Top) Multiple sequence alignment of RCOR1, RCOR2, and RCOR3 linker domain. Highlighted positions represent RCOR interacting residues with LSD1 according to Hwang et al. (2011). (Bottom) Structure and residue interactions of LSD1-RCOR1 and LSD1-RCOR3 at different interaction interfaces (numbered I-III) of tower-linker binding. B) (Top) Structure and residue interactions of LSD1-RCOR1 and LSD1-RCOR3 at interface IV. (Bottom) Multiple sequence alignment of RCOR1, RCOR2, and RCOR3 SANT2 domain. Highlighted positions represent RCOR interacting residues with LSD1.