



Supplementary Figure 1 Sequence Alignment. Alignment of LSD1 homologues from *H. sapiens* (GI:3043726), *C. familiaris* (GI:73950246), *M. musculus* (GI:37360004), *R. norvegicus* (GI:62649867), *D. rerio* (GI:68387817), *G. gallus* (GI:50759643), *P. troglodytes* (GI:55586433), *S. purpuratus* (GI:72031239), and *D. melanogaster* (GI:20151661). The secondary structure is indicated above the sequence as blue cylinders (alpha helices), green arrows (beta sheets), gray lines (coil regions), and gray dots (disordered residues). The numbering below the alignment is relative to human LSD1. Overall sequence conservation at each position is shaded in a color gradient from yellow (70% similarity) to dark red (100% identical). The participation of various residues in the formation of the SWIRM-oxidase interface (magenta dots) active site cavity (green dots) and tower domain interface (purple dots) is indicated below the aligned sequences.