



Supplementary figure 1. Alignment of SMUG1 orthologues. Species are arranged in descending order of sequence similarity to Homo sapiens SMUG1. Gaps and missing residues are denoted by dashes. Secondary structure of xSMUG1 is illustrated above the alignment. Accession numbers of each species are as follows: Hs (Homo sapiens) AAL86910.1; Pt (Pan troglodytes) XP_509109.1; Mm (Mus musculus) Q6P5C5; Bt (Bos Taurus) Q59I47; Rn (Rattus norvegicus) Q811Q1; Cf (Canis familiaris) XP_543623.2; Tn (Tetraodon nigroviridis) CAF95523.1; Xl (Xenopus laevis) Q9YGN6; Gm (Geobacter metallireducens GS-15) YP_383069.1; AE (Azoarcus sp. EbN1) YP_158606.1; Ci (Ciona intestinalis) AK115076.1; Sp (Strongylocentrotus purpuratus) XP_782746.1; Rb (Rhodopirellula baltica SH 1) NP_869403.1; Tc (Tribolium castaneum) XP_971699.1; Ag (Anopheles gambiae str. PEST) XP_312038.2; Am (Apis mellifera) XP_396883.2; Dm (Drosophila melanogaster) NP_650609.1; Dp (Drosophila pseudoobscura) EAL27349.1.