**Figure S1. Sequence similarity between DUBs.** (A) Percentages of amino acid sequence identity within catalytic core domain among the four DUBs was determined using the MUSCLE program (https://www.ebi.ac.uk/Tools/msa/muscle/). The sequence data used for analysis are as follows; human USP7, Q93009; human USP40, Q9NVE5; human USP47, Q96K76. (B) The CLUSTAL multiple sequence alignment by MUSCLE.