Figure S1. Neural network prediction of signal peptides in human DIA1 and DIA1R. The amino acid sequence of (A) human DIA1 or (B) human DIA1R, was evaluated for amino-terminal signal peptides using the neural network (NN) algorithm of SignalP v3.0 [51]. The C-score (cleavage score for each amino acid) is indicated in red, the S-score (signal peptide score) is indicated in green, and the Y-score (derived from the C-score and S-score, and can give a better indication of the cleavage site) is indicated in blue. The significance cut-off value for all probability scores is 0.5, and is indicated by a pink dotted line. Standard single-letter amino acid abbreviations and numbering is provided are provided below the graph.

Fig. S1

A

SignalP-NN prediction (euk networks): HsapiensDIA1

B

SignalP-NN prediction (euk networks): HsapiensDIA1R