



Figure S2. Multiple sequence alignment of IND all known IND variants, visualised using ESPrpt 3.0 online tool [25]. Newly found IND-17 is named IND. Numbers on top of alignment represent amino acid sequence number from N-terminus. BBL numbering of amino acids is presented below the alignment. Lines represent Loop 1 at 60-64 and Loop 2 at 221-241. Dots under alignment mark Zn ions binding amino acids.