‘Q9VYG2’ was entered into the EnsemblMetazoa Genome Browser (EGB) [http://metazoa.ensembl.org/index.html] and the exon transcript for the matching sequence was exported in FASTA format. This sequence was then imported into ExPasy [https://web.expasy.org/translate/], a tool capable of translating nucleotide sequences into amino acid sequences. The open reading frame 5'3' Frame 1 output generated by ExPasy, highlighted in red, was then exported in FASTA format. The amino acid sequence published in UniProtKB for Q9VYG2 was also exported in FASTA format and both the amino acid sequences were aligned using the EMBOSS Needle Pairwise Sequence Alignment tool, which creates global sequence alignment utilising the Needleman-Wunsch algorithm [https://www.ebi.ac.uk/Tools/psa/emboss\_needle/]. To confirm the number of isoforms produced by Q9VYG2 ‘Bap60’ was then searched on the APPRIS web database [http://appris-tools.org/#/seeker], which uses structural, functional and cross species conservation to annotate splice isoforms of protein coding genes. Each of the FASTA files exported in this analysis can be found in Document 2 of the supplementary data.