

Figure S1. Sequence Alignments, Secondary Structure, and Topology of Human ALIX_{Bro1-V}.

Sequence alignments of Bro1/ALIX proteins from five representative species, chosen because they are the most highly studied ALIX/Bro1 proteins. The secondary structure of human ALIX_{Bro1-V} is shown above, together with the numbering scheme. The color coding is the same as in Fig. 1B, with the TSG101 binding site shown in lime green and the Endophilin binding site shown in turquoise. Sequence alignments were performed using the ClustalW server www.ebi.ac.uk/clustalw (Thompson et al., 1994), and match structure-based alignments for the Bro1 domain.