## Supplementary information, Figure S4

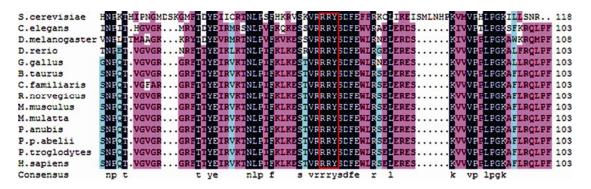


Figure S4 Sequences alignment of the PX domains of Snx3 homologues from different species. Multiple sequences of the PX domains from DSNX3 and related molecules from other species were aligned with DNAMAN software, followed by manual refinement. Amino acid residues conserved in all of the proteins are highlighted in black. The alignment consensus is shown at the bottom. The GenBank accession numbers are as follows: Saccharomyces cerevisiae Snx3p, NP\_015002; Caenorhabditis elegans snx-3, NP\_492437; Drosophila melanogaster CG6359, AAF54838; Danio rerio sorting nexin 3, CAQ14003; Gallus gallus sorting nexin-3, NP\_001006408; Bos taurus sorting nexin-3, DAA26260; Canis familiaris sorting nexin 3, XP\_855006; Rattus norvegicus sorting nexin-3, NP\_001037748; Mus musculus sorting nexin 3, AAI16886; Macaca mulatta sorting nexin-3 isoform 4, XP\_001094537; Papio anubis sorting nexin-3, NP\_001162458; Pongo abelii sorting nexin-3, NP\_001126677; Pan troglodytes sorting nexin 3 isoform 4, XP\_001149032; and Homo sapiens sorting nexin-3 isoform a, NP\_003786. The most conserved motif in the PX domain of SNX3, RRYSDFE, was the PI3P binding motif.