

## Supplementary information, Figure S4

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S.cerevisiae HNEKTHIFNGMDSKGMFTDYEIICRTINLPSFHKRVSKVRRRYSDFEFFRKCITKEISMLNHFQVMVPHLPGKILLSNR.. 118
C.elegans INEITLHGVGGR...MRYTDYEIRMRSNLPEKQKESVRRRYSDFEWVRADPERDS.....KIVVPHLPGKSEKRQLPF 103
D.melanogaster VNEHTTMAAGR...KRYTDYEVRMRTNLPVFKVKESSVRRRYSDFEWLRNEPERDS.....KIVVPHLPGKANKRQMPF 108
D.rerio INEPTLGVGGR...NRETTYEIKLKTINLPIEKLKESVRRRYSDFEWLRGDEPERES.....KVVVPHLPGKALFRQLPF 103
G.gallus GNEPTLGVGGR...GRETTYEIRVKTINLPIEKLKESVRRRYSDFEWLRNEPERES.....KVVVPHLPGKALLRQLPF 103
B.taurus SNEPTLGVGGR...GRETTYEIRVKTINLPIEKLKESVRRRYSDFEWLRSEPERES.....KVVVPHLPGKAFRLQLPF 103
C.familiaris SNEPTLGVFAR...GRETTYEIRVKTINLPIEKLKESVRRRYSDFEWLRSEPERES.....KVVVPHLPGKAFRLQLPF 103
R.norvegicus SNEPTLGVGGR...GRETTYEIRVKTINLPIEKLKESVRRRYSDFEWLRSEPERES.....KVVVPHLPGKAFRLQLPF 103
M.musculus SNEPTLGVGGR...GRETTYEIRVKTINLPIEKLKESVRRRYSDFEWLRSEPERES.....KVVVPHLPGKAFRLQLPF 103
M.mulatta SNEPTLGVGGR...GRETTYEIRVKTINLPIEKLKESVRRRYSDFEWLRSEPERES.....KVVVPHLPGKAFRLQLPF 103
P.anubis SNEPTLGVGGR...GRETTYEIRVKTINLPIEKLKESVRRRYSDFEWLRSEPERES.....KVVVPHLPGKAFRLQLPF 103
P.p.abelii SNEPTLGVGGR...GRETTYEIRVKTINLPIEKLKESVRRRYSDFEWLRSEPERES.....KVVVPHLPGKAFRLQLPF 103
P.troglodytes SNEPTLGVGGR...GRETTYEIRVKTINLPIEKLKESVRRRYSDFEWLRSEPERES.....KVVVPHLPGKAFRLQLPF 103
H.sapiens SNEPTLGVGGR...GRETTYEIRVKTINLPIEKLKESVRRRYSDFEWLRSEPERES.....KVVVPHLPGKAFRLQLPF 103
Consensus np t t ye nlp f s vrrrysdf e r l k vp lpgk

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**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.