

### Supplementary Information.

**Figure S1.** A cartoon showing the domain organisation of full-length myosin VI and a schematic and sequence alignment of C-terminal region of the tail. **(a)** The cartoon depicts the domain organisation of myosin VI highlighting the globular C-terminal tail with the relative positions of the splice inserts (LI: large insert, SI: small insert), the binding sites for Dab2 and GIPC/optineurin [positions 1184aa (W) and 1107-1109aa (RRL) respectively] and the PIP<sub>2</sub> binding site. Black arrowheads (1 and 2) indicate the tryptic cleavage sites and black lines show the positions of domains 1 and 2. The amino acid (aa) numbering refers to the chicken sequence. **(b)** An alignment of the human (H), chicken (C) and mouse (M) myosin VI C-terminal tail sequences (aa 1017 – end) using ClustalW from [www.ch.EMBLnet.org](http://www.ch.EMBLnet.org). The large and small inserts (LI and SI) and the RRL, WWY, and lipid (KSKNKKR) binding sites are shown in bold along with the phosphorylatable TINT sequence<sup>1</sup>. Arrowheads 1 and 2 mark the trypsin cleavage sites. Predicted secondary structure for the chicken myosin sequence obtained by a consensus of 8 prediction algorithms<sup>2</sup> is shown: “c” is random coil, “e” is extended sheet, “h” is a helix and a blank space indicates no consensus.