

## **Supplementary information**

**Isolated pores dissected from human two-pore channel 2 are functional.**

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### **Figure S1. Optimisation of TPC2 pore-only protein expression in *E. Coli*.**

(A-C) Expression, solubilisation and purification trials of *E. coli* cells transformed with a plasmid encoding the hexa-histidine-tagged TPC2 DI pore-only construct containing an extended C-terminus (S212-Q418) (expected size: 20 kDa). (A) Western blot analysis using an  $\alpha$ -poly-histidine antibody against membrane fractions isolated from *E. coli* cells during expression trials at 37°C and 22°C. (B) Western blot analysis using an  $\alpha$ -poly-histidine antibody against membranes solubilised in 10x CMC of the detergents DM, Cymal5 and LDAO or in 1% (w/v) of DDM during solubilisation trials. (C) Coomassie-stained SDS PAGE analysis of the proteins eluted by 500 mM imidazole from washed Ni-NTA or TALON resin beads during affinity chromatography purification trials. (D) Expression trial of shortened TPC2 DI pore-only (S212-A337) (expected size: 14.6 kDa). This construct was used for all subsequent experiments.

### **Figure S2. Co-expression of TPC2 pores with a lysosomal marker**

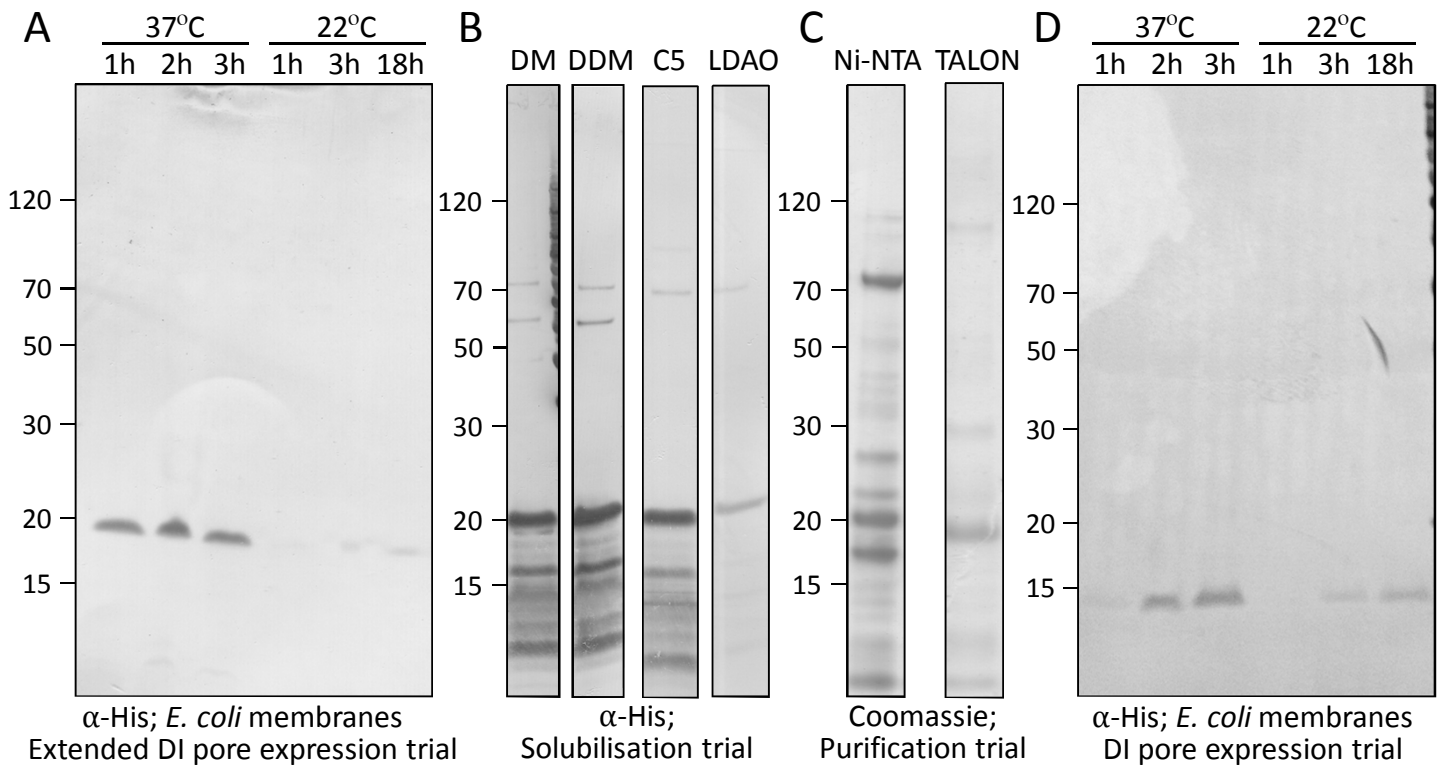
Confocal images of HeLa cells co-expressing a lysosomal marker (LAMP1-RFP, red) and the indicated GFP-tagged pore (green). Nuclei (blue) were stained with DAPI. Scale bar 10  $\mu$ m. Colocalisation plots of red and green fluorescence intensity between arrowheads are shown below.

### **Figure S3. Homology model alignments**

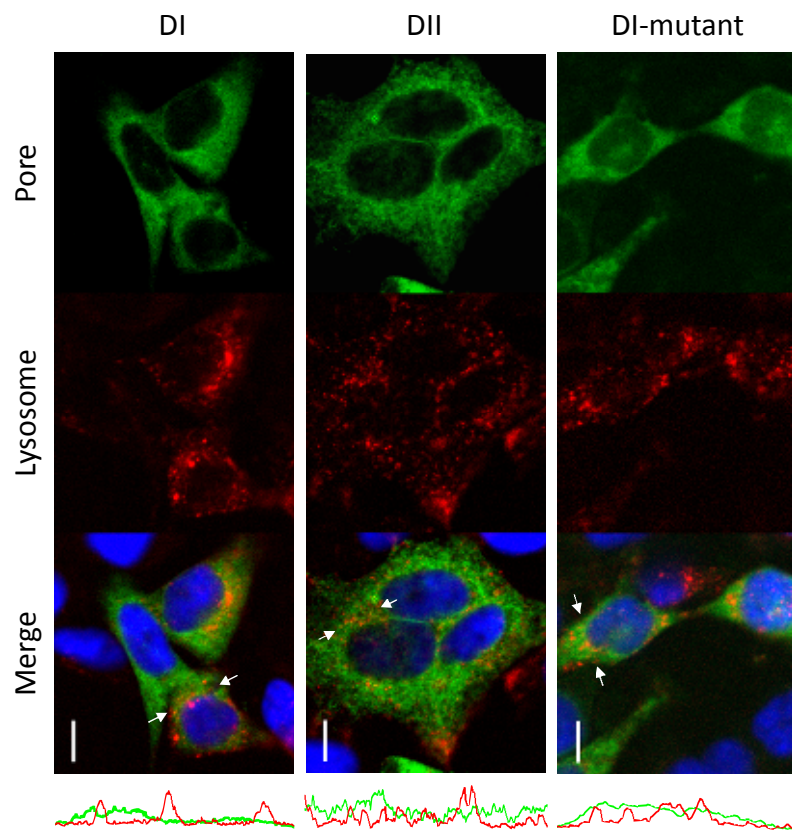
Alignments of human TPC2 (HsTPC2) and TPC1 from *Arabidopsis Thaliana* (AtTPC1) used for the generation of the homology model of the DI pore. For AtTPC1, transmembrane helices are highlighted in yellow and the re-entrant pore helices are highlighted in cyan. For HsTPC2, a short turret loop, denoted by ^ was not modelled.

**Table S1. Primers**

List of forward and reverse primers used to generate the pore-only constructs. Mutagenic bases are underlined. The *E. coli* primers target a codon-optimised plasmid.



**Fig S1**



*Fig S2*

HsTPC2DI	SLPEMASVGLLLAIHLCLFTMFGMLLFAGGKQD^LTYFQNLPESLTSLLVLLTTANNPDV	277
	::         :             :        ::             :                   :        :             :    :              :	
AtTPC1	MLGT <del>YLNILALWMLFLLFASWIAFVMF</del> E <del>DTQQG^LTVF</del> T <del>SYGATLYQMFI</del> L <del>FTTSNNPDV</del>	270
HsTPC2DI	MIPAYSKNRAYAIAFFIVFTVIGSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAA	337
	:             ::         :    :    :    :                  :         :         :                  :              :        :	
AtTPC1	<del>WIPAYKSSRW</del> <del>SSVFFVLYVLI</del> G <del>VYFVTNLI</del> L <del>AVVYDSFKEQLAKQVSGMDQMRR</del> MLEKA	330

*Fig S3*

<b>Cloning Primers</b>		
DI pore (HeLa)	Forward	5'-CACCGAATTCTGGATGGCCTCGCTGCCGAAATG-3'
	Reverse	5'-AGGCTCGAGCATGGAGGATAGGACTTCAAAGG-3'
DII pore (HeLa)	Forward	5'-CACCGAATTCTGGATGGCCCTGGTGCAGAACATGCGT-3'
	Reverse	5'-AGGCTCGAGCCTGCACAGCCACAGGTG-3'
<b>Mutagenic Primers</b>		
DI-mutant (HeLa)	Forward	5'-GTCTCTGACTTCCC <u>C</u> CCTGGTGCTGCTGA-3'
	Reverse	5'-TCAGCAGCACCAGGG <u>G</u> GGAAGTCAGAGAC-3'
DI pore ( <i>E. Coli</i> )	Forward	5'-GTACTCGCGCAGCCTA <u>G</u> GAGGTTTGCCTTGTG-3'
	Reverse	5'-CACAAAGCGCAAACCTC <u>C</u> TAGGCTGCGCGAGTAC-3'

*Table S1*