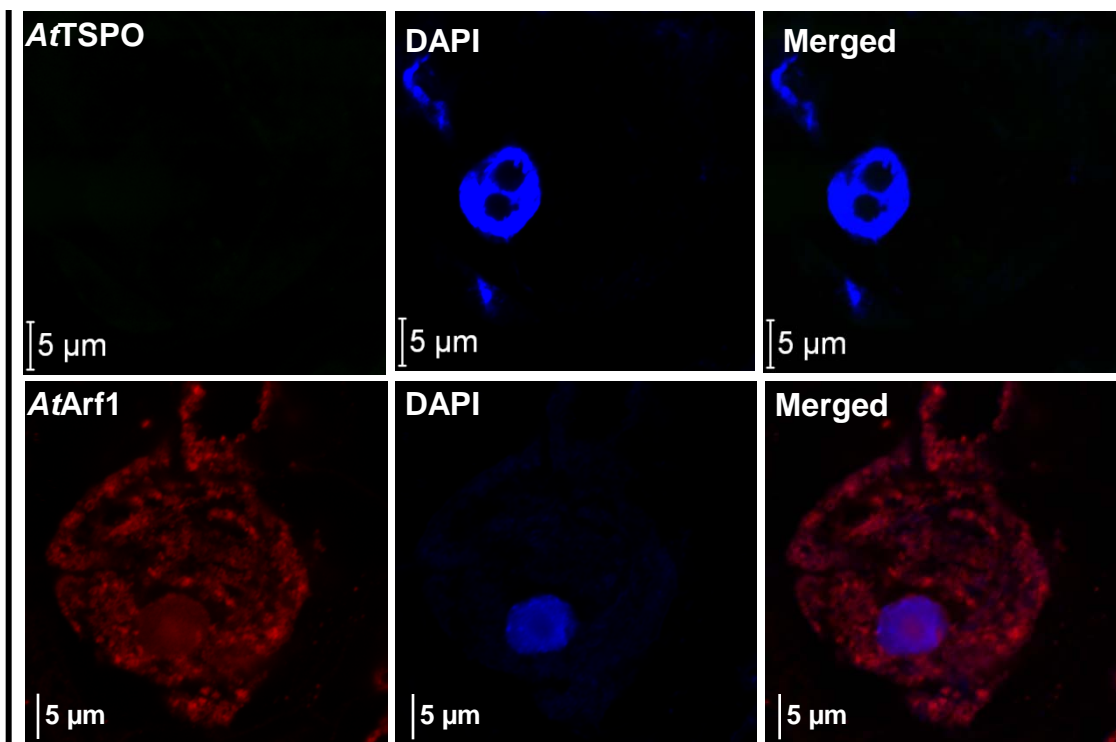


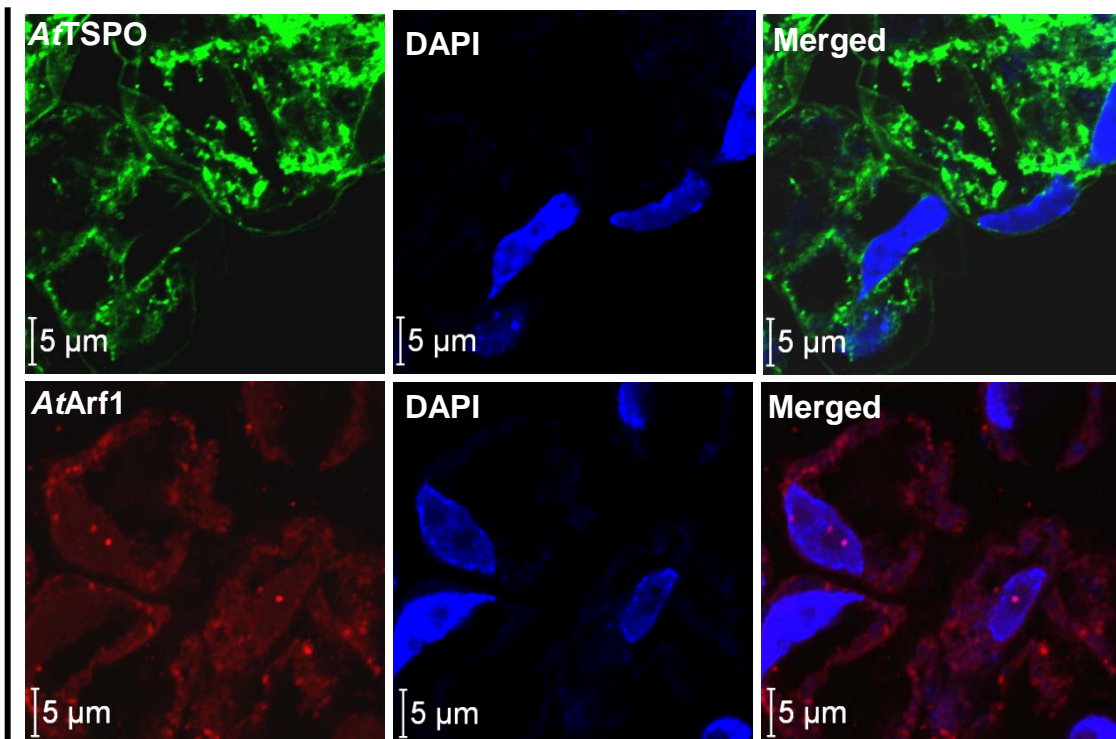
Supplemental table 1: Summary of number of transmembrane domains in human TSPO1 and TSPO2, Arabidopsis AtTSPO and Vitis vinifera VvTSPO using different transmembrane (TM) prediction software.

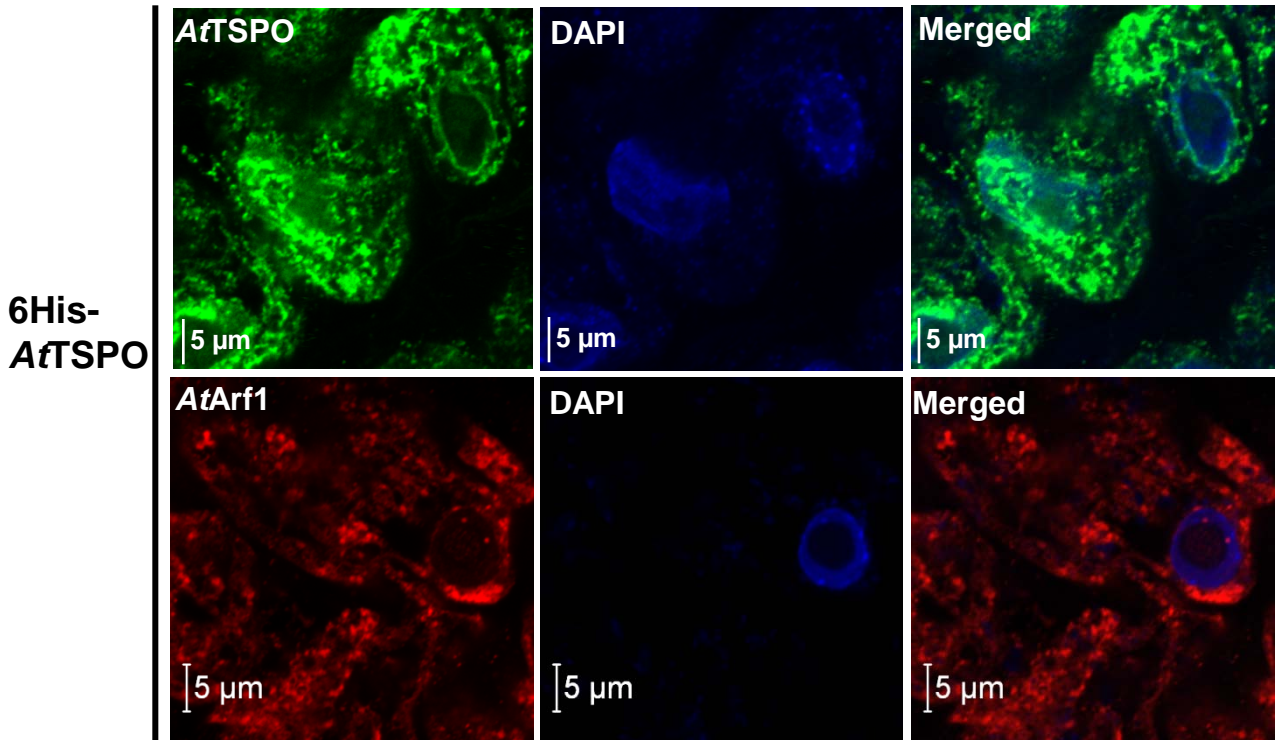
TM Prediction program	Reference	TSPO1	TSPO2	AtTSPO	VvTSPO
TMHMM2	www.cbs.dtu.dk/services/TMHMM	5	5	2	3
HMMTOP2	www.enzim.hu/hmmtop	4	5	4	4
PHOBIUS	http://phobius.sbc.su.se	5	5	4	5
DAS	www.sbc.su.se/~miklos/DAS/maindas.html	5	5	4	5
SPLIT4	www.split.pmfst.hr	5	5	3	4
TMPred	www.ch.embnet.org/software/TMPRED_form.html	5	5	5	4

WT



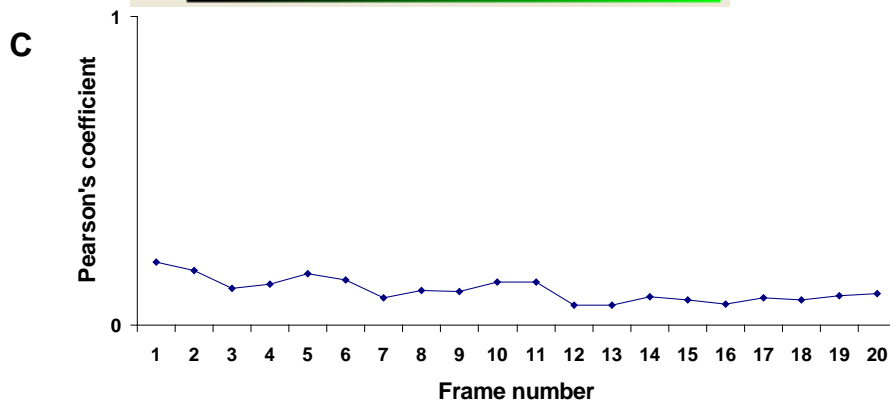
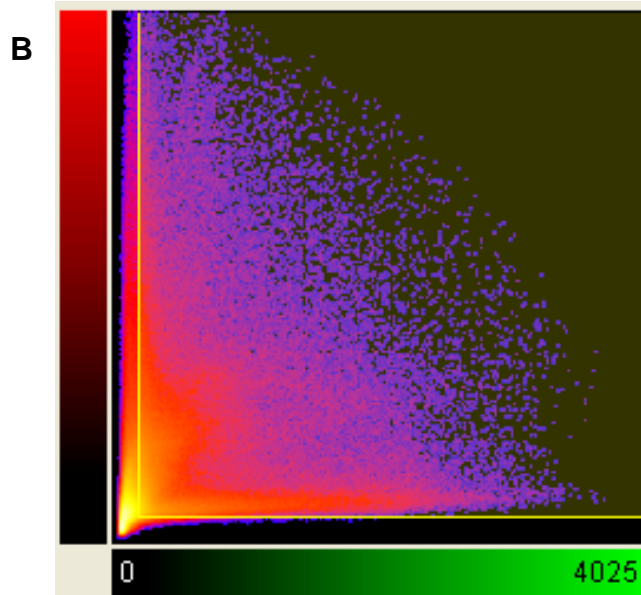
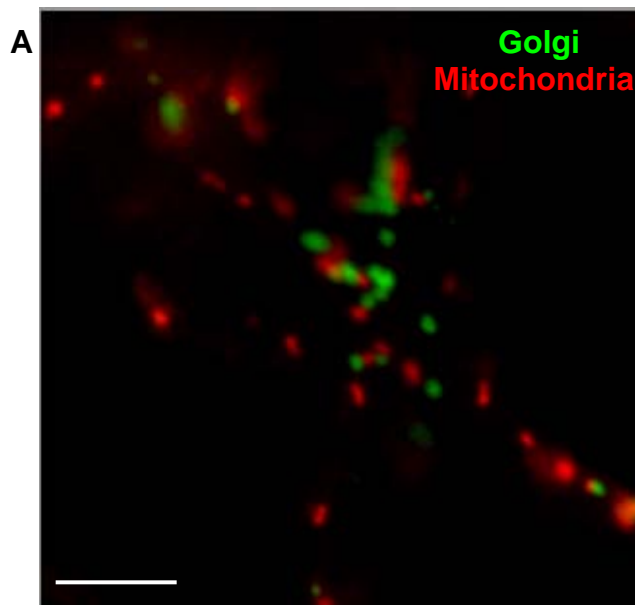
**WT
+
ABA**





SF1: Anti-AtArf1 and anti-AtTSP0 probing of plant cells

Each antibody was used alone to probe wild type cells (WT), wild type cells pre-incubated with ABA (WT + ABA) or a transgenic cell line overexpressing 6xHis-AtTSP0. Nuclei are highlighted by DAPI staining.



SF2: YFP-AtTSPO and Mitotracker-labelled mitochondria do not colocalize

A- single frame from the merge movie shown in supplemental data highlighting the Golgi and the mitochondria. B- colocalization analysis with Imaris (12 bits image)
C- statistical analysis of the colocalization with the Pearson coefficient.

```

HsTSP01 -----MAPPWVPAMGFTLAPSLGC 19
HsTSP02 -----MR---LQGAIFVLLPHLGP 16
AtTSP0  MDSQDIRYRGGDDRDAAATTAMAETERKSADDNKGKRDQKRAMAKRGLKSLTVAVAAPVLV 60
                                         *   : . . . : . :

HsTSP01 FVGSRFVHGEGLRWYAGLQKPSWHPPHWVLGPVWGTLYSAMGYGSYLVWKELGG-FTEEKA 78
HsTSP02 ILVWLFTRDHMSGWCEGPRMLSWCPFYKVLLLVQTAIYSVVGYASYLVWKDLGGGLGWPL 76
AtTSP0  TLFATYFLGTSDGYGNRAKSSSWIPPLWLLHTTCLASSGLMGLAAWLVWVDGGF---HKK 117
      :   : .   :   : ** *   :* .   : . : * . : : * * * : *

HsTSP01 VVPLGLYTGQLALNWAWPPIFFGARQMGWALVDLLLVSGAAAAATTVAWYQVSPLAARLLLY 138
HsTSP02 ALPLGLYAVQLTISWTVLVLFFTVHNPGLALLHLLLLYGLVVSTALIWHPINKLAALLLL 136
AtTSP0  PNALYLYLAQFLLCLVWDPVTFRVGSGVAGLAVWLGQSAALFGCYKAFNEISPVAGNLVK 177
      . * ** * : : .   : * . .   . * * . .   : : . : * . * :

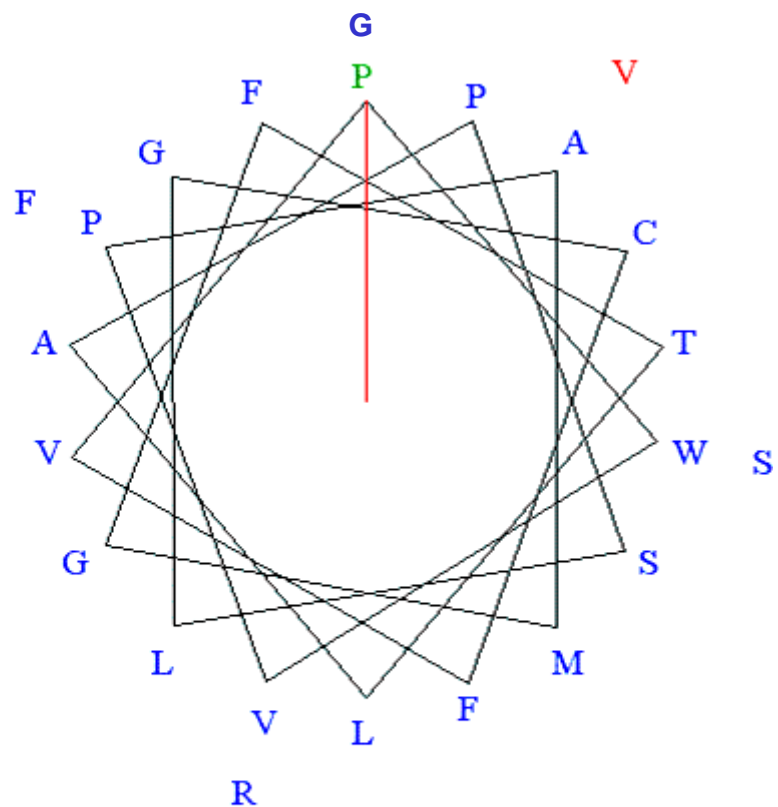
HsTSP01 PYLAWLAFTTTTLNYCVWRDNHGWRGGRRLPE--- 169
HsTSP02 PYLAWLTVTSALTYHLWRDSLCPVHQPQPTEKSD 170
AtTSP0  PCLAWAAFVAAVNVKLAVA----- 196
* *** : . . : : . :

```

SF3:

CLUSTALW alignment of Arabidopsis *AtTSP0* (accession #AAL16286), human *HsTSP01* (accession # NP_000705) and *HsTSP02* (accession # NP_001010873) TspO/MBR domain (IPR004307)-containing membrane proteins. *HsTSP01* is targeted to the mitochondrial outer membrane in mammalian and yeast cells, while *HsTSP02* is targeted to the endoplasmic reticulum in animal cells. Underlined is the Schelman motif (Rone et al., 2009) important for *HsTSP01* import into the mitochondrial outer membrane. Conserved residues are marked in bold, negatively charged residues in red, positively charged residues in green and the predicted transmembrane segments in *HsTSP01* are shaded in grey.

A



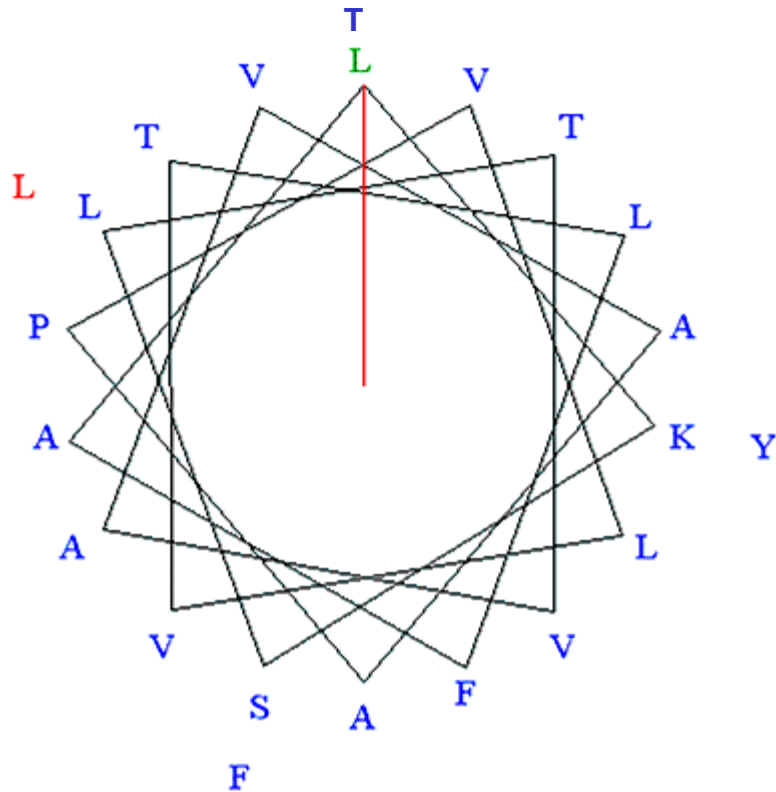
TMS 1: PWVPAMGFTLAPSLGCFVGSRFV

Rotational angle: 330.74

Selected Scale: Pi

Predicted $\Delta G_{app} = 2.672$

B



TMS 1: LKSLTVAVAAPVLVTLFATYFL

Rotational angle: 12.6

Selected Scale: Pi

Predicted $\Delta G_{app} = -0.660$

SF4: α -Helical wheel projection of human TSPO1 (A) and *Af*TSPO (B) predicted first transmembrane segment sequences. The first residues are in green and the last residues in red. The prediction of the corresponding apparent free energy difference, ΔG_{app} , for insertion of each TM sequence into the endoplasmic reticulum membrane by means of the Sec61 translocon was calculated using the ΔG prediction server v1.0 at <http://dgpred.cbr.su.se/index.php?p=home>.