Supplemental Figure S1

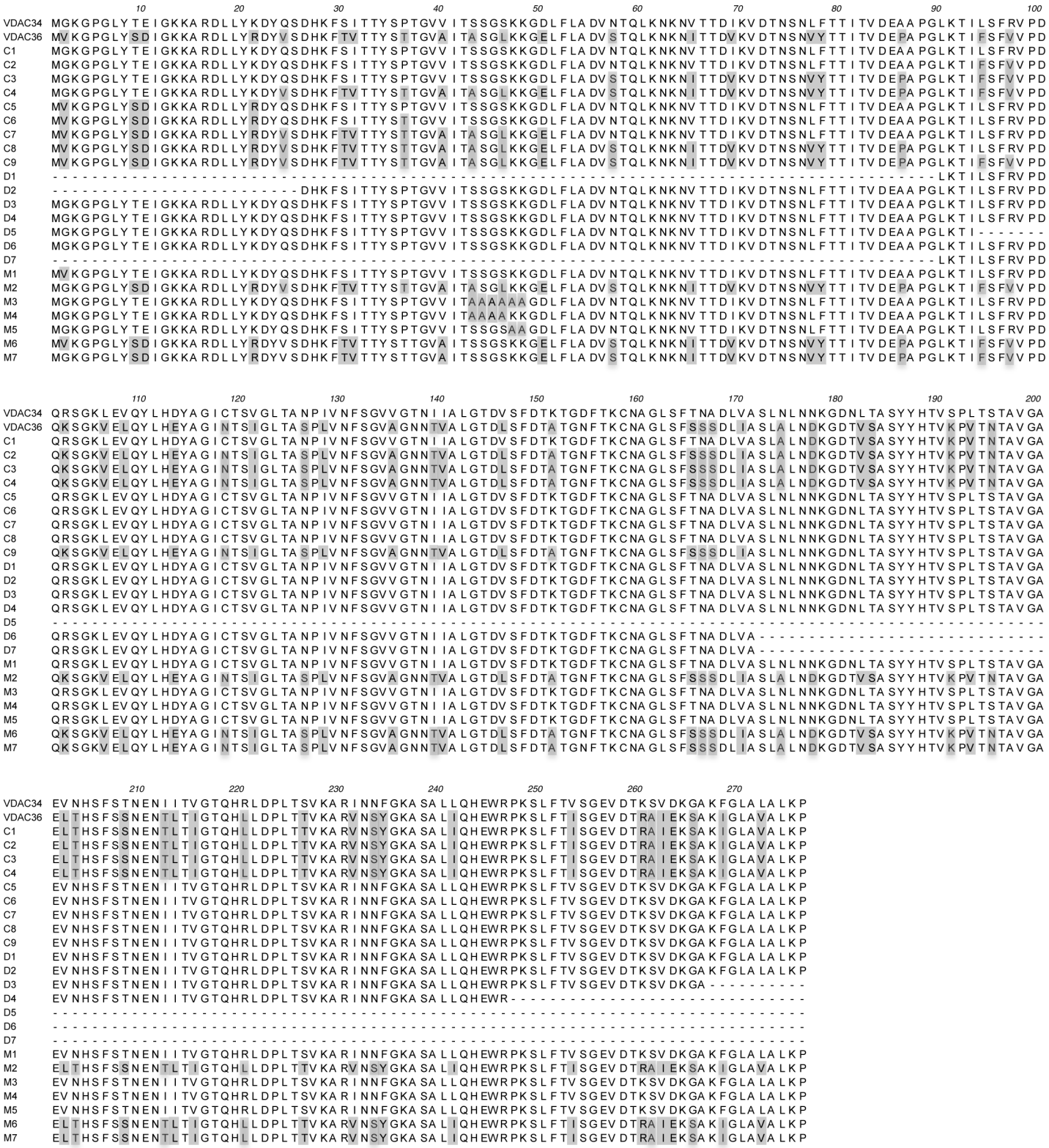

Figure S1. Sequences of VDAC mutants.
Sequence alignment of VDAC34, VDAC36 and the 21 mutants. VDAC34 sequence was used as reference and amino acids differing on the other protein sequences are indicated in grey background.

Supplemental Figure S2

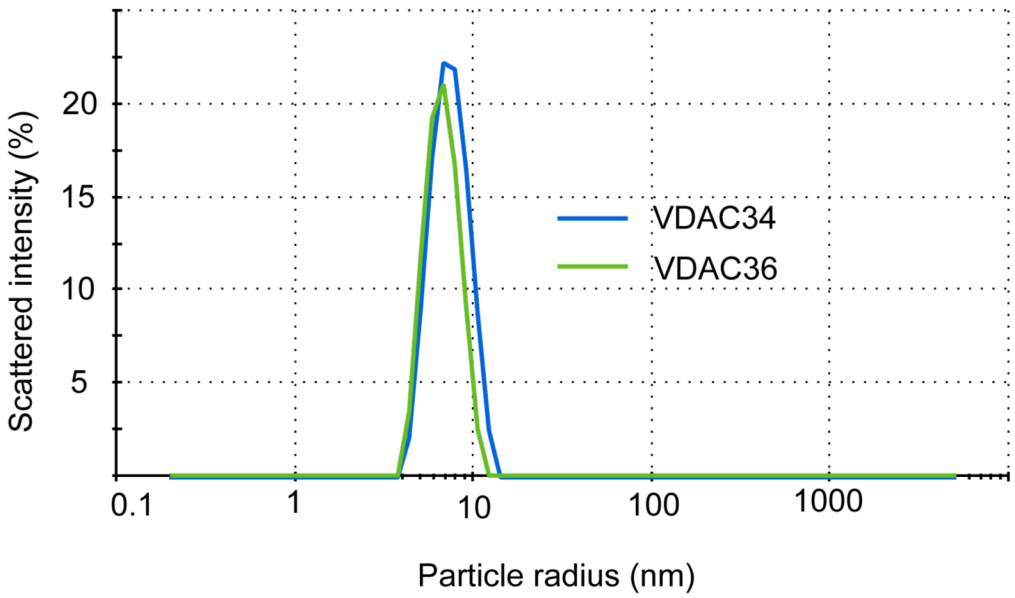

Figure S2. Analysis of stability and homogeneity of VDAC34 and VDAC36 by dynamic light scattering.
VDAC samples (at 14-17 μM) are soluble and stable in the presence of 1% (w/v) octyl-β-D-glucopyranoside. Size distributions derived from respective diffusion coefficients correspond to homogeneous populations of VDAC monomers in solution.

Supplemental Figure S3

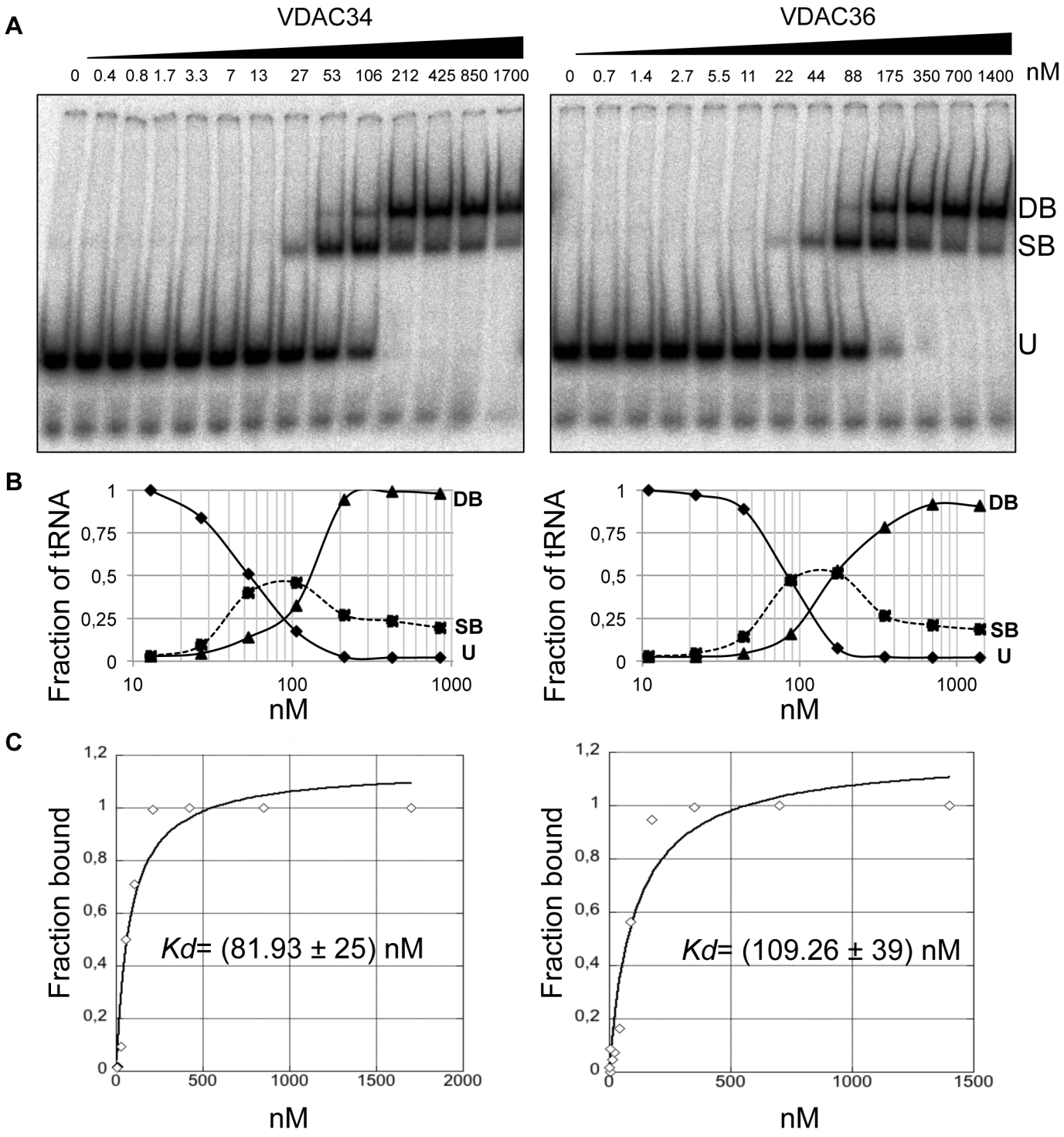

Figure S3. Affinity of VDAC34 and VDAC36 for tRNAs.
Example of gel-shift assays for quantitative analysis of tRNA-VDAC interaction in limiting tRNA conditions. (**A**) Gel-shift with 0.1 nM of tRNA and increasing amounts of VDAC protein. In gel-shift assays performed for quantitative analysis, 3 bands were visible and correspond to the unbound tRNA (U), the single-bound tRNA (SB) and the doubly-bound tRNA (DB). This indicate that the tRNA has 2 binding sites. (**B**) The curves for the 3 bands were plotted with protein concentrations on log scale. At[Protein]=K_d, the fraction of single-bound tRNA is 0.5 and the fraction of unbound and doubly-bound tRNA are 0.25 and this is what is expected for independent binding sites. (**C**) Graphics of binding curves. The apparent constant dissociation (K_d) values were calculated with KaleidaGraph 4.0 software.

Supplemental Figure S4

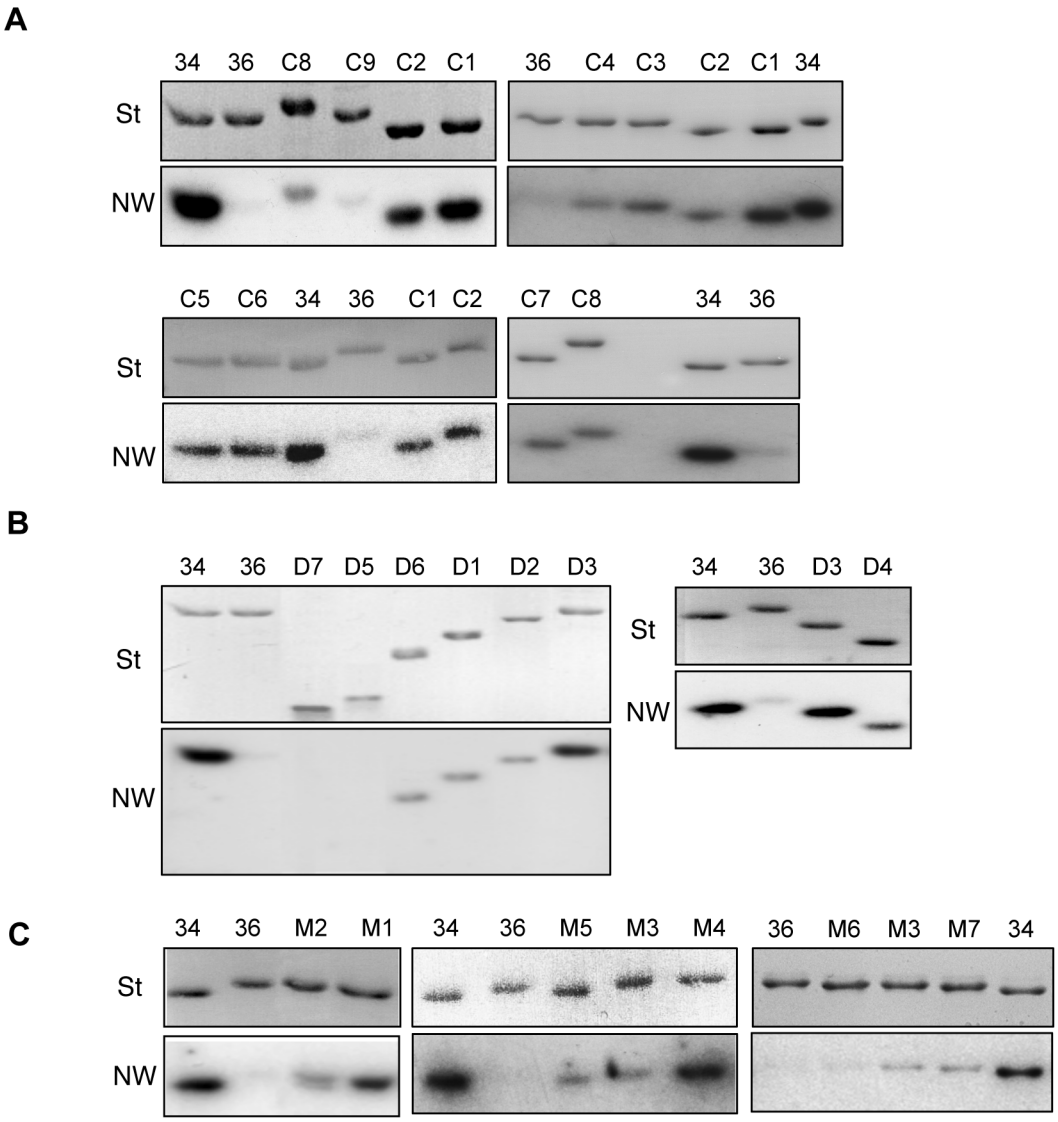

Figure S4. Northwestern analysis with mutant proteins.
Examples of Northwestern analysis with (**A**) chimeric mutants, (**B**) deletion mutants and (**C**) point mutants are given. (St) corresponds to the Coomassie blue staining of overexpressed proteins, fractionated on a SDS-PAGE and electroblotted on Immobilon-P membrane. (NW) corresponds to the Northwestern blot analysis. The proteins fixed on the membrane were renatured and incubated with radiolabeled cytosolic *A. thaliana* $tRNA^{Ala}$ transcripts.

Supplemental Figure S5

BindN

VDAC34

```
Sequence:     MGKGPGLYTEIGKKARDLLYKDYQSDHKFSITTYSPTGVVITSSGSKKGDLFLADVNTQL
Prediction:   ------------+--+--------------------------+-+++------------
Confidence:   55041240124371781652241213215242111313556009079733678868300 5

Sequence:     KNKNVTTDIKVDTNSNLFTTITVDEAAPGLKTILSFRVPDQRSGKLEVQYLHDYAGICTS
Prediction:   --+--+-----------------------------------+--+---------------
Confidence:   00714723504512125432969667546701463605222801931633968587762 1

Sequence:     VGLTANPIVNFSGVVGTNIIALGTDVSFDTKTGDFTKCNAGLSFTNADLVASLNLNNKGD
Prediction:   ------------------------------------------------------------
Confidence:   55517347959457762496686266243200203105132615149677727251103 3

Sequence:     NLTASYYHTVSPLTSTAVGAEVNHSFSTNENIITVGTQHRLDPLTSVKARINNFGKASAL
Prediction:   ---------------------------------------------+-+----------
Confidence:   04041222252272115734473334233436725312305435104738621440725 6

Sequence:     LQHEWRPKSLFTVSGEVDTKSVDKGAKFGLALALKP*
Prediction:   --------------------+---+-------------
Confidence:   83344051144172514207141834056677881 55
```

VDAC36

```
Sequence:     MVKGPGLYSDIGKKARDLLYRDYVSDHKFTVTTYSTTGVAITASGLKKGELFLADVSTQL
Prediction:   ------------+--+--------------------------+--------------+-
Confidence:   69152350123271681563273725526241111112537137250054778978207 4

Sequence:     KNKNITTDVKVDTNSNVYTTITVDEPAPGLKTIFSFVVPDQKSGKVELQYLHEYAGINTS
Prediction:   ------------------------------------------+--+---------------
Confidence:   00014023504411015032859665545702873799543701831633968476731 0

Sequence:     IGLTASPLVNFSGVAGNNTVALGTDLSFDTATGNFTKCNAGLSFSSSDLIASLALNDKGD
Prediction:   ------------------------------------------------------------
Confidence:   53326147948455443214674267364240304105132414122467827773303 3

Sequence:     TVSASYYHTVKPVTNTAVGAELTHSFSSNENTLTIGTQHLLDPLTTVKARVNSYGKASAL
Prediction:   --+-----------------------------------------+--++-+----
Confidence:   04731212151262336746561324210311515434687888104029317727 4146

Sequence:     IQHEWRPKSLFTISGEVDTRAIEKSAKIGLAVALKP
Prediction:   --------------------+----------------
Confidence:   83354051244173526407451025055667781 5
```

Figure S5. *In silico* analysis of VDAC34 protein with BindN software
The results obtained with BindN software correspond to the RNA binding prediction with a specificity equal to 95 %. Binding residues are labeled with (+) and in red. The non-binding residues are labeled with (-) and in green. The confidence is indicated from level 0 (lowest) to level 9 (highest).

Supplemental Figure S6

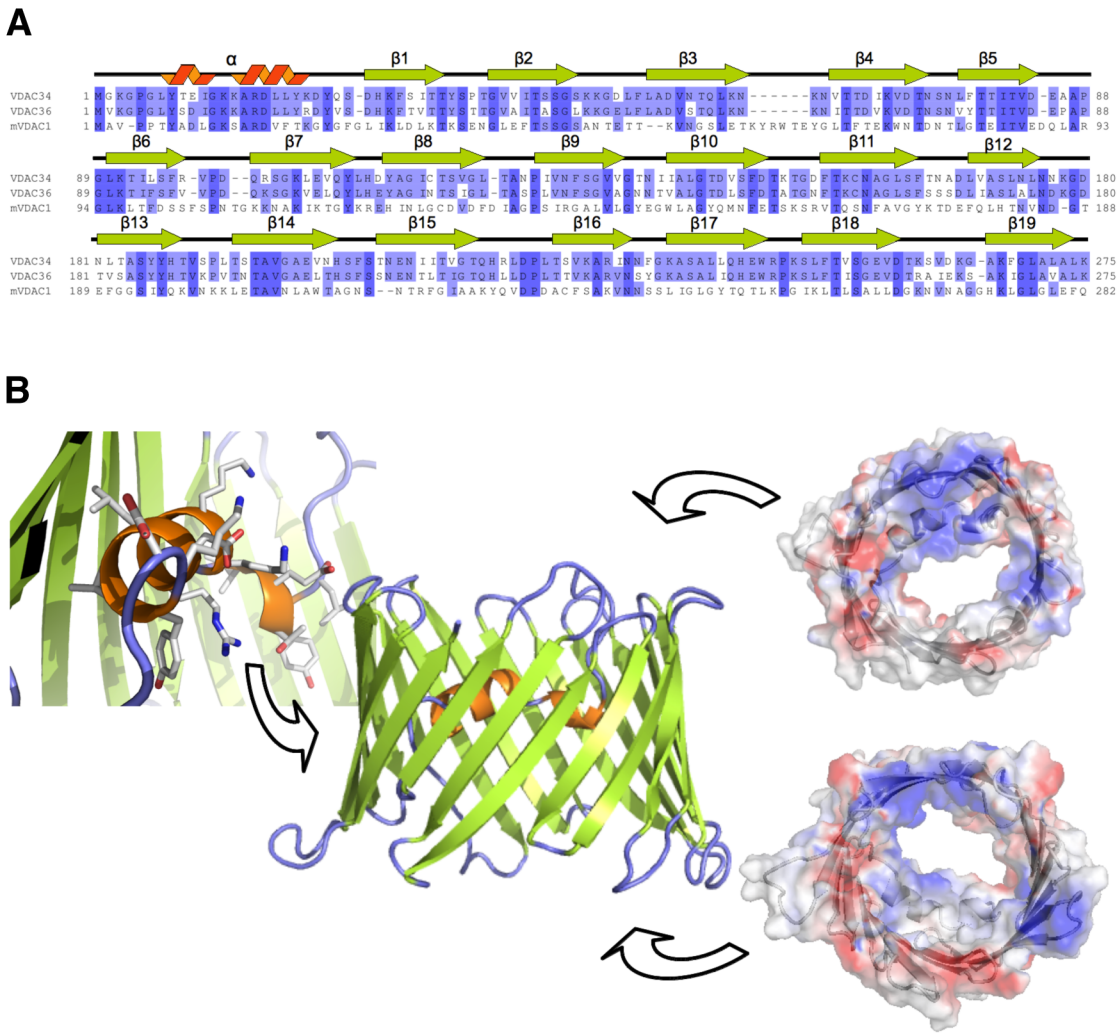

Figure S6. Structural features of *S. tuberosum* VDAC34.
(**A**) Sequence alignment of VDAC34 and VDAC36 with VDAC1 from mouse. Secondary structure elements are indicated above the sequences.
(**B**) 3D comparative model of VDAC34 based on mVDAC1 crystal structure depicted with the same color code (alpha helix in orange, beta-strands in green). On the left, a close up view on the amphiphilic helix making hydrophobic contacts to the channel's wall and pointing polar and charged groups inside the pore. On the right, electrostatic surface potential of channel entries shows high density of electropositive patches inside the channel. Blue indicates positive charges whereas red shows negative charges.

Supplemental Figure S7

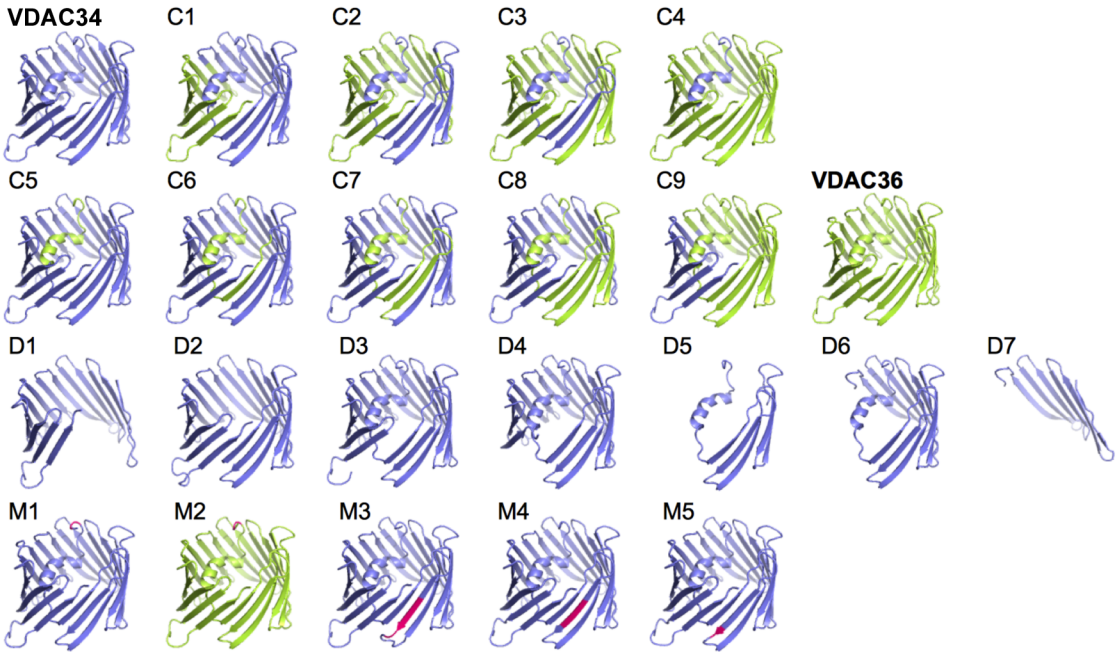

Figure S7. Collection of VDACs and mutants.
The models of VDAC34 and VDAC36 are depicted in blue and green, respectively. The C series corresponds to chimeric mutants and the same color code is used to indicate the origin of sequence segments. The D series corresponds to deletion mutants of VDAC34 and M1-5 represent point mutants of VDAC34 or VDAC36 with mutated positions highlighted in red.