



Figure S6. Analysis of the predicted protein StABCG11 from *Stenocereus thurberi*. **(a)** Phylogenetic tree of StABCG11 and related proteins of the classes ABCG11, ABCG12, and ABCG13 from *Arabidopsis thaliana* (At), *Gossypium arboreum* (Ga), *Citrus sinensis* (Cs), *Medicago truncatula* (Mt), *Solanum lycopersicum* (Sl), *Eutrema halophilum* (Eh), *Beta vulgaris* (Bv), and *Spinacia oleracea* (So). The database accession number next to the protein name is shown. The scale bar of 0.10 represented a sequence divergence of 10%. The number in the branches is the percentage bootstrap value of 1000 replicates. The highest percentages represent higher significant results. The black square beside the protein name shows AtABCG11, AtABCG12, and AtABCG13 from *A. thaliana*. The red circle and red triangle next to the protein name show StABCG11 from *S. thurberi* and a protein from the closest related species, *C. gigantean*, respectively. Neighbor-joining (NJ) phylogenetic tree constructed by MEGA11 software. **(b)** The predicted transmembrane helices of StABCG11. The probability of membrane insertion (Y-axis) and transmembrane region represented by purple color was determined by TMHMM software. **(c)** Multiple sequence alignment of StABCG11 and its homologous from *A. thaliana* (AT1G17840), *S. lycopersicum* (Solyc03g019760), and *C. gigantean* (KAJ8441854). Amino acids are colored according to the chemistry classification of their side-chain. The darkest blue bars below the protein sequences indicate 100% conservation. Black rectangles show the conserved sequence of the Walker A and B motif and the ABC signature, named below the rectangles. Black width lines below the sequence show the predicted transmembrane helices of StABCG11. Alignment was carried out by MUSCLE in MEGA11 and drawn by gmsa in R Studio.