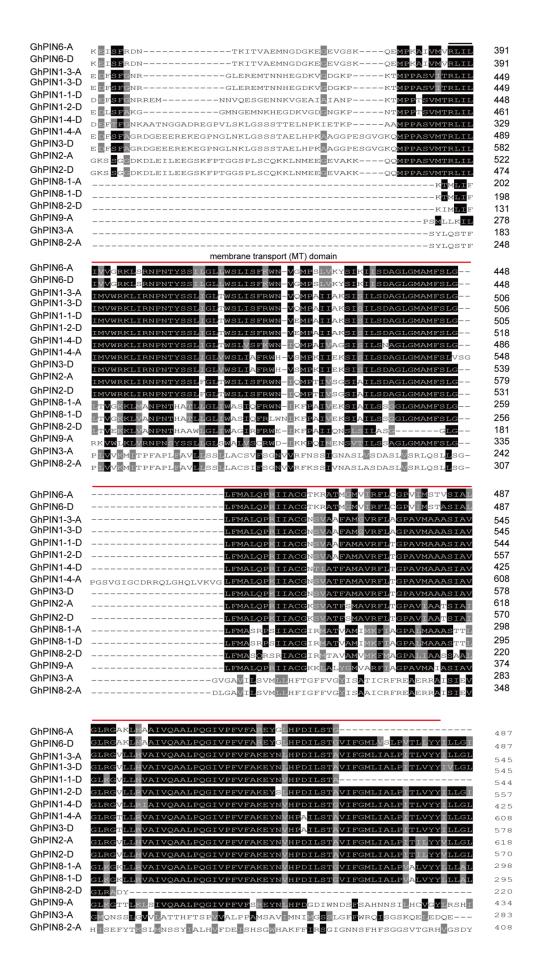


GhPIN6-A GhPIN6-D GhPIN1-3-A GhPIN1-3-D GhPIN1-2-D GhPIN1-4-D GhPIN1-4-A GhPIN3-D GhPIN2-A GhPIN2-A GhPIN8-1-A GhPIN8-1-D GhPIN8-1-D GhPIN8-2-D GhPIN9-A GhPIN3-A GhPIN3-A	ADIFSVNIPGGENNNEIVECNGENGFGYRAVSPR	283 283 287 287 287 290 288 288 299 299 196 192 125 270 176 241
GhPIN6-A GhPIN6-D GhPIN1-3-A GhPIN1-3-D GhPIN1-1-D GhPIN1-2-D GhPIN1-4-A GhPIN3-D GhPIN2-A GhPIN2-D GhPIN8-1-A GhPIN8-1-D GhPIN8-2-D GhPIN8-A GhPIN3-A GhPIN3-A GhPIN3-A	PRASN N	290 290 332 332 329 343 321 338 337 359 359 196 192 125 270 176 241
GhPIN6-A GhPIN6-D GhPIN1-3-A GhPIN1-3-D GhPIN1-1-D GhPIN1-2-D GhPIN1-4-A GhPIN3-D GhPIN2-A GhPIN2-D GhPIN8-1-A GhPIN8-1-D GhPIN8-2-D GhPIN8-A GhPIN9-A GhPIN3-A GhPIN3-A	- EMDVITTAAGNTP WM - EMDVITTAAGNTP WM - EMDVITTAAGNTP WM - ANTKKPNDQAQQKAEDGGRD H FVWS - ANTKKPNDQAPQKAEDGGRD H FVWS - GVKKPNGQAHQKVEDGGGKD H FVWS - N- ANAKRPNGHPQQKSEDGGRD H FVWS - KKANGGOBGGKD H FVWS - QQPVQPQQQPKEKENNKENHDAKD H FVWS - QQQPREKENNKENHDAKD H FVWS MPNKELHMGGRSMSGELYNGGGVPSYPPPNPIFAGSTSGGSKKKEIGAMPNK DI H FVWS MPNK DI H FVWS	306 306 359 359 356 371 341 369 362 419 371 196 192 125 270 176 241
GhPIN6-A GhPIN6-D	R SPVAGGKVFRQPSPVVPPTKMVWDCQDGGGDDNRQGFKDLGE	349



GhPIN6-A		487
GhPIN6-D		487
GhPIN1-3-A		545
GhPIN1-3-D		545
GhPIN1-1-D		544
GhPIN1-2-D		557
GhPIN1-4-D		425
GhPIN1-4-A		608
GhPIN3-D		578
GhPIN2-A		618
GhPIN2-D		570
GhPIN8-1-A		298
GhPIN8-1-D		295
GhPIN8-2-D		220
GhPIN9-A	WKDENINMRNSAALFREIQGYGQNQQQQYSYVFVLS	470
GhPIN3-A		283
GhPIN8-2-A	EYNG	412

Figure S1. Multiple sequence alignment of the deduced amino acid sequences of predicted PINs from *G. hirsutum*.

The graphical view of the alignment was generated by BioEdit using ClustalW. Black under lines indicates the auxin efflux carrier (ACE) domain and red under lines highlight the membrane transport (MT) domain.