Supplementary Material S1: Bioinformatics online tools used in this research.

Name	Function	URL
TMPRED	Prediction of transmembrane domain	http://www.ch.embnet.org/software/TMPREDform.html
PSORT	Prediction of subcellular localization	https://www.genscript.com/psort.html
SignalIP	Prediction of signal peptides	http://www.cbs.dtu.dk/services/SignalIP
ProtScale	Analysis of amino acid affinity/ hydrophobicity	http://web.expasy.org/cgi-bin/protscale/protscale.pl
NCBI Conserved Domains	Prediction of conservative domains	https://www.ncbi.nlm.nih.gov/cdd
SMART		http://smart.embl-heidelberg.de/
NPS@SOPMA	Analysis of protein secondary structure	https://npsa-prabi.ibcp.fr/cgi-bin/npsa_automat.pl?page=npsa_sopma.html
I-TASSER	Construction of protein tertiary structure model	https://zhanggroup.org/I-TASSER/

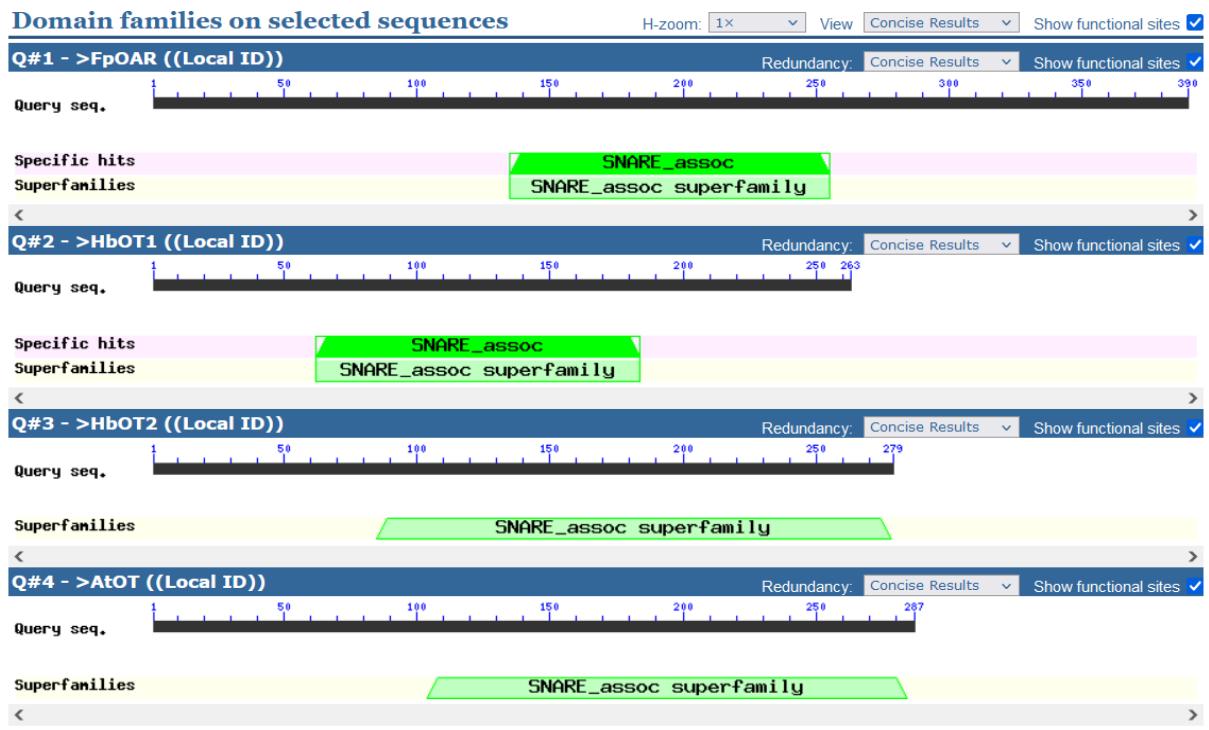Supplementary Material S2: Homology alignment and conserved domain information of FpOAR, HbOT1, HbOT2 and AtOT

1. Homology alignment of *FpOAR, HbOT1, HbOT2 and AtOT.*

Section 1

```
                    1        10        20        30        40        50      64
            (1)     |         |         |         |         |         |       |
FpOAR   (1)  MTDLHRSLQDNRSAYSLATVHDMPSPSASTSLLSHADEPQYG--------TTRPAGPSNKRILF
HhOT1   (1)  ------------------------------------------------------------
AtOT    (1)  ---------------MAAPRNLTGDGGARQLVKDEESPAASSAAKGLLNDDSPTGKRTKSERF
HhOT2   (1)  ---------------MAAARNLMGDAGSNRPTMKDEEKAKE-------DDSPSSKKPKLERF
Consensus (1)                  MAA RNL GDAGS  LL  DEEPA    DDSPSGKK K ERF
```

Section 2

```
                    65       70        80        90        100       110     128
            (65)    |         |         |         |         |         |       |
FnOAR   (57) TATLKMAAIFVVSTLFLGGTLWLALPTLDEEDRPDLRIPKSFAQLOALNTLLKKYRDIYPYRIV
HbOT1   (1)  ---------------MPKWWKVAVVVGIVGIFRELSKQLGWDKDAALQVFALWSDRLGMWAM
AtOT    (49) PLSRWEFAVFFTVFLVFTTGLFCIYLTMPAAEYGKLKVPRTISDLRLLKENLGSYASEYQARFI
HbOT2   (41) PFTRWEFAAALGVFFVFSTGLFCIYLTMPTSVYVNLKLPRTVSDLRLLKEHLATYAKDYPAQFI
Consensus (65) P TRWEFAIFL VFLVFSTGLFCIYLTMP ADY KLKIPRTISDLRLLKELLASYADDYPARFI
```

Section 3

```
                    129      140       150       160       170       180     192
            (129)   |         |         |         |         |         |       |
FnOAR   (121) VCYVTTYLFLQAFSLPGSMYLSILGGAVWGVPRAILLACTCVACGATLCYLISAALGPALLTMP
HbOT1   (48)  PVYVGIHTLTLALCLPYAVFFEAGASLLFGFLPAVLCVFSAKVLGASLSFWIGRLVFKSSSSAM
AtOT    (113) LGYCSTYIFMOTFMIPGTIFMSLLAGALFGVVRGFVLVVLNATAGACSCFFLSKLVGRPLVN-W
HbOT2   (105) LGYCSTYIFMQTFMIPGTIFMSLLAGALFGVVRGLFLVVFNATAGASCFFLSKLIGRPIVN-S
Consensus (129) LGYVSTYIFMOTFMIPGTIFMSLLAGALFGVVRAILLVVSNATAGASSCFFISKLVGRPLVN
```

Section 4

```
                    193      200       210       220       230       240     256
            (193)   |         |         |         |         |         |       |
FpOAR   (185) KYKARADVWSEKISGQRENLISYLIVLRIAPLPPHWVVNVLCPHLGIGIAPFWISTWLGILGVT
HhOT1   (112) EWAORNRYFHLLSRGVERDGWRFVLLARFSPMPSYWINYALAATKVGFLVDFLLPTVIGCLPMI
AtOT    (176) LWPEKLRFFQAEIAKRRDRLLNYMLFLRITPTLPNLFINLSSPIVDIPFHVFFLATLVGLMPAS
HbOT2   (168) LWPEKLRVFQAEIAKRREKLLNYMLFLRVTPTLPNLFINLASPIVDIPFHVFFLATLLGLIPAS
Consensus (193) LWPEKLRVFQAEIAKRREKLLNYMLFLRITPTPPNLFINLLSPIVDIPFHVFFLATLLGLLPAS
```

Section 5

```
                    257      270       280       290       300       310     320
            (257)   |         |         |         |         |         |       |
FpOAR   (249) VIHTTIGGSLDEMTSAAD-FHLISWKNFFMLAAVVVGVMIPVGLRYFFKRELATVVDVEADAAS
HhOT1   (176) LONTSIGSLAGAAVASTSGSOKSKVWSYLFPILGIVSSILISLRIKKYSTDVTMVASSPSNHAG
AtOT    (240) YITVRAGLALGDLRSVKD-LYDFKTLSVLFLIGSISIFPALLKRKRVYE---------------
HbOT2   (232) YITVRAGLALGDLKSVKD-LYDFKTLSMLFLIGSIIIFPTLLKRKRIYE---------------
Consensus (257) YITVRIGLALGDLKSVKD LYDFKTLSVLFLIGSIVIFPILLKRKRIYE DL V    A  A
```

Section 6

```
                    321      330       340       350       360       370     384
            (321)   |         |         |         |         |         |       |
FnOAR   (312) IAEOYRDDESDVILEOGPATGPGKGKDAKLISLSDDEDDYDSDPDEDIILEAGPALVVKADEHM
HhOT1   (240) DCNDVDSSPTLSGRTGGDSLKKSQ-------------------------------------
AtOT    (288) ------------------------------------------------------------
HbOT2   (280) ------------------------------------------------------------
Consensus (321)              S       G A
```

Section 7

```
                    385       399
            (385)   |         |
FnOAR   (376) ESTPDRREWRQEDLL
HhOT1   (264) ---------------
AtOT    (288) ---------------
HhOT2   (280) ---------------
Consensus (385)
```

```
FpOAR  MTDLHRSIQDNRSAYSLATVHDMFSFSASTSILSHADEPQYGTIRFAGPSNKRILFTATLKMAAIFVVSTLFIGCTIWLALPTLEEDRPDLRIFKSFAQIQALNTLLKYRDIYPYRIVVGYVTTYLFL  130
HbOT1  ..................................................................MFKWWKVAVVVGIVGIFRELSKQLGWDKDAALQVFALWSDRLGMWAMFVYVGIHTLT   57
HbOT2  ........MAAARNLMGLAGSNRFTMKLEEKAKE........DLSFSSKKPKLERFPFTRWEFAAAIGVFFVFSTGLFCIYLTMFTSVYVNLKLPRTVSDIRLLKEHLATYAKDYPAQFIIGYCSTYIFM  114
AtOT   ........MAAFRNLTGLGGARQIVKDEESPAASSAAKGILNDLSFTGKRTKSERFPLSRWEFAVFFTVFLVFTTGLFCIYLTMFAAEYGKLKVFRTISDIRLLKENLGSYASEYQARFIIGYCSTYIFM  122

FpOAR  QAFSLFGSMYLSIIGGAVWGVFRAILLACTCVACGATICYLISAALGFALLTMFKYKARALVWSEKISGQRENIISYLIVLRIAFIFPHWVVNVICFHIGIGIAFWISTWLGIIGVTVIHTTICGSLDE  260
HbOT1  IALCLFYAVFFEAGASLLFGFIPAVICVFSAKVIGASLSFWIGRLVFKSSSSAMEWAQRNFYFHLLSRGVERIGWRFVILARFSFMFSYINYALAATKVGFLVFFLLFTVIGCIFMILQNTSIGSIAGA  187
HbOT2  QTFMIFGTIFMSLLAGALFGVVRGLFLVVFNATAGASSCFFISKLIGRPIVNSIWEEKLRVFQAEIAKFRREKILNYMLFLFIFVTPTLFNLFINLASPIVLIIFFHVFFLATILGIIFASYITVRAGLALGDL  244
AtOT   QTFMIFGTIFMSLLAGALFGVVRGFVLVVINATAGACSCFFISKLVGRPLVNWIWFEKLRFFQAEIAKFRERILNYMLFLFITPTLFNLFINISSPIVLIIFFHVFFLATLVGIMFASYITVRAGIAIGDL  252
```

SNARE_assoc Domain

```
FpOAR  MTSAALFHLISWKNFFMLAAVVVGVMIFVGLFYFFKRELATVVEVEALAASIAEQYRFDESDVIIEQGFATGFGKGKDAKLISLSDDELDYDSDFDEDIILEAGFALVVKADEHMESTFDRREWRQEDLL  389
HbOT1  AVASTSGSQRSKVWSYLFPILGIVSSIIISLFIKKYSTDVTMVASSPSNHAGDCNLVLSSFTLSGRTGGDSLKKSQ.......................................  263
HbOT2  KSVKDLYLFRTLSMLFLIGSIIIFPTLLKRKFYE..............................  279
AtOT   RSVKDLYLFFRTLSVLFLIGSISIFFALIKRKFVYE..............................  287
```

2. The SNARE-assoc conserve domain of FpOAR and homology blasted genes HbOT1, HbOT2 and AtOT

3. Similarity analysis of *FpOAR with HbOT1, HbOT2 and AtOT (A) and SNARE protein members from FpOAR, rubber trees and other plants.*