

**Figure 1**

**Figure 1a**

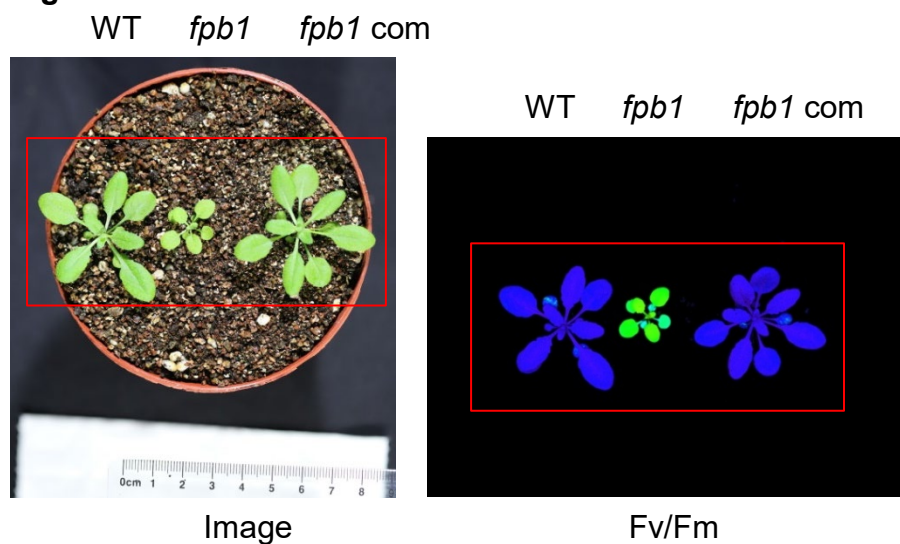


**Figure 1b**

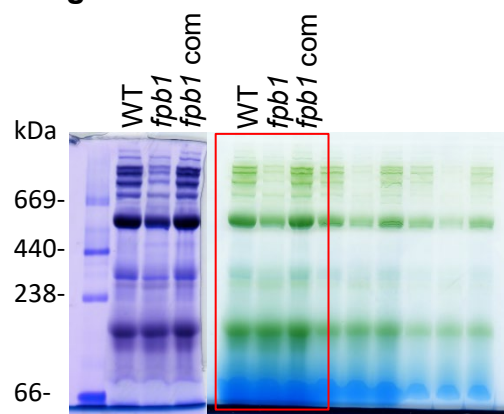
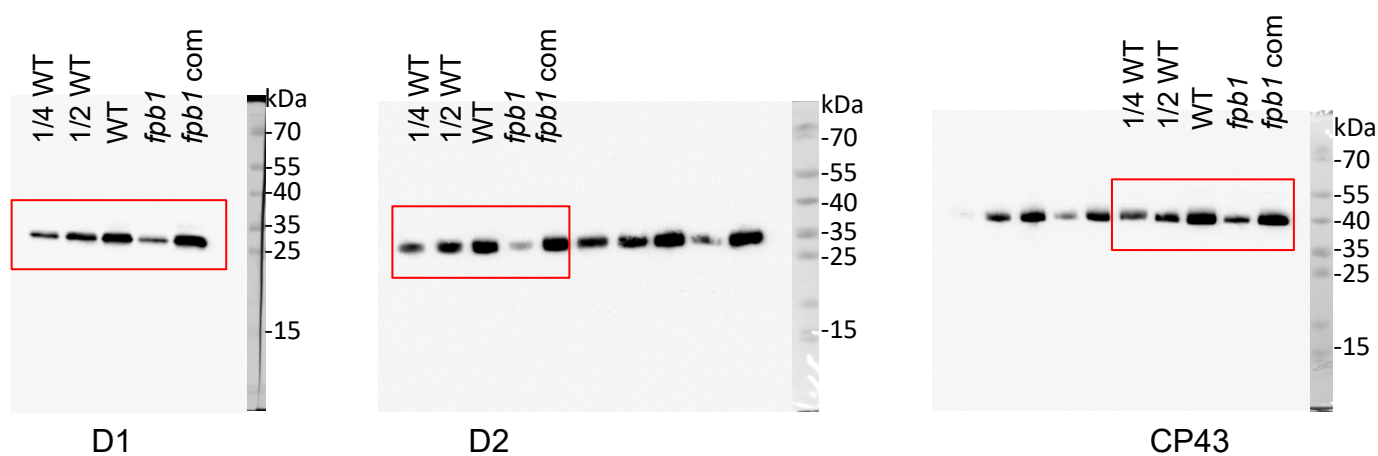


**Figure 1c**

Please note that: Protein ladder from ThermoFisher (Catalog Number 26616) was used throughout the whole study. An unknown band between 15 and 25 kDa was found in SDS-urea-PAGE but not in SDS-PAGE and Tricine-SDS-PAGE.



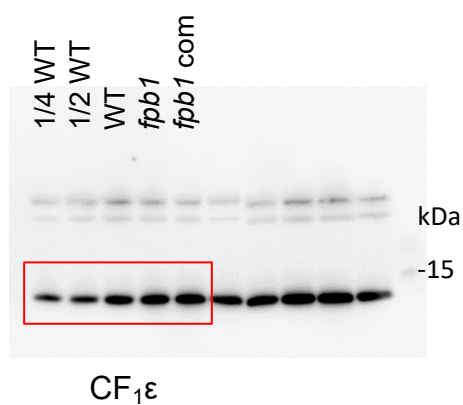
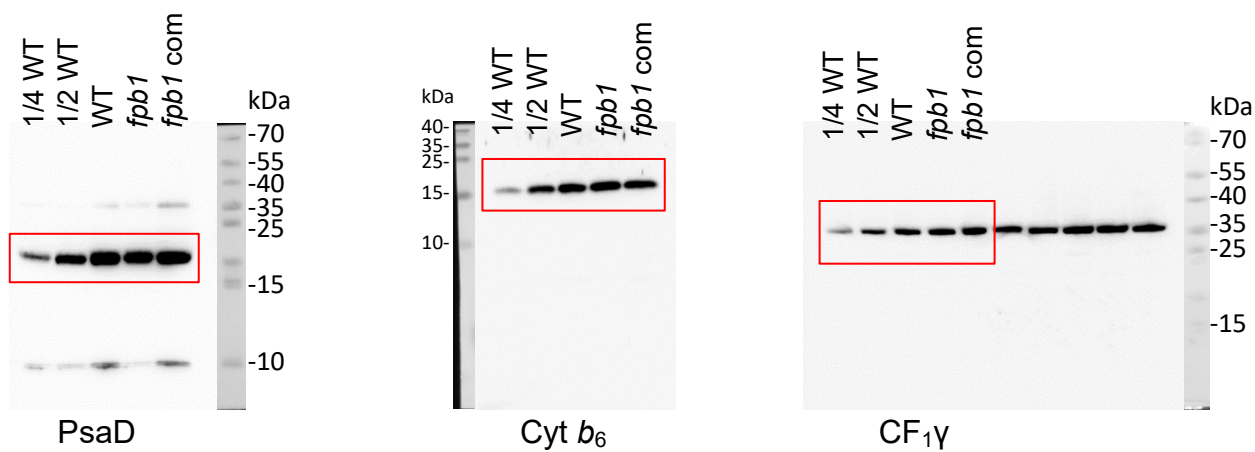
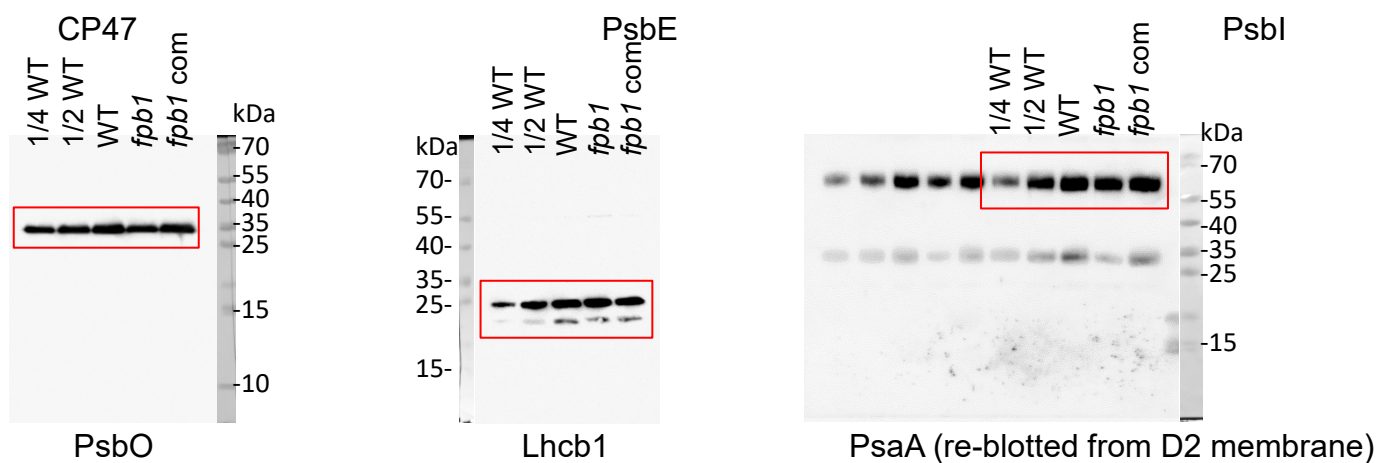
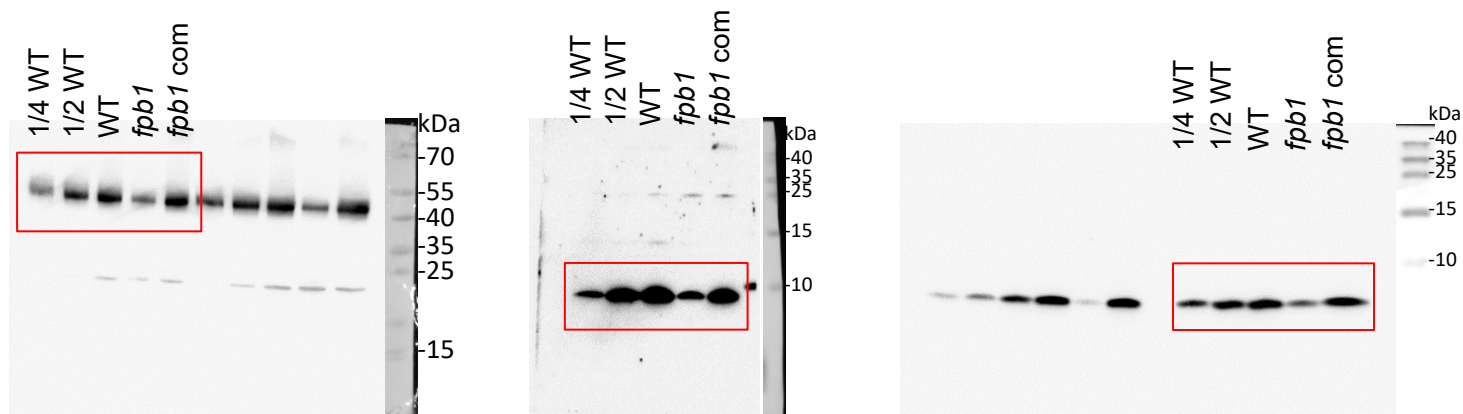
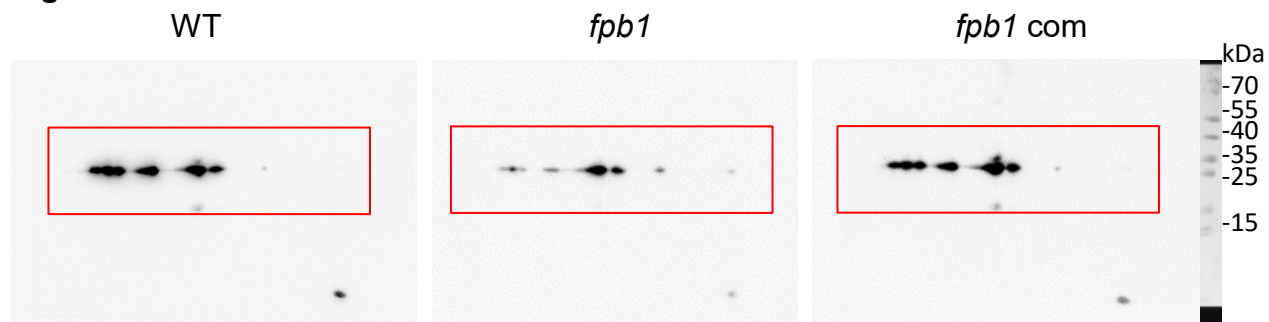
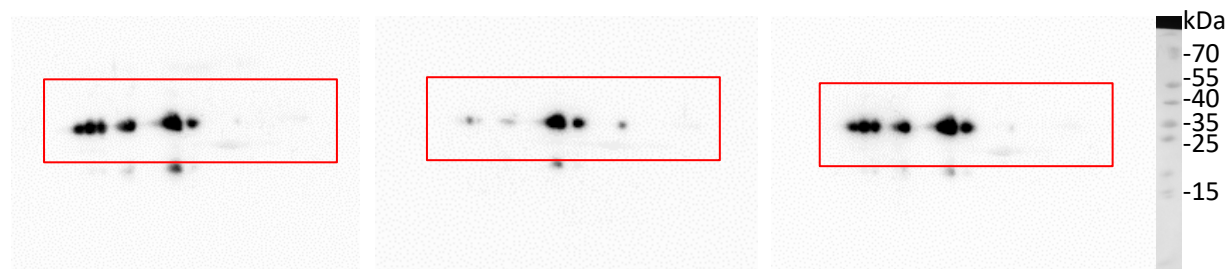


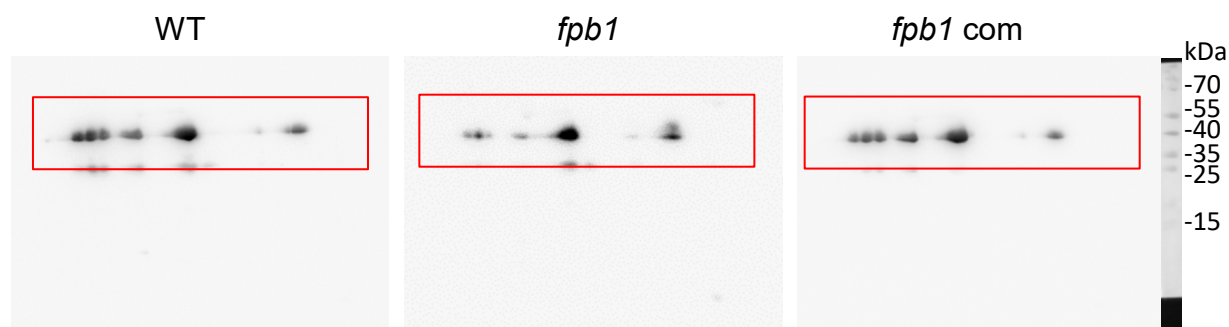
**Figure 1d**



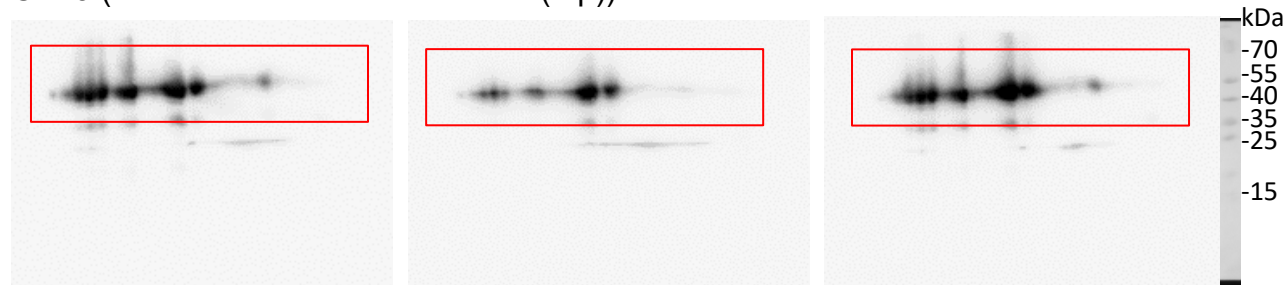
D1



D2



CP43 (re-blotted from D1 membrane (top))

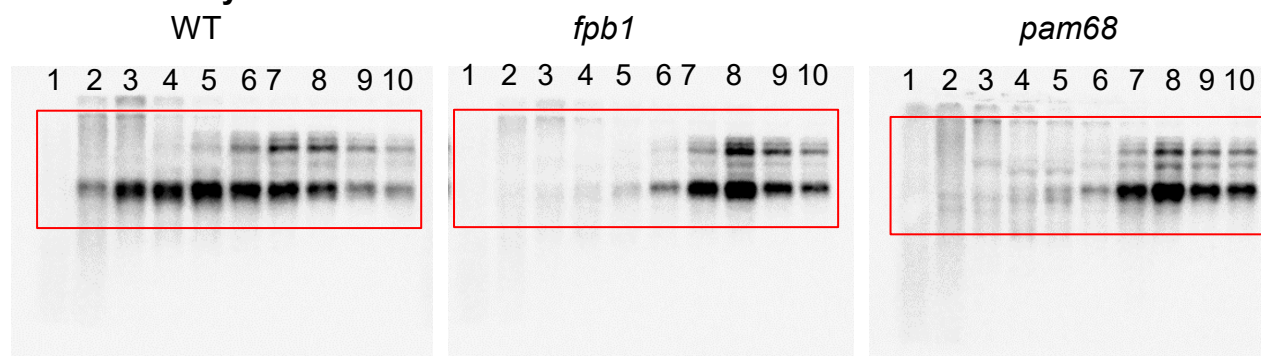


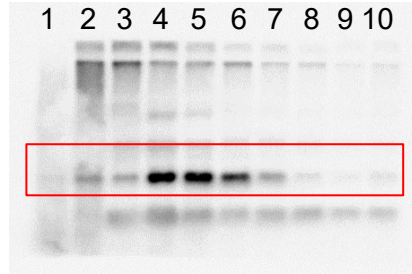
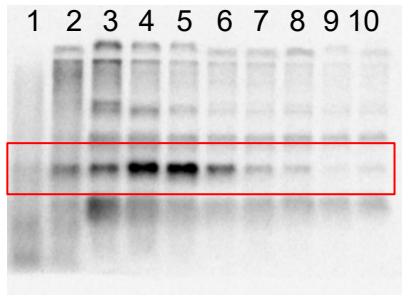
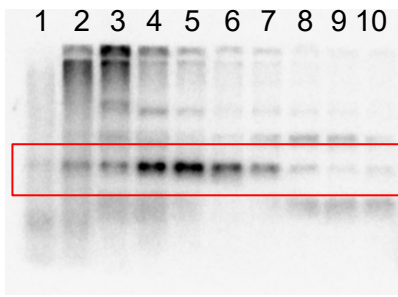
CP47 (re-blotted from D2 membrane (top))

**Figure 2**

**Figure 2a**

**Left -Puromycin**



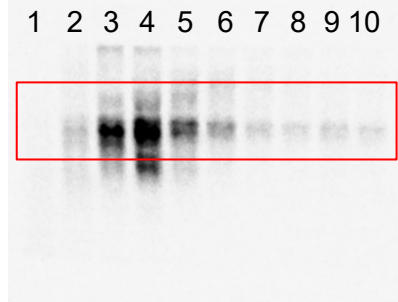
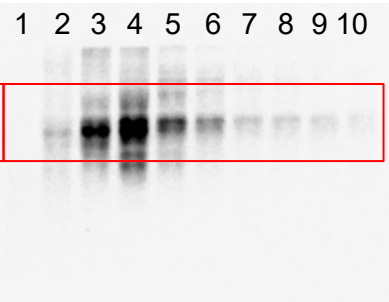
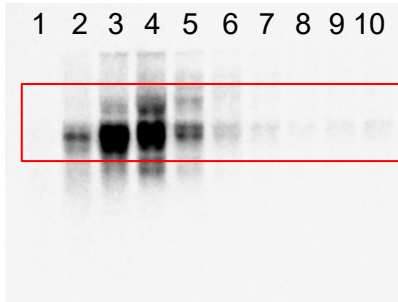


*psbEFLJ*

**Right +Puromycin**  
WT

*fpb1*

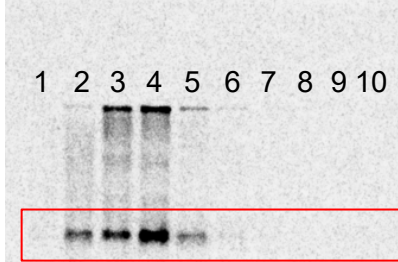
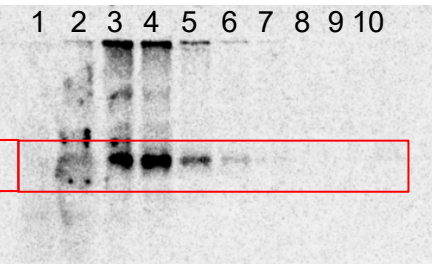
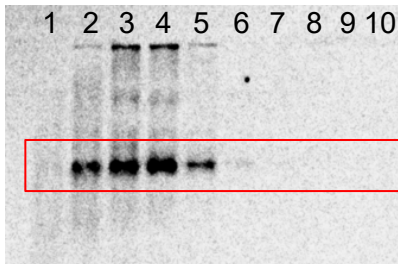
*pam68*



*psbB*  
*psbEFLJ*

WT

*fpb1*



*pam68*

**Figure 2b**

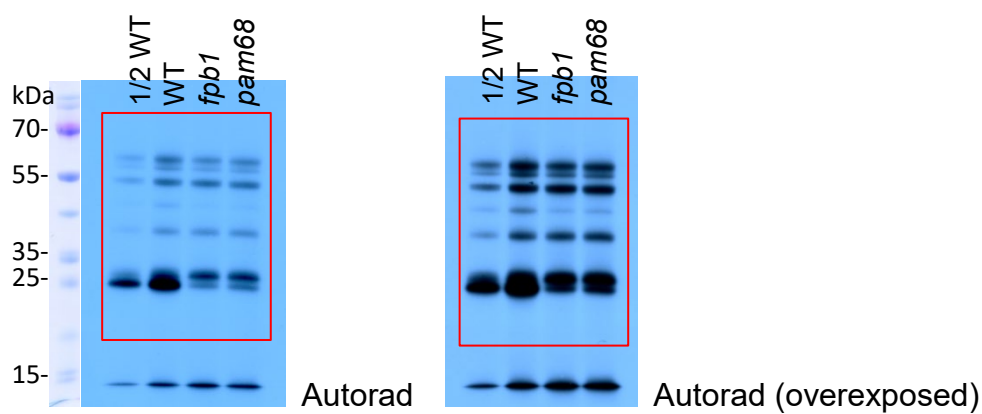


**Figure 2c**

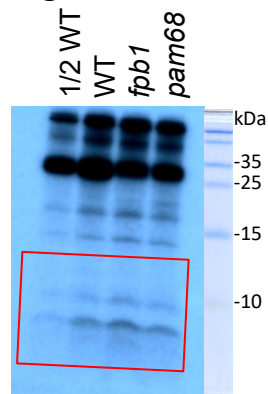


**Figure 2d**

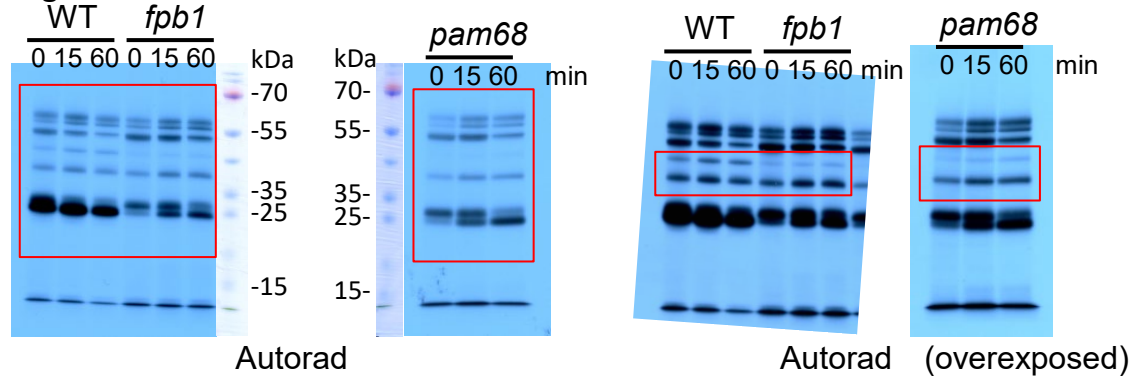


**Figure 2e**

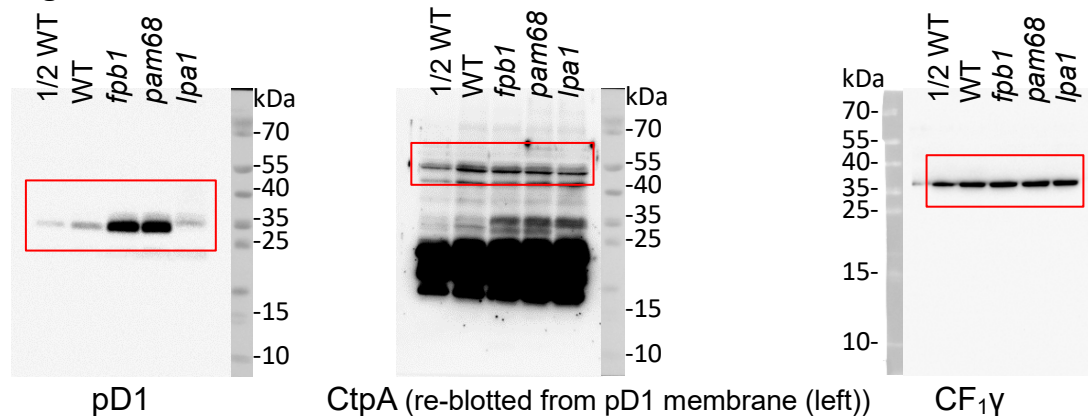
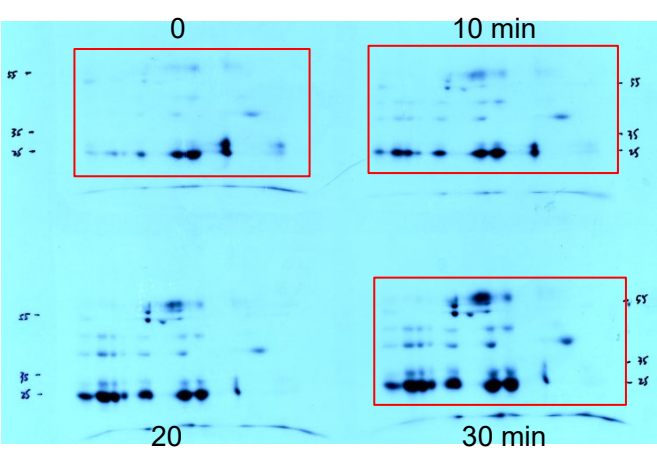
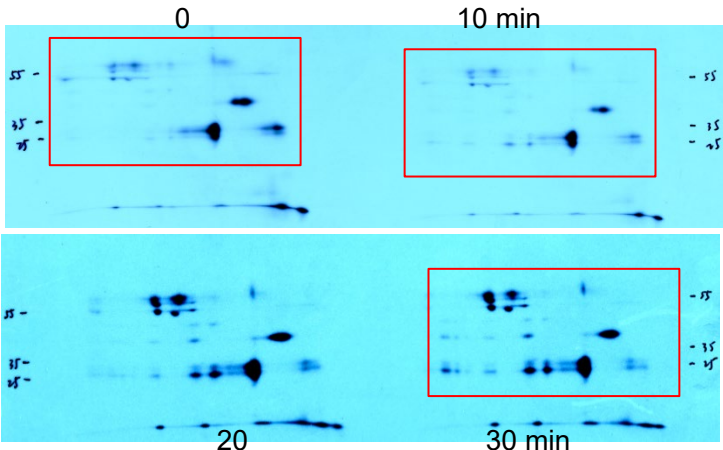


Figure 2f  
WT



*fpb1*



*pam68*

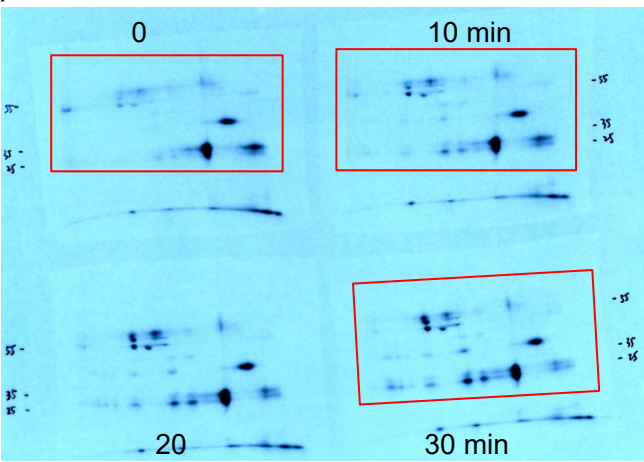


Figure 3  
Figure 3a

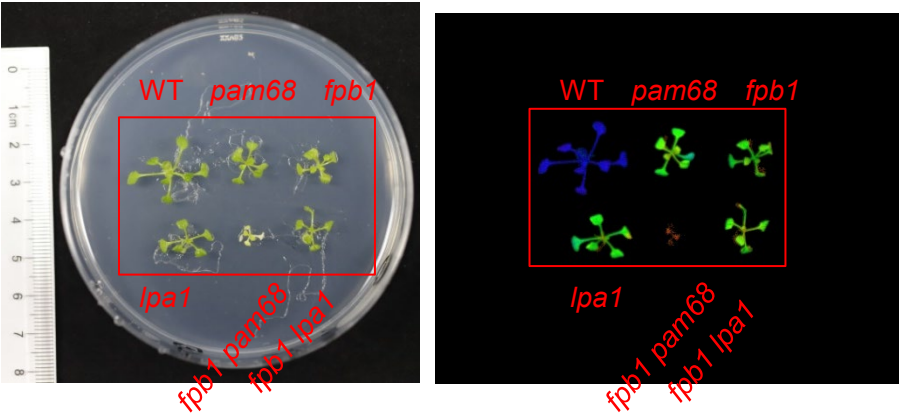


**Figure 3b**

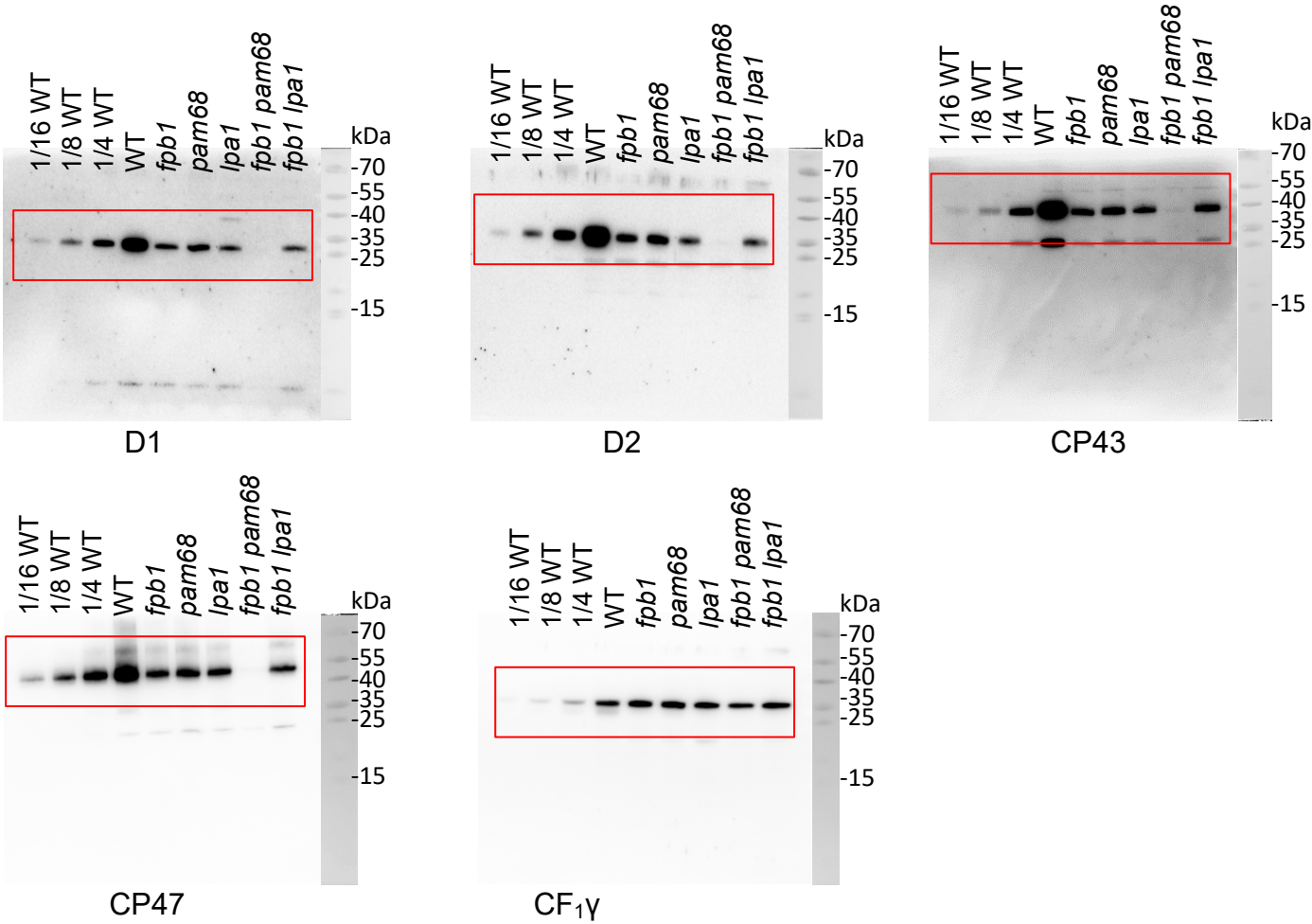
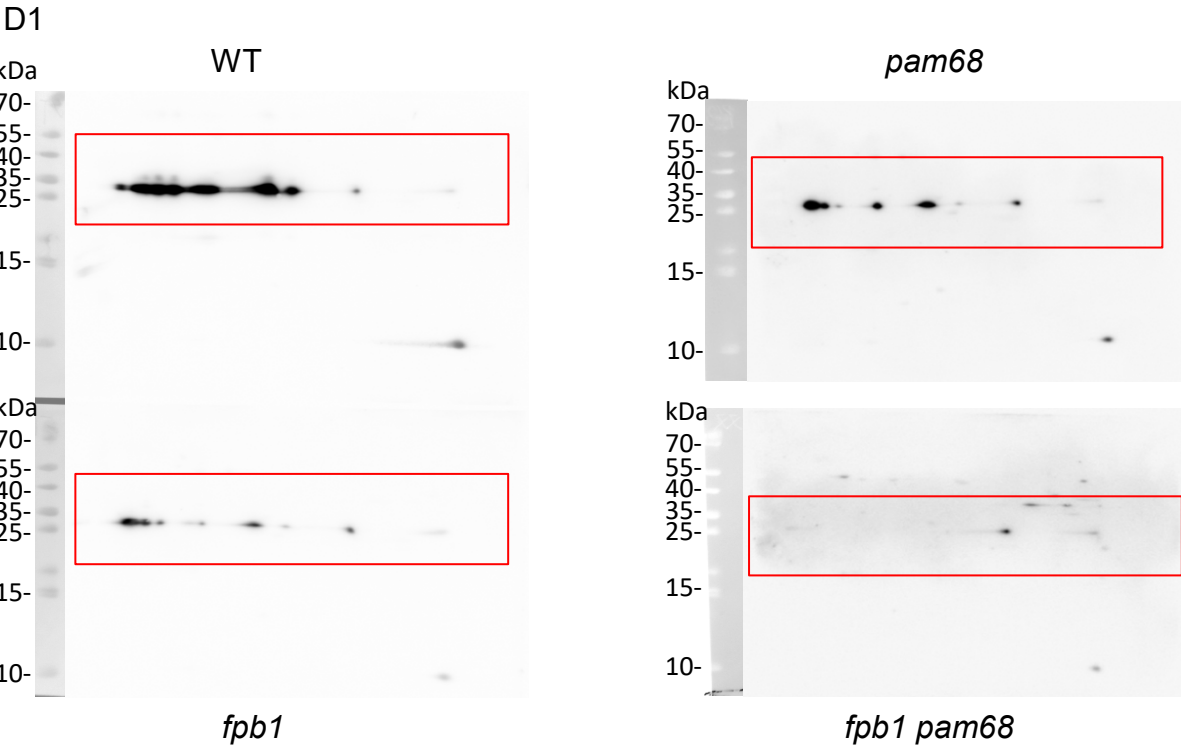
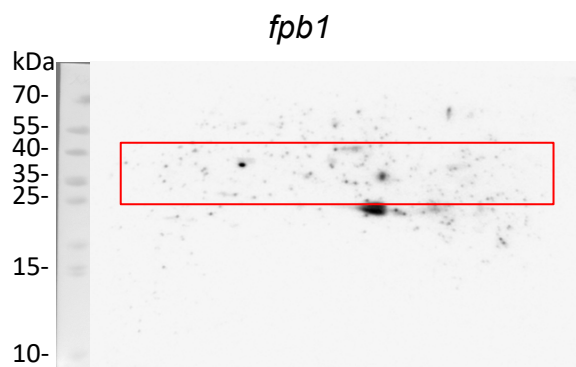
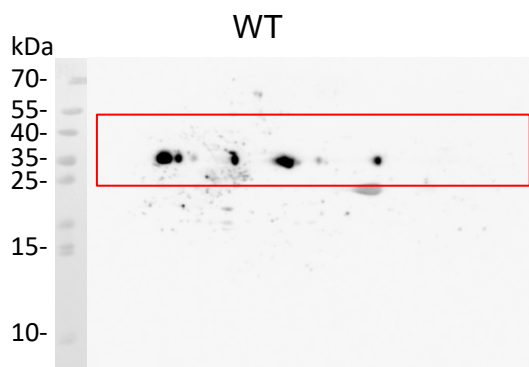
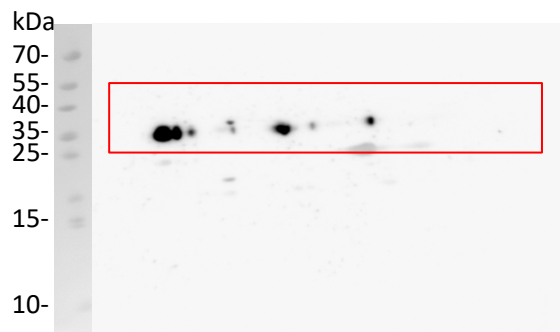
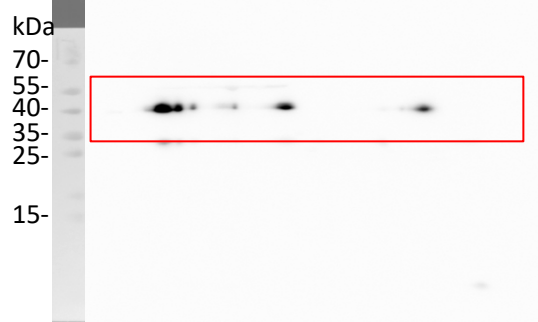
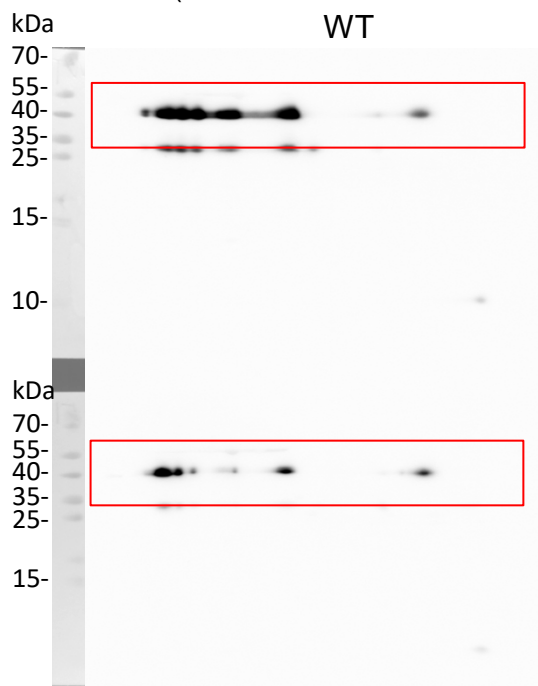


**Figure 3c**

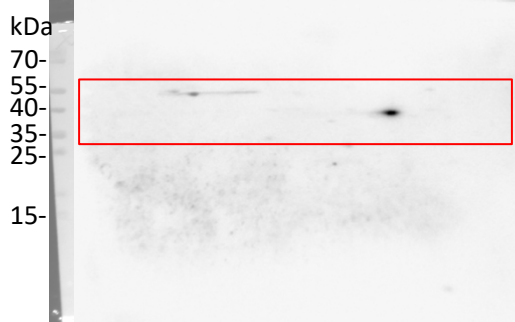
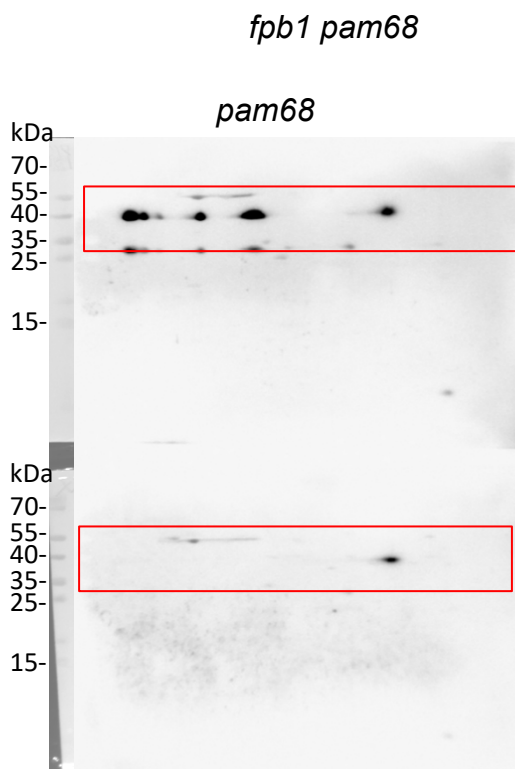




***pam68***  
CP43 (re-blotted from D1 membrane (top))



***fpb1***



***fpb1 pam68***

CP47 (re-blotted from D2 membrane (top))

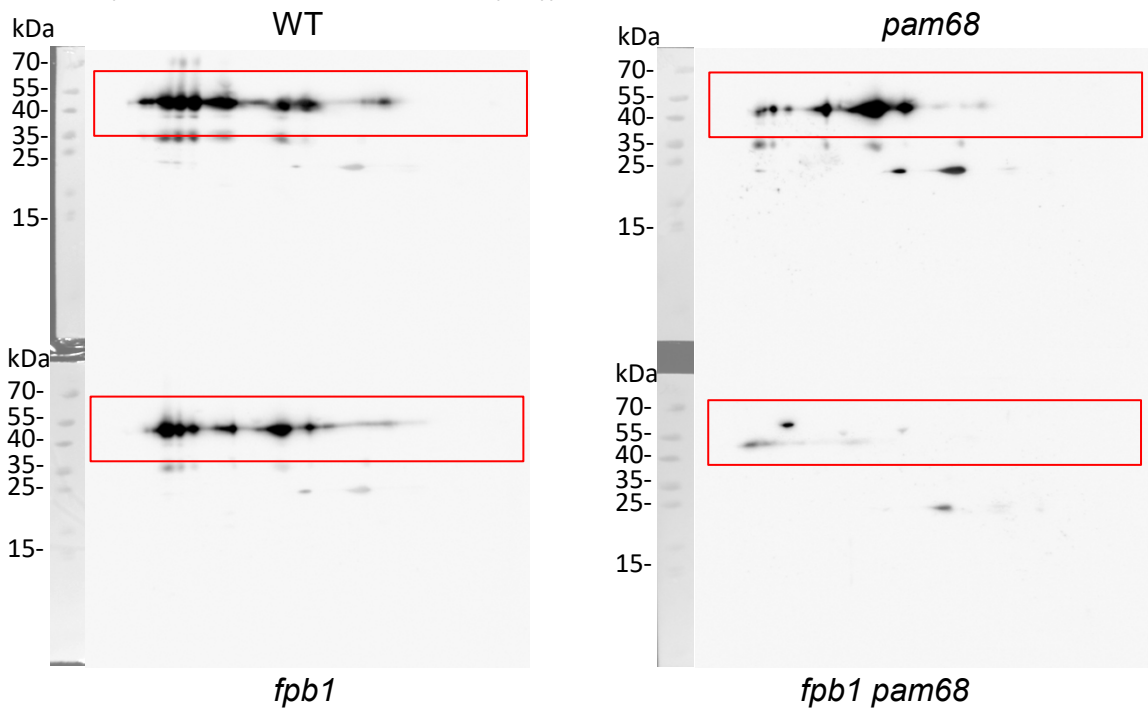


**Figure 4**

**Figure 4a**

### Sequences of FPB1 and its orthologs

>AT3G51510 *Arabidopsis thaliana*

MAASLTSLPTGFCLSHGDECCNRSPKSPFPGHHPLAGRRKGHLLHYERSTVRRLLVTAATEGSKKSKESEPSWANPDS  
DEPPPWARNEGRSSTSQESFEVPFFVYLLASAITAIAAIGSVFEYTSKNPVFGILESDSIFYTPVLGFFALTGIPTSVFLWFKS  
VEAANKAEQEQDKRDGFL

>Potri.001G455900.1 *Populus trichocarpa*

MAAATLLCWCNSDLIIHGSCSRLFVRNKMDSNQSTVKSRSYYAYQKQKKFFVCAATEGSAKSSKSEETIPSWAKPDSD  
EPPPWAKGEGKENSCKQNFVPPFFVYLLASAITAIAAIGSIFYVNQRPVFGVNPDSIFYAPLLGFFAFTGIPFSAFLWFKSV  
QAANKEAEEQDRRDGFF

>GRMZM2G117558\_T01 *Zea mays*

MAAAVAISTSVCTSSRRSTGCPNVRPQARPLLGMPSLRRLQTALAATGKTPGEAEEQVPAWAKPGADEPPPWEREGG  
AARGQEARQVPFYAYLLASTITAIAAIGSIFYTNQRPVFGIVGPDSALYAPLLGFFVFTGIPTSAFLWFKAVQTANREAEQD  
RRDGFL

>LOC\_Os05g41190.1 *Oryza sativa*

MAAAVSACSSRCLRLILGRPPRARLASVVEVVEKRRRGGLVAVAATEGSAKSSGEADEQVPSWARPGSDEPPPWAREGG  
GGGGQQEPGAVELPFFAYLLASAITAIAAIGSIFYANQRPVFGVVSPDSALYAPLLGFFVFTGIPTSGFLWFKAVQTANKEA  
EEQDRRDGFS

>69021 *Selaginella moellendorffii*

PEWAKPGSDVPPPWASGEKKQVSSEGFQDLPIYIVYLVASCLVAIAAVGSIFYFNKNPVFGVIQPDSPFYTPVLGFFSITGIP  
VSAFLWFRAIKLANKDAERQDKEDGY

>Pp3c12\_25230V3.1 *Physcomitrella patens*

MTFAAALAASLAGPHLSIPSFSSSRTKVRAQSSSSCALPLTSRRRDIQRQWRVQSQSDQAPGSSKTEDKPTENEPTPSWA  
KPGTEELPPWARNEAAAPVDSSGDLPPVYLIGSCLVAIAAVGSIFYFNQNPFGVVPDSPLWAPILGVFAITGFPSAGFL  
FYKAISLANKASEEADRADGFDP

>Cre16.g679300.t1.2 *Chlamydomonas reinhardtii*

MCVTIGRFSSGVSARSLQTQVRAQPEQKTPPTVPGSEDELPPWVRREKERELQAKDGVSGLPWGLCLLFSVFTAIAAVGS  
IFEVDRNAIFGVIQPDSPWLAPILLFFGVTGFPTAGYLFIKGVNGFNEEAERQDKLDGYL

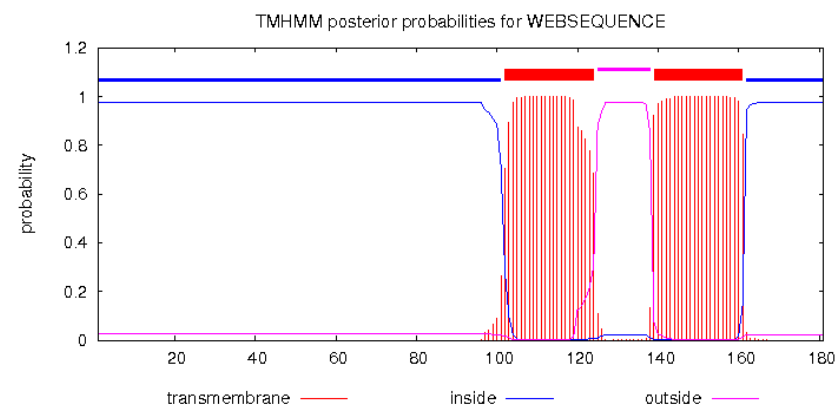
Prediction of transmembrane domains

AT3G51510

TMHMM result

# WEBSEQUENCE Length: 181  
# WEBSEQUENCE Number of predicted TMHs: 2  
# WEBSEQUENCE Exp number of AAs in TMHs: 45.07206  
# WEBSEQUENCE Exp number, first 60 AAs: 0  
# WEBSEQUENCE Total prob of N-in: 0.97536

|             |          |         |     |     |
|-------------|----------|---------|-----|-----|
| WEBSEQUENCE | TMHMM2.0 | inside  | 1   | 101 |
| WEBSEQUENCE | TMHMM2.0 | TMhelix | 102 | 124 |
| WEBSEQUENCE | TMHMM2.0 | outside | 125 | 138 |
| WEBSEQUENCE | TMHMM2.0 | TMhelix | 139 | 161 |
| WEBSEQUENCE | TMHMM2.0 | inside  | 162 | 181 |



Prediction of cleavage site

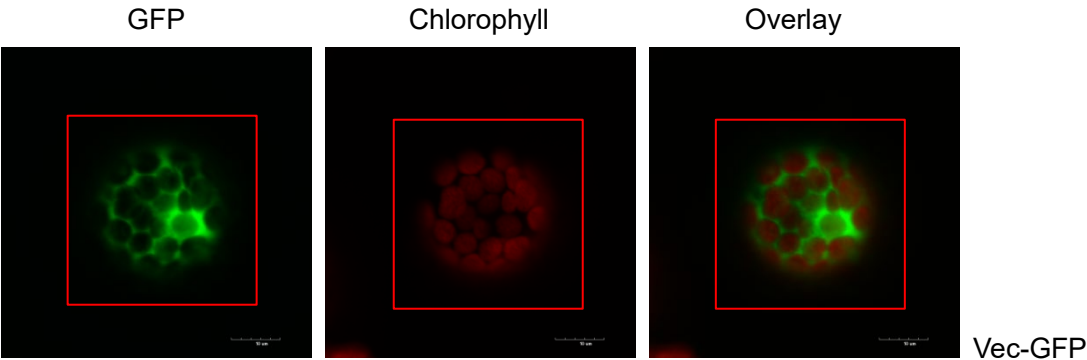
AT3G51510

chlorop v1.1 prediction results

Number of query sequences: 1

| Name     | Length | Score | cTP | CS-<br>score | cTP-<br>length |
|----------|--------|-------|-----|--------------|----------------|
| Sequence | 181    | 0.479 | -   | 2.999        | 36             |

Figure 4b



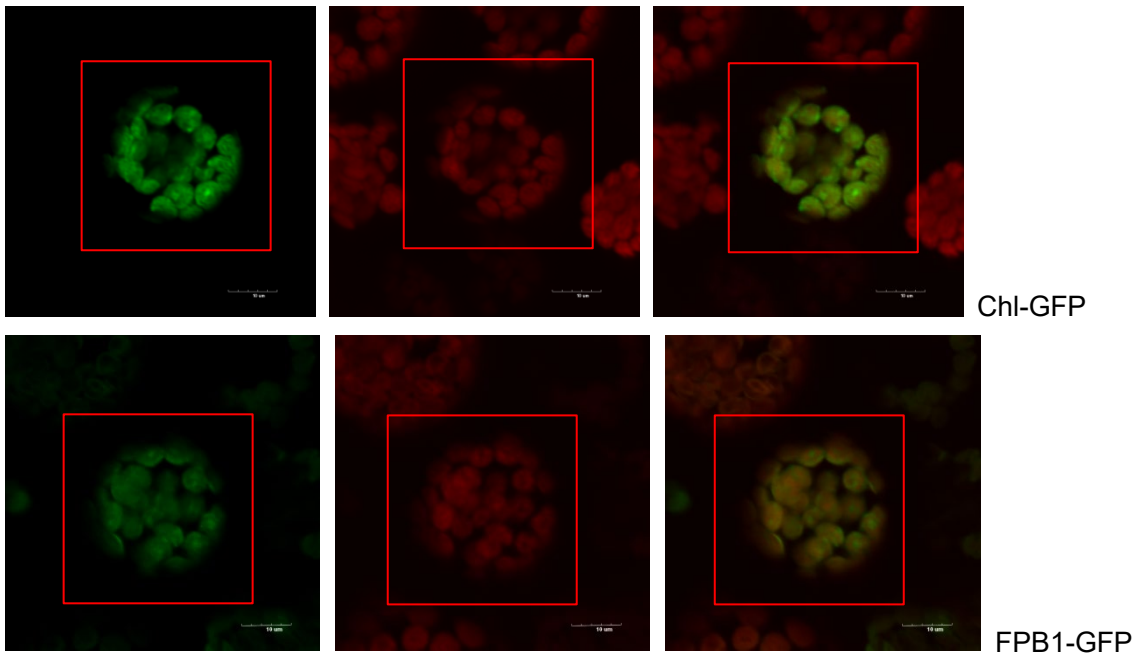


**Figure 4c**

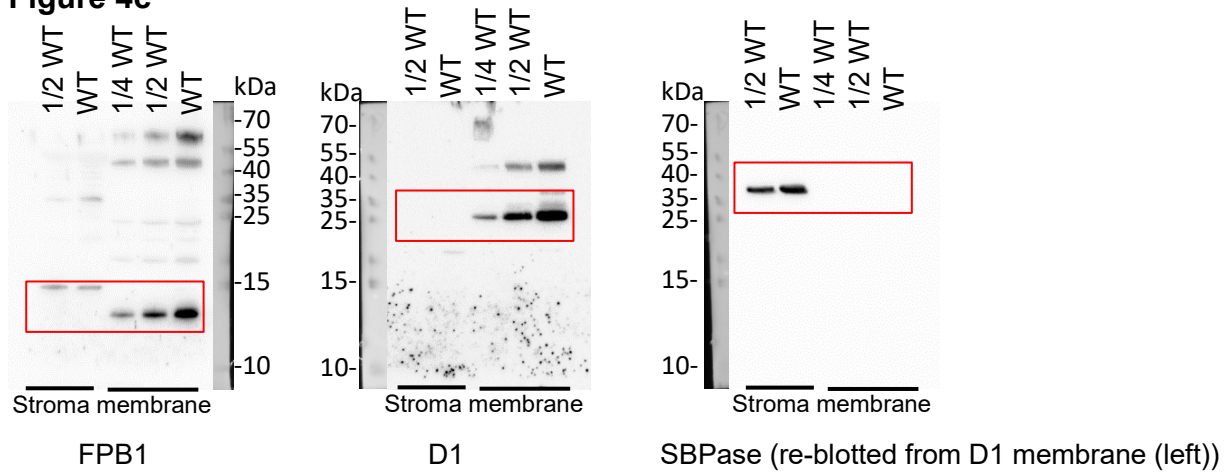


**Figure 4d**

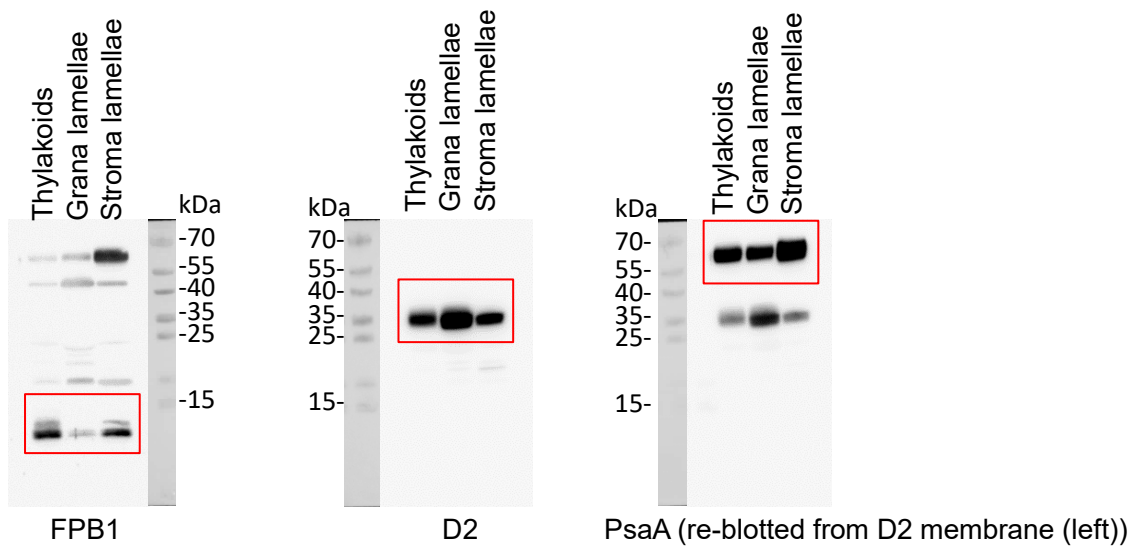


**Figure 4e**

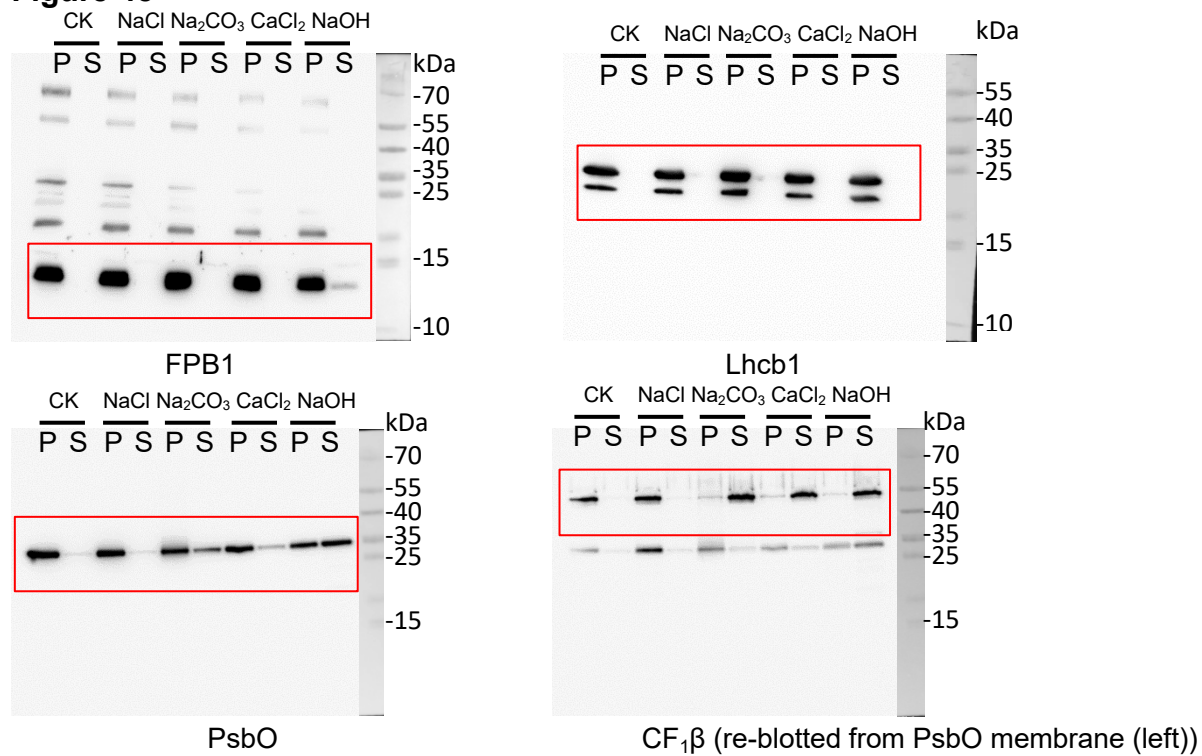


**Figure 4f**

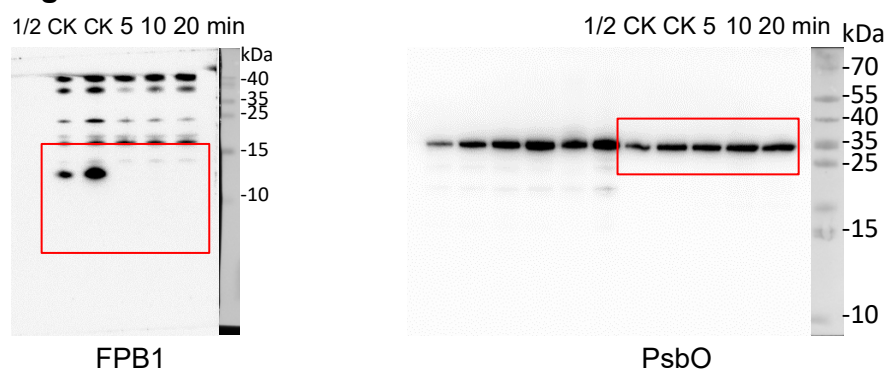
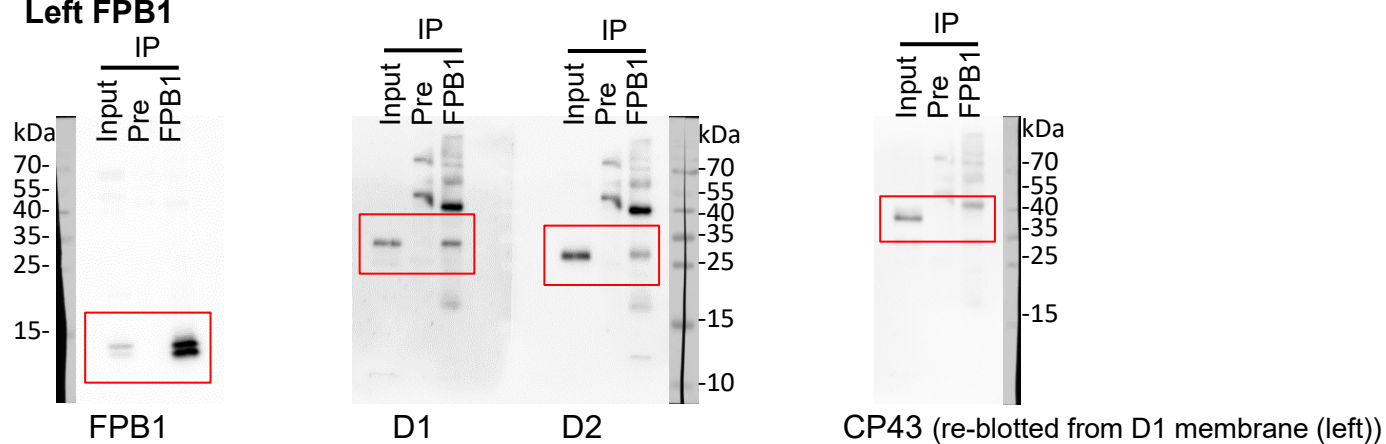
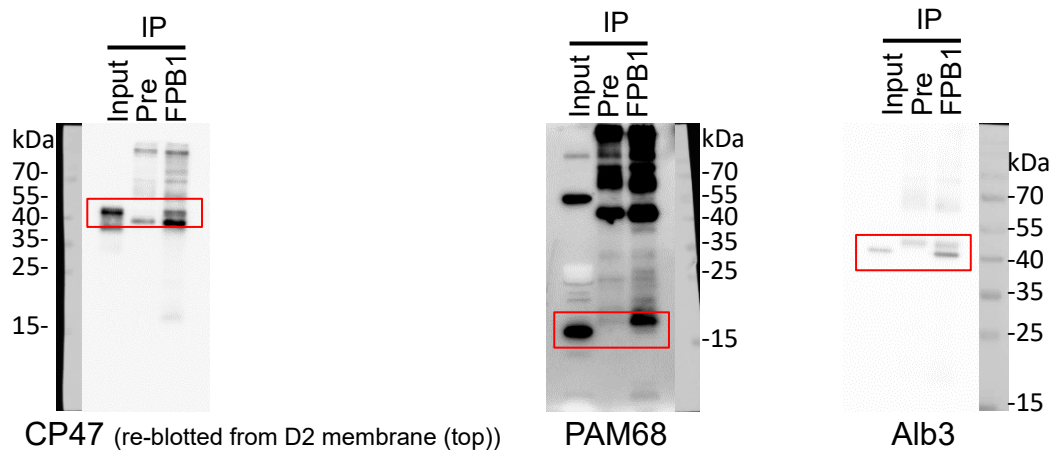


**Figure 5**

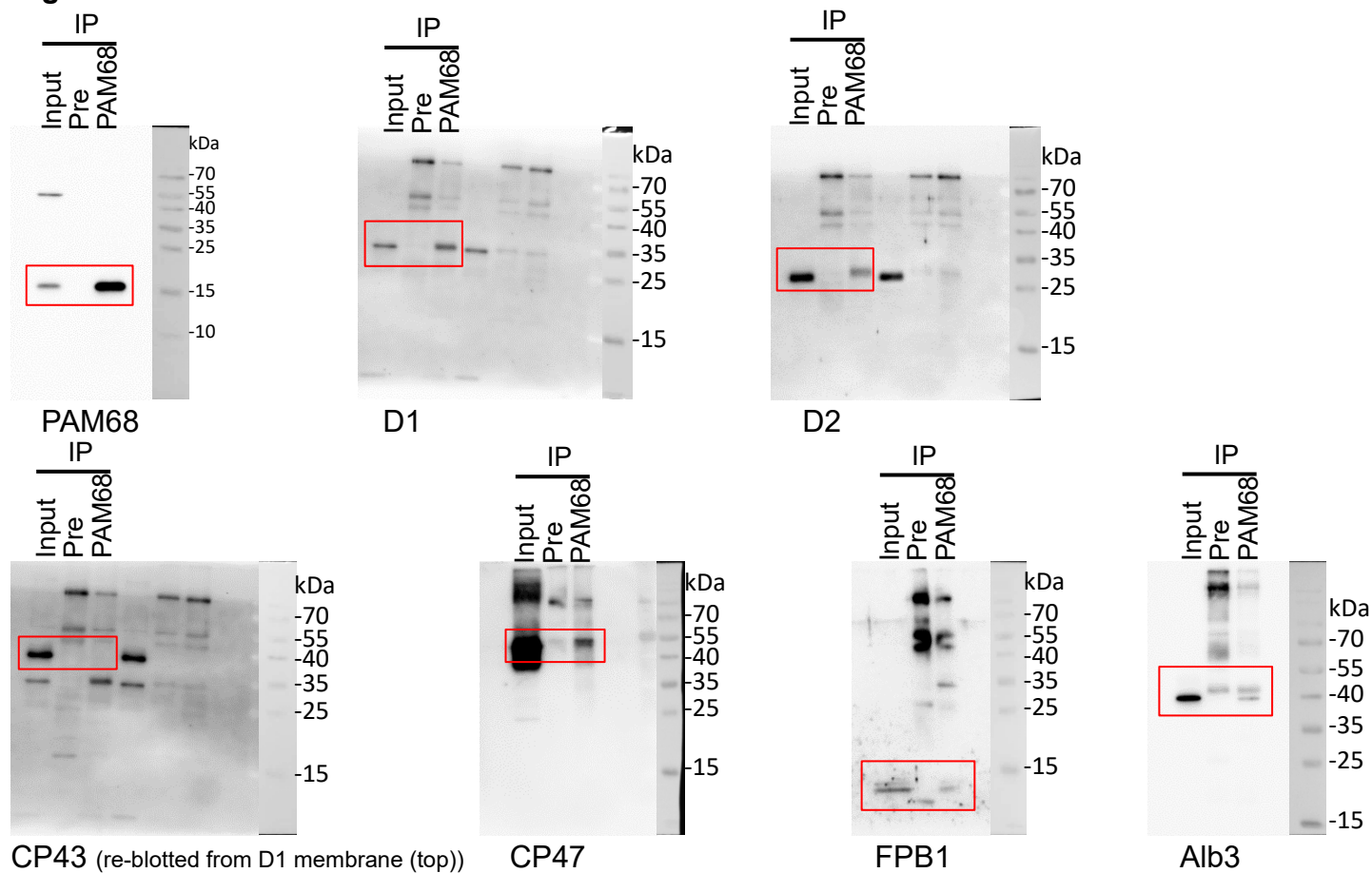
**Figure 5a**

**Left FPB1**



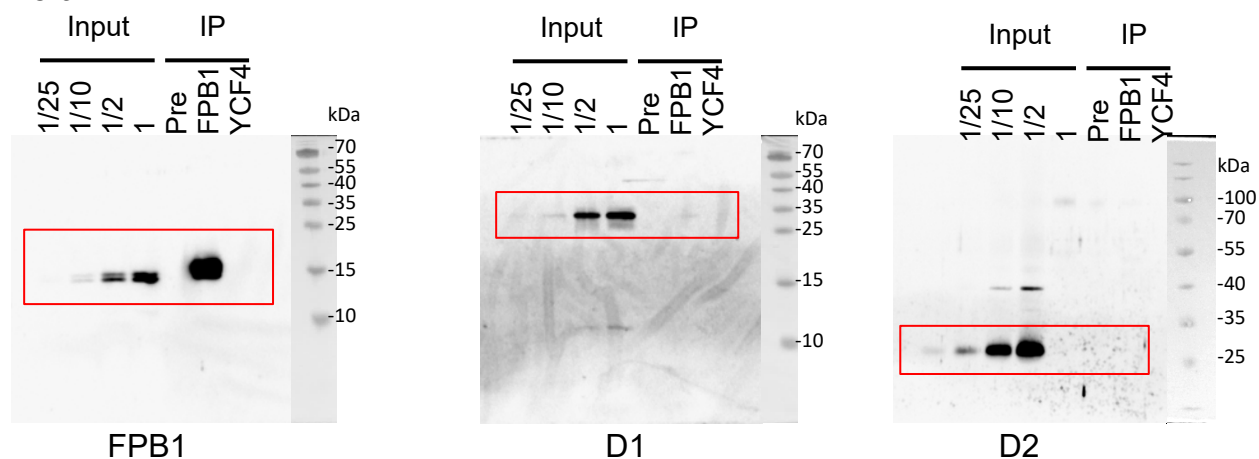


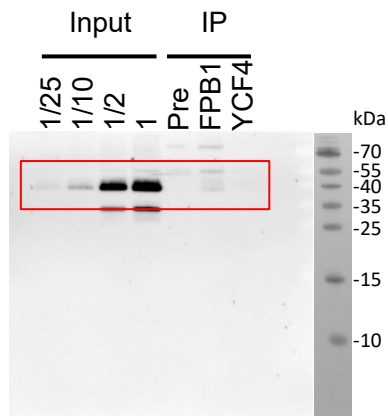
### Right PAM68



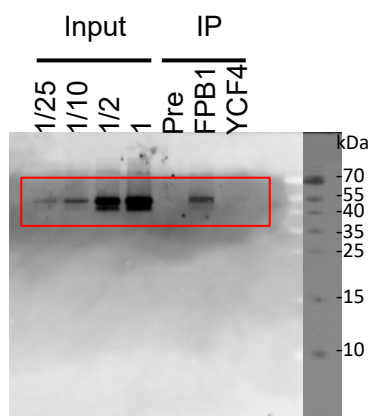
### Figure 5b

#### Left FPB1

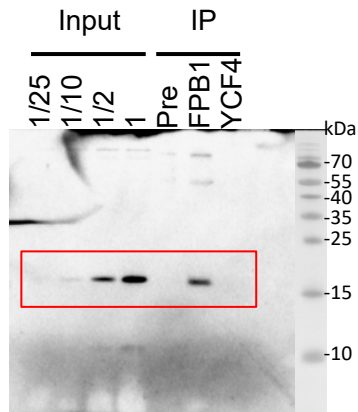




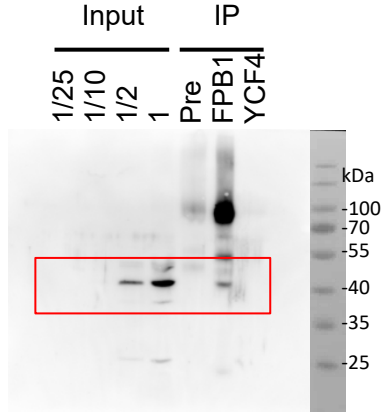
CP43 (re-blotted from D1 membrane (top))



CP47

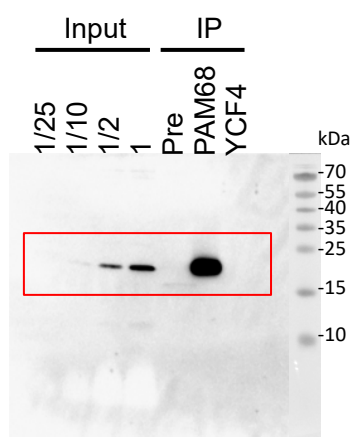


PAM68

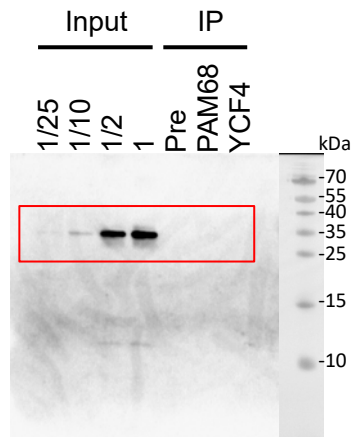


Alb3

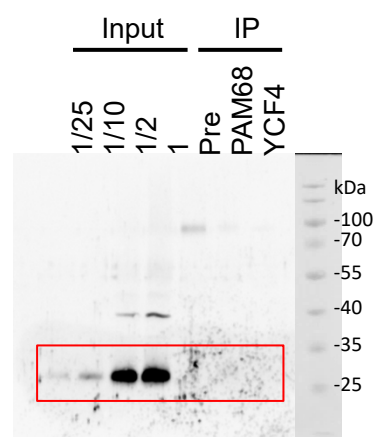
## Right PAM68



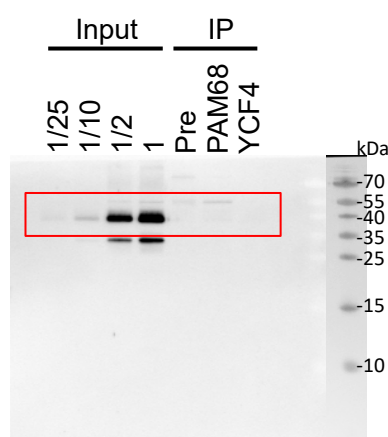
PAM68



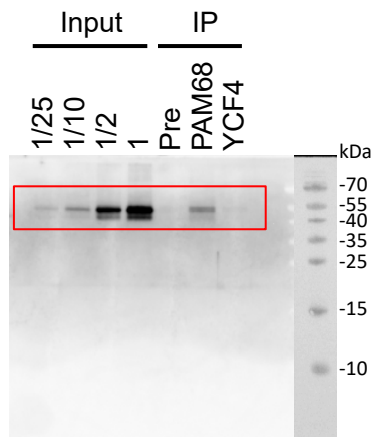
D1



D2



CP43 (re-blotted from D1 membrane (top))



CP47

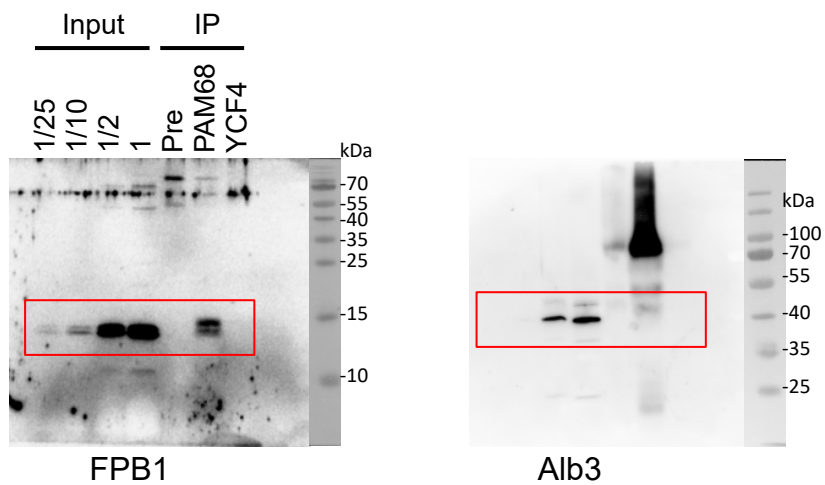


**Figure 5c**

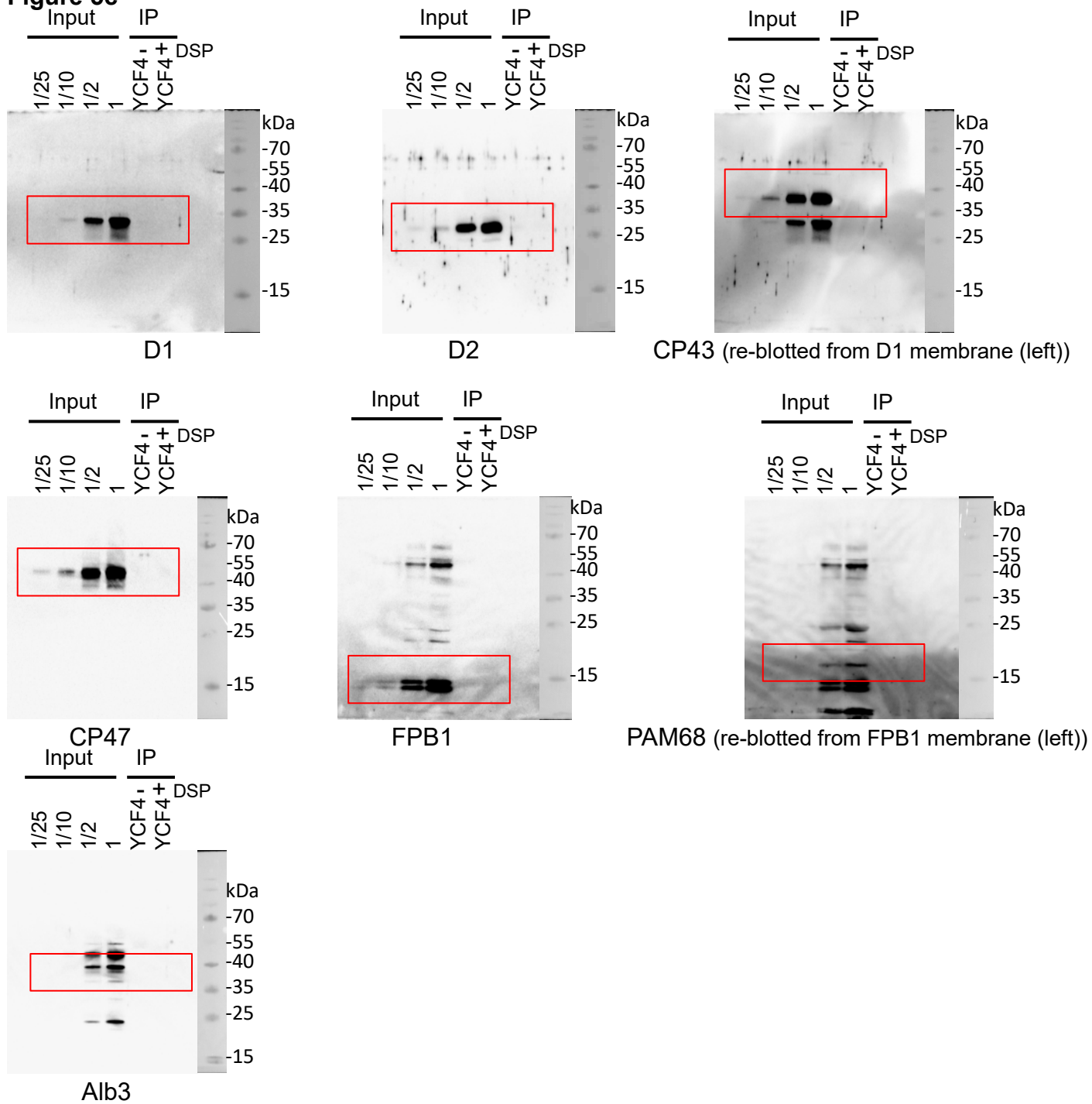


Figure 5d  
Cub-FPB1

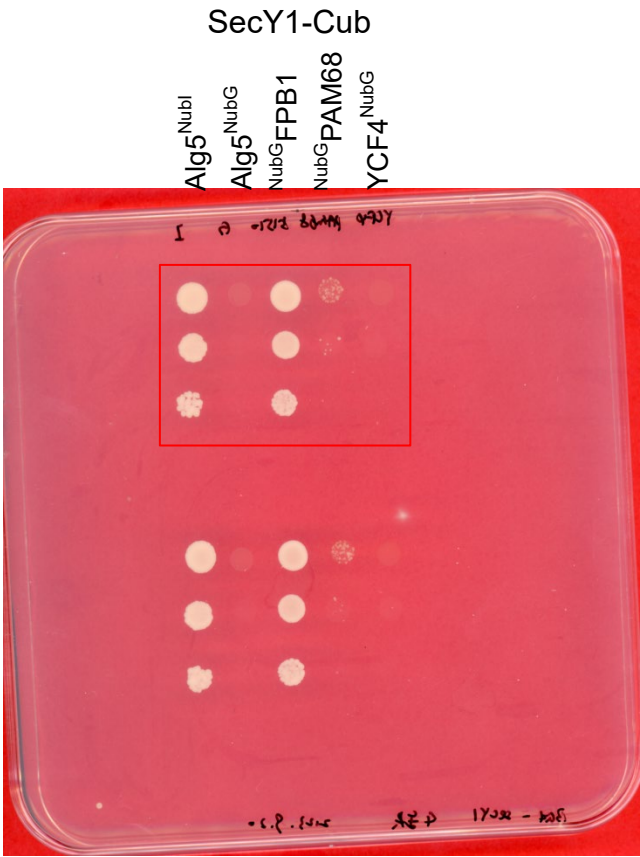
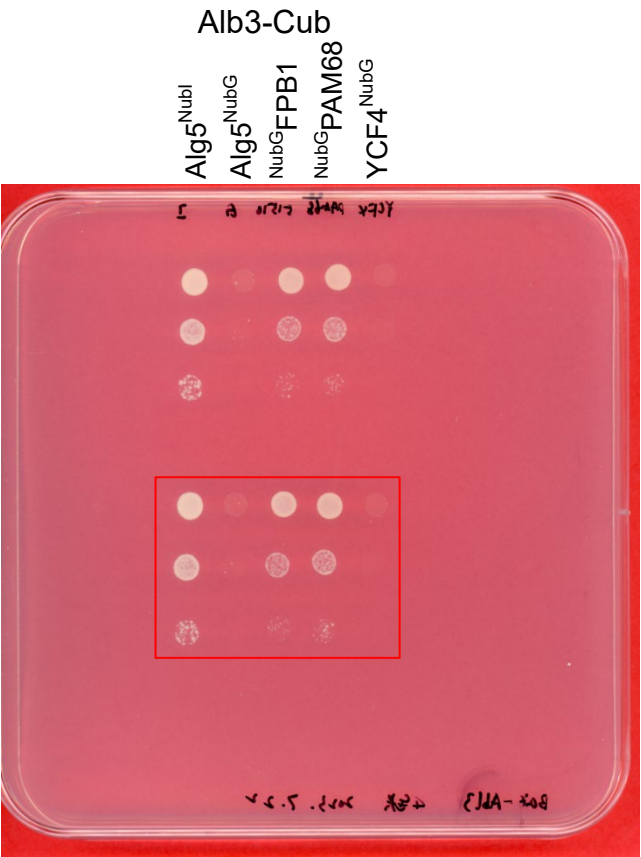
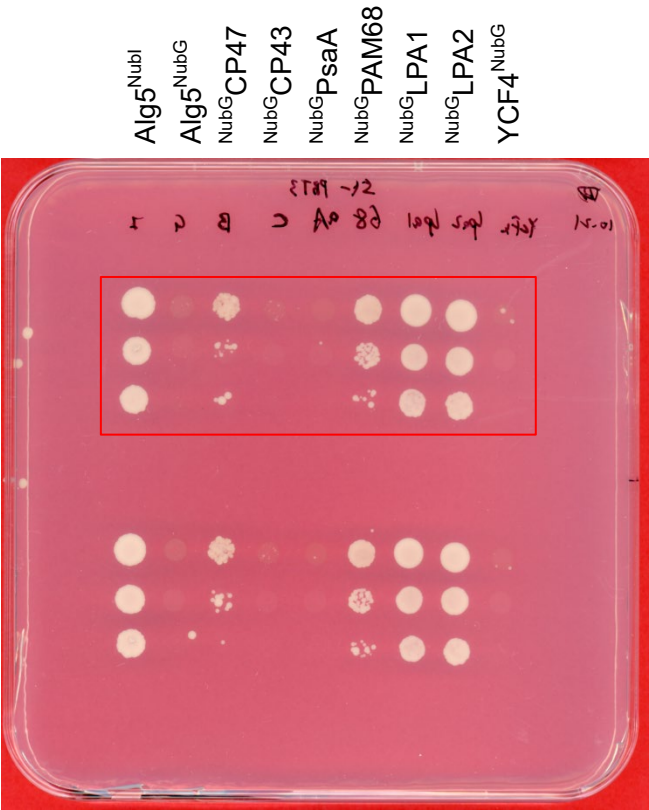


Figure S2

Figure S2a

Sequencing with SALK-LBa1 primer:

AGATTCGCTTTGAGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACAC  
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CAGGATTTTCGCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGGCCAG  
GCGGTGAAGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCCAGTACATT  
AAAAACGTCCGCAATGTGTTATTAAGTTGTCTAAGCGTCAATTTGTTTACACCACAATATAGCTGTT  
GCGTCATTATTAAGTTTAA//ACCTCCTTGGGCTAGAAACGAAGGTCGTTCTTCTACGTCCCAAGAG  
AGCTTTGAGGTTCCCTTTCTTTGTTTATCTGCTAGCTTCCGCGATTACTGCCATTGCTGCTGTATGC  
TTCTTCTTCTCTCTCTTTCACTCCTTTTGTTGTTTGCATTGCTGATTCTCATATCAAAGATGTTATCT  
TAATTATGCATCGTTTGGTCACTGTAGATTGGTTCTGTTTTTCGAGTACACAAGCAAGAATCCAGTTT  
TCGGGATCTTGGAATCTGACAGCATCTTTTATACTCCTGTGCTTGGATTCTTTGCTCTTACTGGAAT  
CCCCCACTTCTGA

Blast:

>AT3G51510.1 | Symbols: no symbol available | no full name available | chr3:19108990-19110372

FORWARD LENGTH=1383

Length=1383

Score = 581 bits (643), Expect = 2e-164

Identities = 325/326 (99%), Gaps = 1/326 (0%)

Strand=Plus/Plus

|       |     |                                                               |     |
|-------|-----|---------------------------------------------------------------|-----|
| Query | 347 | ACCTCCTTGGGCTAGAAACGAAGGTCGTTCTTCTACGTCCCAAGAGAGCTTTGAGGTTCC  | 406 |
|       |     |                                                               |     |
| Sbjct | 374 | ACCTCCTTGGGCTAGAAACGAAGGTCGTTCTTCTACGTCCCAAGAGAGCTTTGAGGTTCC  | 433 |
| Query | 407 | TTTCTTTGTTTATCTGCTAGCTTCCGCGATTACTGCCATTGCTGCTGTATGCTTCTTCTT  | 466 |
|       |     |                                                               |     |
| Sbjct | 434 | TTTCTTTGTTTATCTGCTAGCTTCCGCGATTACTGCCATTGCTGCTGTATGCTTCTTCTT  | 493 |
| Query | 467 | CTCTCTCTTCACTCCTTTTGTTGTTTGCATTGCTGATTCTCATATCAAAGATGTTATCT   | 526 |
|       |     |                                                               |     |
| Sbjct | 494 | CTCTCTCTTCACTCCTTTTGTTGTTTGCATTGCTGATTCTCATATCAAAGATGTTATCT   | 553 |
| Query | 527 | TAATTATGCATCGTTTGGTCACTGTAGATTGGTTCTGTTTTTCGAGTACACAAGCAAGAAT | 586 |
|       |     |                                                               |     |
| Sbjct | 554 | TAATTATGCATCGTTTGGTCACTGTAGATTGGTTCTGTTTTTCGAGTACACAAGCAAGAAT | 613 |
| Query | 587 | CCAGTTTTCGGGATCTTGGAATCTGACAGCATCTTTTATACTCCTGTGCTTGGATTCTTT  | 646 |
|       |     |                                                               |     |
| Sbjct | 614 | CCAGTTTTCGGGATCTTGGAATCTGACAGCATCTTTTATACTCCTGTGCTTGGATTCTTT  | 673 |
| Query | 647 | GCTCTTACTGGAATCCCCACTTCTG                                     | 672 |
|       |     |                                                               |     |
| Sbjct | 674 | GCTCTTACTGGAAT-CCCCACTTCTG                                    | 698 |

**Figure S2b**

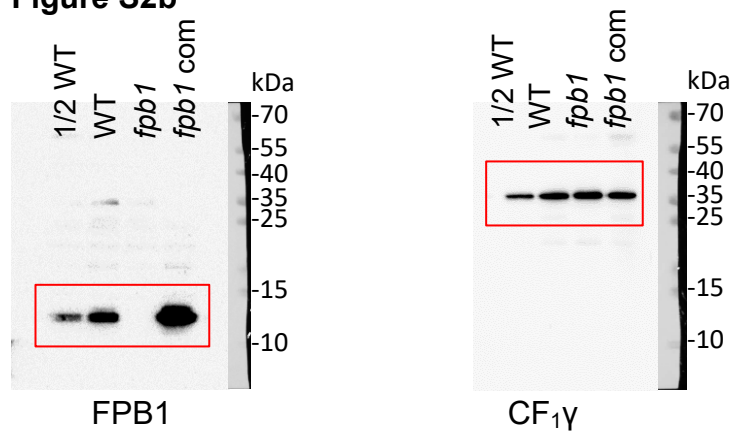
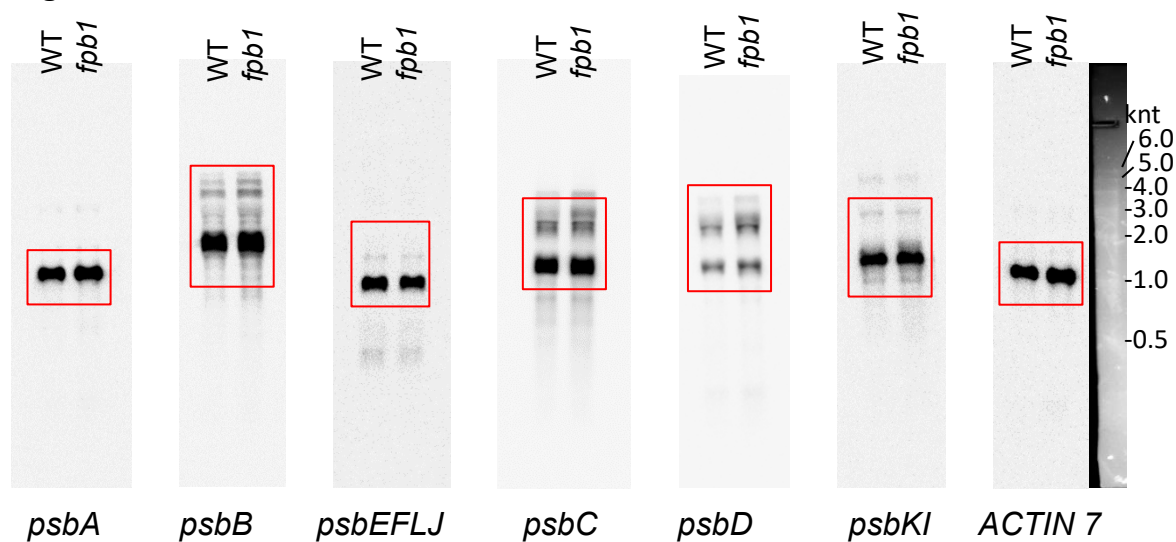


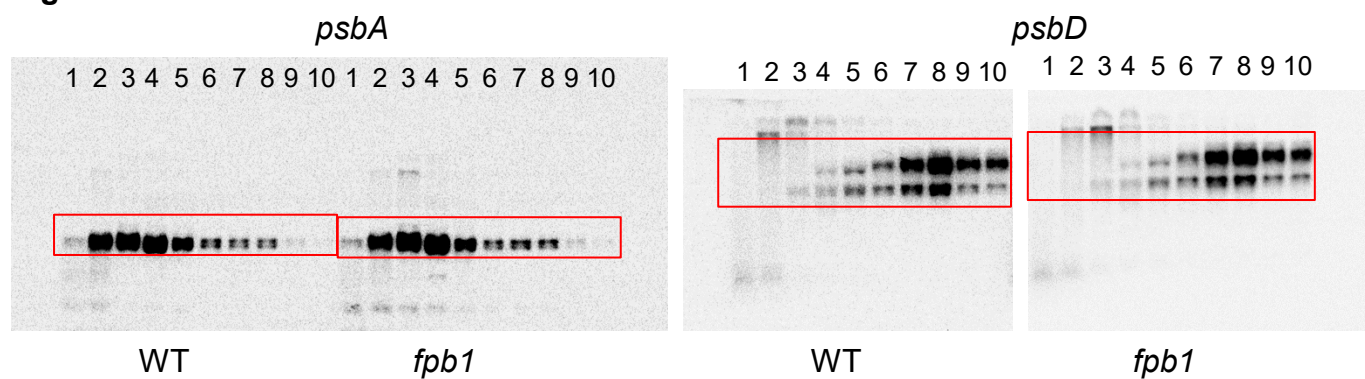
**Figure S4**

**Figure S4a**



Staining

**Figure S4b**



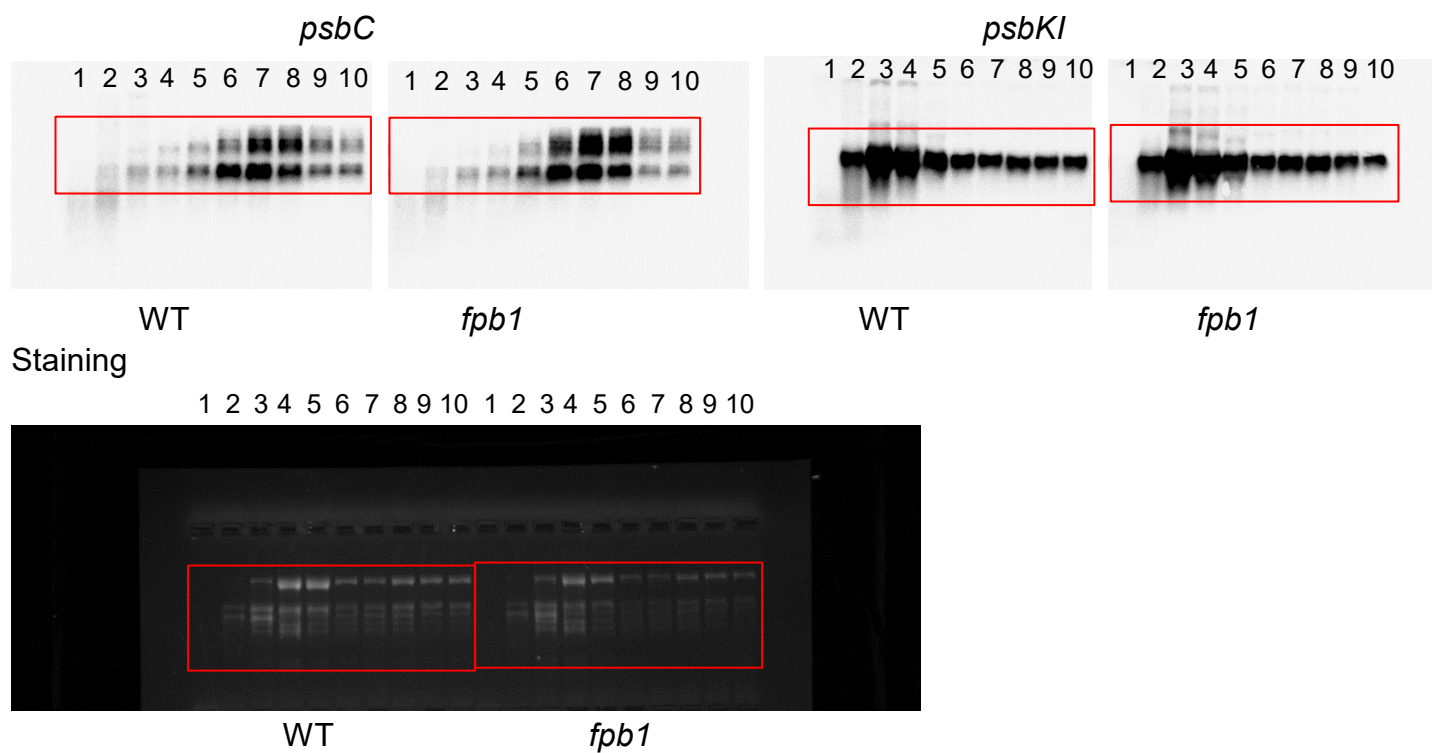
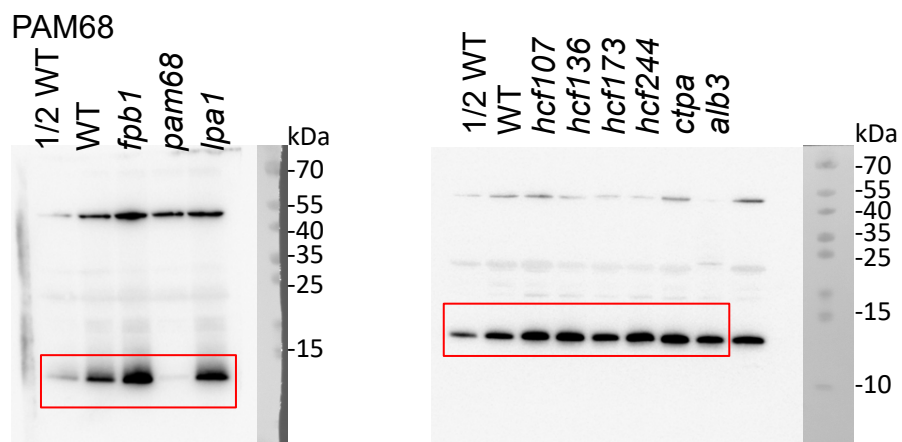
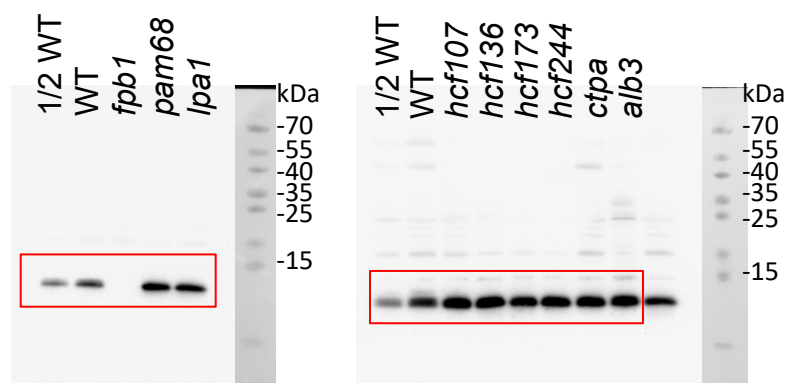
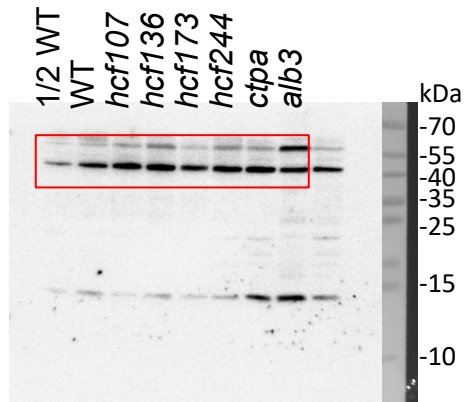
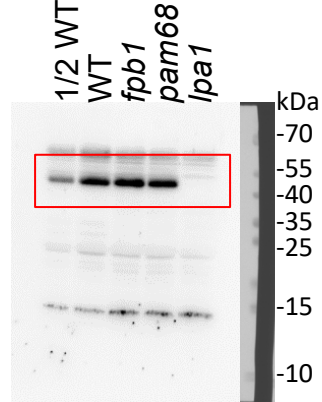


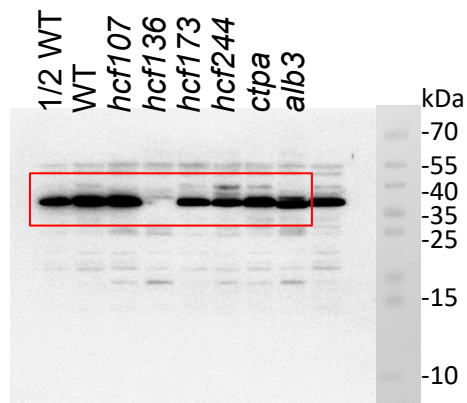
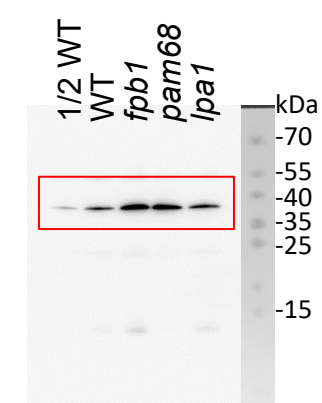
**Figure S5**  
**Figure S5a**  
**FPB1**



# LPA1



# HCF136



# HCF244

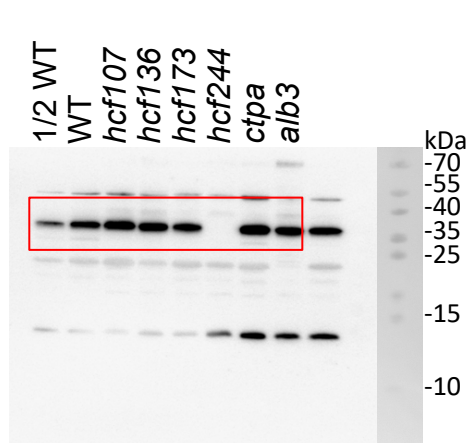
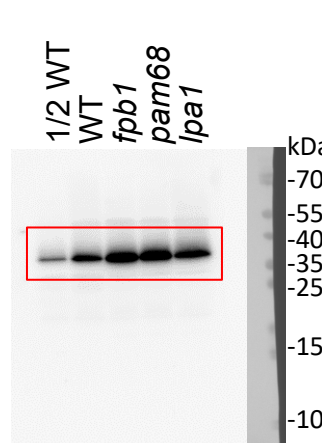
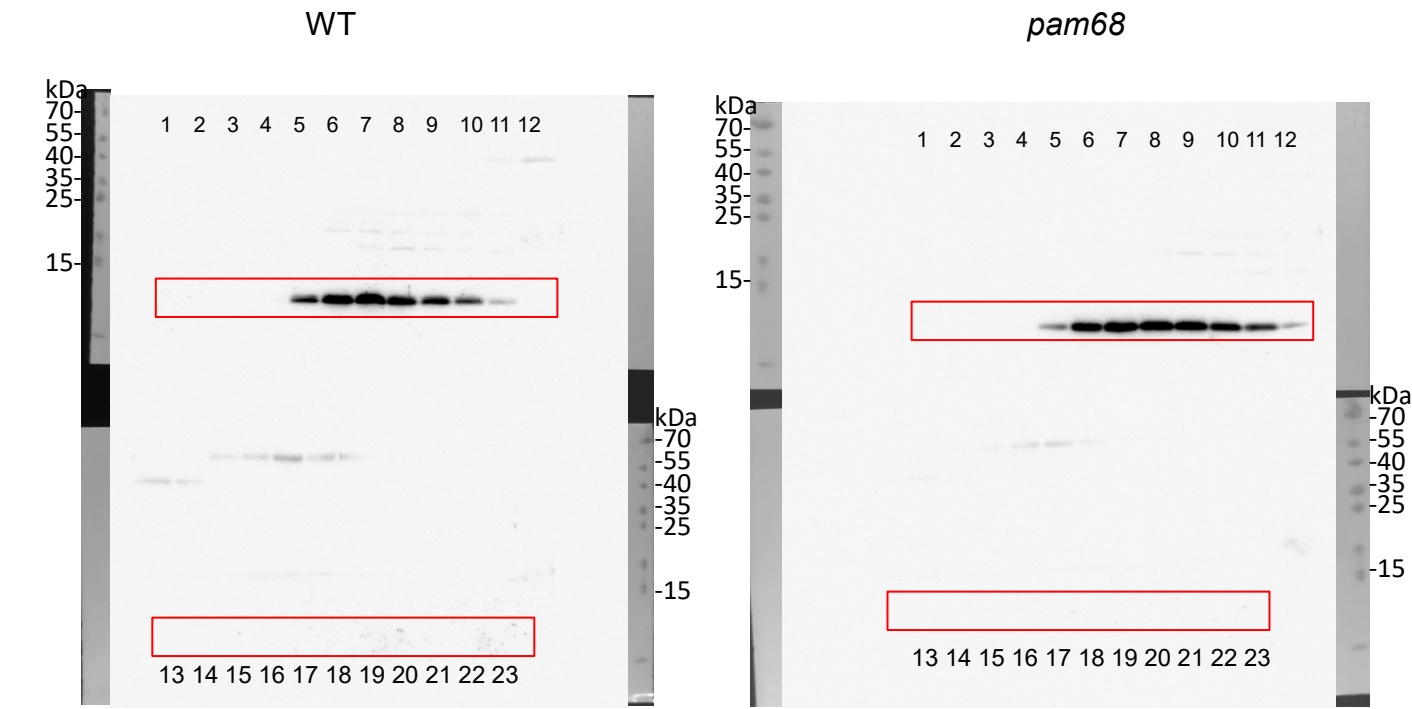
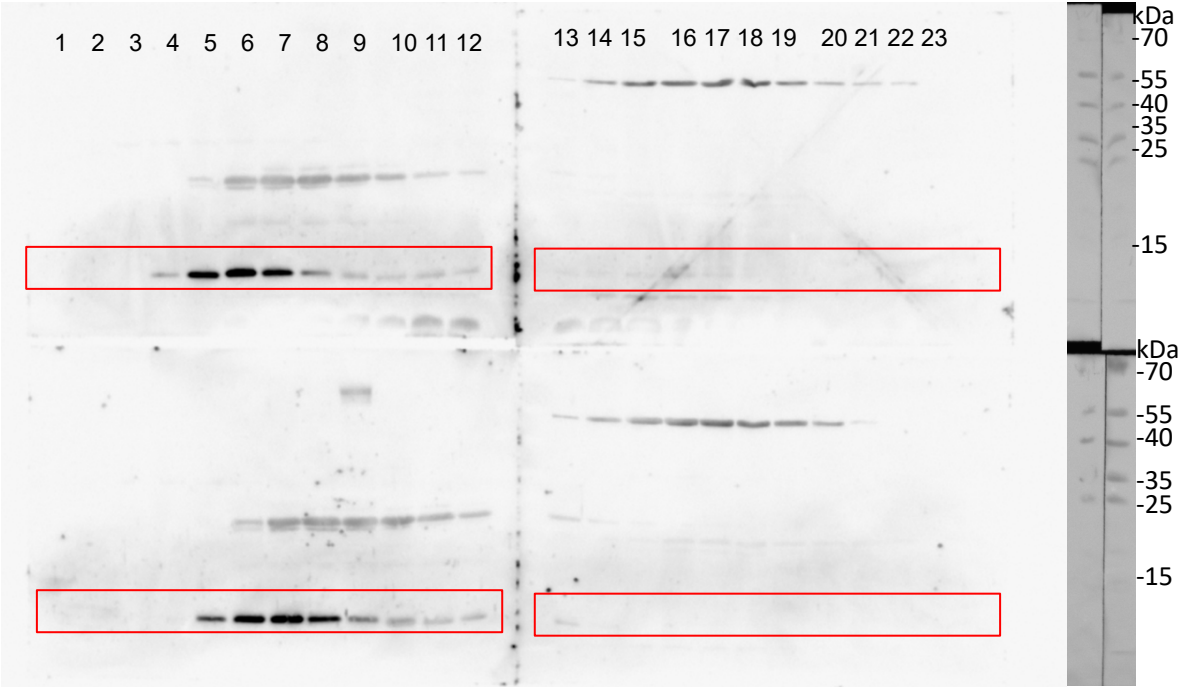


**Figure S5b**  
**FPB1**



PAM68

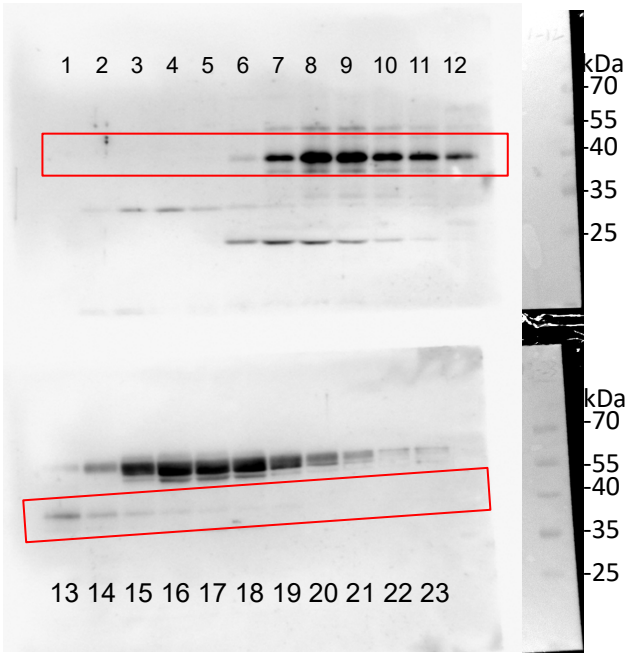
WT



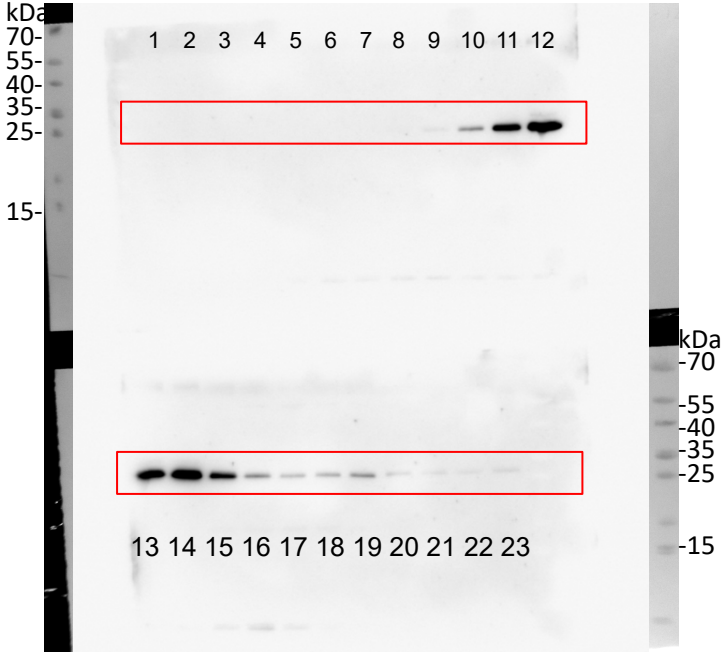
*fpb1*

WT

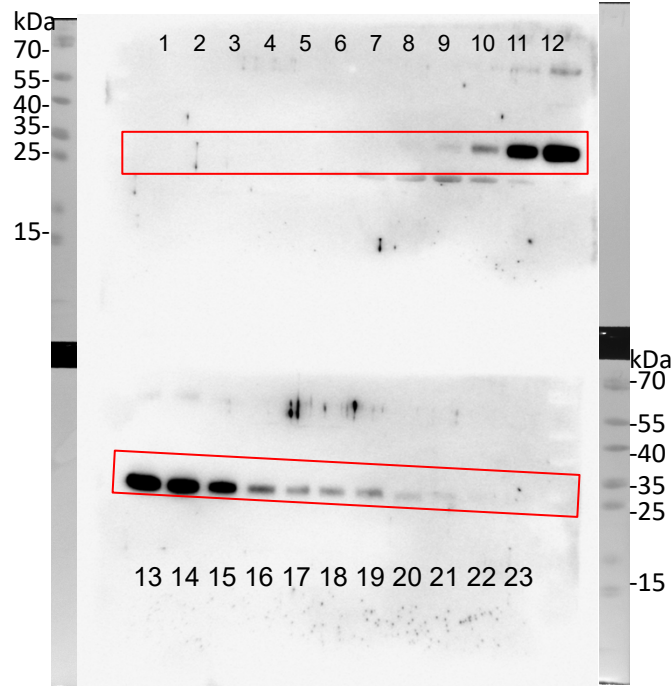
Alb3



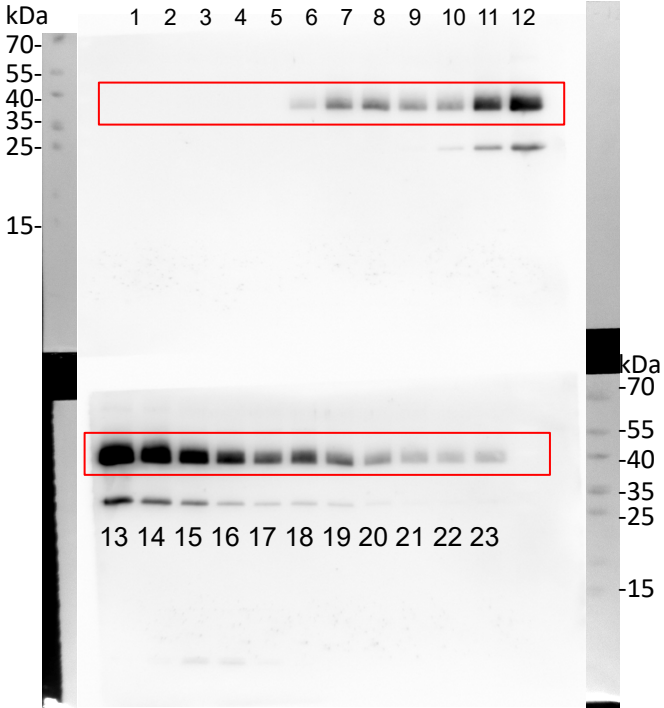
D1



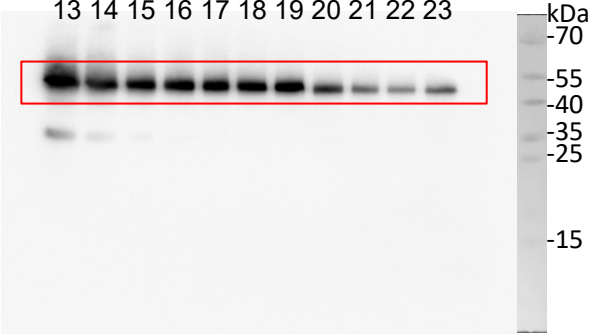
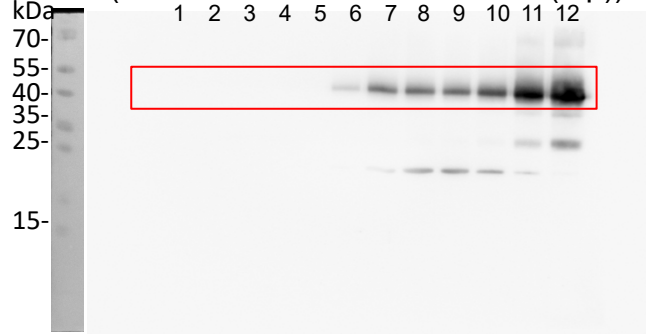
D2



CP43 (re-blotted from D1 membrane (top))



CP47 (re-blotted from D2 membrane (top))



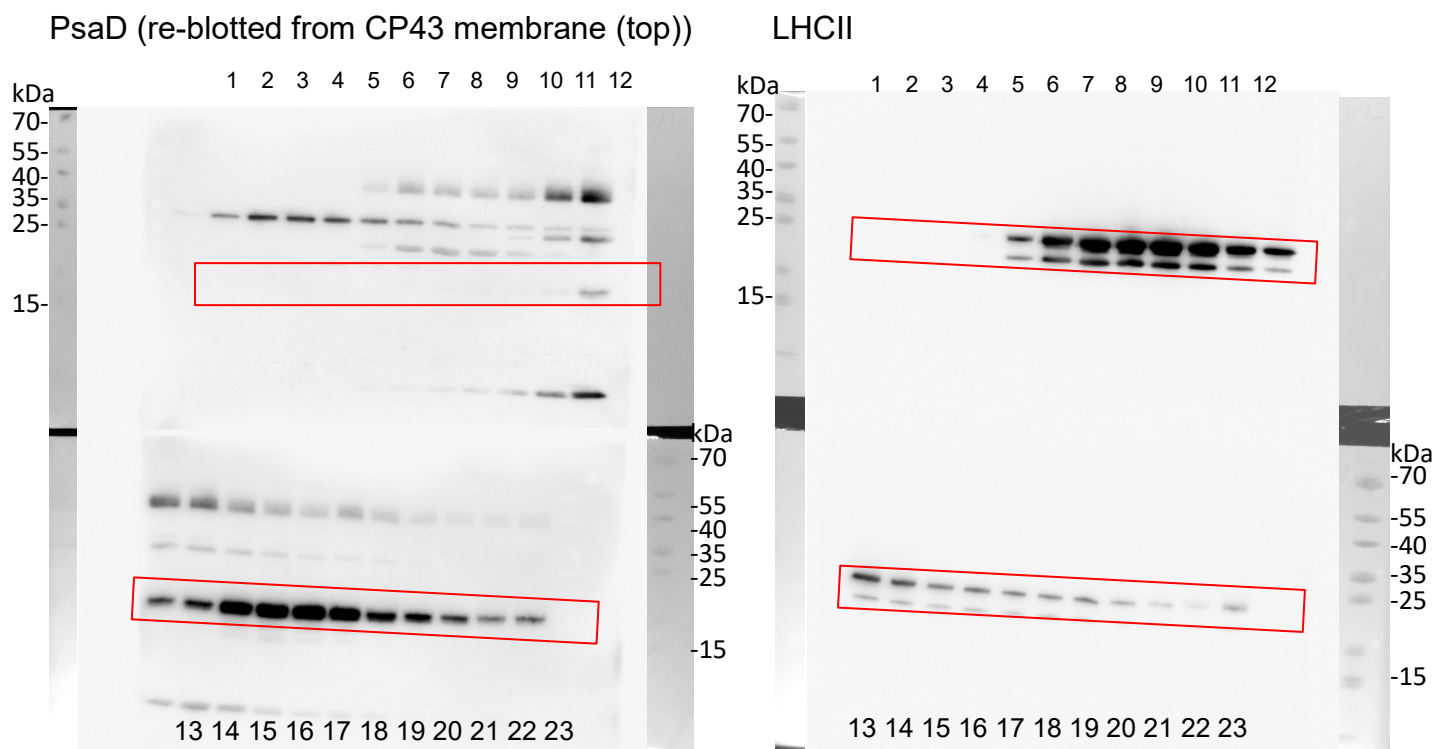


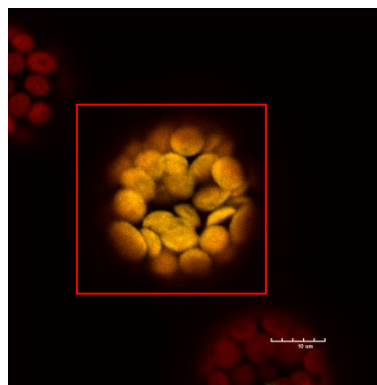
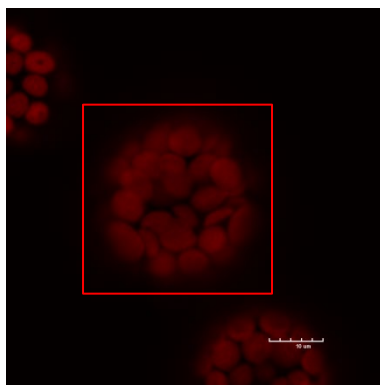
**Figure S6a**

**Left**

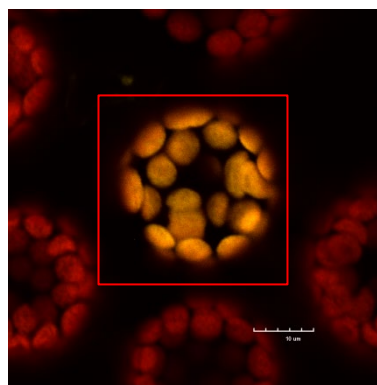
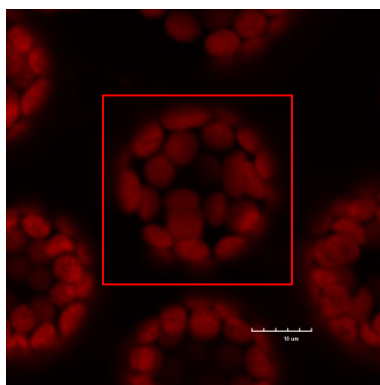
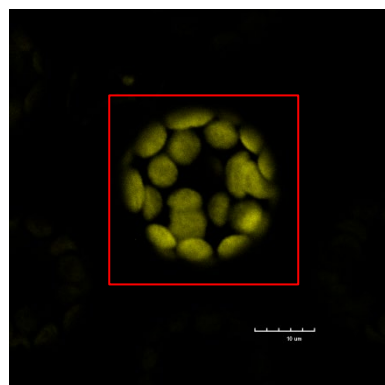
YFP  
FPB1-YFP<sup>N</sup>+PAM68-YFP<sup>C</sup>

Chl.

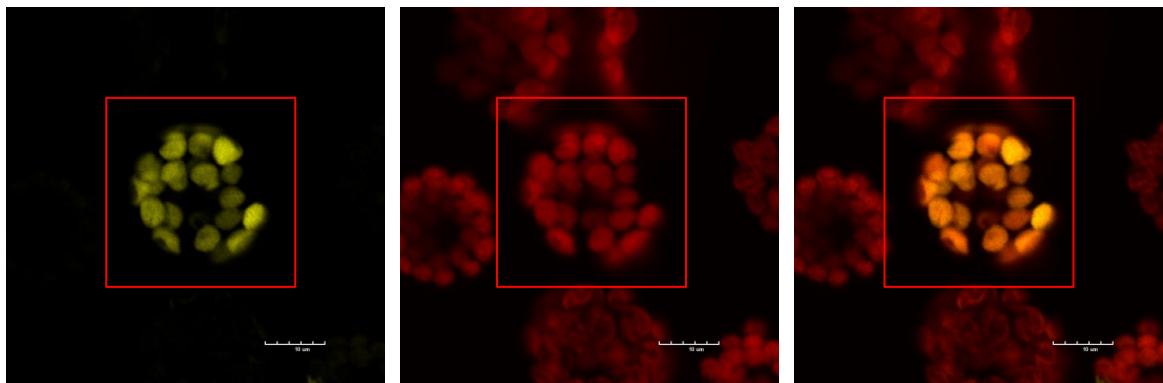
Merged



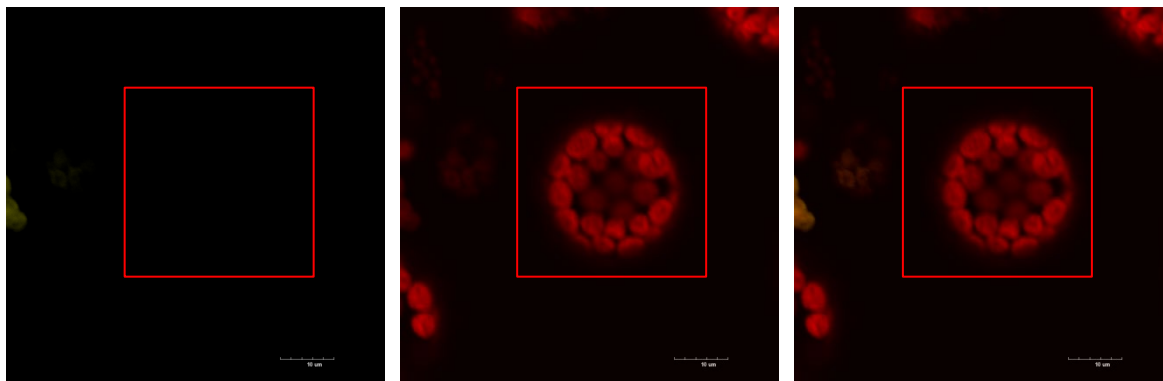
FPB1-YFP<sup>N</sup>+LPA1-YFP<sup>C</sup>



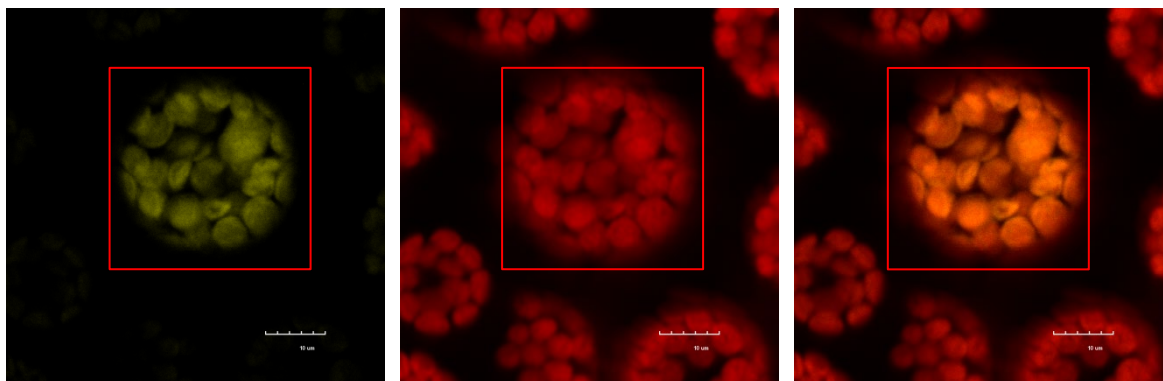
FPB1-YFP<sup>N</sup>+LPA2-YFP<sup>C</sup>



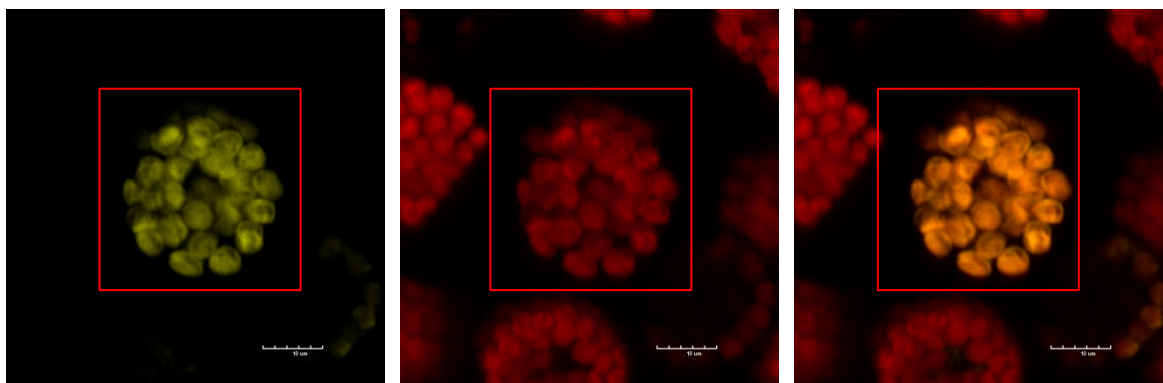
FPB1-YFP<sup>N</sup>+YFP<sup>C</sup>-SecY1



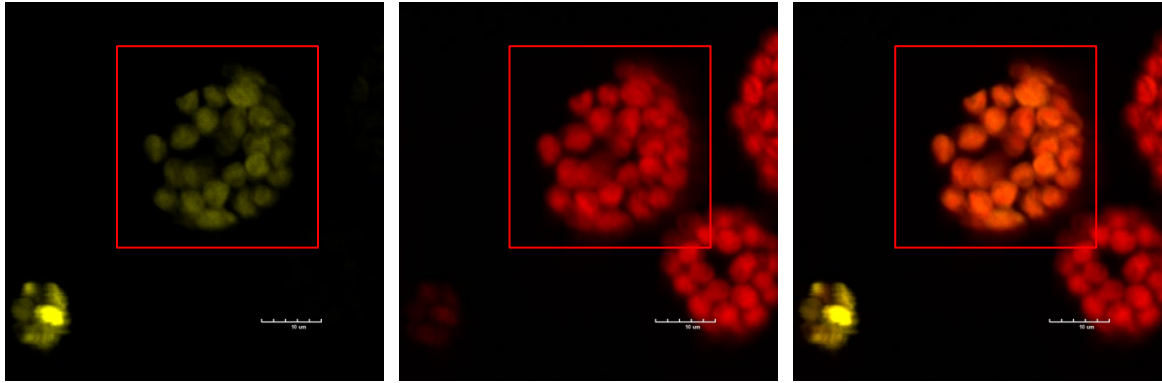
FPB1-YFP<sup>N</sup>+YFP<sup>C</sup>-SecE1



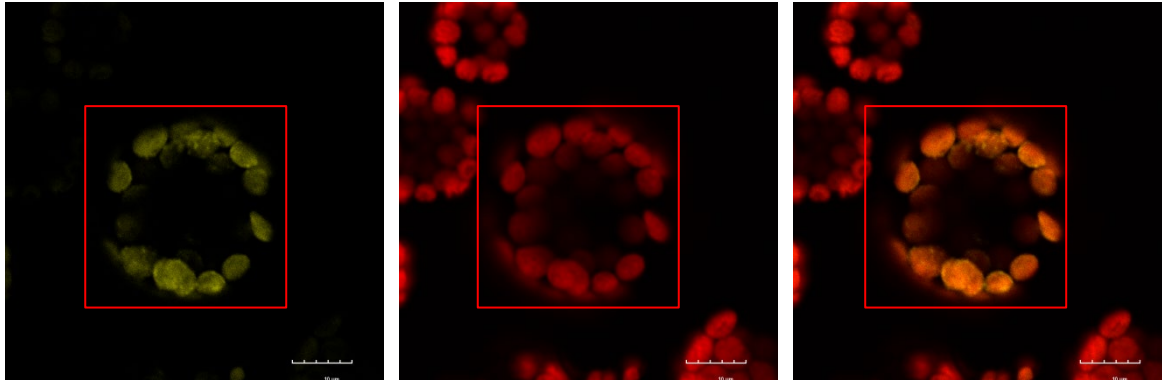
FPB1-YFP<sup>N</sup>+FtsY-YFP<sup>C</sup>



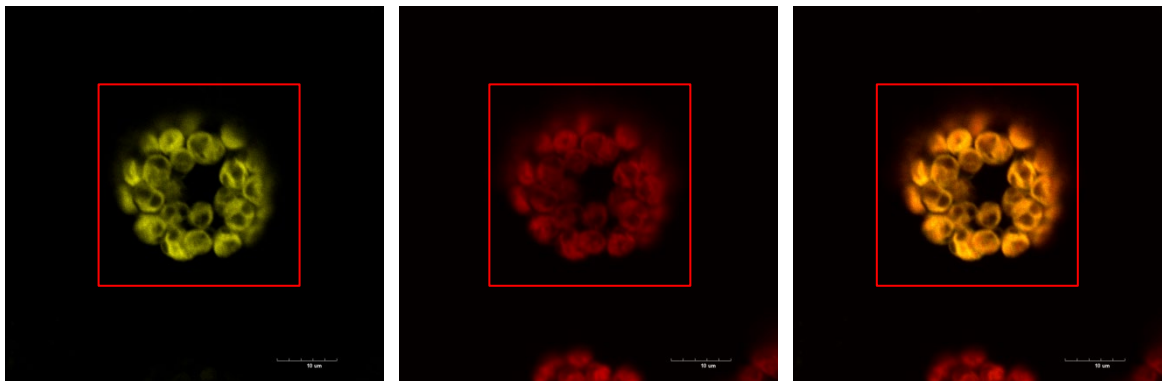
FPB1-YFP<sup>N</sup>+cpSRP54-YFP<sup>C</sup>



FPB1-YFP<sup>N</sup>+Alb3-YFP<sup>C</sup>



FPB1-YFP<sup>N</sup>+SecA1-YFP<sup>C</sup>



FPB1-YFP<sup>N</sup>+YCF4-YFP<sup>C</sup>

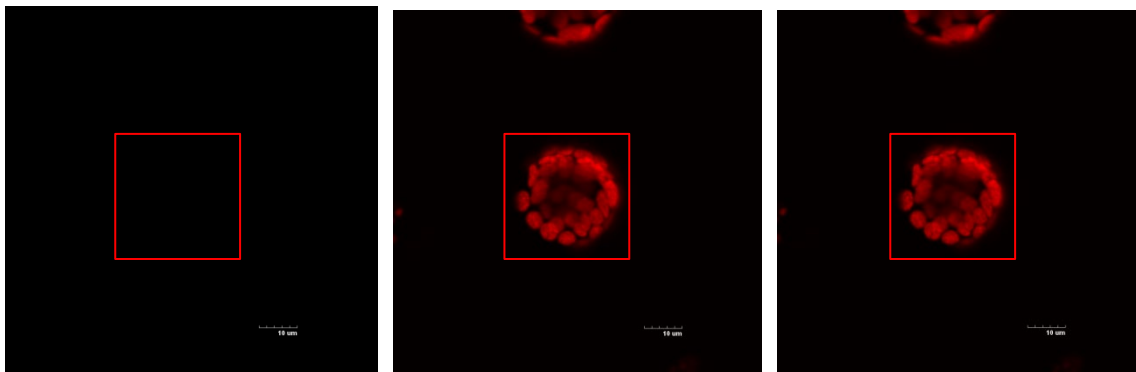


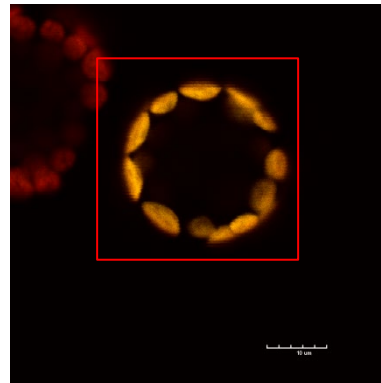
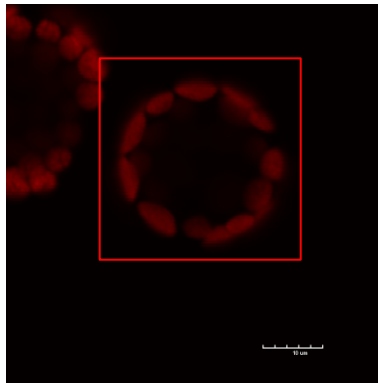
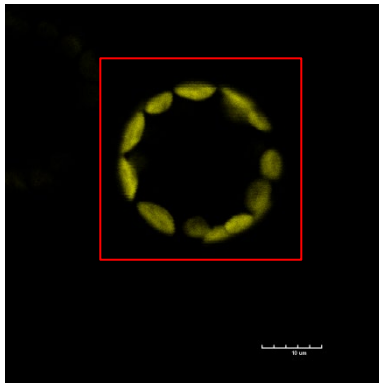
**Figure S6a**

**Right**

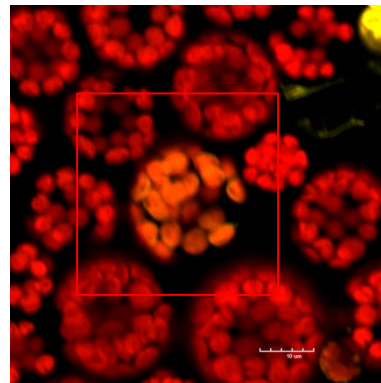
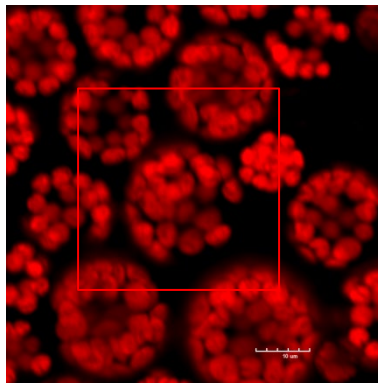
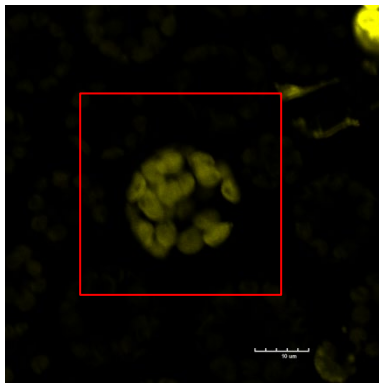
YFP  
PAM68-YFP<sup>N</sup>+FPB1-YFP<sup>C</sup>

Chl.

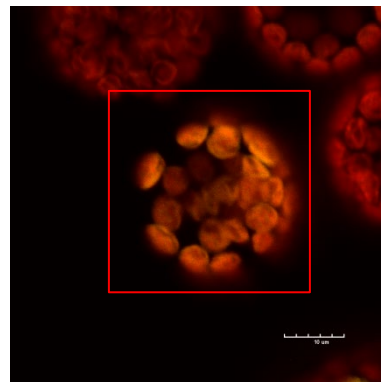
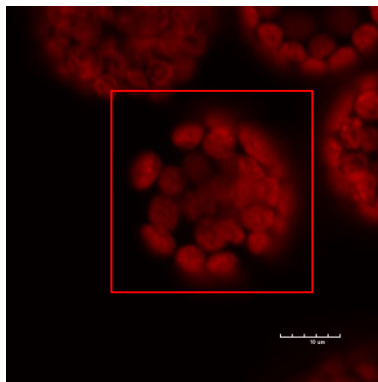
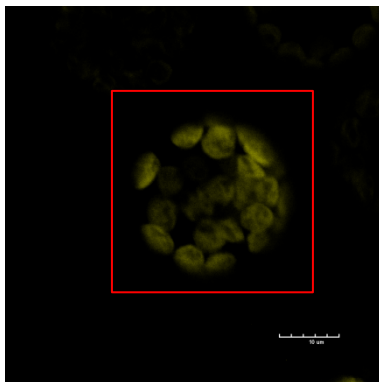
Merged



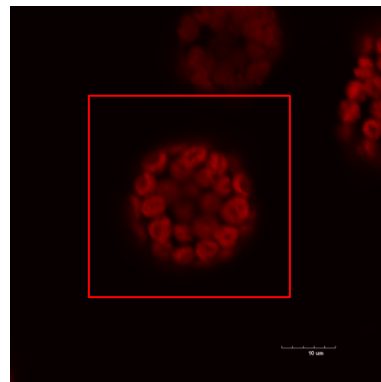
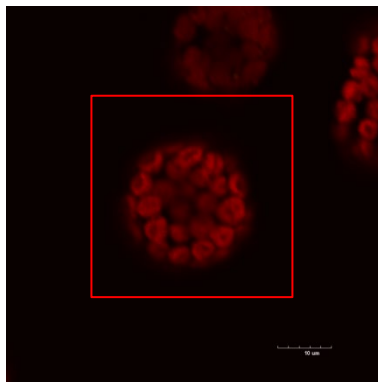
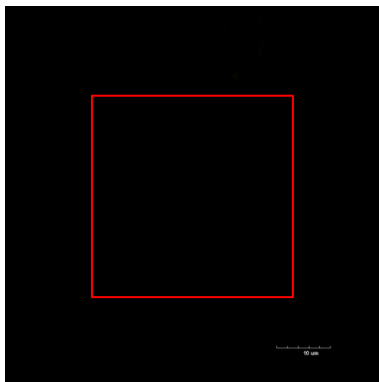
PAM68-YFP<sup>N</sup>+LPA1-YFP<sup>C</sup>



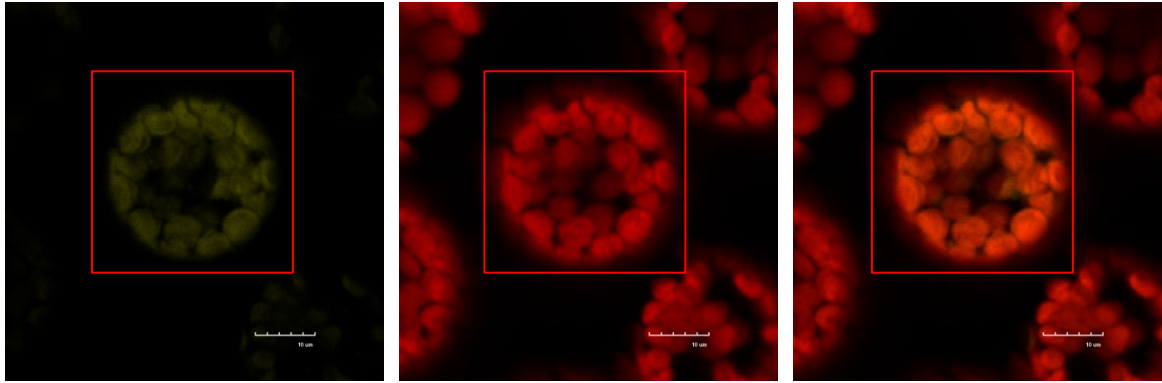
PAM68-YFP<sup>N</sup>+LPA2-YFP<sup>C</sup>



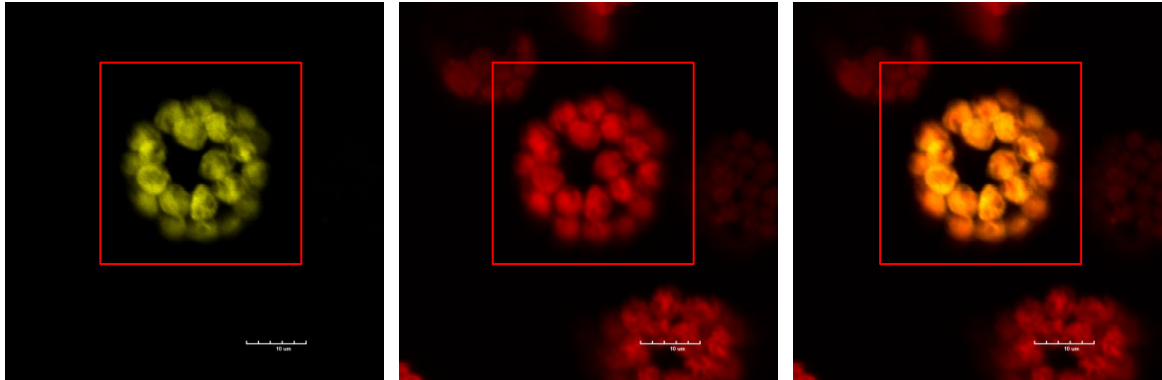
PAM68-YFP<sup>N</sup>+YFP<sup>C</sup>-SecY1



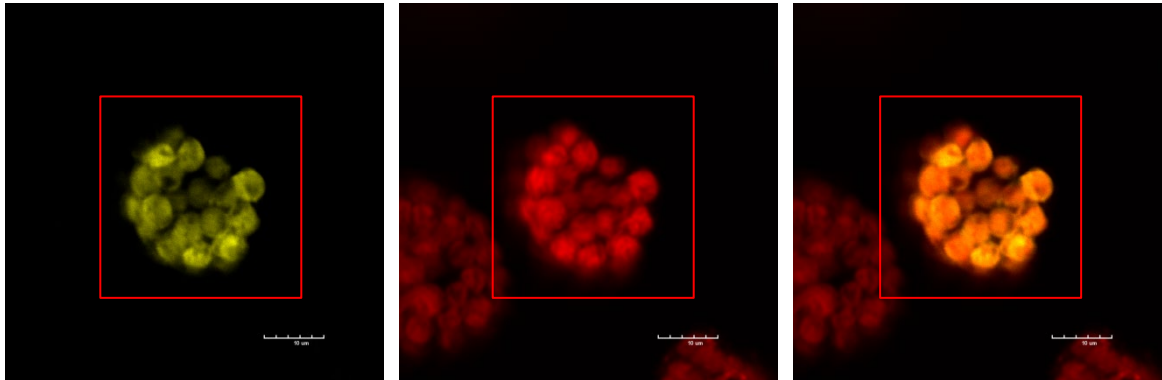
PAM68-YFP<sup>N</sup>+YFP<sup>C</sup>-SecE1



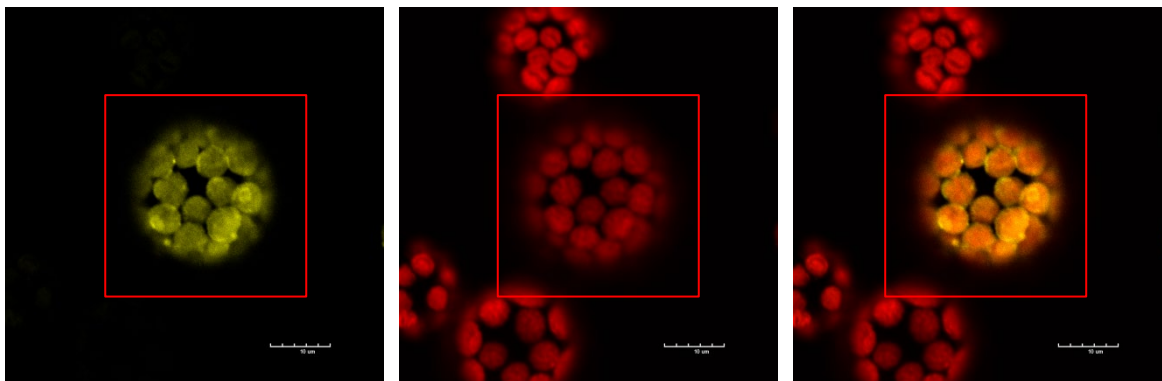
PAM68-YFP<sup>N</sup>+FtsY-YFP<sup>C</sup>



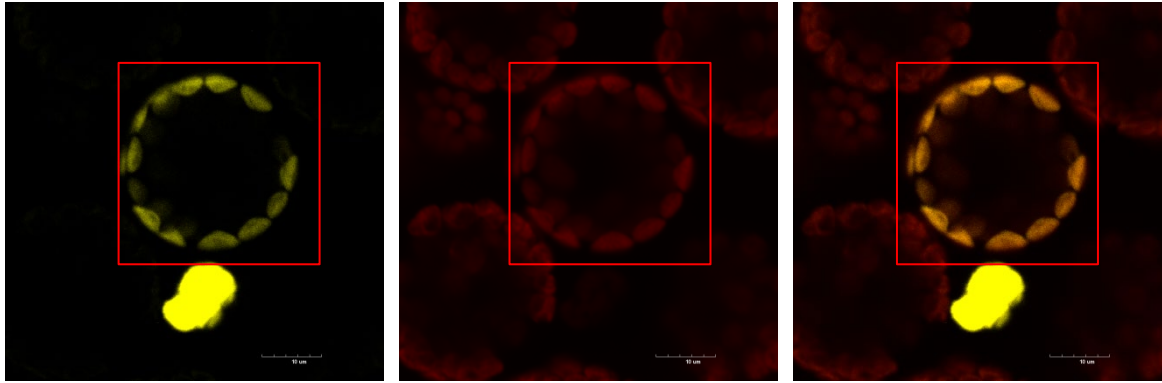
PAM68-YFP<sup>N</sup>+ cpSRP54-YFP<sup>C</sup>



PAM68-YFP<sup>N</sup>+Alb3-YFP<sup>C</sup>



PAM68-YFP<sup>N</sup>+SecA1-YFP<sup>C</sup>



PAM68-YFP<sup>N</sup>+YCF4-YFP<sup>C</sup>

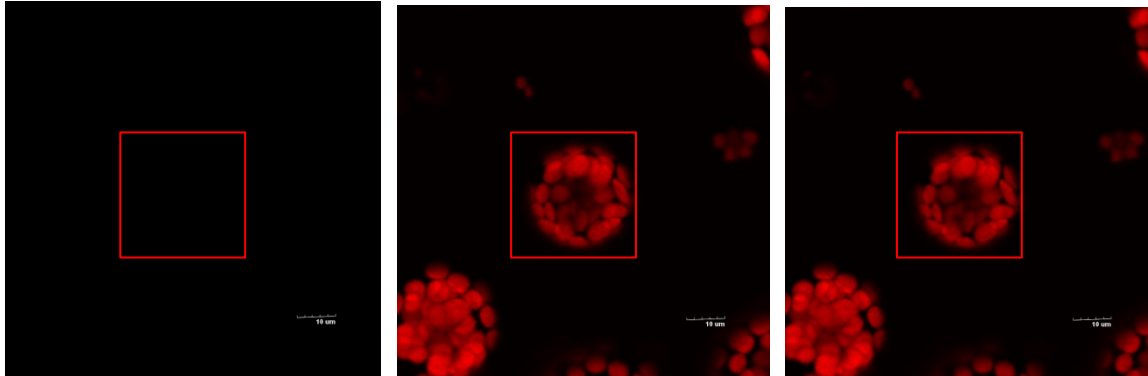


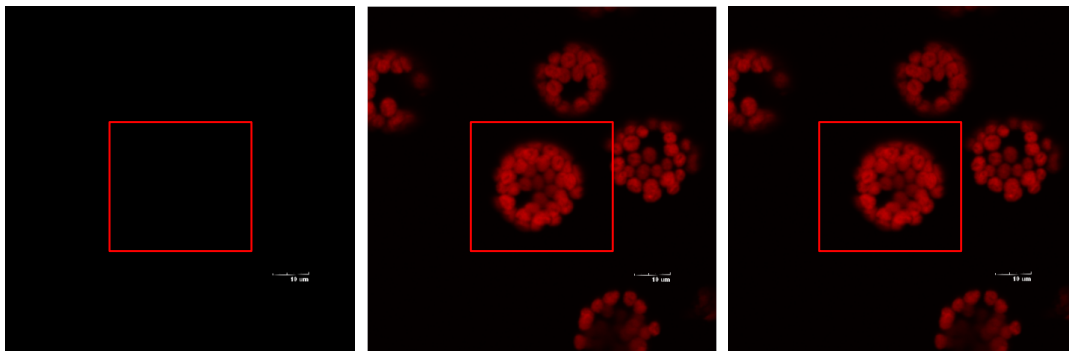
**Figure S6b**

**Left**

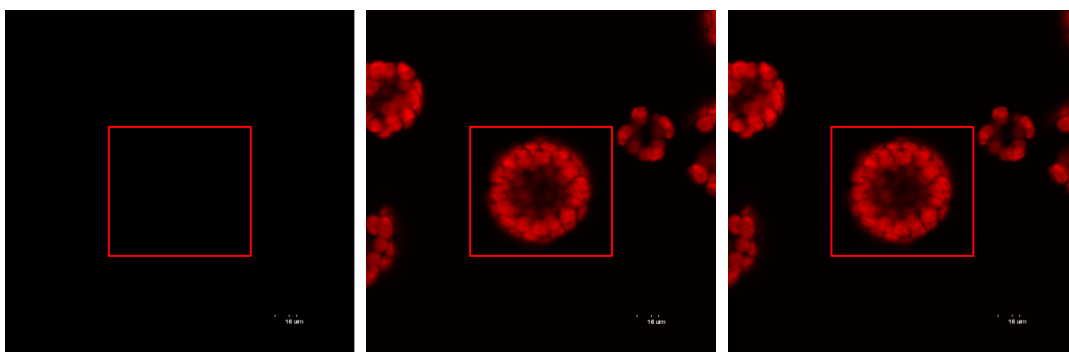
YFP  
YFP<sup>N</sup> +FPB1-YFP<sup>C</sup>

Chl.

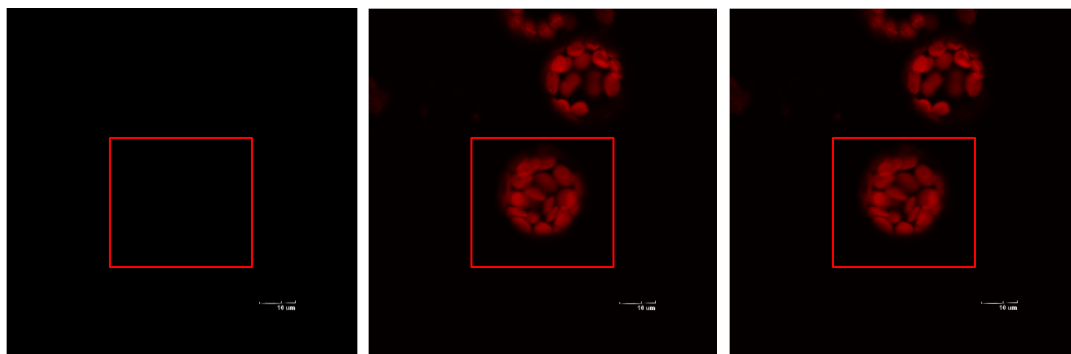
Merged



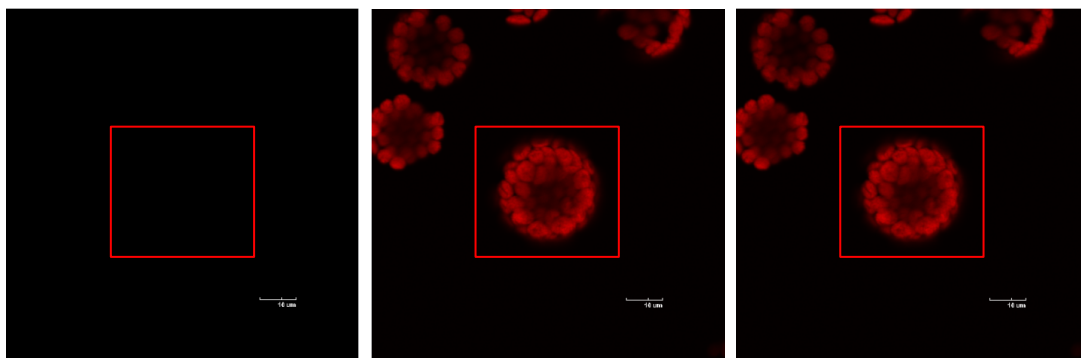
YFP<sup>N</sup> +PAM68-YFP<sup>C</sup>



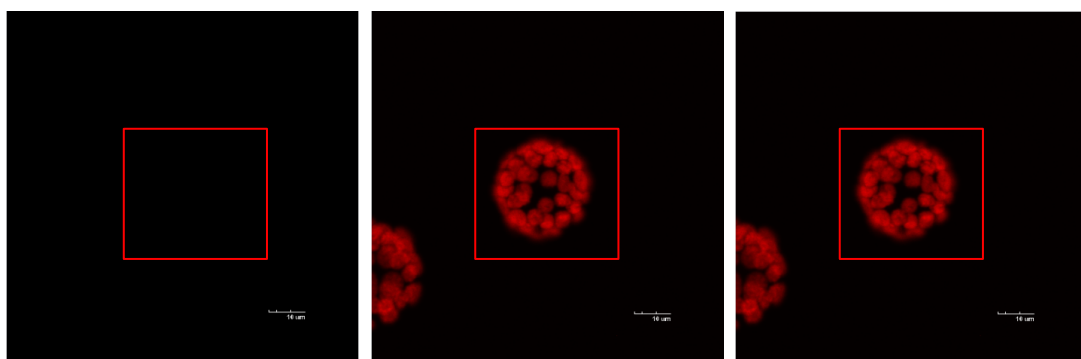
YFP<sup>N</sup> + LPA1-YFP<sup>C</sup>



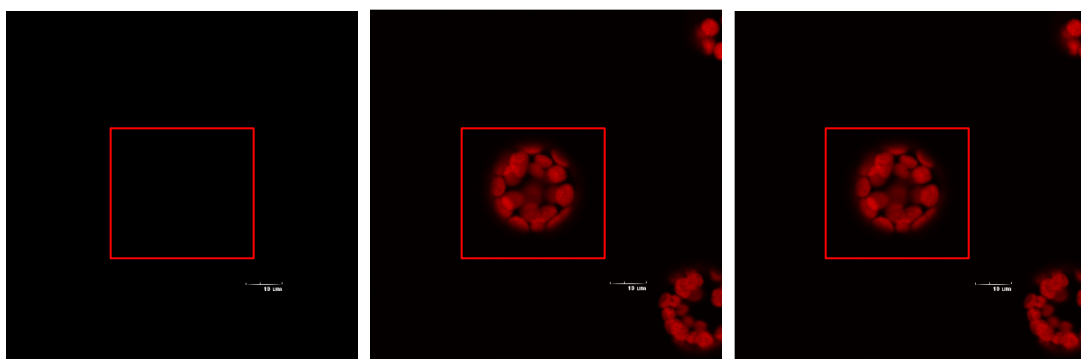
YFP<sup>N</sup> + LPA2-YFP<sup>C</sup>



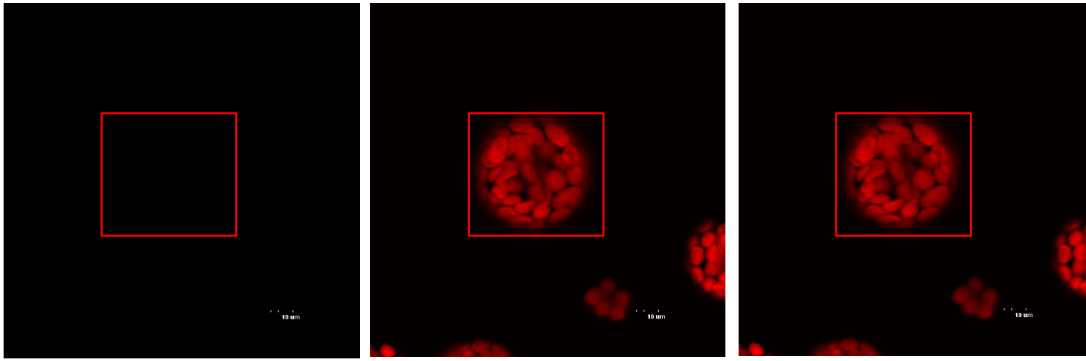
YFP<sup>N</sup> + YFP<sup>C</sup>-SecY1



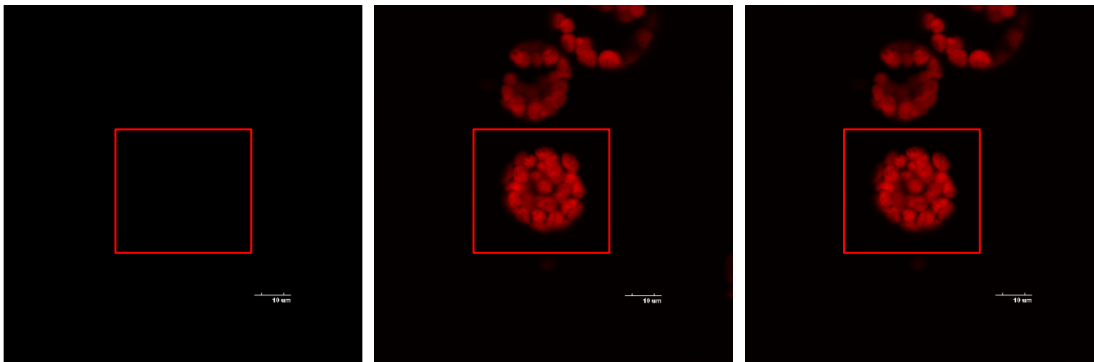
YFP<sup>N</sup> + YFP<sup>C</sup>-SecE1



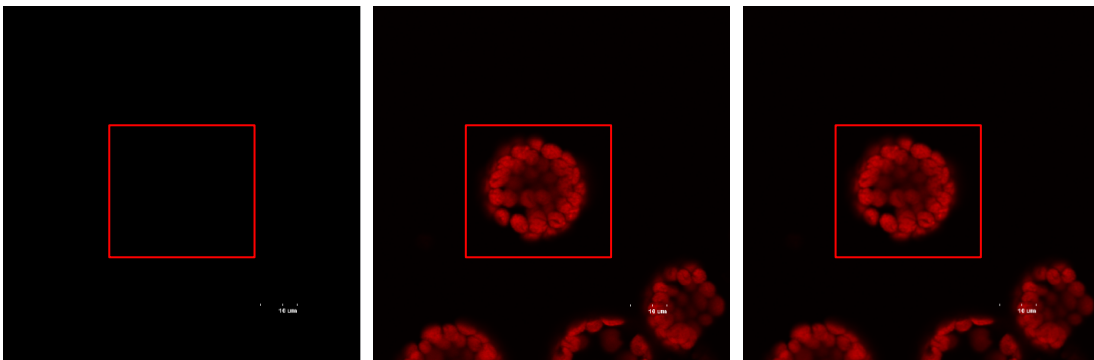
YFP<sup>N</sup> + FtsY-YFP<sup>C</sup>



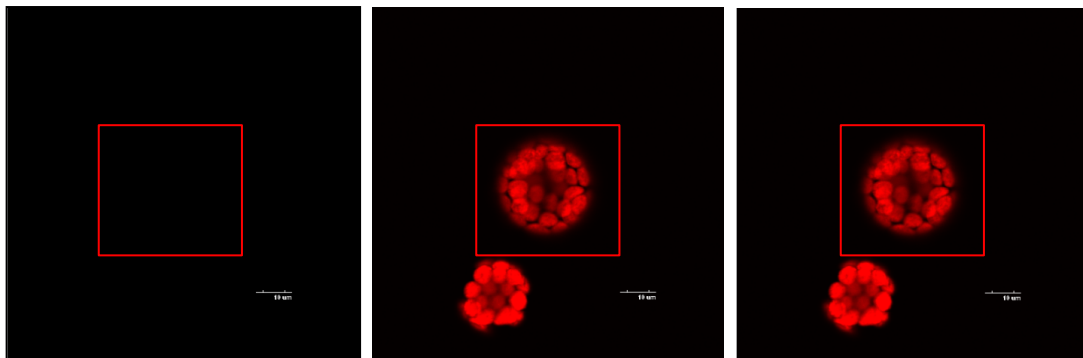
YFP<sup>N</sup> + cpSPR54-YFP<sup>C</sup>



YFP<sup>N</sup> + Alb3-YFP<sup>C</sup>



YFP<sup>N</sup> + SecA1-YFP<sup>C</sup>



YFP<sup>N</sup> + YCF4-YFP<sup>C</sup>

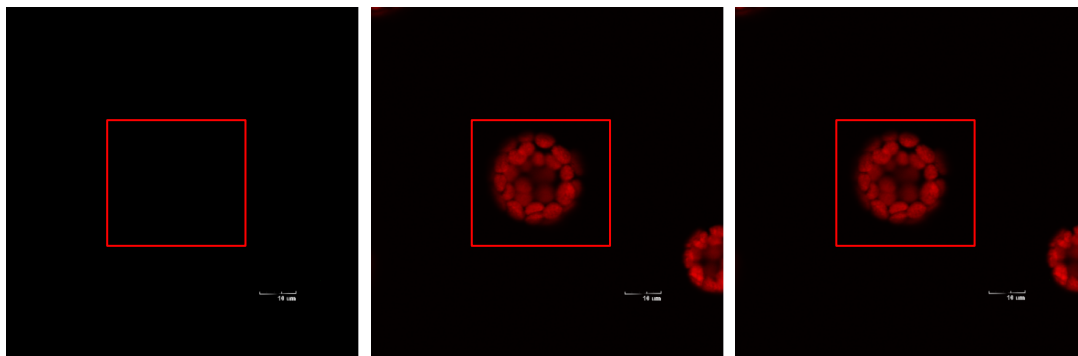
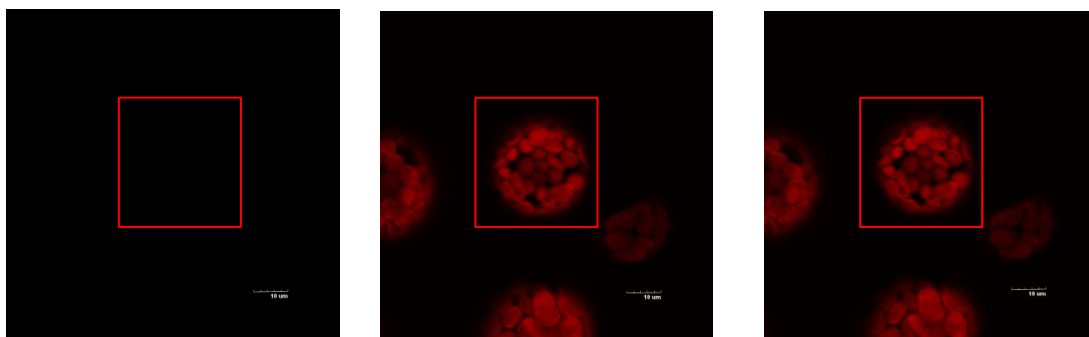


**Figure S6b**  
**right**

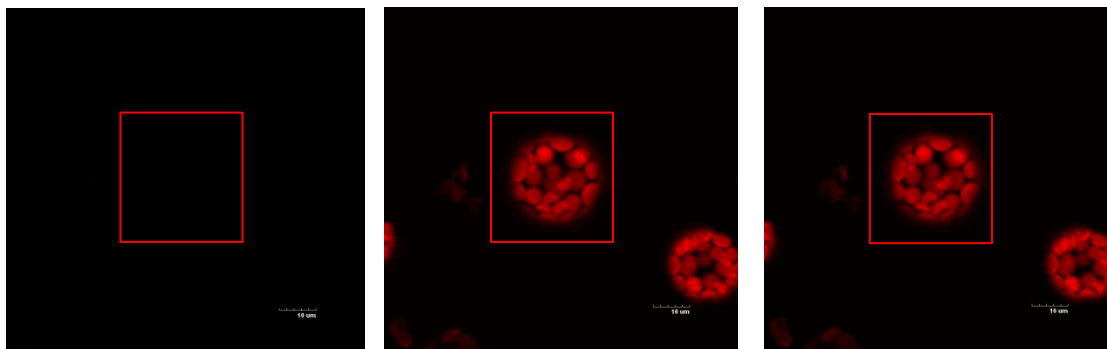
YFP  
YCF4-YFP<sup>N</sup>/FPB1-YFP<sup>C</sup>

Chl.

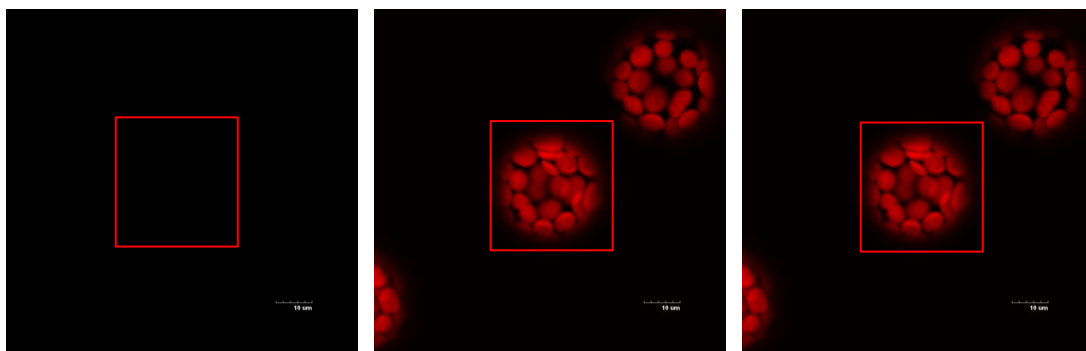
Merged



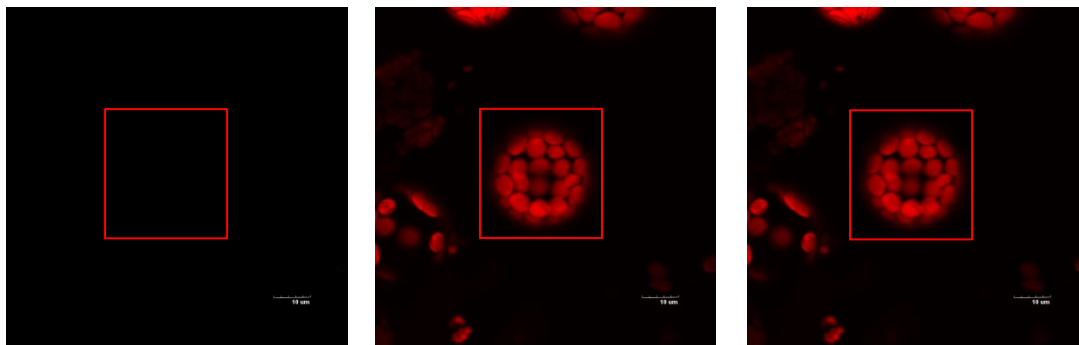
YCF4-YFP<sup>N</sup>/PAM68-YFP<sup>C</sup>



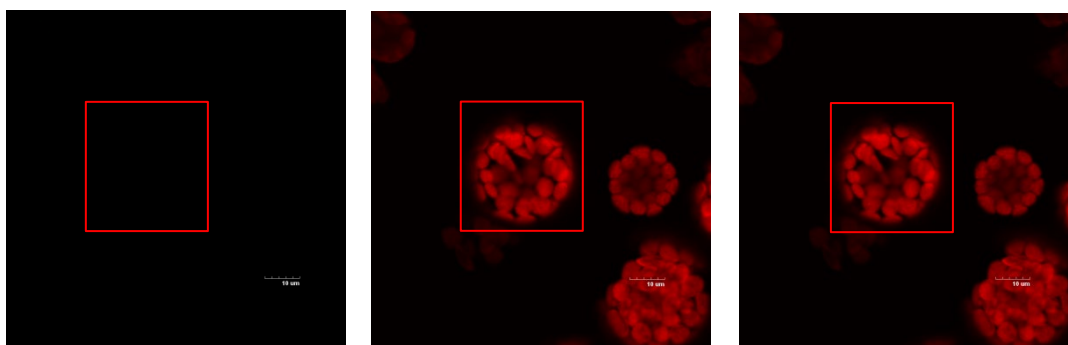
YCF4-YFP<sup>N</sup>/LPA1-YFP<sup>C</sup>



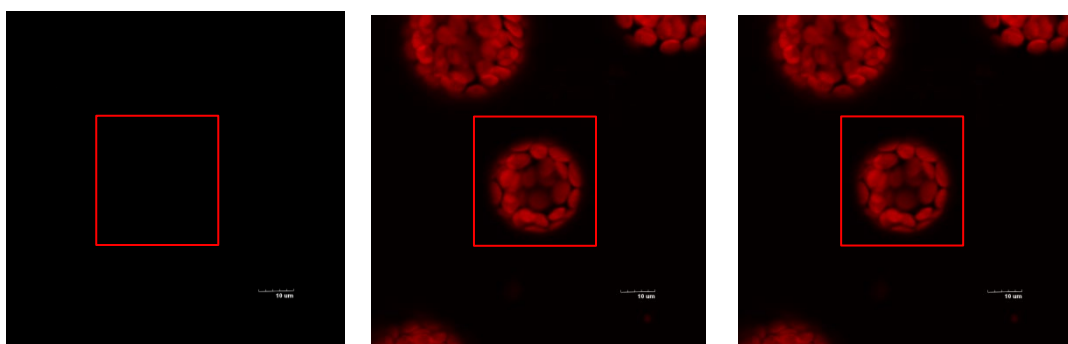
YCF4-YFP<sup>N</sup>/LPA2-YFP<sup>C</sup>



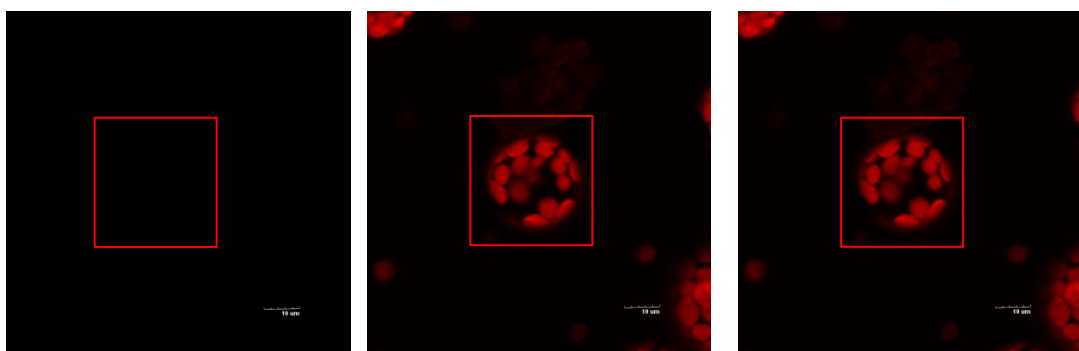
YCF4-YFP<sup>N</sup>/YFP<sup>C</sup>-SecY1



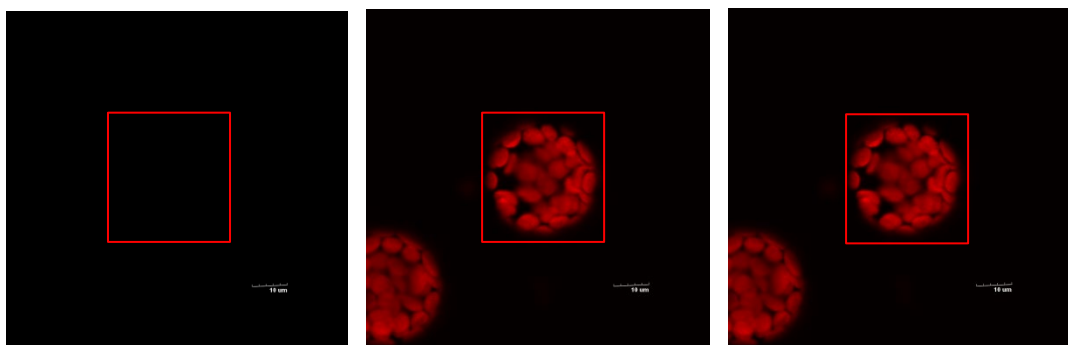
YCF4-YFP<sup>N</sup>/YFP<sup>C</sup>-SecE1



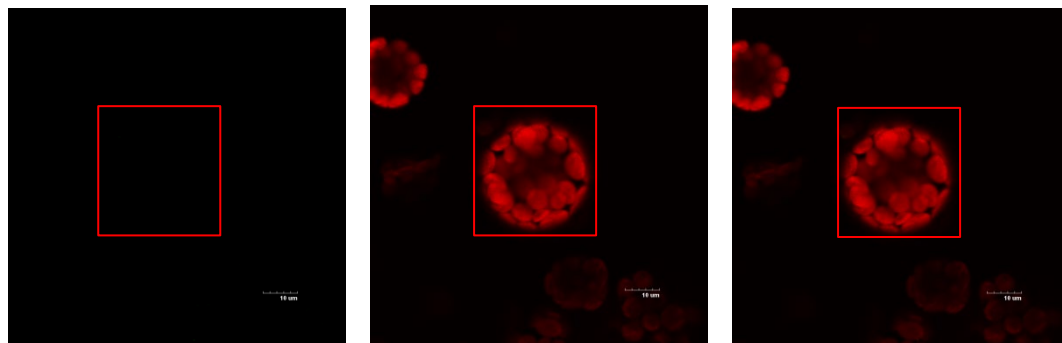
YCF4-YFP<sup>N</sup>/FtsY-YFP<sup>C</sup>



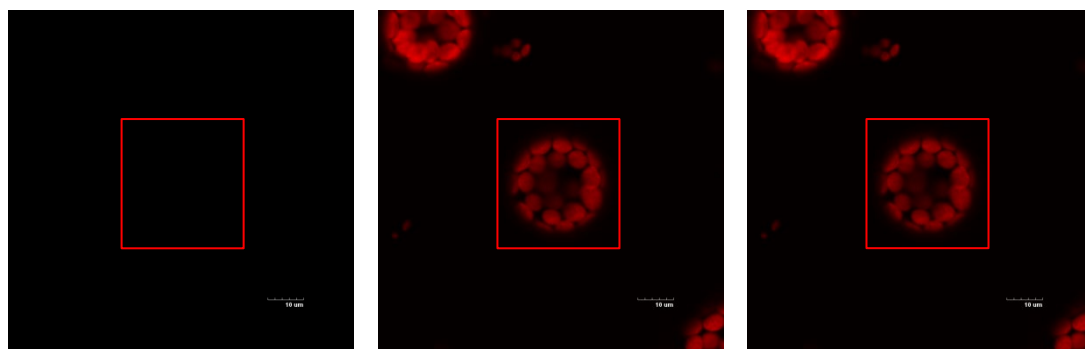
YCF4-YFP<sup>N</sup>/cpSRP54-YFP<sup>C</sup>



YCF4-YFP<sup>N</sup>/Alb3-YFP<sup>C</sup>



YCF4-YFP<sup>N</sup>/SecA1-YFP<sup>C</sup>



YCF4-YFP<sup>N</sup>/PYG7-YFP<sup>C</sup>

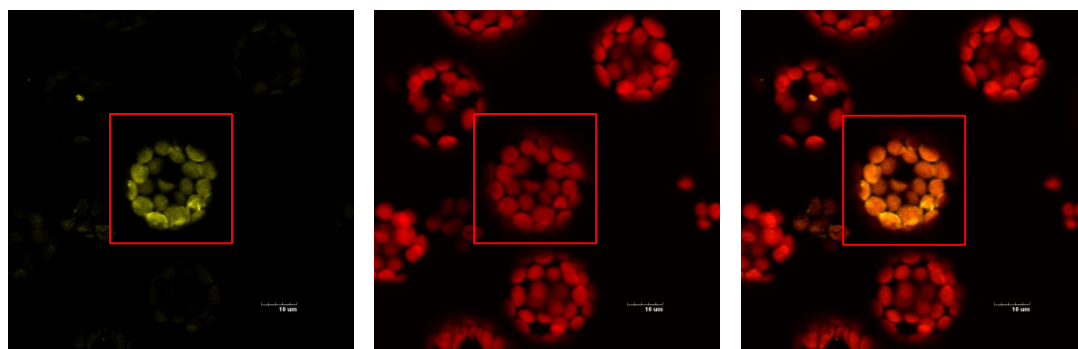


**Figure S6c**

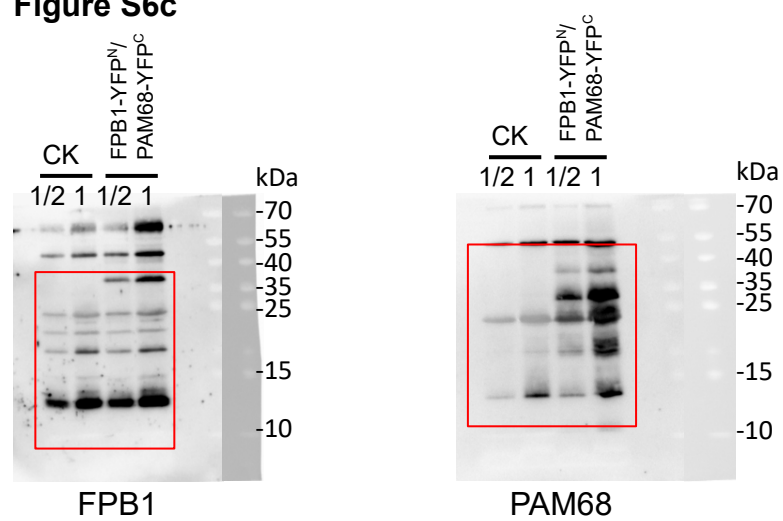


**Figure S6d**

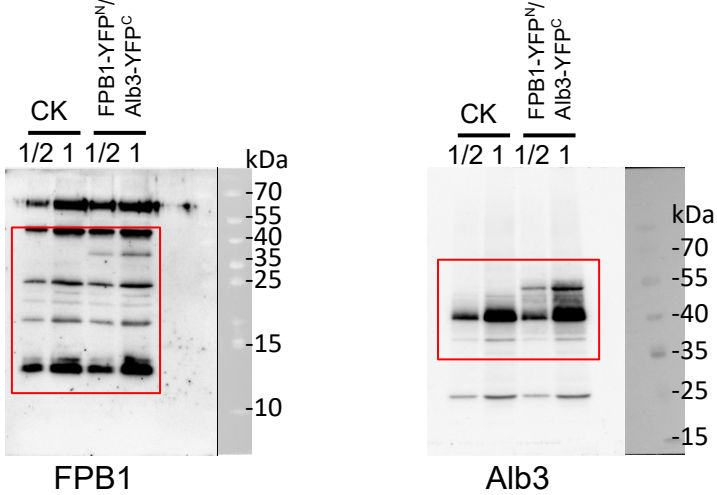


**Figure S11**  
**Figure S11a**

*AtpsbB* (ATCG00680)

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CAATGTGGAGACAAGGTATGTTCTGTTATACCTTTTCATGACTCGTTTAGGAATAACCAATTCTTGGGGCGGTTGGAATATT  
ACAGGGGGGACTATAACGAATCCGGGTCTTTGGAGTTACGAAGGGGTAGCCGGAGCACATATAGTGTTTTCTGGTTTG  
TGCTTCTTGGCAGCTATTTGGCATTGGGTATATTGGGATCTAGAAATTTTTGTGATGAACGTACAGGAAAACCTTCTTT  
GGATTTGCCCAAGATTTTTGGAATTCATTTATTTCTTTCAGGAGTGGCTTGCTTCGGTTTTGGCGCATTTCATGTAACAG  
GATTATATGGTCCTGGAATATGGGTATCCGACCCTTATGACTAACCAGGAAAGGTACAACCCGTAAACCCGGCGTGGG  
GCGTGGAGGGTTTTGACCCTTTTGTCCGGGAGGAATAGCCTCTCATCATATTGCAGCAGGGACGTTGGGTATATTAG  
CGGGCCTATTCCATCTTAGTGTTCTCGTCCGCCTCAACGTCTATACAAAGGATTACGTATGGGCAATATTGAAACCGTCCT  
TTCCAGTAGTATTGCTGCTGTCTTTTTTGCAGCTTTTGTGTTGCTGGAACATATGGGTATGGTTCTGCACTACTCCCA  
TCGAATTATTTGGTCCTACTCGTTATCAATGGGATCAGGGATACTTTCAACAAGAAATATATCGAAGAGTTAGTGCTGGA  
CTGGCTGAAAATCAAAGTTTATCAGAAGCTTGGGCGAAAATTCCTGAAAATTAGCTTTTTATGATTATATTGGTAATAAT  
CCAGCAAAGGGGGGTTATTCCGAGCGGGTTCATGGACAATGGGGATGGAATAGCTGTTGGATGGTTAGGCCACCC  
CGTCTTTAGAAATAAAGAAGGGCGTGAACTTTTTGTACGCCGCATGCCTACTTTTTTTGAACTTTTCCGGTAGTTTTG  
GTAGACGGAGACGGAATTGTTAGAGCTGACGTCCCGTTTAGAAGGGCAGAATCAAATATAGTGTCGAACAAGTAGGT  
GTAACGTGTTGAGTTTTATGGTGGTGAACCTCAATGGAGTGAGTTATAGTGATCCCGCAACTGTGAAAAAATATGCTAGAC  
GGGCTCAATTGGGTGAGATTTTTGAATTAGATCGTGCGACTTTGAAATCTGATGGTGTTTTTCTGATGAGCCCAAGAG  
GTTGGTTTACGTTTGGACATGCTTCGTTTGTCTACTTTTCTTCTTTGGACACATTTGGCATGGTGCTAGAACCCTCTT  
CAGAGATGTTTTTGTGTTGTTGATCCAGATTGGATGCTCAAGTGGAAATTCGGGGCATTCCAAAACTTGAGATCCA  
ACTACAAAACGACAAGCAGTCTGA

*ZmpsbB* (NC\_001666.2)

ATGGGTTTGCCTTGGTATCGTGTTCACTGTCGATTGAATGATCCGGGTCGATTGCTTTCGGTGCAATATAATGCACAC  
AGCTCTAGTTTCTGGTTGGGCTGGTTCGATGGCTTTATACGAATTAGCGGTTTTTATCCCTCTGATCCTGTTCTGGAT  
CCAATGTGGAGACAAGGTATGTTCTGTCATCCCTTCATGACTCGTTTAGGAATAACGAATTCGTGGGGTGGTTGGAGT  
ATTTAGGAGGAACGTGAACGAATCCGGGTATTTGGAGTTATGAAGGTGTGGCAGGTGCGCATATTGTGTTTTCTGGC  
TTGTGTTTCTTGGCAGCTATCTGGCATTGGGTATATTGGGACCTAGAAATATTCTGTGATGAGCGGACGGGAAAACCTT  
CTTTGGATTTGCCCAAGATCTTTGGAATTCATTTATTTCTTGCAGGGGTGGCTTGTTTTGGCTTTGGTGCAATTCATGTA  
ACGGGTTTATATGGCCCTGGGATATGGGTGTCCGATCCTTACGGACTCACTGGAAAAGTACAAGCTGTAAATCCTGCG  
TGGGGTGCAGAAGGTTTTGATCCTTTCTGTTCCGGGAGGAATAGCTTCGCATCATATTGCTGCGGGTACTTTGGGCATA  
TTAGCGGGCCTATTCCATCTAAGTGTCCGTCCGCCTCAACGTCTATACAAAGGGTTACGTATGGGCAATATTGAACTG  
TACTTTCCAGTAGTATCGCTGCTGTTTTTTTTGCTGCTTTCTGATGTTGCCGGAACATATGTGGTATGGATCAGCAACTACC  
CCAATCGAATTATTTGGGCCTACTCGTTATCAGTGGGATCAGGGATACTTTAGCAAGAAATATATCGAAGAGTTAGCGA

TGGGTTAGCCGAAAATCTTAGTTTATCAGAAGCTTGGTCTAAAATTCCCGAAAAATTAGCCTTTTATGATTATATTGGTAA  
TAATCCGGCAAAGGGGGGATTATTCAGAGCAGGCTCAATGGACAATGGGGATGGCATAGCTGTTGGATGGTTAGGACA  
TCCCGTCTTTAGAGATAAAGAAGGACGCGAGCTTTTTGTACGTCGTATGCCTACTTTTTTTGAAACATTTCCGGTCGTTT  
TGGTAGATGAAGAGGGAATTGTGAGAGCGGACGTTCCTTTTAGAAGAGCAGAATCCAAATATAGTGTTGAACAAGTAG  
GCGTAACGGTGGAGTTCTATGGTGGCGAACTTAATGGAGTAAGTTATTCTGATCCTGCTACTGTAAAAAATATGCGCG  
GCGTGCTCAATTAGGGGAAATTTTTGAATTAGATCGAGCTACTTTGAAATCAGATGGTGTTCGACAGTCCAAGG  
GGTTGGTTCACTTTTGGTCATGCTACCTTTGCTTTGCTCTTCTTTTTCGGACACATTTGGCATGGCGCTCGAACCTTGT  
TCCGAGATGTTTTTGTGGTATTGATCCAGACTTGGATGCTCAAGTGGAATTTGGAACATTCCAAAAAGTTGGAGATCC  
AACTACAAGGAGACAGGCAGCCTGA

### Figure S11b

AtCP47 (ATCG00680)

MGLPWYRVHTTVLNDPGRLLAVHIMHTALVAGWAGSMALYELAVFDPSDPVLDPMWRQGMFVIPFMTRLGITNSWGGWN  
ITGGTITNPGLWSYEGVAGAHIVFSGLCFLAAIWHWVYWDLEIFCDERTGKPSLDLPKIFGIHLFLSGVACFGFGAFHVTGLY  
GPGIWVSDPYGLTGKVQPVNPAWGVGFDPFVPGGIASHHIAAGTLGILAGLFHLSVRPPQRLYKGLRMGNIETVLSSSIAA  
VFFAAAFVAGTMWYGSATTPIELFGPTRYQWDQGYFQQEIYRRVSAGLAENQSLSEAWAKIPEKLAFYDYIGNNPAKGGLF  
RAGSMDNGDGIAGVWLGHVPFRNKEGRELFVRRMPTFFETFPVVLVDGDGIVRADVPFRRAESKYSVEQVGVTVEFYGG  
ELNGVSYSYPATVKKYARRAQLGEIFELDRATLKSDGVFRSSPRGWFTFGHASFALLFFFGHIWHGARTLFRDVFAGIDPD  
LDAQVEFGAFQKLGDPPTTKRQAV

ZmCP47 (NP\_043049.1)

MGLPWYRVHTTVLNDPGRLLSVHIMHTALVSGWAGSMALYELAVFDPSDPVLDPMWRQGMFVIPFMTRLGITNSWGGW  
SISGGTVTNPGIWSYEGVAGAHIVFSGLCFLAAIWHWVYWDLEIFCDERTGKPSLDLPKIFGIHLFLAGVACFGFGAFHVTG  
LYGPGIWVSDPYGLTGKVQAVNPAWGAEGFDPFVPGGIASHHIAAGTLGILAGLFHLSVRPPQRLYKGLRMGNIETVLSSSI  
AAVFFAAAFVAGTMWYGSATTPIELFGPTRYQWDQGYFQQEIYRRVSDGLAENLSLSEAWSKIPEKLAFYDYIGNNPAKGG  
LFRAGSMDNGDGIAGVWLGHVPFRDKEGRELFVRRMPTFFETFPVVLVDEEGIVRADVPFRRAESKYSVEQVGVTVEFY  
GGELNGVSYSYPATVKKYARRAQLGEIFELDRATLKSDGVFRSSPRGWFTFGHATFALLFFFGHIWHGARTLFRDVFAGID  
PDLDAQVEFGTFQKVGDPPTTRRQAA