

Supplementary Information for

Establishing super-resolution imaging for proteins in diatom biosilica

Philip Gröger¹, Nicole Poulsen¹, Jennifer Klemm¹, Nils Kröger^{1,2}, Michael Schlierf^{1*}

¹B CUBE – Center for Molecular Bioengineering, TU Dresden, Arnoldstr. 18, 01307 Dresden,
Germany

²Department of Chemistry and Food Chemistry, TU Dresden, Arnoldstr. 18, 01307 Dresden,
Germany

*correspondence: schlierf@bcube-dresden.de

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SI Methods

*SEM imaging of *Thalassiosira pseudonana**

Diatoms were lysed (as described under *Biosilica Isolation* in the main methods), dehydrated with ethanol and afterwards critically point dried in a Leica-CPD 300. The dry diatoms were spread onto a carbon conductive adhesive tape and sputter coated with platinum in a Baltec SCD 050. Imaging was performed using a JEOL JSM-7500F scanning electron microscope with a SE2 detector and an acceleration voltage of 15kV.

ThunderSTORM settings

Image filtering was performed using the “à trous” undecimated wavelet transform with a B-spline order of 3 and scale of 2. For localization approximation a local threshold (in an 8-connected neighborhood) of 1x the standard deviation of the filtered image was chosen. The sub-pixel localization was performed via maximum likelihood fitting of the integrated form of a symmetric 2D Gaussian function with a radius of 3 pixel. The initial sigma was 1.6 pixel.

Super-resolution image reconstruction

The visualization of the localized molecules was performed by drawing a normalized symmetric 2D Gaussian for each of them and summing up all the Gaussians to form a final image. As the standard deviation, the localization precision (calculated via the Thompson-Larson-Webb formula as mentioned in the supplementary note for ThunderSTORM) was chosen.

Filter Sets used for imaging

Excitation WL	Laser bandpass	Dichroic	Emission bandpass
405	390/40 BrightLine HC (Semrock)	H 405 LPXR superflat (AHF)	460/50 ET (Chroma)
488	475/35 BrightLine HC (Semrock)	H 488 LPXR superflat (AHF)	525/45 BrightLine HC (Semrock)
561	555/25 ET (Chroma)	H 560 LPXR superflat (AHF)	609/54 BrightLine HC (Semrock)
647	628/40 BrightLine HC (Semrock)	H 643 LPXR superflat (AHF)	700/75 ET (Chroma)

Table S1. Fluorescent proteins used and their core parameter

Abbreviations: λ_{ex} & λ_{em} ... excitation and emission spectrum peak position, t_{mature} ... maturation time at 37°C, Brightness refers to the product of the extinction coefficient (in $\text{Mol}^{-1} \text{cm}^{-1}$) and the quantum yield divided by 1000. The first three FPs are photo-activatable FPs, meaning their non-fluorescent ground state can be activated, irreversibly. MEOS3.2 and Dendra2 are photo-convertible FPs and can be irreversibly switched from green to orange fluorescence. Dronpa is a photo-switchable FPs and can be reversibly switched between a fluorescent and non-fluorescent state.

FP	Transitions	State	λ_{ex} (nm)	λ_{em} (nm)	Brightness	t_{mature} (min)
PATagRFP	Off → Orange, 405 nm	Orange	562	595	25.1	75
PAmCherry1	Off → Orange, 405 nm	Orange	564	595	9.3	23
PA-GFP	Off → Green, 400 nm	Green	504	517	13.7	27
mEOS3.2	Green → Orange, 405 nm	Green	507	517	53.2	20
		Orange	572	593	17.7	
Dendra2	Green → Orange, 480 nm	Green	490	507	22.5	90
		Orange	553	573	19.3	
Dronpa	Off → Green, 400 nm	On	503	518	80.7	40
	Green → Off, 503 nm					

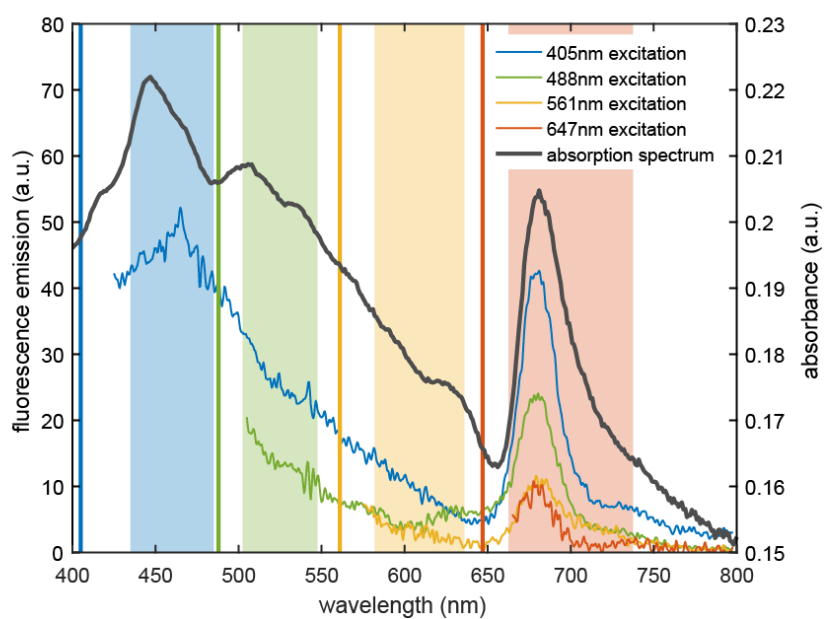


Figure S1. Emission spectra of live diatom

Emission spectra of *T. pseudonana* for different excitation wavelengths. Vertical lines represent the laser lines. The shaded area depict the detection window. The absorption spectrum is plotted in black on a separate y-axis. Clearly visible are the absorption peaks for chlorophyll a at around 670nm and chlorophyll c and fucoxanthin around 450nm.

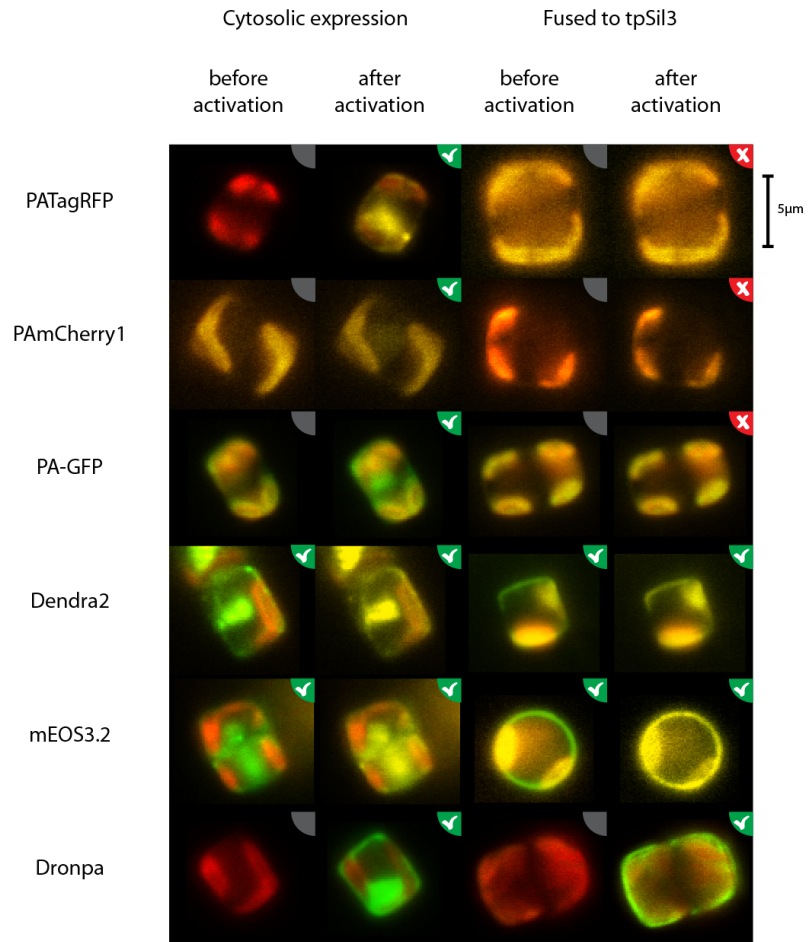


Figure S2. Screening of all fluorescent proteins and their activation capability

Each row displays the activation of a different fluorescent protein. The activation was performed with the appropriate laser light as specified in Table S1. The colors represent the four different excitation wavelengths 405nm (blue), 488nm (green), 561nm (yellow) and 647nm (red). Chloroplasts are always visible in the red channel.

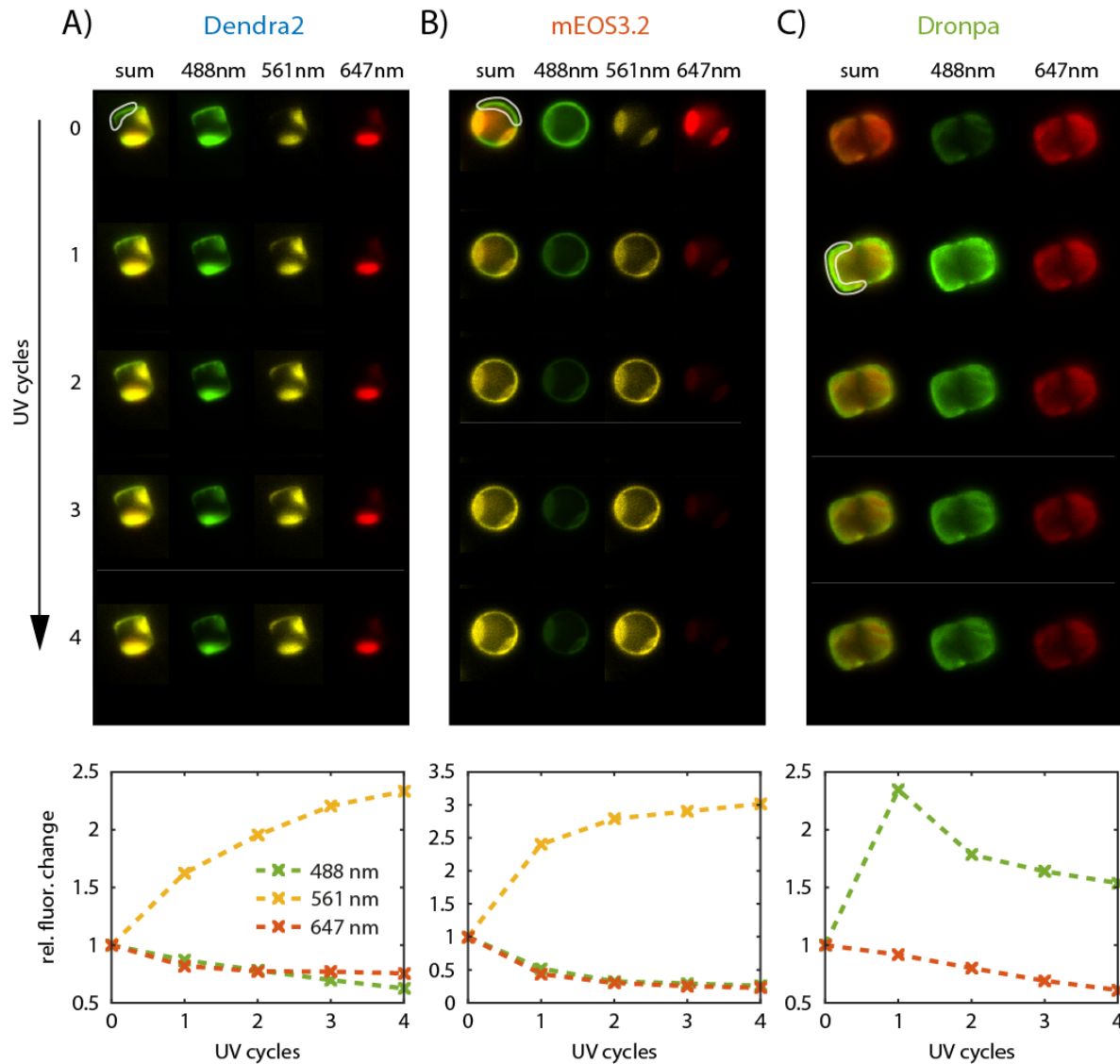


Figure S3. Photo-conversion analysis of active tpSil3 clones

Photo-conversion statistics for Dendra2 (A), mEOS3.2 (B) and Dronpa (C). The top panel show the individual imaging channels during conversion. Each UV cycle equals one second of 405nm illumination at 20mW. To analyze the conversion quantitatively, a region containing the biosilica cell wall and overlapping as little as possible with chloroplasts was selected (depicted in white). The intensity in this region was summed up and the relative intensity change with 488 nm, 561 nm and 647 nm excitation is plotted in the lower panels, showing the clear photo-conversion or –activation of the probes.

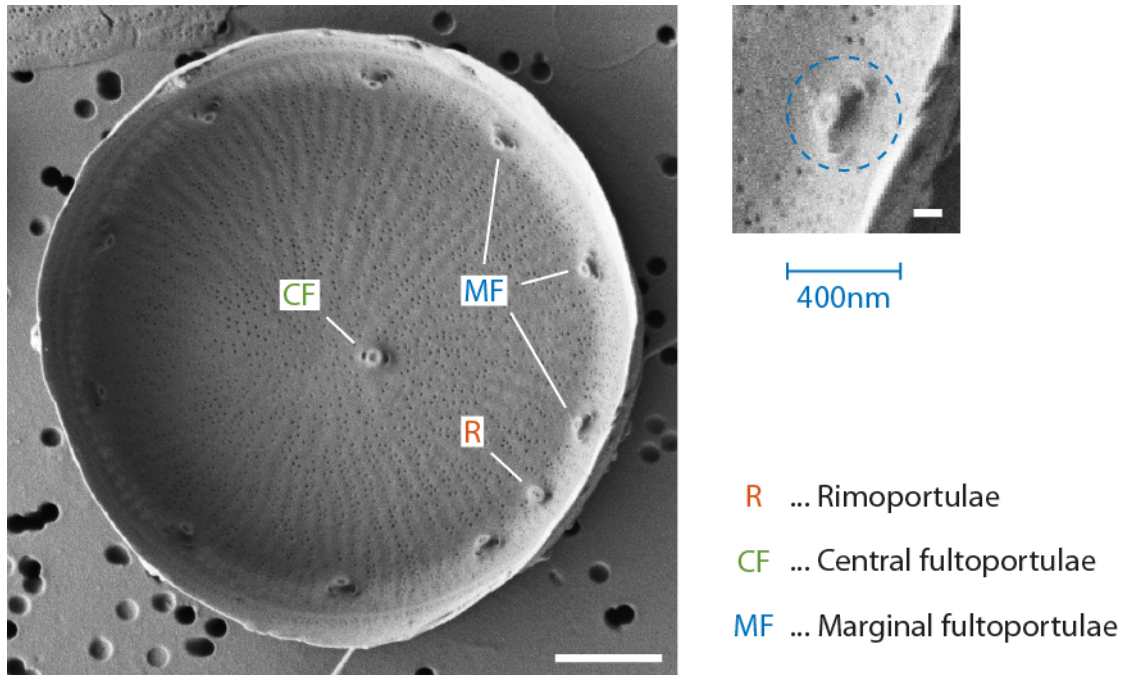


Figure S4. SEM micrograph of the inside of the valve biosilica

SEM image of isolated biosilica valve of *T. pseudonana*. The inside of the valve shows the thick basal chamber of the fultoportulae. A zoomed image shows a diameter estimate of the outer region of the fultoportulae basal chamber of around 400 nm. Scale bars are 1 μm and 100 nm for the zoomed image.

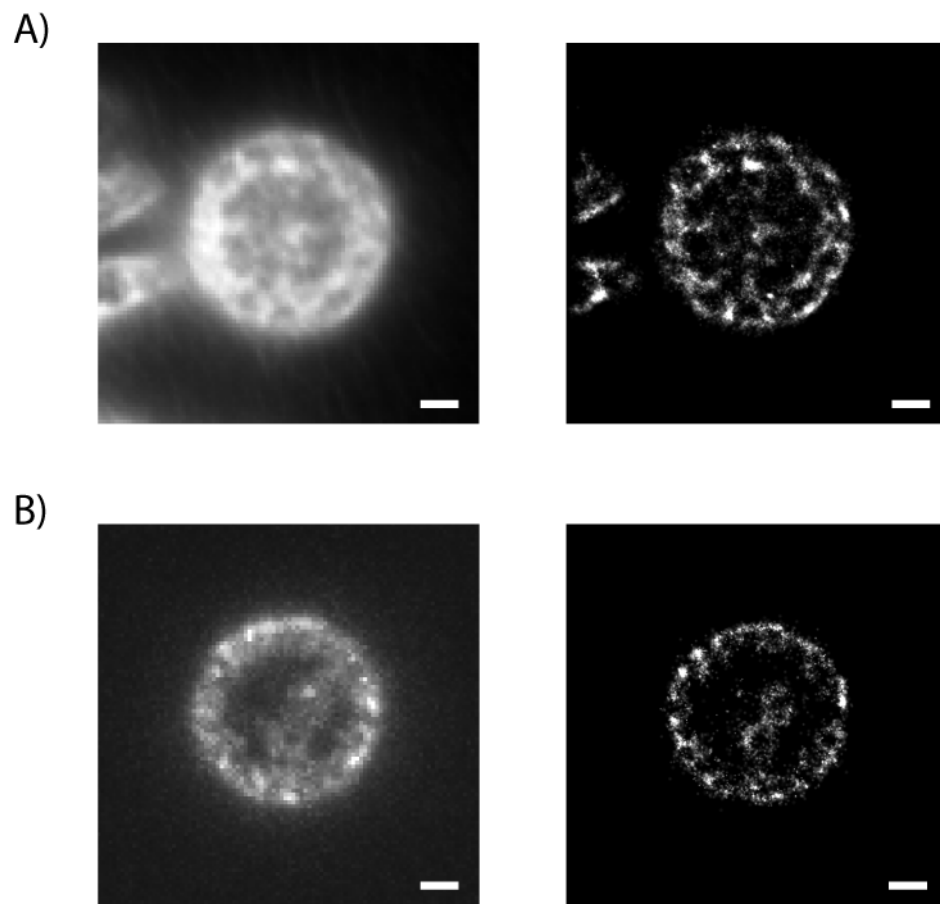


Figure S5. Additional PALM images on tpSil3-Dendra2 and tpSil3-mEOS3.2

Comparison of epifluorescence images (left) and the reconstructed super-resolution image (right) of (A) tpSil3-Dendra2 and (B) tpSil3-mEOS3.2 with z-focus on the valve region of the diatom. All scale bars are 1 μ m.

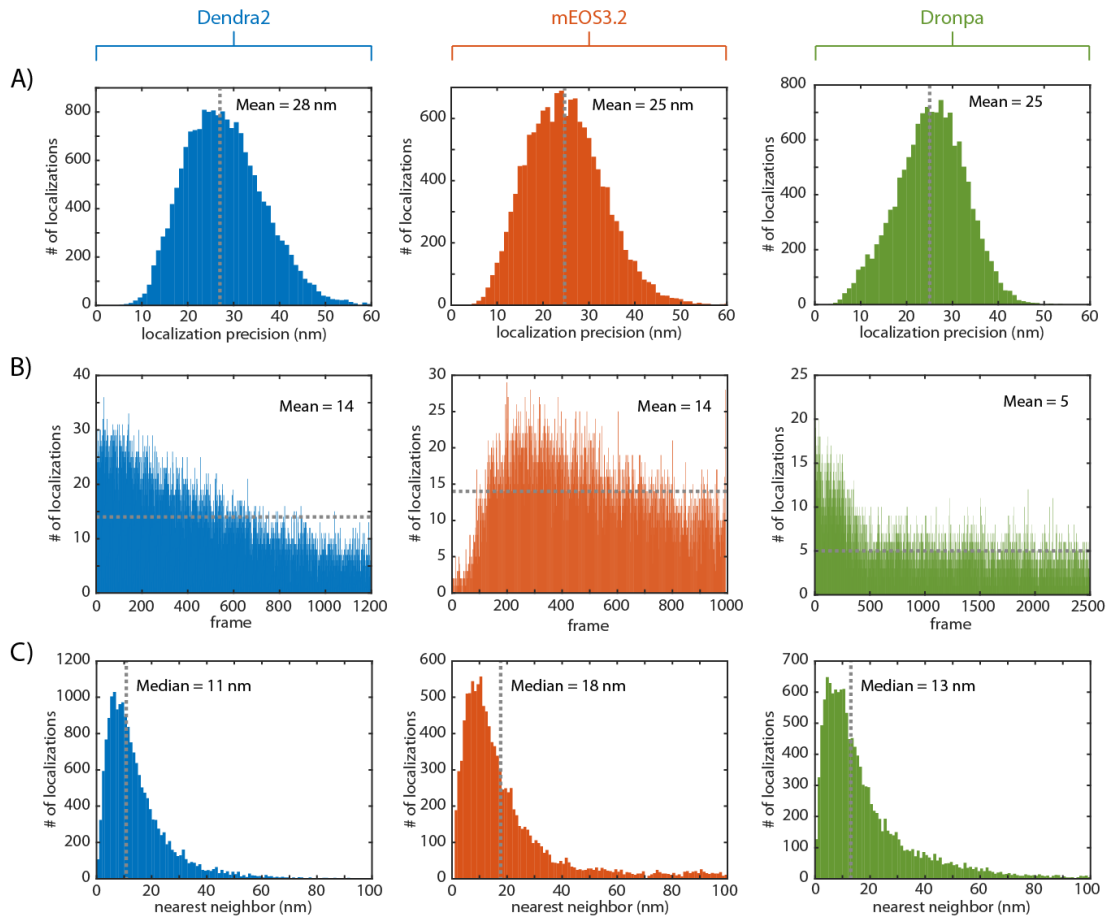


Figure S6. Localization parameter for tpSil3-Dendra2, mEOS3.2 and Dronpa

Parameter of the reconstructed super-resolution image in Figure 2D, E and F for Dendra2, mEOS3.2 and Dronpa, respectively. **(A)** Localization precision of all localizations. **(B)** Number of localized events per frame. **(C)** Nearest neighbor distribution of all localized events.

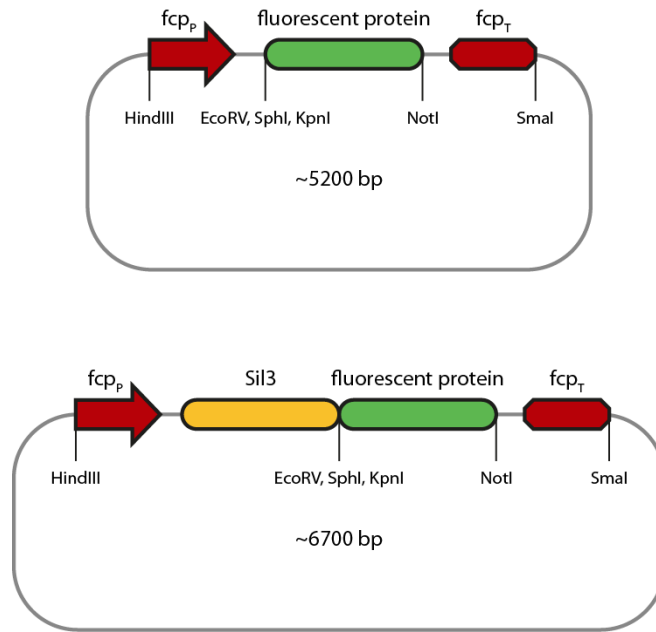


Figure S7. Vector design for cloning

(Top) Cytosolic expression featuring the fluorescent protein in between the fcp promoter and terminator.

(Bottom) Sil3 fusion constructs, with an N-terminal Sillafin 3 followed by the C-terminal FPs

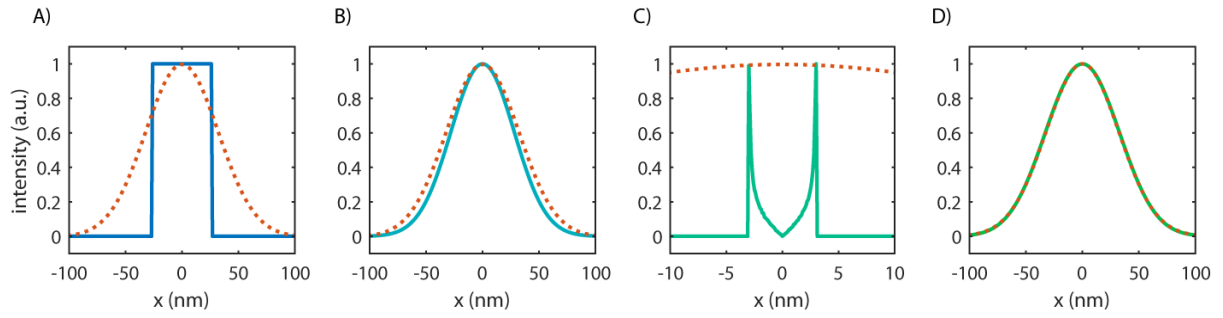


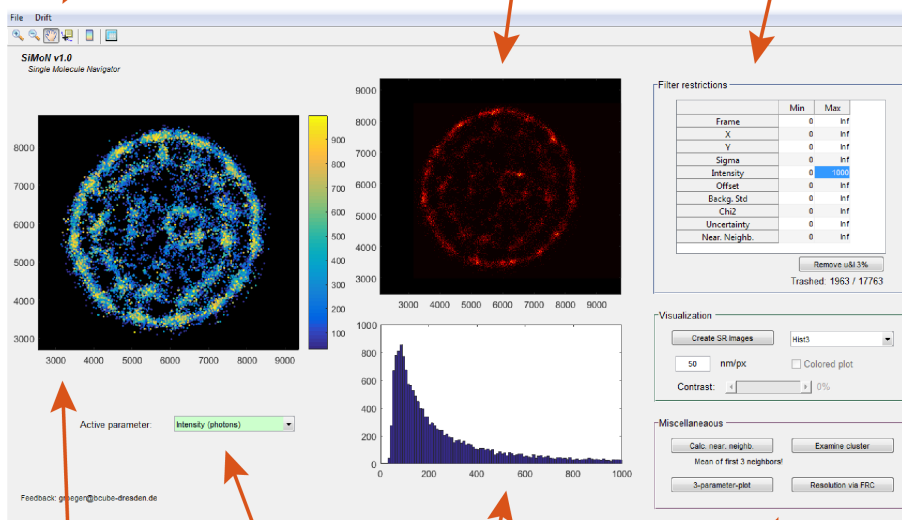
Figure S8. Convolution to estimate tpSil3-Dendra2 filament thickness

Convolution process to estimate the underlying filament thickness based on a measured filament thickness of 76nm (FWHM) in the super-resolution image. The gauss profile of the measured filament is displayed in red in all plots. **(A)** Underlying filament with a thickness of 53nm. **(B)** The first convolution contribution: Fluorophore localization uncertainty of 28nm. **(C)** The second convolution contribution: Linker length between protein and fluorophore of 3nm. Assumed as points on a sphere of 3nm radius. **(D)** Final convolution of A) to C) resulting in the desired width of 76nm.

Options to remove linear drift or load a drift file from an external source

Preview of the resulting super-resolution image

Filter out certain localizations by specifying parameter thresholds



Multiple options to form a super-resolution image, including coloring by the active parameter

Scatter plot of all localizations colored by the active parameter

The active localization parameter to display

A histogram of the current active parameter

More display options, including
 - calculation of the nearest neighbor distribution
 - a simple cluster identification script
 - plotting multiple localization parameter against each other
 - resolution estimation via fourier-ring-correlation

Figure S9. MATLAB GUI to visualize super-resolution data from thunderSTORM
 Screenshot of the custom written MATLAB GUI for super-resolution data visualization with several features annotated.

Table S2. Codon optimized sequences for the fluorescent proteins

DNA sequences of all the fluorescent proteins used in this study - plus their translation. Codon optimized for expression in *T. pseudonana*.

PATagRFP
702 nucleotides, 234 amino acids

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1 ATGTCGGATGATCAAAAGAAACATGCAC ATGAAGTTGATCATGGAAGTACTGTGAAC AACCCACCTTCAAGTGCATCAGAGGGC GAGGAAAGCCATACGAGGAAACAAACA ATGCGTATCAAGTGGTGAAGTGGACCA
1 M S E L I K E N M H M K L Y M E G T V N N H H F K C T S E G E G K P Y E G T Q T M R I K V V E G G P
151 TTGGCATTTCGCATTCGACATCTGGCCAGC AGCTTATGTACGGATCTCCATTCATC AACCCACCGAGGAGTCCGACATCTCGG AAGCAATCATTCCAGAGGGATTCACATGG GAGCGTGTGACAAACATACGAGAGTGGTGT
51 L F F A A D D I L A T S F M Y G S S T F I N H T Q G I F D F W K Q S F P E G F T W E R V T Y E D G G
301 GTTTTACAGCGCAACCAAGACCCCTATTG CAGACCGAGTGTGTATTCACACCTGAG ATCAGGGGAGTGCACCTCCCATCAACCGA CCAGTGTAGAGAAAGACGTGGATGG GAGCCATCCAGGAGTGGAGCCAGCA
101 V L T A T Q D T S L Q D G C L I Y N V K I R G V N F P S N G P V M K R K T L G W E P S T E K L K P A
451 GATGGTGAATGGAGGAGATGGATGATG GCATTGAAGTTGGTGGAGGTGGACCTGT ATCTGCAACTTCAAGACGACTACCTTCC AAGAAGCCAGCAAGAACTTGAAGTGCCT GGTGTTTACTACGTGACCCCTGTTGGAG
151 D G G L E G R V D M A L K L V G G G H L I C N F K T T Y R S K K P A K N L K M P G V Y Y V D R R L E
601 ATCATCAAGAGGGCCACCAAGACATAC TGGGACCAACATGAGTGGCAGTGGCAAGA TACTCCGATTCGCAAAATGGGGAC AAGTTGAACGA
201 I I K E A D K E T Y W E Q H E V A V A R Y S D L P S K L G H K L N *
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PamCherry
711 nucleotides, 237 amino acids

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1 ATGGTGTCAAAGGTTGAAGAGCAACATG GCCATCATCAAGAATTCTAGCGTTTCAAG GTGCACATGAAGGATCCGTGAACGACAT GTGTTTGAAGTGGAGGTGAAGGCAAGGA CGACCATACGAGGAAACAGACAGCAAG
1 M V S K G E E D N M A I I K E F M R F K V H M E G S V N G H V F E I E G E G E G R P Y E G T Q T A K
151 TTGAAGTGCAGAGGTTGACCATTCGCAAC TTACGCTGGGATTTTGTGCCACAGTAT ATGTCAGGATCAACGCATACGTGAAGCAC CCAGCAGATTTCCAGACTACTCAAGTTG TCCTCCAGAGGATTCAGTGGGAGCGTT
51 L E V T E G G F L F F F W D I L S F Q F M Y G S N A Y V K H P A D I P D Y F K L S F P E G F K W E R
301 GTGATGAAGTTGAGGATGGTGTGTGTG ACCCTGACCGAGATTCATCTTGCAGAC AGGTAAATTCATCTCAATFAGTGTGCGT GGAACCACTTCCATCCGATGACCCAGTG ATCCGAAAGAACATGGATGGAGGCC
101 V M K F E D G G V V T V T Q D S S L Q D G E F I Y K V K L R G T N F P S D G P V M Q K K T M G W E A
451 TTGTCAGAGAAATGACCCAGAGGATGTT GCCTTGAAGGTTGAAGTTAAGCCAGTGTG AAGTTGAAGGATGGGACACTACGATGCA GAAGTCAAGCAGACTACAAGCAAGAAG CCAGTTCACTTGGTGGTATACACAGCTG
151 L S E R M Y P E D D A L K G E V K P R V K L K D G G H Y D A E V K T T Y K A K K P V Q L P G A Y N V
601 AACCCAAAGTGGACATCCACATCCAGC GAGGATTCACAGATCGTTGACAAACAG AGAGCAGAGGACATAGTACAGTGGGA ATGGACGAGTTGACAAATGA
201 N R K L D I T S H N E D Y T I V E Q Y E R A E G R H S T G G M D E L Y K *
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PAGFP
720 nucleotides, 240 amino acids

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1 ATGGTGAAGAGGCGAGGAGCTGTTCCAC GGGTGTGCCCATCTGTTGAGAGTGGAC GGGCAGTAAAGGCCCAAGTTCAGCGTG TCCGGCAGGGCGAGGGCGATCCACCTAC GGCAGCTACCCCTGAAGTTCATCTGCACC
1 M V S K G E E L F T G V V P I L V E L D G D V N G H K F S V S G E G E G D A T Y G K L T L K F I C T
151 ACCGCAAGCTCCCGCTCCCTGGCCACCC CTGCTGACACCTTCAGTCCGGCGTGCAG TGTTCAGCGCTACCCCGACCATGCAAG CAGCAGACTTCTCAAGTCCGCGATGCC GAGCGTACGTCGAGGAGCCACCATCTTC
51 T G K L P V P W T L Y T T F S Y G V Q C F S R Y P D H M K Q H D P F K S A M P E G Y V Q E R T I F
301 TTCAGGACAGCCCACTCAAGACCCCGC GCCAGGTGAAGTTCGAGGGCCACCCCTG GTCAACCGACTCGAGTGAAGGCATCGAC TTCAGGAGGAGCCCAACTCTTGGGCGAC AAGTGGATACACTCAACACAGCCACAC
101 F K D D G N Y K T R A E V K F E G D T L V N R I E L K G I D F K E D G N I L G H K E D G N I L G H
451 GTCTATATCATGGCCGACAGCAGAAAGAC GGCATCAAGCCCACTCAAGATCCGCCAC AACCTGCAAGAGCGGTGACACTACGATGCA GAAGTCAAGCAGACTACAAGCAAGAAG CCAGTTCACTTGGTGGTATACACAGCTG
151 V Y I M A D K Q K N G I K A N F K I R H N I E D G S V Q L A D H Y Q Q N T P I G D G P V L P L P D N H
601 TACTGAGCCACCTCAAGCTGAGCAAA GACCCCAAGGAGGCGCATCACATGGTC CTGCTGGAGTCTGTCAGCCGCGGGGATC ACTCTGGCATGGACGAGCTGTCAAGTAA
201 Y L S K L S K L S K L R H M V L L E F V T A A G I T L G M D E L Y K *
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mEos3.2
681 nucleotides, 227 amino acids

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1 ATGTCTGCATCAAGCCAGACATGAAGATC AAGTTGCGTATGGAAGGCAACGTGAACGGA CACCATTCTGTCAGCGGTGATGGAAC TGGAAAGCCATTCAGGGAAGCAGTCCATG GATTTGGAAGTGAAGAGGTTGACCATTTG
1 M S A I K F P D M K I K L R M E E G N V N G H H F V I D G D G T G R P F E G F Q S M D L E V K E G G P L
151 CCATTCGACATTCGACATTCGACAGGAC CTGCTGACAGCAACCGTGTGTCCGCAAG TACCGACAGCACTCCGACCATGCAAG CAGTCTCCGAAAGGATCTCCCTGGGAG AGATCATGACATTCGAGGAGCCGAGTTC
51 P E A F D I L T A F F H Y G N R V F A E Y P D N I Q D D Y F K Q S F P K G Y S W E F S L T F E D G G I
301 TGCAAGCAGCTAACGATATTACGATGGAA GCGCACAGCTTCTACACCAAGTCCGATTC TACGCAAGCACTCCGACCAAGCAGCA GTGATCGAGAAAGACATTGAAGTGGAG CCATCCACCGAAGATGTACGTGGTGTAT
101 C N A R N D I T M E G D T F Y N K V R F Y G T N F P A N G P V M Q K K T L K W E P S T E K M Y V R D
451 GGTGCTTTCAGCGGTGATATTGAGATGCC TTGTTGTGGAGGAAACCCACATACCCT TCGGATTCCTGACGACTACAAGGCCAAA GAAAGGGTGTAAAGTTCAGGCTGACAC TCGTGGATCATCTGATCGAGATTTGTC
151 G V L T G D I E M A L L L E G N A H Y R C D F R T T Y K A K E R G V K L P G A H F V D H C I E I L S
601 CAGCAGAGGATATAACCAAGTGAAGTTG TACGAGCAGCAGTGGCAGACTCAGGATTC CCAGATAACCGCAAGCGTTGA
201 H D K D Y N K V K L Y E H A V A H S G L P D N A R R *
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Dendra2
693 nucleotides, 231 amino acids

```
1 ATGACACACCTGGAATCACTTGCATCAAA GAAGATATGCGGATGGAAGTGCACATGGA GGCACCTGAAGGACATGCTGCTGATT GAGGGCAGGGAAGGAAACCATACGAG GGAACACAGCCGCAACTGCAGTGAAG
1 M H T P G I N L I R E D M R V K V H M E G N V N G H R F V I E G E G K G E F Y E G T Q T A N L T V K
151 GAGGCTACCACTTCCATTTCTGACGAC ATTTTGCACACCGCGTGCATTCAGGAAC CGTGTGTTTACAAAGTACCCGAGCAGCATC CCAGACTACTCAAGCAATCATCCAGAG GGATCTCGTGGGAGCTCAAGTCAATTC
51 E G A P L P F S Y D I L T T A V H Y G N R V F T K Y P E D I P D Y F K Q S F P E G Y S W E R T M T F
301 GAGGATGAAGTTCGACATCCGTTCC GACTTTCATGGAGGGCGACTTGTCTCTC CAGAAGCTCGTTTCAAGGAAACGACTTT CCACCAGGAGCAGTGTGAGCAAAAAG ACATGAAGTGGAGCCATCCACGAGAG
101 E D K G I C T I R S D I S L E G D C F F Q N V R F K G T N F P P N G P V M Q K K T L K W E P S T E K
451 TTGACTGTCGACGGTTTGTGGTGGAA AACATCAACATGGCCTTGTGTTGGAGGTT GGTGGACACTACTTGTGCGATTTCAGAGC ACGTACAAGGCCAAGAGGTTGGTCAATTG CCAGATGCACATTTCTGGATCCAGCTATC
151 L H V R D G L V G N I N M A L L L E G G S H Y L C D F K T T Y K A K K V V Q L P D A H F V D H R I
601 GAGTCTTGGAAACCTCCACATCAAC AACGTGAGTTTACGACCCACCTGGCC TGAATCTTCCATGCCATCAACTCTGG TGA
201 E I L G N D S D Y N K V K L V E H A V A R Y S P L P S Q V W *
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Dronpa
678 nucleotides, 226 amino acids

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1 ATGGTGTCAAGTGAAGCAGACATGAAG ATCAAGTTCGCTATGGAAGTGCAGTGAAC GGACATCCATTCGCAATTCAGGTTGTTGA TTGGAAAGCCATTCAGGGAAGCAGCTGG ATGACTTGAAGTGAAGAGGTTGGACCA
1 M V S V I K P D M K I K L R H E G A V N G H P P A I E G V C L G K P F E G K Q S N D L E V K E G G P
151 TTGGCATTTCGCATTCGACATCTGGCCAGC GTGTTCTGCTACGAAACCGTGTGTTGCA AAGTCAAGCAGACACTGCGACTACTTC AAGCAGTCAATCCAGAGGATACCTGCTGG GAGATCAAAAGCAACAGAGCCGTTGCA
51 L P F A Y D I L T T V F C Y G N R V F A K Y P E N I V D Y F K Q S F P E G Y S W E R S M N Y E D G G
301 ATCTGCAAGCAGCAACGATATTACGTTG GACGTGACTGCTACATCTACGAGATCCGT TTCGATGGTCAACTTCCAGCAAAACGGA CCAGTGTGAAAAGCCTACAGTGAAGTGG GAGCCATCCAGAGAGAGTGTACGTGGCT
101 I C N A T N D I T L D G D C Y I Y E I R F D G V N F P A N G P V M Q K R T V K W E P S T E K L Y V R
451 GATGGTGTTCGAGGTTGACCTGAACATG GCATTTCATGGAGGTTGGTGGACACTAC CTTTGGATTTCAAGACGACTCAAGGCA AAGAAGTGTTCCAATTCAGCAGTACCAT TTCGTGGATCCACATCGAGATCAAGTCC
151 D C V L E G D V N W A L S L E G G H Y R C D F K T T Y K A K K V V Q L P D Y H F V D H H I E I K S
601 CAGCAGAGGATCTCAAGCTGAAGTGTG CATGAGCAGCAGGAGCAGATTCAGGTTG CCACCTCAAGCAAAAGA
201 H D K D Y S N V N L H E H A E A H S E L P R Q A K *
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(see attached movie file)

Movie S1. Raw movie of tpSil3-Dendra2, -mEOS3.2 and Dronpa

The movie contains the first 500 frames of the raw movie used to create the PALM images shown in this study (Fig. 2). From left to right: Dendra2, mEOS3.2 and Dronpa. One pixel equals 106.7 nm.