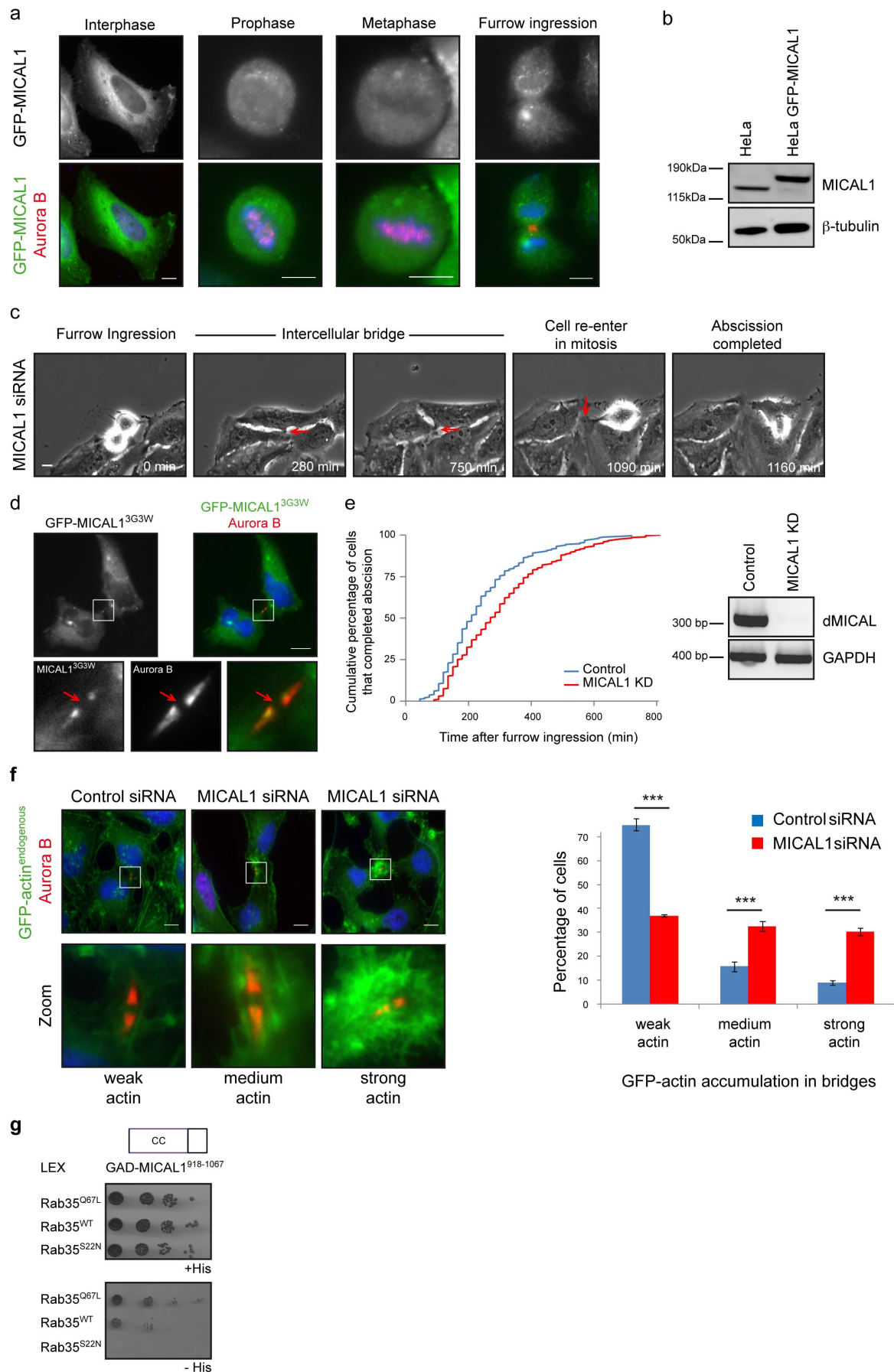
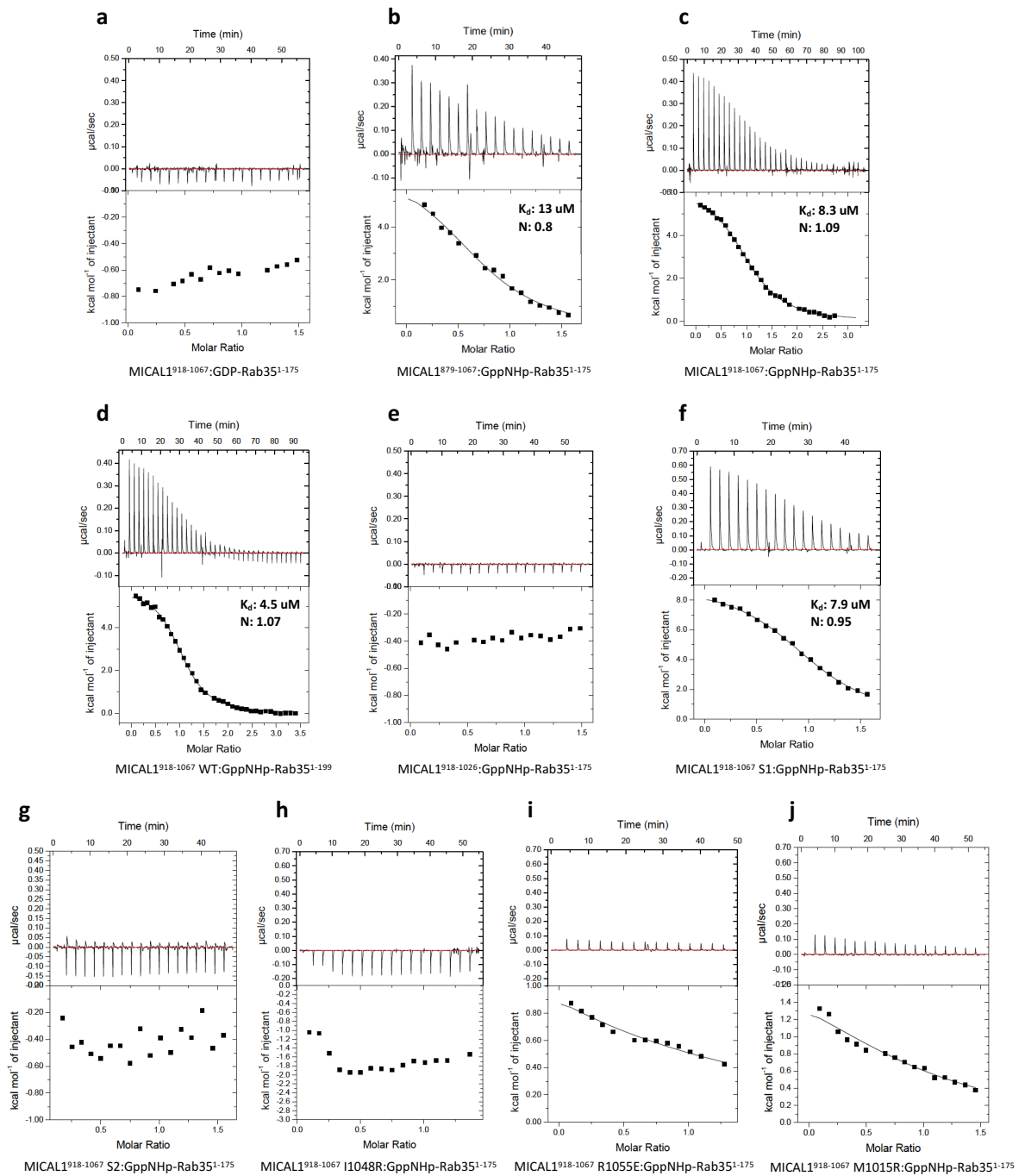


SUPPLEMENTARY INFORMATION



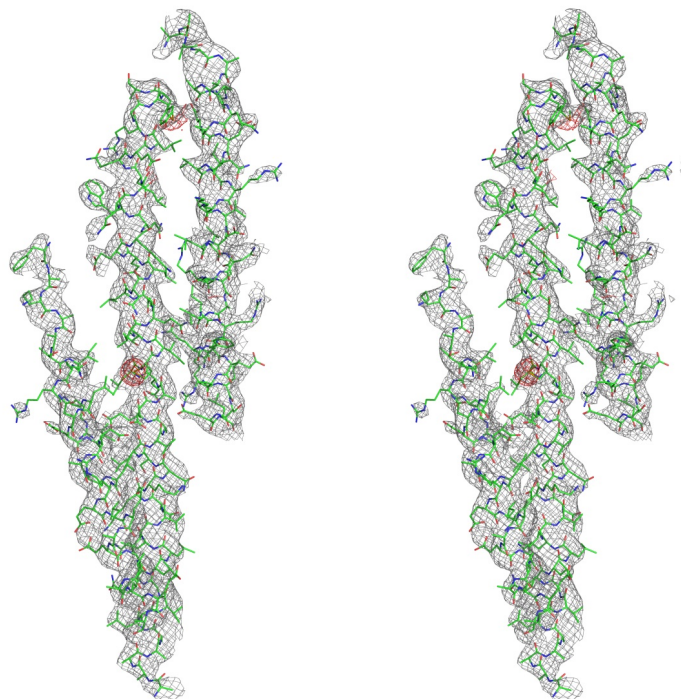
Supplementary Figure 1: Function of MICAL1 and dMICAL in cytokinesis

- (a) HeLa transfected with GFP-MICAL1 (green) were stained with Aurora B (red). Scale bars, 10 μm .
- (b) Western blot from HeLa (parental cell) and HeLa GFP-MICAL1^{endogenous} cell line extracts. Loading control: β -tubulin.
- (c) Snapshots from a time-lapse phase-contrast microscopy movie of MICAL1-depleted cells. Scale bars, 10 μm .
- (d) HeLa cells transfected with GFP-MICAL1^{3G3W} catalytically-dead mutant (green) were stained with Aurora B (red). Scale bars, 10 μm .
- (e) Distribution of the abscission times in control- and MICAL1-depleted *Drosophila* S2 cells (N= 3). $p = 0.000$ between red and blue curves (KS test). $n = 249\text{-}272$ cells per condition. RT-PCR for *GAPDH* and *dMical* at Day6.
- (f) Left: HeLa cell line expressing actin tagged by GFP following TALEN excision and homologous recombination at the endogenous locus (GFP-actin^{endogenous}) were stained with AuroraB (red) and DAPI (blue) in control- or MICAL1-depleted cells. Right: Quantification of the intensity of the GFP-actin^{endogenous} in bridges after control and MICAL1 depletion (N= 3). Error bars represent standard deviations. ***: $p < 0.001$ (two-way ANOVA). $n = 192\text{-}234$ cells per condition. Scale bars, 10 μm .
- (g) *S. cerevisiae* reporter strain expressing indicated GAD- and LEX fusion proteins, and grown on selective medium with or without Histidine.
- In all figures, Red arrow: Flemming body.

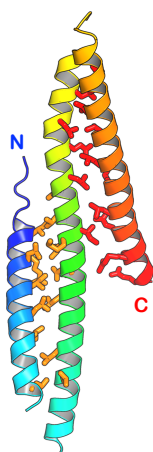
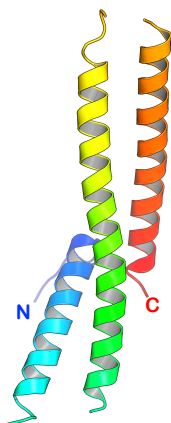
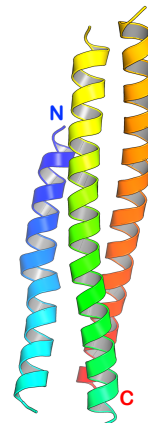


Supplementary Figure 2: Rab35 / C-terminal MICAL1 constructs Interaction by Isothermal Titration Calorimetry (ITC)

The top panels show the baseline corrected titration data, and the bottom panels show the binding isotherm fitted for the interactions between GDP-Rab35¹⁻¹⁷⁵ and MICAL1⁹¹⁸⁻¹⁰⁶⁷ wild-type (a) or GppNHp-Rab35¹⁻¹⁷⁵ and: MICAL1⁸⁷⁹⁻¹⁰⁶⁷ wild-type (b), MICAL1⁹¹⁸⁻¹⁰⁶⁷ wild-type (c), MICAL1⁹¹⁸⁻¹⁰²⁶ (e), MICAL1⁹¹⁸⁻¹⁰⁶⁷ S1 mutant (E946K, V950D, E953K, V971E, L975R, V978E) (f), MICAL1⁹¹⁸⁻¹⁰⁶⁷ S2 mutant (R1012E, M1015R, L1034K, V1038E) (g), MICAL1⁹¹⁸⁻¹⁰⁶⁷ I1048R (h), MICAL1⁹¹⁸⁻¹⁰⁶⁷ R1055E (i) or MICAL1⁹¹⁸⁻¹⁰⁶⁷ M1015R (j). Moreover, titration of GppNHp-Rab35¹⁻¹⁹⁹ with MICAL1⁹¹⁸⁻¹⁰⁶⁷ wild-type (d) was tested and show that the Rab35 tail doesn't contribute much to the affinity. The results were fitted using one site binding mode resulting in estimation of the complex dissociation constants (K_d) and interaction stoichiometry (N).

a**b**

MICAL1 C-terminal domain

lactoferrin-binding domain of
Pneumococcal surface protein AN-terminal region of type III secretion
major translocator SipB from Salmonella

Supplementary Figure 3: MICAL1 C-terminal domain crystal structure

(a) The MICAL1 C-terminal domain structure is shown in stereo view with a sigma-weighted 2Fo-Fc map at 3.3Å resolution, contoured at 1.0 σ (grey) and anomalous difference map contoured at 4 σ (red). (b) The structure of MICAL1 corresponds to a sheet of three anti-parallel helices. Note that it is difficult to predict whether helical regions form a single alpha-helix¹ or pack as anti-parallel or parallel helices². This structure provides insights about how alpha-helices that have characteristic coiled-coil repeat patterns can pack. The first (H1) and the last helices (H3) of MICAL1 bind to the helix-2 (H2) through coiled-coil interaction (shown with side chains in sticks). The distribution of hydrophobic residues on the central H2 helix orients the other two helices. Thus, the MICAL1 C-terminal domain assembles in an original, flat, alpha-helical sheet structure, rather than a three-helix bundle. This C-terminal domain is compared with two three-helix fold of closest topology found with the PDB fold server (<https://www.ebi.ac.uk/msd-srv/ssm/cgi-bin/ssmserver>): lactoferrin-binding domain of Pneumococcal surface protein A (PDB ID 2PMS)³, and N-terminal region of type III secretion major translocator SipB from Salmonella (PDB ID 3TUL)⁴. The three protein folds consist of three consecutive helices shown in rainbow colors that interact in an antiparallel manner, but in MICAL1, the H1 and H3 helices do not interact and orient themselves to form a flat curved sheet.

-----H1-----
a-d-a-d-a-d-a-d

MICAL1_Human 911 RTLLRRAKEEEMKRFCKAQTIRRLNEIEAALRELEAGVKLELALRRQ-----SSS--- 962
MICAL1_Mouse 898 RTLMRRAKEEEMKRFCKAQTIRRLNEIEATMRELEAGVKLELALRRQ-----SSS---
MICAL1_Chicken 992 RTLNRRHAREAQMKRFCKAQTIRRLNEIEVTFRELEQQGKLEKFLRED-----SDS---
MICAL1_Zebrafish 1046 KTLERKAKMTEIQRFHKAQSIRRLNEIEVTFKLEEKGVLEERLALRGE-----TGT---
MICAL_FruitFly 4543 RAISKASQAELKRLRIAQEIQRQEETIEVQLKLEARGVLEKALRGEAQNIENLDA-----
MICAL_ApisFloreia 2595 KTTKRIARQAQLKRLRMAQEIQRKLEETIEVQKRELSRGVSEKALRGE-----GE---C
MICAL3_Human 1834 KAARRQAKQEELKRLHRAQIIRQLQVEERQRLLEERGVAVEKALRGE-----AGM---
MICAL3_Mouse 1825 KAARRQAKQEELKRLHRAQIIRQLQVEERQRLLEERGVAVEKALRGE-----AGM---
MICAL3_Chicken 2018 KAARRQAKQEELKRLHRAQIIRQLQVEERQRLLEERGVAVEKALRGE-----AGM---
MICAL3a_Zebrafish 1488 RAARRQAKQEELKRLHRAQIIRQLQVEEVQRLLEEKGVAVEKALRGEADFWEDS-----S---TSVLLDVHLCGM---
MICAL3b_Zebrafish 1809 KAARRQAKQEELKRLHRAQIIRQLQVEERQRLLEERGVAVEKALRGEADYWGES-----N---YSEILDHLHLCGM---
MICAL3_Lizard 2065 KAARRQAKQEELKRLHRAQIIRQLQVEERQRLLEERGVAVEKALRGEAVEPNAG-----TPRRRPLSFCCPAHEGM---
MICAL-L1_Human 674 -----QADQYIPEEDIHGEMDTIERRLDALEHHRGVLEEKLRGGLN-----
MICAL-L1_Mouse 681 -----QADQYIPEEDIYGEMDNIERQLDALEHSGVLEEKLRGGAN-----
MICAL-L1_Chicken 764 -----QTDQYIPEEDIYGEMDAIEHQDLDEHHRGVLEEKLRSSSEN-----
MICAL-L_FruitFly 772 -----KVLQRLPLQEIIRHFEIITAVQGLEKQGVLEKMRDRCCERS--LDATDTDGP-----ESAEVLT
MICAL-L_Lizard 733 -----QSDQYVPVEDIYGEMDSIEQQLDELEHHRGVLEERKLRSMENVRERLNCSSLKRWEQDISFISQLHSLGEV--
MICAL-L2_Human 730 -----LHPDYLSPEEIQRQLQDIERRLDALELRGVLEEKLRRAAEG-----
MICAL-L2_Mouse 836 -----LHPDYIPQEEIQRQLQDIERQLDALELRGVLEEKLRRAAEG-----
MICAL-L2_Xenopus 784 -----ARPEYIPEEEIQRQLQIEQEQLDALEQQGVMEKQLRICDG-----
: : : : : * * * * *

-----H2-----
d-a-d-a-d-a-d-a-d-a-d-a-d-a-d

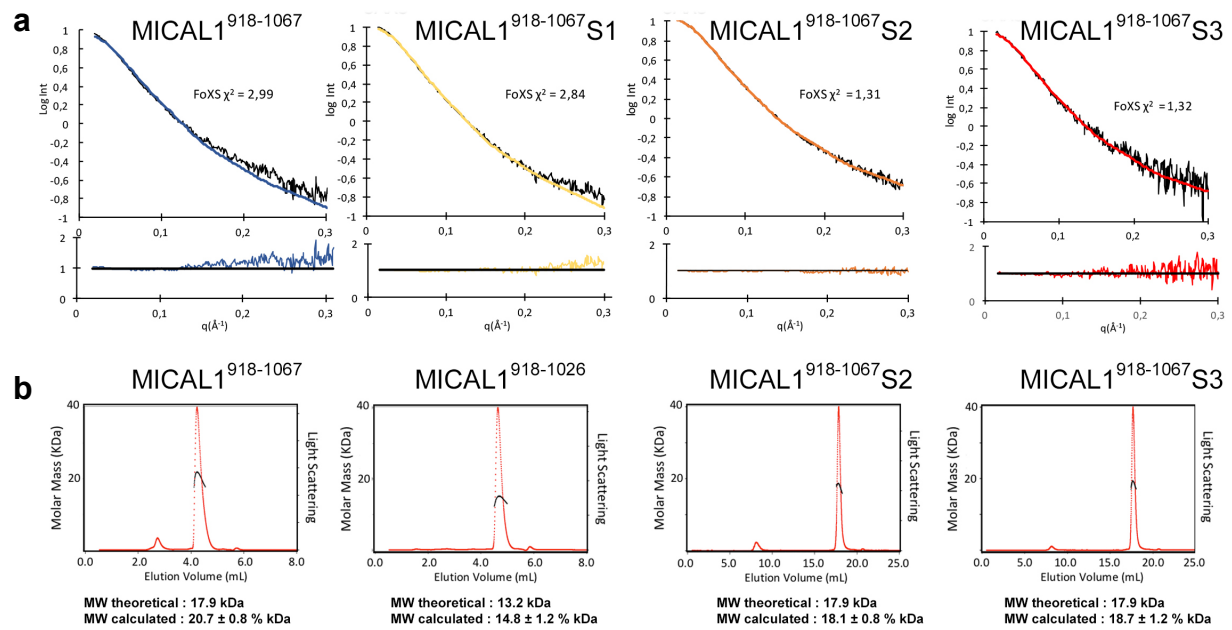
MICAL1_Human 1021 PEQKKKLVGGQLLQVVKNSLVAEAEALMITVQELNLEEKQWLDQELRGYMNREENL
MICAL1_Mouse PEQKKKLVGGQLLQVVKNSLVTEAEALMITVQELNLEEKQWLDQELRGYMNREETM
MICAL1_Chicken PADQKKLVGGQLLQVVKNSLVTEAEALMITVQELNLEEKQWLDQELRGYNIETEEAL
MICAL1_Zebrafish GD---PTIIDQWIELVQEKNNLLSEESDLVVASRQLELEDKQSMLEMLERRRYMEMDDSE
MICAL_FruitFly TKDNDKELKLELLEIWRNITALKKRDEELTIRQQLLEQYRHAQKEELNLRSCNKL
MICAL_ApisFloreia SDREEADLLREWFLLMKEKTELRRYKELLLVRAQEVQLLEDRHERLQQLERLADDDNK
MICAL3_Human GKDDPKLMQEWFKLVQEKNNLVRYESELMIFARELELEDQSRQLQQLERMAVEDHL
MICAL3_Mouse GKDDPKLMQEWFKLVQEKNNLVRYESELMIFARELELEDQSRQLQQLERMAVEDHL
MICAL3_Chicken GKDDPKLMQEWFKLVQEKNNLVRYESELMIFARELELEDQSRQLQQLERMAVEDHL
MICAL3a_Zebrafish GKDDPKLMQEWFKLVQEKNNLVRYESELMIFARELELEDQSRQLQQLERMAVEDHL
MICAL3b_Zebrafish GKDDPKLMQEWFKLVQEKNNLVRYESELMIFARELELEDQSRQLQQLERMAVEDHL
MICAL3_Lizard GKDDPKLMQEWFKLVQEKNNLVRYESELMIFARELELEDQSRQLQQLERMAVEDHL
MICAL-L1_Human -EGREDDMLVDWFKLIHEKHLVRRSEELIYVFKQQLNQRQADVEYELRCLLNKPEKD
MICAL-L1_Mouse -EGSEDDMLVDWFKLIHEKHLVRRSEELIYVFKQQLNQRQADVEYELRCLLNKPEKD
MICAL-L1_Chicken -DSPEDSLLVDWFKLIHEKHLVRRSEELIYVFKQQLNQRQADVEYELRCLLNKPEKD
MICAL-L_FruitFly NSKEVEDLLIQFLFELVNEKNEFLRRQAELMYLRRQHRLEQEQADIEHEIRVLMGQPEHN
MICAL-L_Lizard MEAPEDGGLVDWFKLIHEKHLVRRSEELIYVFKQQLNQRQADVEYELRCLLNKPEKE
MICAL-L2_Human -DDAEDSLMVDWFKLIHEKQLLLRQSEELMYKSKAQRLLEEQLDIEGELRLMAKPEAL
MICAL-L2_Mouse -DASEDSLMVDWFKLIHEKQLLLRQSEELMYKSKAQRLLEEQLDIEGELRLMAKPEAL
MICAL-L2_Xenopus -DESEDLLMVDWFKLIHEKQLLLRQSEELMYKSKAQRLLEEQLDIEGELRLMAKPEAL
: : : : : * * * * *
▲ ▲ ▲ ▲ ▲

-----H3-----
d-a-d-a-d-a-d-a

MICAL1_Human 1067 KTAADRQAEQVLRKLVLDLVNQDRLIRFOEERRLSEELALGTGAQG---
MICAL1_Mouse KTEADQLSENQVLRKLVLDLVNQDRLIRFOEERRLREMPA-----1048
MICAL1_Chicken KTFEDRAAEQQILAQLLKVVDKRNALHMQEERKLSLELHP-----1142
MICAL1_Zebrafish KSPFQQKHAEAILQEMLDVVDMDSLVAFLEEKRLKEVNDQFNSSL-15-1214
MICAL_FruitFly KSSADVAAGAIENEMLEIVAKRAALRPASQDLDTAAGSASTSAE-18-4720
MICAL_ApisFloreia KTSADVKKEGEILTEMLEIVAKRDSLIALLEEBRQRYQDEDRDLEA-21-2672
MICAL3_Human KTEELSEKQILNEMLEVVEQRDSLVALLLEEOQLREKEEDKDLEA-12-2002
MICAL3_Mouse KTEELSEKQILNEMLEVVEQRDSLVALLLEEOQLREKEEDKDLEA-12-1993
MICAL3_Chicken KTEELSEKQILNEMLEVVEQRDSLVALLLEEOQLREKEEDKDLEA-12-2186
MICAL3a_Zebrafish KGEELAEERRISEMLDVVEQRDALVALLLEEOQLREKEEDSDLEA-12-1673
MICAL3b_Zebrafish KTEELAEKQILNEMLEVVEQRDSLVALLLEEOQLREKEEDKDLEA-12-1994
MICAL3_Lizard KTDDELSEKQILNEMLEVVEQRDSLVALLLEEOQLREKEEDKDLEA-12-2255
MICAL-L1_Human WTEEDRARKEVLMQELVTITIEQRNAIINCLDEDQREEEEDKMLEA-45-863
MICAL-L1_Mouse WTEEDRARKEVLMQELMTITIEQRDAIINCLDEDQREEEEDKMLET-45-870
MICAL-L1_Chicken WTEEDVRKEVLMQELVTITIEQRNAIINCLDEDQREEEEDKMLEA-45-953
MICAL-L_FruitFly KTDSDKAHEVLLINLVKVVEMRNEVDSLETDRVREAREDMMSIKN-71-1010
MICAL-L_Lizard WTDDDRVRKEVLMQELVTITIEQRNAIINCLDEDQREEEEDKMLEA-45-952
MICAL-L2_Human KSLQERRREQEELLEQYVSTVNDRSDIVDCLDEDRLREQEEDQMLRD-30-904
MICAL-L2_Mouse KSPQDRQREQEELLEQYVSTVNDRSDIVDCLDEDRLREQEEDQMLRN-29-1009
MICAL-L2_Xenopus KTPGESERKEKELLDQLLLIVNDRSEIVDCLDEDRLREKEEDMMNA-39-967
: * : : : * : :
▲ ▲ ▲ ▲ ▲

Supplementary Figure 4: MICAL C-terminal domain fold conservation

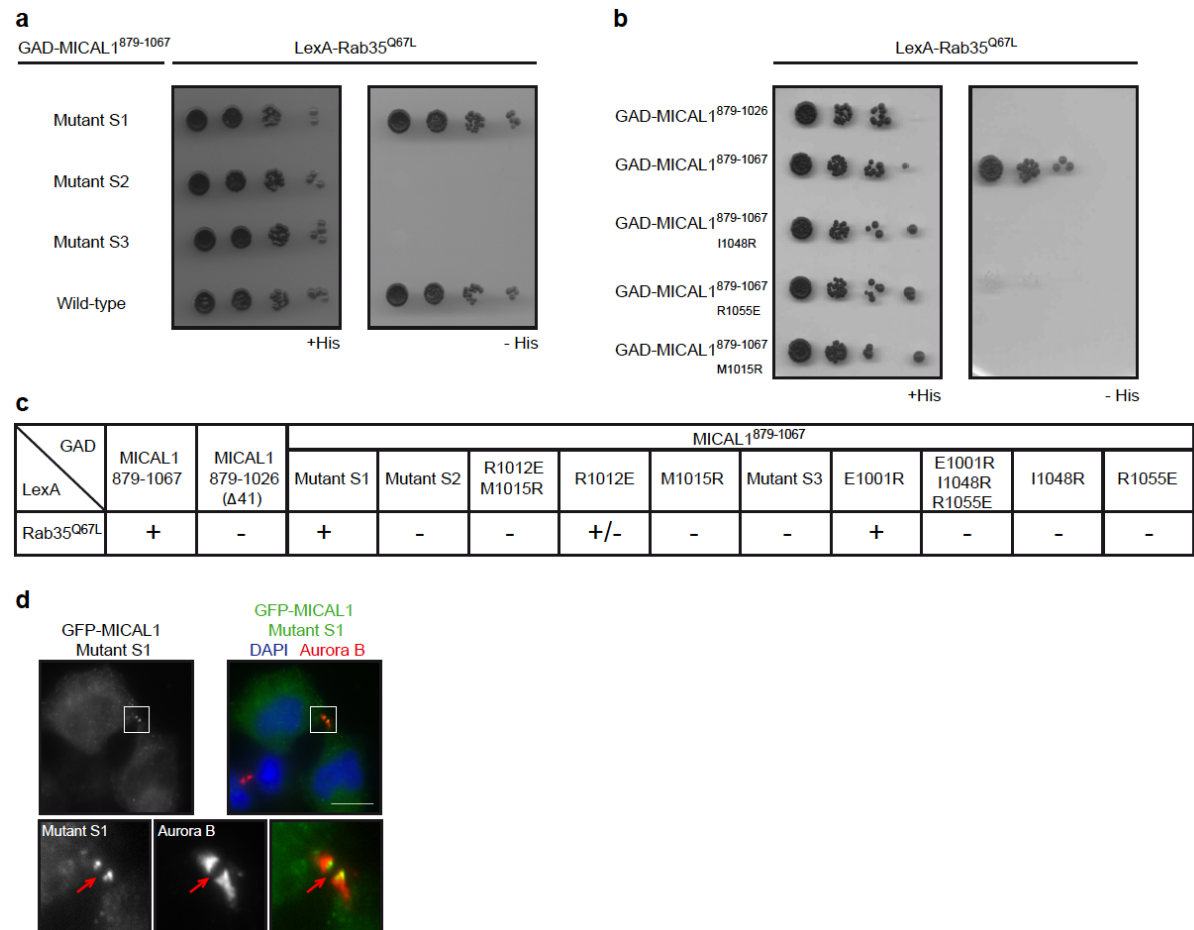
Alignment of C-terminal regions of selected MICAL sequences. The output reflects the degree of sequence similarity among the proteins. Orange letters: conserved residues implicated in interaction between Helix-1 and Helix-2 and red letters: residues implicated in interaction between Helix-2 and Helix-3. Glycine and proline residues frequently found in loop structures of proteins are shown in brown. Residues matching the consensus pattern of heptad repeat motif for canonical coiled-coils are annotated above the sequence for MICAL1 with *a* and *d* letters. Residues mutated to define the surface S1 and S2 are indicated with highlights using a color code as defined in Fig.5a (Surface 1 in yellow (S1: E946, V950, E953, V971, L975, V978) and Surface 2 in orange (S2: R1012, M1015, L1034, V1038). The side chains of aa I1048 and R1055 essential for Rab35 interaction are displayed in white with highlighted red contour). Conserved residues on the surface of Helix-2 and Helix-3 (as defined in Fig. 5b) are indicated with green triangles below the sequences.



Supplementary Figure 5: SAXS and MALS analysis of MICAL1 constructs

(a) Comparison of SAXS profiles calculated from atomic model (colored lines) against SAXS experimental data (black curve). The residual plots are for $q(\text{\AA}^{-1})$ (x axis) versus experimental intensity divided by model calculated intensity (y axis). The SAXS data of the S1 mutant (E946K, V950D, E953K, V971E, L975R, V978E), S2 mutant (R1012E, M1015R, L1034K, V1038E) and S3 mutant (E1001R, V1038E, V1041E, I1048R, R1055E) are consistent with a conserved fold despite the introduction of mutations.

(b) SEC-MALS elution profiles displaying the plots of the UV signal (red line) at 280 nm and plot of molar mass (black dashed line) vs. elution volume. Molar masses determined by MALS analysis (dotted lines) across the peaks of eluted protein from a Superdex 200 (for MICAL1⁹¹⁸⁻¹⁰⁶⁷-S2 and MICAL1⁹¹⁸⁻¹⁰⁶⁷-S3) size exclusion column or X-Bridge BEH SEC 200 $\text{\AA}$ (for MICAL1⁹¹⁸⁻¹⁰⁶⁷ and MICAL1⁹¹⁸⁻¹⁰²⁶) column. All the proteins are eluted as single molecular species.

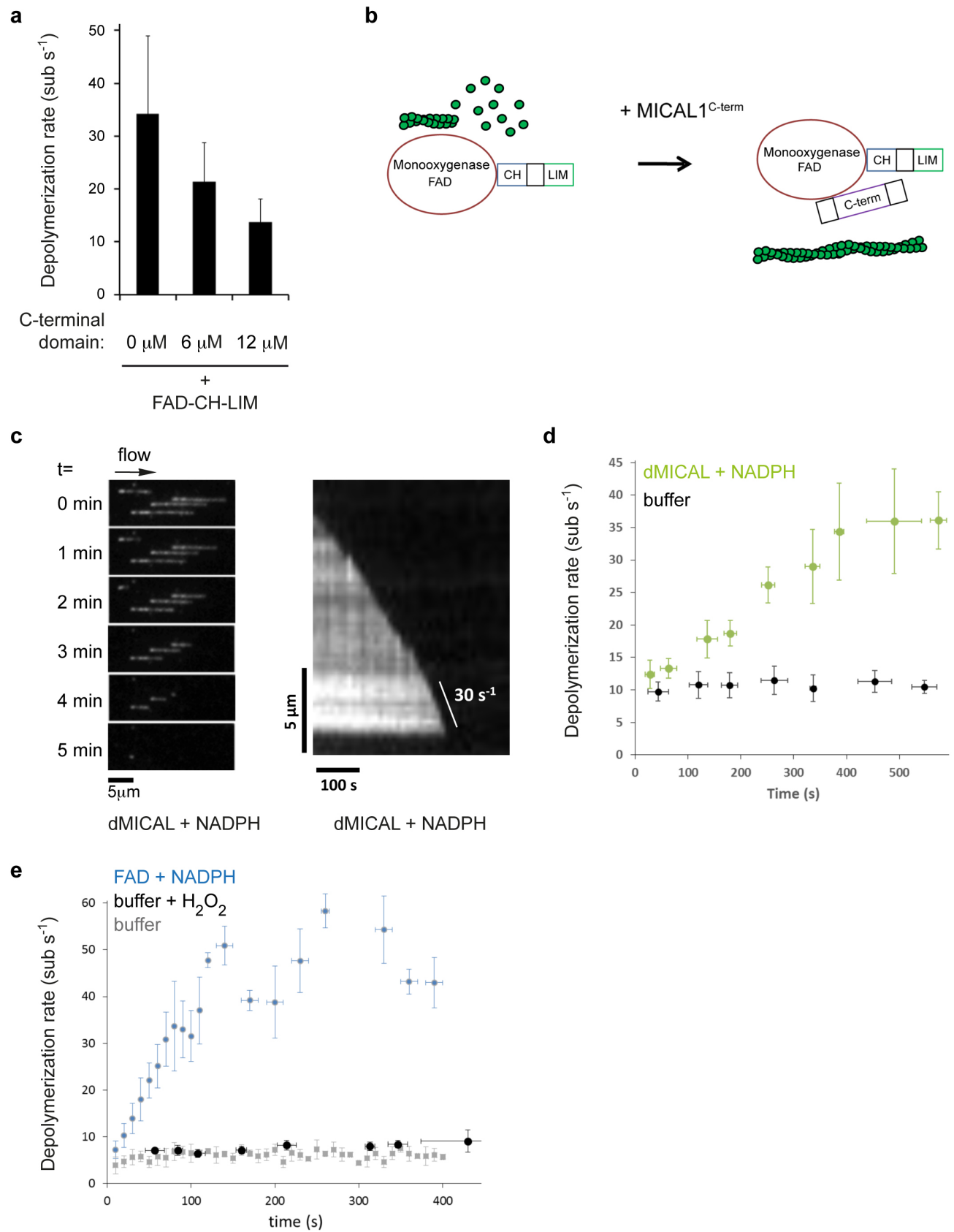


Supplementary Figure 6: Interactions between Rab35 and WT or mutant MICAL1

(a-b) *S. cerevisiae* reporter strain expressing indicated GAD- and LEX fusion proteins were grown on selective medium with or without Histidine.

(c) Summary of all the interaction between Rab35^{GTP} and MICAL1 mutants tested by yeast-two hybrids.

(d) HeLa cells transfected with GFP-MICAL1 Mutant S1 (green) were stained with Aurora B (red) and DAPI (blue). Scale bar, 10 μm.



Supplementary Figure 7: *Drosophila* MICAL has the same effects as human MICAL1 on actin filaments

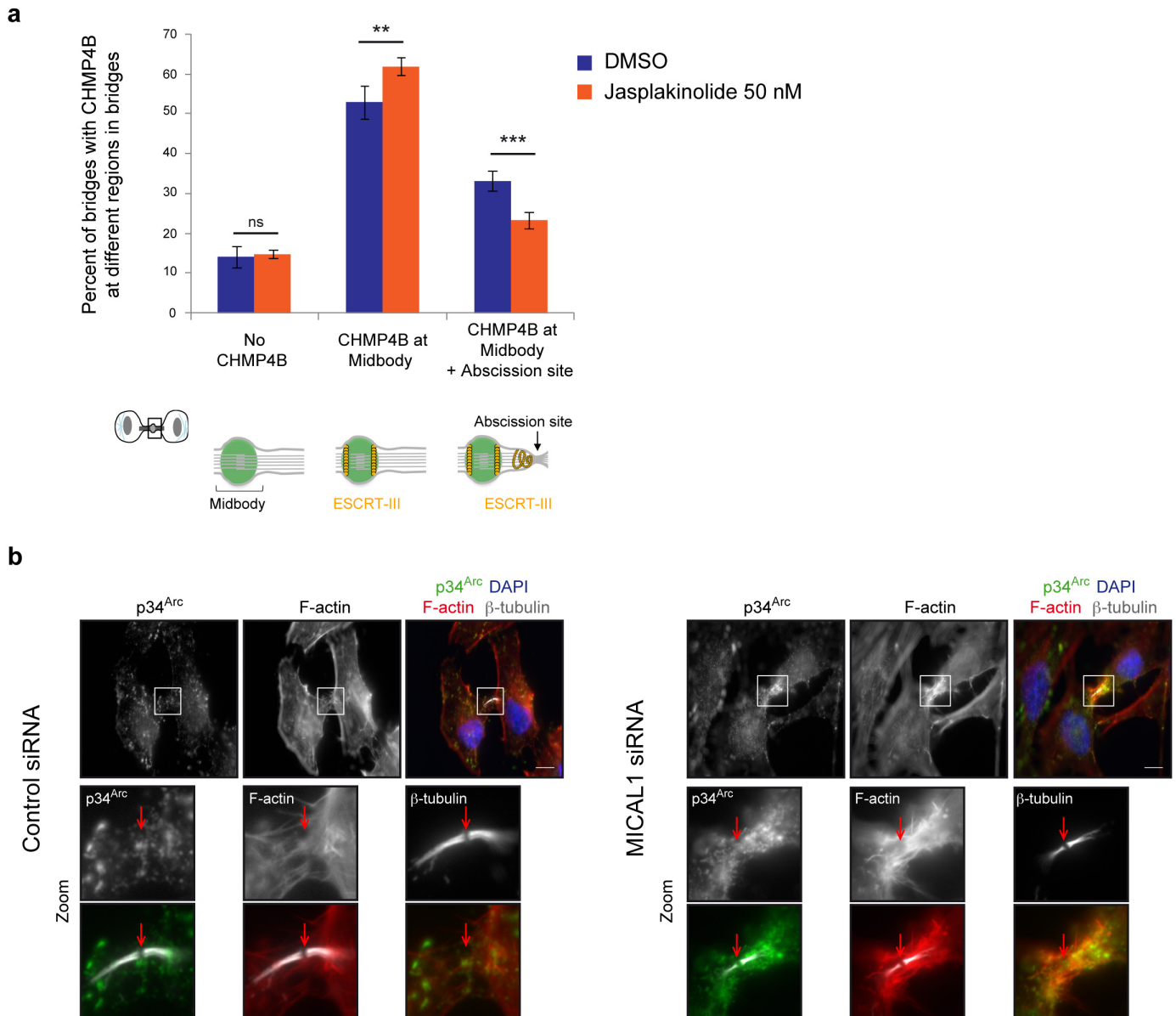
(a) Depolymerization rates measured on ADP-actin filaments anchored on to the surface by inactivated myosins (as in Fig. 6d and f). Depolymerizing filaments are exposed to 120 μ M NADPH, with 600 nM human FAD-CH-LIM and (from left to right) 0, 6 or 12 μ M human MICAL1-C-terminal domain. 10-13 filaments quantified per condition. Error bars represent standard deviations.

(b) Model for inactivation of the redox enzyme MICAL1 by its C-terminal domain. Actin is in green.

(c) Timelapse images showing a typical set of ADP-actin filaments exposed to 600 nM dMICAL FAD-CH + 120 μ M NADPH, in our microfluidics setup. The flow runs from left to right, the filament pointed ends (left hand side) are anchored to the coverslip surface, and the barbed ends (right hand side) depolymerize freely (left). Kymograph of a depolymerizing filament from the same experiment (right).

(d) Average depolymerization rates over time, for ADP-actin filaments exposed to 600 nM dMICAL FAD-CH + 120 μ M NADPH (green) or to buffer alone (black). Error bars are standard deviations (right). 19-25 filaments quantified per condition.

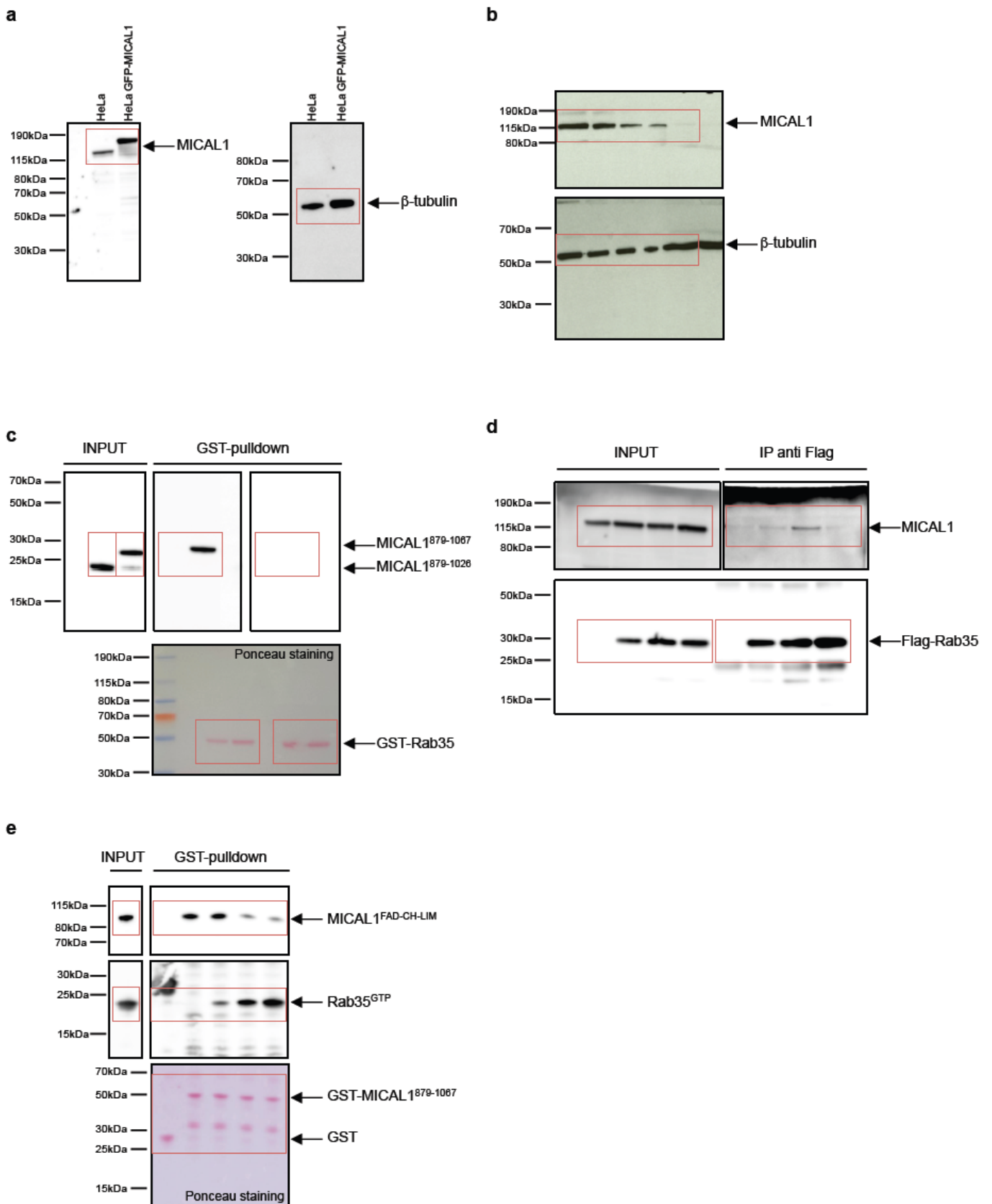
(e) Using our microfluidics setup we monitored the barbed end depolymerization of ADP-F-actin in the presence of 40 mM H_2O_2 (black) and compare it to data from Fig. 6B for filaments depolymerizing in the presence of buffer (gray) and in the presence of 600 nM human FAD + 120 μ M NADPH (blue). We also verified the potency of our H_2O_2 (data not shown) by monitoring the elongation of filaments from 1 μ M G-actin incubated with 40 mM H_2O_2 for 20 minutes at 20°C and found that, in agreement with previous reports⁵, H_2O_2 oxidizes G-actin and hinders polymerization: filaments elongated from H_2O_2 -treated monomers at 2.4 ± 0.3 sub/s (StdDev, N=12), compared to 7.8 ± 0.8 sub/s (StdDev, N=12) in control experiments.



Supplementary Figure 8: F-actin stabilization impairs the recruitment of CHMP4B at the abscission site. MICAL1 depletion induces accumulation of Arp2/3 complex protein p34^{Arc} at the bridge

(a) Percentage of bridges with no CHMP4B, with CHMP4B only at the midbody, and with CHMP4B at the midbody + at the abscission site in cells treated with either DMSO or Jasplakinolide (N=4). Error bars represent standard deviations. **: $p < 0.01$; ***: $p < 0.001$ (two-way ANOVA). $n = 330$ - 347 cells per condition.

(b) Staining of p34^{Arc} (green), F-actin (phalloidin, red), β -tubulin (gray) and DAPI (blue) in control- or MICAL1-depleted cells. Scale bars, $10\mu\text{m}$.



Supplementary Figure 9: uncropped images for presented Western Blots

(a) corresponds to Supplementary Fig. 1b; (b) corresponds to Fig. 2a; (c) corresponds to Fig. 4c; (d) corresponds to Fig. 4d; (e) corresponds to Fig. 6e.

C-term MICAL1	Rab35	Kd1	Kd2	mean Kd	N
MICAL1 ⁹¹⁸⁻¹⁰⁶⁷	GDP-Rab35 ₁₋₁₇₅	n.b.*	n.b.*	-	-
MICAL1 ⁹¹⁸⁻¹⁰⁶⁷	GppNHp-Rab35 ₁₋₁₇₅	8,3	4,5	6.4	1.09
MICAL1 ⁹¹⁸⁻¹⁰⁶⁷	GppNHp-Rab35 ₁₋₁₉₉	4,5	5	4.8	1.07
MICAL1 ⁸⁷⁹⁻¹⁰⁶⁷	GppNHp-Rab35 ₁₋₁₇₅	13	13	13	0.8
MICAL1 ⁹¹⁸⁻¹⁰²⁶	GppNHp-Rab35 ₁₋₁₇₅	n.b.*	n.b.*	-	-
MICAL1 ⁹¹⁸⁻¹⁰⁶⁷ S1 ^a	GppNHp-Rab35 ₁₋₁₇₅	7,9	6,4	7.2	0.95
MICAL1 ⁹¹⁸⁻¹⁰⁶⁷ S2 ^b	GppNHp-Rab35 ₁₋₁₇₅	n.b.*	n.b.*	-	-
MICAL1 ⁹¹⁸⁻¹⁰⁶⁷ I1048R	GppNHp-Rab35 ₁₋₁₇₅	n.b.*	n.b.*	-	-
MICAL1 ⁹¹⁸⁻¹⁰⁶⁷ R1055E	GppNHp-Rab35 ₁₋₁₇₅	w.b. ⁺	w.b. ⁺	-	-
MICAL1 ⁹¹⁸⁻¹⁰⁶⁷ M1015R	GppNHp-Rab35 ₁₋₁₇₅	w.b. ⁺	w.b. ⁺	-	-

Equilibrium dissociation constants (K_d) and stoichiometry constant (N) values were determined by ITC measurements.

* no binding

⁺ very weak binding, fitting is not reliable

^a S1 mutant (E946K, V950D, E953K, V971E, L975R, V978E).

^b S2 mutant (R1012E, M1015R, L1034K, V1038E).

Supplementary Table 1: Isothermal Titration Calorimetry measurements for Rab35 and C-terminal MICAL1 constructs

	Peak SAD SeMet
Data collection	
Space group	P 4 ₃ 22
Cell dimensions	
<i>a</i> , <i>b</i> , <i>c</i> (Å)	52.78, 52.78, 157
α , β , γ (°)	90, 90, 90
Wavelength	0.978870
Resolution (Å) ^a	43.8 - 3.3 (3.49 - 3.3)
<i>R</i> _{sym}	3.7 (32.1)
<i>R</i> _{meas}	4 (34.8)
<i>I</i> /σ(<i>I</i>)	26.56 (4.67)
<i>CC</i> _{1/2}	100 (98.4)
Completeness (%)	99.6 (97.9)
Redundancy	7 (6.6)
Refinement	
Resolution (Å)	37.32 - 3.3 (3.418 - 3.3)
No. reflections	3730 (356)
<i>R</i> _{work} / <i>R</i> _{free}	0.2715 (0.3131)/0.3068 (0.4240)
No. atoms protein	956
<i>B</i> factors protein	120.59
R.m.s deviations	
Bond lengths (Å)	0.005
Bond angles (°)	0.62
Favoured/allowed/outlier	96%/4.3%/0%
Ramachandran angles	

^a Values in parentheses are for highest-resolution shell.

The crystallized MICAL1 fragment corresponds to residue range: 918-1067. The loops: 918-924, 955-963, 1017-1019 and 1060-1067 - are missing in the structure.

Supplementary Table 2: Data collection and refinement statistics for the MICAL1 C-terminal domain (PDB ID code 5IE0)

Supplementary References

1. Knight, P.J. *et al.* The predicted coiled-coil domain of myosin 10 forms a novel elongated domain that lengthens the head. *The Journal of biological chemistry***280**, 34702-34708 (2005).
2. Sievers, F. *et al.* Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. *Molecular systems biology***7**, 539 (2011).
3. Senkovich, O. *et al.* Structure of a complex of human lactoferrin N-lobe with pneumococcal surface protein a provides insight into microbial defense mechanism. *Journal of molecular biology***370**, 701-713 (2007).
4. Barta, M.L. *et al.* The structures of coiled-coil domains from type III secretion system translocators reveal homology to pore-forming toxins. *Journal of molecular biology***417**, 395-405 (2012).
5. DalleDonne, A. & Milzani, R. H₂O₂-treated actin: assembly and polymer interactions with cross-linking proteins. *Biophysical journal***69**, 2710-2719 (1995).