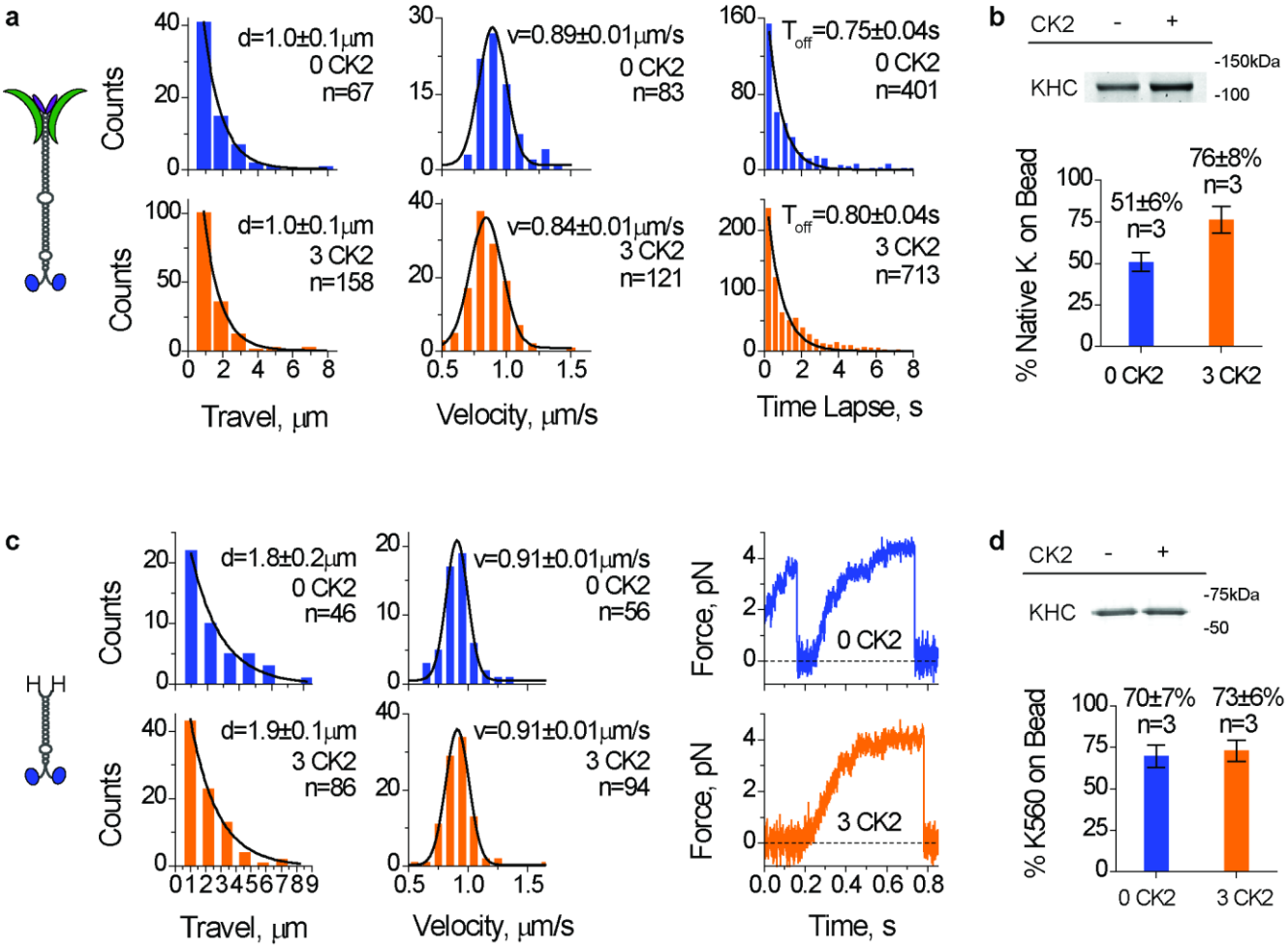
Supplementary Figure



Supplementary Figure S1. Effect of CK2 treatment on the single motor function of active kinesin, and motor:bead recruitment. Native or truncated kinesins were incubated with or without CK2 for 40 at 30°C prior to functional studies. "3 CK2" indicates an incubation ratio of 3 kinase molecules per motor. "0 CK2" indicates CK2-blank samples. (**a**) Distributions of travel distance, velocity, and time lapse for beads carried by single native kinesins. "Time lapse" denotes the time interval between consecutive binding events when a bead, carried by a single active kinesin, was spatially confined to the vicinity of a microtubule. CK2-treated kinesin (orange) required significantly more dilution relative to the untreated kinesin (blue) to reach the single motor range (~ 30% binding fraction[11]). (**b**) Effect of CK2 treatment (3:1 CK2:motor) on motor-bead association for the native kinesin, assayed by

Coomassie stain. Carboxylated polystyrene beads were used to evaluate non-specific binding between the native kinesin and the bead. Values shown were determined as the fraction of bead-bound motors *vs.* total input amount (mean ± SEM, n = 3 each). (**c**) Distributions of travel distance and velocity, and representative force traces of beads carried by a single K560 (~ 30% binding fraction). CK2-treated K560 again required significantly more dilution relative to the untreated sample to reach the single motor range. (**d**) Effect of CK2 on K560-bead association, assayed by Krypton IR stain (Thermal Scientific). Carboxylated polystyrene beads were used to evaluate non-specific binding between K560 and the bead. Values shown were determined as the fraction of bead-bound motors *vs.* total input amount (mean ± SEM, n = 3 each).

Supplementary Table S1

	Accession Number	Unique Peptides		% Coverage		Protein Name
		Exp. 1	Exp. 2	Exp. 1	Exp. 2	
K560	P33176	61	49	47.7	42.9	Kinesin-1 heavy chain
	Q86YZ3	1	n/a	0.6	n/a	Hornerin
	P07900	1	n/a	1.5	n/a	Heat shock protein HSP 90-alpha
	P68400	1	n/a	4.6	n/a	Casein kinase II subunit alpha
K560+CK2	P33176	57	73	47.0	51.1	Kinesin-1 heavy chain
	P68400	37	32	72.1	67.8	Casein kinase II subunits alpha
	P67870	24	22	88.4	71.6	Casein kinase II subunits beta
	P11021	1	n/a	2.4	n/a	78 kDa glucose-regulated protein
	Q5H9R7	1	n/a	1.5	n/a	Serine/threonine-protein phosphatase 6 regulatory subunit 3

Table S1. Purity of K560 and CK2 samples examined via liquid chromatography-mass spectrometry. Two independent experiments were carried out for K560, and K560+CK2. No significant contamination was detected for either CK2 or K560. The potential contaminants were not meaningful: they were identified by only one unique peptide each (with less than 4.5% sequence coverage), and were detected in only one of the two parallel experiments. Tubulin β and α isoforms associated with the final microtubule affinity step in K560 purification (Fig. 2b), were present in both K560 and K560+CK2 samples, and are not included in this table. Activation of kinesin (native or truncated) was independently verified using this particular CK2 lot; the same magnitude of activation was observed across three different lots of CK2 used in the current study.

Supplementary Table S2

(i)	TKEYELLS(Phospho)DELNQK+2
m/z	**Ion**
275.136	y2(-0.035)
341.173	b3-H2O(-0.0089)
359.102	b3(-0.091)
372.136	y3-NH3(-0.052)
389.183	y3(-0.031)
502.211	y4(-0.087)
522.322	b4(0.066)
580.328	b9+2(0.078)
613.347	y5-H2O(0.017)
631.312	y5(-0.029)
651.254	b5(-0.044)
693.325	b11-NH3+2(0.53)
746.35	y6(-0.018)
764.27	b6(-0.11)
815.27	y7-H3PO4(-0.12)
847.096	MH-H3PO4+2(0.67)
877.352	b7(-0.11)
896.408	y7-NH3(0.068)
913.227	y7(-0.14)
928.303	y8-H3PO4(-0.17)
1041.328	y9-H3PO4(-0.23)
1061.167	b9-H3PO4(-0.35)
1139.388	y9(-0.15)
1159.345	b9(-0.15)
1303.443	b11-H3PO4(-0.20)
1401.615	b11(-0.0035)
1431.54	y11(-0.10)

(ii)	TKEYELLSDELNQK+2
m/z	**Ion**
258.218	y2-NH3(0.073)
275.188	y2(0.017)
341.293	b3-H2O(0.11)
359.267	b3(0.074)
372.235	y3-NH3(0.047)
389.242	y3(0.028)
485.262	y4-NH3(-0.0098)
502.187	y4(-0.11)
516.784	b4(-0.062)
614.262	y5-NH3(-0.052)
631.284	y5(-0.057)
651.256	b5(-0.042)
746.349	y6(-0.019)
764.237	b6(-0.15)
816.373	y7-NH3(-3.9e-4)
833.385	y7(-0.015)
846.728	MH-NH3+2(-0.19)
859.285	b7-H2O(-0.17)
877.407	b7(-0.060)
946.344	y8(-0.14)
964.393	b8(-0.11)
1059.489	y9(-0.079)
1079.324	b9(-0.20)
1188.499	y10(-0.11)
1208.521	b10(-0.047)
1321.586	b11(-0.066)
1351.665	y11(-0.0090)
1435.595	b12(-0.10)
1480.668	y12(-0.049)
1563.783	b13(0.029)

Table S2. Corresponding m/z values of each y- and b- ions for LC-MS/MS spectra (Fig. 3d) of tryptic phosphopeptide (**i**, TKEYELLS(phospho)DELNQK) and non-phosphopeptide (**ii**, TKEYELLSDELNQK). m/z values are highlighted in black. b-ions are highlighted in red, with mass errors for the assigned ion types in parenthesis.

Supplementary Discussion

Binding fraction measurements detect/reflect the presence of active motors.

In binding fraction measurements, beads were held by the optical trap in the vicinity of a microtubule for 30 seconds, and binding events were scored only if the bead bound to, and processed along the microtubule. A wait time of 30 sec is sufficient for binding if there is any active kinesin present. Kinesin's on-rate when confined to the vicinity of a microtubule is typically 2-5 per second[12], allowing repeated opportunities for the motor to bind in this trial time. Svoboda and Block[11] demonstrated that the probability of a bead binding/moving along the microtubule is negligible in repeated trials if the bead failed to bind and move in the first trial. We obtained similar results when we extended the wait time from 30 to 120 sec. Here the overall binding fraction of untreated kinesin was kept below 30%, and no more than 2% of moving beads were simultaneously transported by more than one active motors[11]. Of the thirty beads that we tested that didn't interact with microtubules within the first 30 sec wait time, only one bound and moved after the first 30 sec. The resulting 2.5 % increase in overall binding fraction measured using 30 *vs.* 120 sec wait time is within the 7 % measurement error ($\sqrt{[p(1-p)/n]}$, where p is the measured binding fraction, n is the number of trial beads[11]). Taken together, binding fraction measurements are sufficient to detect the presence of the active, untreated motor(s) on the bead. An increase in binding fraction thus necessarily reflects an increase in the number of active motors on the bead, rather than an increase in the microtubule association rate of the active kinesin.

Kinetic calculation for equilibrium microtubule-kinesin association at 4 mM AMPPNP.

The dissociation constant, K_d, for the kinesin-microtubule interaction in the presence of 1 mM AMPPNP has been measured by Crevel, Lockhart, and Cross[28] to be 0.27±0.15 μM. Since the microtubule concentration (5 μM) in our microtubule pelleting assay was in significant excess than our kinesin concentration (~7.5 nM), we can estimate that

$$\frac{[Kin*MT]_{eq}}{[Kin]_{tot}} = \frac{[MT]_{tot}}{K_d + [MT]_{tot}} \approx \frac{5}{0.27\mu M + 5\mu M} = 0.948,$$

where $[Kin*MT]_{eq}$ is the concentration of kinesin bound to microtubules at equilibrium, $[Kin]_{tot}$ is the total concentration of active kinesin, and $[MT]_{tot}$ is the total concentration of tubulin-heterodimer. This equilibrium kinetic calculation suggests that 94.8% of all kinesins that are active ought to co-sediment with microtubule pellet at 4 mM AMPPNP. Thus microtubule pull-down assays provides a direct read out for the amount of active motors present.

Assuming that the entire motor population is active (as was assumed for these calculations), any potential effect of CK2 to increase kinesin's on rate, or decrease kinesin's off-rate, cannot result in a significant increase in kinesin binding to microtubules under our assay conditions (with 4 mM AMPPNP present). For example, a 100-fold increase in K_{on} could only increase the kinesin bound to microtubules from 94.8% to 99.9% of the total active population.

Time scale for the tail-independent inactivation/reactivation of K560.

To approximate the rate of tail-independent kinesin inactivation, we carried out microtubule pulldown assays of microtubule affinity purified K560 as rapidly as experimentally allowed for (Fig. 2d): within four hours of ATP release from the microtubule (Fig. 2b), and without any freeze-thaw cycles. This freshly purified K560 was placed on ice for 2.5 hours while we determined the motor concentration using Coomassie stained SDS-PAGE gel and BSA standards, and was then incubated with or without CK2 (3:1 CK2:K560 molar ratio) on ice for 1.5 hrs, followed by microtubule pulldown assays. More than half of the initially active K560 became incapable of binding/interacting with microtubule within four hours of the final purification step (ATP-release from microtubules), despite being kept on ice. CK2 increased the fraction of microtubule-bound K560 from the untreated 45 ± 6 % to 78 ± 5 % (mean ± SEM, n = 3, Fig. 2d). We were experimentally limited by the time necessary to assay for motor

concentration and the CK2-treatment. The tail-independent inhibition (and CK2-mediated activation) identified in this study, may occur more rapidly than the 4 hr (and 1.5 hr) reported here.

Supplementary Methods

Proteins

Functional Tail-less K560[1], monomer K339[2], and phospho-mutant S520A were constructed using the plasmid pET17b_k560[3] (Addgene) as template. Protein was bacterially expressed and Ni-NTA purified as previously reported[1]. To specifically select for motor activity, unless otherwise noted Ni-eluted K560 was further purified by microtubule affinity purification[4] prior to flash freezing in 10% sucrose and storage at -80°C.

In vitro CK2 pre-treatment

75 nM purified kinesin (native or truncated) was incubated with recombinant CK2 (up to 250nM, New England Biolabs) in 20μL of reaction buffer (20mM Tris-HCl pH7.5, 50mM KCl, 10mM $MgCl_2$, 0.5mM EGTA, plus 500μM ATP) at 30°C for 40 min (optimal for CK2 kinase activity), or 0°C for 1.5 hr. Reactions from which CK2 had been omitted served as controls. To block CK2 kinase activity, 100μM CK2-specific inhibitor TBCA[5] (EMD Chemicals, Inc.) was introduced to these assays, with ethanol as a control. For functional characterizations (bead assay, microtubule pulldown, and quantum dot assay), samples were placed on ice after allotted incubation time without further quenching of CK2 kinase activity.

To assay for phosphate incorporation, motor/kinase reactions (0.5μg kinesins per 250U CK2, 30°C for 40 min as suggested by manufacture) were supplemented with 1μCi of [γ-^{32}P]-ATP (Perkin Elmer), quenched with reducing SDS sample buffer, separated by SDS-PAGE, and visualized by PhosphorImager (Amersham).

In vitro CK2 re-activation

CK2-blank kinesins (thawed aliquot, 150nM native or truncated dimer, or 300nM monomer) were first incubated on ice for 1.5 hours. This ice incubation does not impact the active fraction of native kinesin (~20% immediately after thawing), but significantly reduced the active fraction of truncated kinesins (dimer or monomer, down to ~20%). After ice incubation, 10μL each of the kinesin samples were identically transferred to two sets of new eppendorf tubes. For one set, 10μL CK2-blank reaction buffer was added, followed immediately by a microtubule pulldown assay to determine the active motor fraction. For the second set containing identical kinesin samples, 10μL CK2 (500nM) was added, followed by 1.5 hr kinase:motor incubation on ice, then assayed for active motor fraction via microtubule pulldown.

Microtubule affinity pull-downs[6]

Kinesin (20μL of 75nM native or truncated dimer or 150nM monomer, with indicated amounts of CK2 holoenzyme or subunit, and indicated incubation conditions) was incubated with microtubule binding solution (180μL of 5μM microtubule, 80mM Pipes pH6.9, 50mM CH_3CO_2K, 4mM $MgSO_4$, 1mM DTT, 1mM EGTA, 20μM taxol), supplemented with 4mM AMPPNP (EMD), for 15 minutes at room temperature (RT). The reaction was centrifuged in a TLS55 rotor for 10 min at 170,000g at 25°C. The resulting microtubule pellet was dissolved in 30μL 1x reducing SDS sample buffer, separated by SDS-PAGE, and analyzed by immunoblot. Addition of 1mg/ml casein in the microtubule binding solution did not alter CK2-mediated kinesin activation.

Liquid Chromatography-Mass Spectrometry (LC-MS/MS)

Monoisotopic masses of parent ions and corresponding fragment ions, parent ion charge states and ion intensities from LC-MS/MS spectra were extracted using in-house software based on Raw_Extract script from Xcalibur v2.4. Following automated data extraction, the resultant peak lists for each LC-MS/MS experiment were submitted to the development version (5.0.0) of Protein Prospector (UCSF) for database searching using a Swiss-Prot database (11/07/2007, 574100 sequence entries). *Homo*

sapien was selected as the restricted species. Trypsin was set as the enzyme with a maximum of two missed cleavage sites. Chemical modifications such as protein N-terminal acetylation, methionine oxidation, N-terminal pyroglutamine, and deamidation of asparagine were selected as variable modifications. Since cysteine was reduced and alkylated, carbamidomethylation was chosen as a fixed modification. To map phosphorylation sites, phosphorylation of serine and threonine were chosen as variable modifications. The mass errors for parent ions were set as +/- 20ppm and for fragment ions as +/- 0.8Da. Search Compare program in Protein Prospector was used for summarization, validation, and comparison of results.

Motor-bead association

Kinesin was first incubated with CK2 *in vitro* (26μL of 75nM native kinesin or K560, 0nM or 250nM CK2, 30°C for 40min), then incubated with carboxylated polystyrene beads (0.5μm, Polysciences) at 160:1 beads:motor ratio in 80mM Pipes (pH6.9, 70μL total volume) for15 min at RT, followed by centrifugation at 2000g for 15 min at 4°C. Bead pellets were washed thrice (80mM Pipes pH6.9, 70μL), boiled in 30μL 1x reducing SDS sample buffer for 15 minutes, and then centrifuged at 16,000g for 10 minutes at 4°C. Elute was separated by SDS-PAGE, analyzed by immunoblot or sypro stain (Invitrogen).

Co-immunoprecipitation

K560 was first incubated with CK2 *in vitro* (20μL of 75nM motor, 0nM or 65nM CK2 holoenzyme or catalytic subunits, 0°C for 1.5hr), then incubated with 50μL μMACS microbeads (Miltenyi Biotec) at 0°C for 30min. For immunoprecipitatation against the motor's C terminal His-tag, we used μMACS anti-His microbeads. For immunoprecipitation against kinesin's heavy chain, we used μMACS protein A microbeads, and preincubated 50μL protein A microbeads each with 2μg of SUK4 at 0°C for 30min before mixing with protein samples. Protein/microbeads mixture was washed in four times in 200μL each of ice cold RIPA buffer (50mM TrisHCl pH8, 150mM NaCl, 1% NP-40, 0.5% $C_{24}H_{39}O_4Na$, 0.1%

SDS), then rinsed in 100µL of ice cold low salt wash buffer (20mM TrisHCl pH7.5), and incubated with 20µL of 95°C elution buffer (50mM TrisHCl pH6.8, 50mM DTT, 1% SDS, 1mM EDTA, 0.005% bromphenol blue and 10% glycerol) for 5min at RT. Proteins were eluted with an additional 50µL of 95°C elution buffer. Elutes were separated by SDS-PAGE, analyzed by immunoblot.

Gel filtration

500µg Ni-purified K560 (expressed in Terrific Broth for scaled-up protein production[7]) was analyzed using a Superdex-200 gel filtration column (Amersham Biosciences) in buffer A (50mM sodium phosphate pH8.0, 100mM NaCl), supplemented with 1mM DTT.

Dialysis

Ni-purified K560[7] (one freeze-thaw cycle) was dialyzed using Thermo Scientific Slide-A-Lyzer MINI Dialysis Unit (20K MWCO), for two hours on stir plate at 4°C. Dialysis buffer (80mM Pipes pH7.0, 5mM EDTA) was exchanged thrice (1L each, 40 min interval) for each dialysis.

***In vitro* optical trap**[8]

Kinesin was first incubated with CK2 (75nM native or K560, indicated CK2 amount and conditions), then titrated (see below) and incubated with 0.6pM carboxylated polystyrene beads (0.5µm, Polysciences) in 100µL motility buffer (80mM Pipes pH6.9, 50mM CH_3CO_2K, 4mM $MgSO_4$, 1mM DTT, 1mM EGTA, 10µM taxol, 1mg/ml casein) for 15min at RT for non-specific recruitment. Here, bead concentration was chosen to optimize the number of beads in our field of view, and was kept constant while we varied kinesin concentration (up to ~2000-fold dilution starting from 75nM) to vary motor:bead incubation ratio, and thereby control motor presence on individual beads. In case of K560, we also used anti-his beads[9] (0.4µm) to specifically recruit the motor via its C-terminal his-tag. Anti-his beads[9] were prepared by incubating 20µL penta-His biotin conjugate (Qiagen) with 10µL streptavidin-coated polystyrene beads (1% solids, Spherotech) in 100µL 1xPEM80 buffer for 30min at 4°C, and washed five times in 1xPEM80 buffer containing 8mg/ml BSA or 5.55mg/ml casein before

use. K560 concentration was titrated after indicated treatment (starting at 75nM) and incubated with 1μL anti-his beads in total 15μL motility buffer for 15min at RT. After incubation, motor-bead mixture were flown into flowcells with preassembled microtubules[8], and all measurements were carried out at RT in motility buffer, supplemented with 1mM ATP, and an oxygen-scavenging system (250μg/ml glucose oxidase, 30μg/ml catalase, 4.5mg/ml glucose). Bead-microtubule binding was tested using an optical trap (K_{trap} ~ 0.005pN/nm) to position each bead near a microtubule. A binding event is scored if the bead processes away from the trap within a wait time of 30 sec (see Supplement Discussions). Extending wait times (up to 2 minutes) had no effect on binding fraction measured. Bead force production was monitored by the bead positions in the trap (K_{trap} = 0.0436 ± 0.001pN/nm). Bead motility was measured with trap turned off upon a binding event. Where appropriate, travel distributions were fitted to a single exponential decay to extract the characteristic run length and associated uncertainties. For measurements where CK2-treatment significantly increased the population walking out of the 8μm field view, algorithmic mean (and associated error) was used to determine the minimum average travel and associated error. Stall force distributions were fitted to Gaussians to extract mean one- and two-motor forces, and the associated errors. Error on binding fractions (p) was determined as $\sqrt{[p(1-p)/n]}$, for n beads tested.

***In vitro* quantum dot (qDot)**

QDot motility was measured in the same motility buffer and flow chamber (with preassembled microtubules) as for bead assays. QDots (qDot-655 Carboxyl, Invitrogen) were excited with 488nm laser (Ti:Sapphire, Coherent) and imaged via a custom through-objective Total Internal Reflection Fluorescence (TIRF) microscope (Nikon 1.49NA, 100x), recorded at 4.25fps (Photmetrics Quantem 512SC). Motility analysis was carried out using a custom-tracking program (Gross Lab) that identifies qDot positions via two-dimensional Gaussian fitting of their brightness profile.

For CK2 pretreatment, K560 was first incubated with CK2 (75nM K560, 0 or 250nM CK2, 1hr on ice), then diluted (25-fold) to incubate with qDots at 4.3:1 qDot:motor ratio in 6μL motility buffer for 12min at RT. The reaction was then brought up to 20μL in motility buffer, supplemented with 1mM ATP and oxygen-scavenging system, followed by motility experiments.

For CK2 effect on motors already in complex with qDot, 75nM K560 was first incubated with qDots at 4.3:1 qDot:motor ratio in 6μL moltility buffer for 30 minutes at 4°C. The kinesin/qDot mixture was then divided into equal 3μL portions and incubated with 3μL each of 0 or 250nM CK2 for 1 hr at 4°C. The reaction was then diluted (35-fold) in motility buffer, and 20μL each was supplemented with 1mM ATP and oxygen-scavenging system, followed by motility experiments.

Cell culture and CK2α knockdown

Cos-1 cells were grown in DMEM (Invitrogen) supplemented with 10% fetal bovine serum (FBS) at 37°C in 5% CO_2. Gene silencing was achieved by transfection with two different commercially available CK2α siRNAs, from Qiagen (with sense strand 5'-CAUUGAAGCUGAAAUGGUATT-3') and Santa Cruz Biotechnology, Inc (a pool of 3 different siRNA duplexes with sense strands 5'-GAAGCCAUCAACAUCACAATT-3', 5'- GAUCCACGUUUCAAUGAUATT-3' and 5'-CCUCAGUCUUGUAAAUGUATT-3'), using the Hiperfect transfection reagent and according to manufacturer's instructions. Non-silencing siRNA and non-transfected cells were included as controls. Final dosing concentrations of all siRNAs provided were 50nM, unless otherwise noted, and the cells were incubated with the siRNA transfection complexes for 24 hours in complete media at normal growth conditions. After 24 hr in complete media at normal growth conditions (additional 50μM TBCA in growth media for TBCA-treatment), the cells were treated with 60μg/ml of fatty acid-albumin complex to induce the lipid droplet formation. The cells were then exposed to DMEM without glucose and fatty acid for 16 hr, before immediate lipid droplet trapping experiments.

For cell lysates, scrapped off cells were washed with PBS and lysed in ice cold lysis buffer (25mM TrisHCl pH7.5, 150mM NaCl, 1% NP40, 1mM EDTA, 1mM PMSF, 1mM Na_3VO_4, and 1x protease inhibitor cocktail).

Immunofluorescence imaging

Cos-1 cells were fixed (4% paraformaldehyde, 10 min at RT), permeabilized (2mg/ml BSA, 0.2% Triton X-100in PBS, 10 min on ice), blocked (3% BSA, 0.02% TritonX100 in PBS, 30 min at RT), and stained with primary (SUK4 or CK2α, 1:100 in blocking buffer for 1 hr at RT) followed by addition of Alexa Fluor (488nm and/or 546/610nm, goat anti-mouse and/or goat anti-rabbit IgG; Invitrogen) conjugated secondary antibodies (1:100 in blocking buffer for 1hr at RT), and imaged using LSM 510 confocal microscope or TIRF.

To quantify potential KHC/CK2α colocalization in Cos-1 cystosol, we used DAPI-stained images to generate masks for nuclei, and the JACoP plugin[10-11] (utilizing both intensity correlation and object-based colocalization coefficients) in ImageJ to analyze the nuclei-masked fluorescence images of KHC and CK2α.

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