Supplemental Materials

Molecular Biology of the Cell

Vasudevan et al.

Video - 13BC-KO cells grown with shaking move slower than wildtype cells

Wildtype (WT) and double knockout (13BC-KO) cells are grown with shaking at 160 rpm and a video is recorded for 10 sec at a maximal speed by Axiocam HS camera mounted on a Nikon Observer.A1 microscope with 10X lens and are shown side by side.

Video - Wildtype cells increase their motility upon treatment with IBMX

Video of wildtype cells without or with IBMX (1 mM, 20 min) recorded under a dissecting microscope with 40X magnification for 10 seconds using Moticam 480 digital camera.

Video - 13BC-KO cells increase their motility upon treatment with IBMX

Video of 13BC-KO cells without or with IBMX (1 mM, 20 min) recorded under a dissecting microscope with 40X magnification for 10 seconds using Moticam 480 digital camera.

Video - Cilia of wildtype cells have an apparently normal waveform

High-speed video recording of motile cilia in a wildtype cell acquired at 500 frames/s by a Photronics 1280 PCI FastCam on a Nikon Eclipse E600 microscope and replayed here at 30 frames/s.

Video - Cilia of wildtype cells have a less coordinated waveform

High-speed video recording of motile cilia in a 13BC-KO cell acquired at 500 frames/s by a Photronics 1280 PCI FastCam on a Nikon Eclipse E600 microscope and replayed here at 30 frames/s.

Video - GFP-Kin13Bp localizes to basal bodies, cortical microtubules and subset of cilia in 13BC-KO rescue B cell

Video of 13BC-KO cell rescued with GFP-Kin13Bp transgene (13BC-KO rescue B) captured using a TIRF system home-built around a Nikon eclipse Ti-U inverted microscope equipped with a 60 × NA 1.49 TIRF objective. GFP-Kin13Bp is seen to localize to the basal body, contractile vacuole pore, cortical microtubules and cilia (marked with red arrow at 9 s mark)

Video - GFP-Kin13Cp localizes to basal bodies, cortical microtubules and subset of cilia in 13BC-KO rescue C cell

Video of two 13BC-KO cells rescued with GFP-Kin13Cp transgene (13BC-KO rescue C) captured using a TIRF system home-built around a Nikon eclipse Ti-U inverted microscope equipped with a 60 × NA 1.49 TIRF objective. GFP-Kin13Cp localizes to the basal body and contractile vacuole pore in the first cell whereas in the second cell, GFP-Kin13Cp localizes to the basal body and cilia (marked with red arrow on 6 - 9 s mark)

Video - GFP-Kin13Bp localizes to the basal body, cortical microtubules and in assembling cilia of regenerating 13BC-KO rescue B cell

Video of 13BC-KO rescued with GFP-Kin13Bp cell that was deciliated and allowed to regenerate for 0, 30 and 100 minutes captured using a TIRF system home-built around a Nikon eclipse Ti-U inverted microscope equipped with a 60 × NA 1.49 TIRF objective.. GFP-Kin13Bp is seen to localize to the basal body, and cortical microtubules at 0 min whereas at 30 min, GFP-Kin13Bp is seen to localize to the basal body, cortical microtubules and in assembling cilia (marked with red arrows) and at 100 min, GFP-Kin13Bp localizes to the basal body and cortical microtubules but not in cilia.

Video - GFP-Kin13Bp localizes to the basal body, cortical microtubules and in assembling cilia of regenerating 13BC-KO rescue C cell

TIRF video of 13BC-KO rescued with GFP-Kin13Cp cell that was deciliated and allowed to regenerate for 0, 30 and 100 minutes captured using a TIRF system home-built around a Nikon eclipse Ti-U inverted microscope equipped with a 60 × NA 1.49 TIRF objective. GFP-Kin13Cp is seen to localize to the basal body, and cortical microtubules at 0 min whereas at 30 min, GFP-Kin13Cp is seen to localize to the basal body, cortical microtubules and assembling cilia (marked with red arrows) and at 100 min, GFP-Kin13Cp localizes to the basal body and cortical microtubules but not in cilia.

Homologs of kinesin-13 in Tetrahymena themophila are well conserved

Multiple sequence alignment of members of kinesin-13 family from Tetrahymena thermophila (KIN13A, KIN13B and KIN13C), Homo sapiens (KIF2A, KIF2B and MCAK), Mus musculus (KIF2A, KIF2B and MCAK), Xenopus laevis (KIF2A and MCAK), Giardia intestinalis, Leishmania major (KIN13-2), Trypanosoma brucei (KIN13-2) and Chlamydomonas reinhardtii (CrKIN13) using ClustalW (1.8.3) tool.

Loss of Kin13Ap causes defects in the nuclear composition

(A) Confocal immunofluorescence images of cells labeled with a mixture of anti-α-tubulin mAb (12G10) and anti-polyglycylation antibodies (polyG) (red), and DAPI (blue) for DNA. Bar = 20µm. (B) A graph showing the nuclear organization in wildtype and 13A-KO cells. N = 50 cells. Abbreviations: mic, micronucleus; mac, macronucleus.

13BC-KO cells swim slowly, have reduced rates of phagocytosis and outer doublet microtubules of 13BC-KO cells have a normal density of outer dynein arms

Paths traced by cells swimming for 10 seconds of wildtype cells grown without (A) or with shaking (B) and 13BC-KO cells grown without (C) and with shaking (D). (E) A graph showing the percentage of cells that have taken up India Ink after 20 min and 60 min. (F) The axonemes of wildtype and 13BC-KO cells were reactivated with 1mM ATP, negatively stained with uranyl acetate and viewed in TEM. Bar = 0.2 µm

Cells lacking Kin13Bp and Kin13Cp have a normal ultrastructure of cilia

Images of wildtype and 13BC-KO cells obtained using transmission electron microscopy showing cross-sections of the middle segments of cilia (A and B), cross-section of the distal segments with singlet peripheral microtubules (C and D), longitudinal sections of axonemes (E and F), and cross-sections of oral ciliary membranelles (G and H). Bar = 20 µm.

Coomassie gel image showing the amount of loading for total cilia, axoneme and M+M fractions

Total cilia, axoneme and M+M fractions of wildtype and 13BC-KO cells loaded onto 10% SDS-PAGE gels stained with Coomassie blue.

Deletion of MEC17, KIN13B and KIN13C is synthetically lethal

(A). Immunofluorescence images of progeny recovered from mating of either wildtype strains or knockout heterokaryons, fixed at different time points after the induction of mating and labeled with an anti-α-tubulin antibody 12G10 and anti-acetyl-K40 α-tubulin antibody 6-11 B-1. Note that by 48 hr the triple knockout cells have lost most their cilia. (B). TIRFM images of the triple knockout cells lacking KIN13B, KIN13C and MEC17 that were rescued by introduction of either GFP-KIN13B or GFP-KIN13C. Arrowheads mark cilia. Abbreviations: bb, basal body; cvp, contractile vacuole pore. (C) Viabilities of progeny of double and triple knockout heterokaryons (more details in Table 1 in the main text).

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CLUSTAL W (1.83) multiple sequence alignment

T.THERMOPHILA_KIN13A  MFDYPAVVI----------DNGSERCKAG---IAGEYAPRADFPS-------------------IVGRPKYQNLMLQGKE 48
T.THERMOPHILA_KIN13B  MLRKQIN-----------------NILQNQQIARTEYD---ESPQN-------------------VQIQQLDSFDSQN-- 39
T.THERMOPHILA_KIN13C  MKGTAAEK-------------HKERLKNA---RDVQMS---KKEAQINKLTDEEVVNEL------KDKALPVYGTRQEKL 55
H.SAPIENS_KIF2A       MATAN-----------------FGKIQIG---IYVEIK---RSDGRIHQA----MVTSLNEDNESVTVEWIENGDTKGKE 53
H.SAPIENS_KIF2B       MASQFCLPESPCLSPLKPLKPHFGDIQEG---IYVAIQ---RSDKRIHLA----VVTEINRENYWVTVEWVEKAVKKGKK 70
H.SAPIENS_MCAK        MAMDSSL---------------QARLFPG---LAIKIQ---RSNGLIHSA----NVRTVNLEKSCVSVEWAEGGATKGKE 55
M.MUSCULUS_KIF2A      MATAN-----------------FGKIQIG---IYVEIK---RSDGRIHQA----MVTSLNEDNESVTVEWIENGDTKGKE 53
M.MUSCULUS_KIF2B      MASQFCLPLAPRLSPLKPLKSHFTDFQVG---ICVAIQ---RSDKRIHLA----VVTEINRENSWVTVEWVEKGVKKGKK 70
M.MUSCULUS_MCAK       MESLH------------------ARLFPG---LSINIQ---RSNGLIHPA----NISTVNVEKSCVSVEWIEGGTTKGKE 52
C.REINHARDTII_KIN13   MVSSSVA----------------RG---------------------------------------------LEDAGLK--- 16
G.INTESTINALIS_KIN13  MSDLVYQ--------------------------------------------------------------WLESANLQ--- 15
L.MAJOR_KIN13.2       MRAESSGS----------------E---------------------------------------------SQSRQ----- 14
T.BRUCEI_KIN13.2      MTSL---------------------------------------------------------------------------- 4
                      *

T.THERMOPHILA_KIN13A  FYIGDDALANKALFNLQYPIENGLVTNYDNMEQIWRHCFDNELQVDPSQQPCM-LT--ESAMTPK--LYREKMTNIMFET 123
T.THERMOPHILA_KIN13B  -----------------------------------------------------------SGRL----------------- 43
T.THERMOPHILA_KIN13C  DRLKKYMGIIPNPVQQQQ-QQ--------------------------G-NNLP-PS-NNNGGL----------------- 88
H.SAPIENS_KIF2A       IDLESIFSLNPDLVPDEEIEP--------------------------S-PETP-PPPASSAKVNKIVKNRR--------- 96
H.SAPIENS_KIF2B       IDLETILLLNPALDSAEHPMP--------------------------P-PPLSPLALAPSSAI----RDQR--------- 110
H.SAPIENS_MCAK        IDFDDVAAINPELLQLLPLHP--------------------------K-DNLP-LQ--ENVTIQK--QKRR--------- 94
M.MUSCULUS_KIF2A      IDLESIFSLNPDLVPDEDIEP--------------------------S-PELP-PP-SSSSKVNKIVKNRR--------- 95
M.MUSCULUS_KIF2B      IELETVLLLNPALASLEHQRS--------------------------R-RPLRPVSVVPSTAI----GDQR--------- 110
M.MUSCULUS_MCAK       IDIDDVAAINPELLQLLPLRP--------------------------K-DSLP-LQ--ENVTVPK--QKRK--------- 91
C.REINHARDTII_KIN13   --------------RFV--------------------------PAF---SGVS-DQ--AFLGLMM--SDYASY------- 41
G.INTESTINALIS_KIN13  --------------QYY--------------------------PAFEQ-QGIT-PQ--RFITITI--QDYGAL------- 42
L.MAJOR_KIN13.2       -------------------------------------------------------------------------------- 14
T.BRUCEI_KIN13.2      -------------------------------------------------------------------------------- 4


T.THERMOPHILA_KIN13A  FDVPSFYVQIQAVLSLYSSCGVTGIVLDSGEGVTN---AVPIFEGCALRHAIQKNY--------LAGRDLTDYCMKLMYE 192
T.THERMOPHILA_KIN13B  ------------------------------------------------------------------------------EY 45
T.THERMOPHILA_KIN13C  -------------------------------------------------------------------------------- 88
H.SAPIENS_KIF2A       -------------------------------TVASIKNDPPSRDN----------RVVGSARARP----------SQFPE 125
H.SAPIENS_KIF2B       -------------------------------TATK----------------------------WV----------AMIPQ 121
H.SAPIENS_MCAK        -------------------------------SVNS---KIPAP-K----------ESLRSRSTRM----------STVSE 119
M.MUSCULUS_KIF2A      -------------------------------TVAAVKNDPPPRDN----------RVVGSARARP----------SQLPE 124
M.MUSCULUS_KIF2B      -------------------------------TATK----------------------------WI----------AMIPH 121
M.MUSCULUS_MCAK       -------------------------------SVNS---KIPAL-K----------EGLRSRSTRM----------STVSE 116
C.REINHARDTII_KIN13   --------GVVE---------------------------LED-------------------------------------- 48
G.INTESTINALIS_KIN13  --------GIQA---------------------------LPD-------------------------------------- 49
L.MAJOR_KIN13.2       -------------------------------------------------------------------------------- 14
T.BRUCEI_KIN13.2      -------------------------------------------------------------------------------- 4


T.THERMOPHILA_KIN13A  VGLNFQSSVEREVIR-DIKE-KYCYVALDYEAELKAYQNNSSKHKQYQFPDGKMITIQDQRFRVPELLFKPDFIGNEQKG 270
T.THERMOPHILA_KIN13B  DSE--------------RYQ-Q-----VDNVVDQGNQNN-N--------------------------------------- 65
T.THERMOPHILA_KIN13C  NQ---------------NFNNN-----NINVNDFNDQQ------------------------------------------ 106
H.SAPIENS_KIF2A       QSS--------------SAQ-Q-----NGSVSDISPVQA-AK--KEFGP------------------------------- 151
H.SAPIENS_KIF2B       KNQ--------------TAS-G-----DSLDVRVP--------------------------------------------- 136
H.SAPIENS_MCAK        LRI--------------TAQ-E-----NDMEVELPAAAN-SR--KQFSVPPAP--------------------------- 149
M.MUSCULUS_KIF2A      QSS--------------SAQ-Q-----NGSVSDISPVQA-AK--KEFGP------------------------------- 150
M.MUSCULUS_KIF2B      RNE--------------TPS-G-----DSQTLMIP--------------------------------------------- 136
M.MUSCULUS_MCAK       VRI--------------PAQ-E-----NEMEVELPVPTN-SR--KQFAIPSHP--------------------------- 146
C.REINHARDTII_KIN13   ------KQRLFRLIKSIAA---------SVKSS-DAPA-----------P------------------------------ 71
G.INTESTINALIS_KIN13  ------KQKLFRLITTLKSR-EN-----ILEQQPSAPNTG---ATPQSVPS----------------------------- 85
L.MAJOR_KIN13.2       -------------------------------------------------------------------------------- 14
T.BRUCEI_KIN13.2      -------------------------------------------------------------------------------- 4


T.THERMOPHILA_KIN13A  ISELAFHSIMSCDIDLRRNLYENIVLSGGTTMFDGFAERISKDINALAPLSIKAE------------------------- 325
T.THERMOPHILA_KIN13B  -------------------------------------------------------------------------------- 65
T.THERMOPHILA_KIN13C  -------------------------------------------------------------------------------- 106
H.SAPIENS_KIF2A       -------------------------------------------------------------------------------- 151
H.SAPIENS_KIF2B       -------------------------------------------------------------------------------- 136
H.SAPIENS_MCAK        -------TRPSCP-----------------------------------------AVAEIPLRMVSEEMEEQVHSIRGSSS 181
M.MUSCULUS_KIF2A      -------------------------------------------------------------------------------- 150
M.MUSCULUS_KIF2B      -------------------------------------------------------------------------------- 136
M.MUSCULUS_MCAK       --------RASCS-----------------------------------------TVTELPLLMVSEEAEEQAHSTRSTSS 177
C.REINHARDTII_KIN13   -------------------------------------------------------------------------------- 71
G.INTESTINALIS_KIN13  -------------------------------------------------------------------------------- 85
L.MAJOR_KIN13.2       -------------------------------------------------------------------------------- 14
T.BRUCEI_KIN13.2      -------------------------------------------------------------------------------- 4


T.THERMOPHILA_KIN13A  -VIALPQRKYSAFIGGSILSSLSSFQSKWITKAEYDEEEIQKKQ-INETKKEKEKN-----SED--M--MQQE------- 387
T.THERMOPHILA_KIN13B  ---KKKQTK----------------KSSLLQNMEKMEQKRQERREK-----------------------------MNQMK 97
T.THERMOPHILA_KIN13C  ---KKQNAF----------------KDPTVEKIQKMEQKREERRAK-----------------------------MEEAK 138
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H.SAPIENS_KIF2A       -----PSRR----------------KSNCVKEVEKLQEKREKRRLQ-----------------------------QQELR 181
H.SAPIENS_KIF2B       SKPCLMKQK----------------KSPCLWEIQKLQEQREKRRRL-----------------------------QQEIR 171
H.SAPIENS_MCAK        ANPVNSVRR----------------KSCLVKEVEKMKNKREEKKAQ-----------------------------NSEMR 216
M.MUSCULUS_KIF2A      -----PSRR----------------KSNCVKEVEKLQEKREKRRLQ-----------------------------QQELR 180
M.MUSCULUS_KIF2B      SNPCLMKRK----------------KSPCLREIEKLQKQREKRRRL-----------------------------QLEIR 171
M.MUSCULUS_MCAK       ANPGNSVRR----------------KSCIVKEMEKMKNKREEKRAQ-----------------------------NSELR 212
C.REINHARDTII_KIN13   ----------------------------ALEKPNAL-IDLDEN-------DG-----------D-----LLAD------- 92
G.INTESTINALIS_KIN13  -------SH----------------VSPHVAQGDRFVGDKQKQNDIQQAQDMSLYESYDGGYEPPYVSAQGSGPANGDDY 142
L.MAJOR_KIN13.2       -----------------------------------------------------SER------------------------ 17
T.BRUCEI_KIN13.2      -------------------------------------------------------------------------------- 4

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                                                             NECK DOMAIN

T.THERMOPHILA_KIN13A  ------------------------------------F-NIDD----------------LSNEPRIKVVIRKRPVNKKEQA 414
T.THERMOPHILA_KIN13B  QQKLEKEQMNKESNRNVDIDFEMLIEQERLN-----FSLQHV----------------PISNNRLSVIVRKRPLFSKEEE 156
T.THERMOPHILA_KIN13C  REREEKIMEHQALGKNIDVDFEILIEKNRFK---EPLQQNHT----------------PASHLKLCVCVRKRPIFKKEET 199
H.SAPIENS_KIF2A       EKRAQDV---DATN--PNYEIMCMIRDFRGSLDYRPL-TTAD----------------PIDEHRICVCVRKRPLNKKETQ 239
H.SAPIENS_KIF2B       ARRALDV---NTRN--PNYEIMHMIEEYRRHLDSSKI-SVLE----------------PPQEHRICVCVRKRPLNQRETT 229
H.SAPIENS_MCAK        MKRAQEY---DSSF--PNWEFARMIKEFRATLECHPL-TMTD----------------PIEEHRICVCVRKRPLNKQELA 274
M.MUSCULUS_KIF2A      EKRAQDV---DATN--PNYEIMCMIRDFRGSLDYRPL-TTAD----------------PIDEHRICVCVRKRPLNKKETQ 238
M.MUSCULUS_KIF2B      ARRALDI---NTGN--PNFETMRMIEEYRRRLDSSKM-SSLE----------------PPEDHRICVCVRKRPLNQRETT 229
M.MUSCULUS_MCAK       IKRAQEY---DSSF--PNWEFARMIKEFRVTMECSPL-TVTD----------------PIEEHRICVCVRKRPLNKQELA 270
C.REINHARDTII_KIN13   ---------------------------AGVNFQLSPL-ANQNPKAPVPSGGGGVPPSEGEDPPKIRVVVRKRPISKKERE 144
G.INTESTINALIS_KIN13  VIPTIPY---HPNA--PNPPNPRGIPTVNRTV-VPPV-DLFL----------------NQIQSRIRVVIRKRPINPKELS 199
L.MAJOR_KIN13.2       ------------------------------TCGVSPG-GPGG----------------PGASPSIVVAVRKRPRIPGR-E 49
T.BRUCEI_KIN13.2      -----------------------------------------C----------------PI-TSSITVAIRKRPIANNG-N 25
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                                        NECK DOMAIN
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                                                                                          MOTOR DOMAIN

T.THERMOPHILA_KIN13A  KSDVDIIEV--KT-GQSVIVKEMKYVQLFILSAAKTDKLIRKHQIDDIFINRQKVD-LTKYVEEHLFNFDHAFGENCTNE 490
T.THERMOPHILA_KIN13B  EGELDSISC--S--NPIIRVHEPK----------------------------YKVDGITKYVENQDFQFDNAFSEKESTE 204
T.THERMOPHILA_KIN13C  NGEIDSVSV--S--NPQIRVLAPK----------------------------FKVDGITKYVENYDFTFDNSFNENEETQ 247
H.SAPIENS_KIF2A       MKDLDVITI--PS-KDVVMVHEPK----------------------------QKVD-LTRYLENQTFRFDYAFDDSAPNE 287
H.SAPIENS_KIF2B       LKDLDIITV--PS-DNVVMVHESK----------------------------QKVD-LTRYLQNQTFCFDHAFDDKASNE 277
H.SAPIENS_MCAK        KKEIDVISI--PS-KCLLLVHEPK----------------------------LKVD-LTKYLENQAFCFDFAFDETASNE 322
M.MUSCULUS_KIF2A      MKDLDVITI--PS-KDVVMVHEPK----------------------------QKVD-LTRYLENQTFRFDYAFDDSAPNE 286
M.MUSCULUS_KIF2B      MKDLDIITI--PS-HNVVMVHESK----------------------------QKVD-LTRYLENQTFCFDHAFDDKASNE 277
M.MUSCULUS_MCAK       KKEIDVISV--PS-KCLLLVHEPK----------------------------LKVD-LTKYLENQAFCFDFAFDETASNE 318
C.REINHARDTII_KIN13   RGDDDVVDV--LAKNNTVVVNEEK----------------------------VKVD-LTKYLEKHAFKFDESLDENVSNE 193
G.INTESTINALIS_KIN13  QNQRDVVTA--DG-WNQVSIHEPK----------------------------VKVD-LTKYTDLHTFKFDHVFNEQSDNQ 247
L.MAJOR_KIN13.2       DDENDVVRCGENG-GPSVTVYEPR----------------------------TKLD-LTPIIEPSSFSYDHVFGEACTNE 99
T.BRUCEI_KIN13.2      SGDKDIVTC--ED-CRTISVHEPK----------------------------TRVD-LKAVVETSAFAFDYVFDESVAND 73
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                                MOTOR DOMAIN

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                                                                        KVD DOMAIN

T.THERMOPHILA_KIN13A  EVFINYFKDTIYLKHFSYLKWSQHSSQLISVSIQVYMTCVRPIVTAAFQRARVTCFAYGQTGSGKTHTMLGSVA----NR 566
T.THERMOPHILA_KIN13B  D---------------------------------VYKYSLQPLIKCIFEHGVVTCFAYGQTGSGKTFTMRG--------- 242
T.THERMOPHILA_KIN13C  D---------------------------------VYKYSLRPLLDHIMNQGVITCFAYGQTGSGKTFTMKG--------- 285
H.SAPIENS_KIF2A       M---------------------------------VYRFTARPLVETIFERGMATCFAYGQTGSGKTHTMGGDFSGKNQDC 334
H.SAPIENS_KIF2B       L---------------------------------VYQFTAQPLVESIFRKGMATCFAYGQTGSGKTYTMGGDFSGTAQDC 324
H.SAPIENS_MCAK        V---------------------------------VYRFTARPLVQTIFEGGKATCFAYGQTGSGKTHTMGGDLSGKAQNA 369
M.MUSCULUS_KIF2A      M---------------------------------VYRFTARPLVETIFERGMATCFAYGQTGSGKTHTMGGDFSGKNQDC 333
M.MUSCULUS_KIF2B      L---------------------------------VYQFTARPLVESIFRKGMATCFAYGQTGSGKTHTMGGAFLGKAQDC 324
M.MUSCULUS_MCAK       V---------------------------------VYRFTARPLVQTIFEGGKATCFAYGQTGSGKTHTMGGDLSGKSQNA 365
C.REINHARDTII_KIN13   A---------------------------------VYQLTVGPLVRTLFRNGRASCFAYGQTGSGKTYTMSP--------- 231
G.INTESTINALIS_KIN13  E---------------------------------IYQYAAKPLIRSVFEGKNCTVFAYGQTGSGKSFTMMHK-------- 286
L.MAJOR_KIN13.2       E---------------------------------VYRGCCQPLLQNVREGGGAVIFAFGQTGSGKTHTMLGTGE------ 140
T.BRUCEI_KIN13.2      V---------------------------------VYKVCCQPLLSDVQNGGSVVVIAFGQTGSGKTHTMLGHGS-----K 115
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                                                        MOTOR DOMAIN

T.THERMOPHILA_KIN13A  VPGMYVLASHDIFTALQRPQ-----FSH--LQIFVSFYEIYCGKLFDLLNDRQILHPREDGKQNINIIGLMEQRITNVDQ 639
T.THERMOPHILA_KIN13B  ---LQQHYINDIFSIIQK---------NHQFQLIMSYFEIYGGKCFDLLNERNQLNILEDKNNNVQIQNLIEKPVRDQLE 310
T.THERMOPHILA_KIN13C  ---LQNQYVTDMYKLSTHQN-----YSSMNLKFFISFFEIYGGRCYDLLNNKNQLVILEDKNGYVQIQNIVEKQAMSAEE 357
H.SAPIENS_KIF2A       SKGIYALAARDVFLMLKKPN-----YKKLELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLQEREVKCVED 409
H.SAPIENS_KIF2B       SKGIYALVAQDVFLLLRNST-----YEKLDLKVYGTFFEIYGGKVYDLLNWKKKLQVLEDGNQQIQVVGLQEKEVCCVEE 399
H.SAPIENS_MCAK        SKGIYAMASRDVFLLKNQPC-----YRKLGLEVYVTFFEIYNGKLFDLLNKKAKLRVLEDGKQQVQVVGLQEHLVNSADD 444
M.MUSCULUS_KIF2A      SKGIYALAARDVFLMLKKPN-----YKKLELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLQEREVKCVED 408
M.MUSCULUS_KIF2B      SKGIYALVAQDVFLLLKTPA-----YEKLELKVYGTFFEIYGGKVYDLLNWKKKLQVLEDGNQQVQVVGLQEQEVSCVEE 399
M.MUSCULUS_MCAK       SKGIYAMASRDVFLLKNQPR-----YRNLNLEVYVTFFEIYNGKVFDLLNKKAKLRVLEDSRQQVQVVGLQEYLVTCADD 440
C.REINHARDTII_KIN13   ---LPIRASADIFTFMAQQQ-----YRD--ISLCVSCFEIYGNKVFDLLNARKKLNILEDGKKKVVVVGLKEFGVDDVDG 301
G.INTESTINALIS_KIN13  DNGIYVLACFDILEYLRVYNGSQGNNSK-FLVPVVSFFEIYGGKLFDLLNNRQRLQALEDGKGNVQITGLTEKQISSVDA 365
L.MAJOR_KIN13.2       RPGLYSLAVTELLTMTE----------H--STMTASFYEAYGAKLYDLLNDRAEVKMLQDEYQNVHIVGITEQIVSSVDD 208
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T.BRUCEI_KIN13.2      TIGLYGYAIRELIGEET----------T--RKLAVSFYEVYGSKLFDLLNGRTQLKMMQDEADNLRIVGLSEKVVTCDKE 183
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                                                        MOTOR DOMAIN

T.THERMOPHILA_KIN13A  LLKIIEFGMSARVTAQNSANTDSSRSHAILQIQLKE----------------QNNVY-GKISFIDLAGSERGADVIDQNK 702
T.THERMOPHILA_KIN13B  MIEIIEQAAIIRTTHATEANEESSRSHAICQIVVKDT---------------NGSTR-GKLIMVDLAGSERAQDCQSNSK 374
T.THERMOPHILA_KIN13C  MIQLIEYGHNIRTTHATASNDTSSRSHAICQIMLRND---------------KDKQV-GKLVLVDLAGSERAQDCQSNNR 421
H.SAPIENS_KIF2A       VLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR----------------KGKLH-GKFSLIDLAGNERGADTSSADR 472
H.SAPIENS_KIF2B       VLNLVEIGNSCRTSRQTPVNAHSSRSHAVFQIILKS----------------GRIMH-GKFSLVDLAGNERGADTTKASR 462
H.SAPIENS_MCAK        VIKMLDMGSACRTSGQTFANSNSSRSHACFQIILRA----------------KGRMH-GKFSLVDLAGNERGADTSSADR 507
M.MUSCULUS_KIF2A      VLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR----------------KGKLH-GKFSLIDLAGNERGADTSSADR 471
M.MUSCULUS_KIF2B      VLNLVELGNSCRTSGQTSVNAHSSRSHAVFQLILKA----------------GGKLH-GKFSLVDLAGNERGADTAKATR 462
M.MUSCULUS_MCAK       VIKMINMGSACRTSGQTFANSNSSRSHACFQILLRT----------------KGRLH-GKFSLVDLAGNERGADTSSADR 503
C.REINHARDTII_KIN13   VKALIEESAKNRSTGSTAANADSSRSHSIMQFALKRAAPAPAGGFRRGEDAPEPRVV-GKISFIDLAGSERGADTFDNNR 380
G.INTESTINALIS_KIN13  MLNLIDSGLTLRAVGATGANADSSRSHAILQIALKYT--------------KSGKEY-SRISFIDLAGSERASDVQNSDR 430
L.MAJOR_KIN13.2       VNALMMRGQQLRAIGTTHANDRSSRSHAVLEIKLKLADS------------SSESQL-GRITFVDLAGSERASDTAETDA 275
T.BRUCEI_KIN13.2      VYKLISKGESLRSSGSTLANDTSSRSHAVLEIKVLNY---------------QGEPHGGRVTLIDLAGSERAADTTSSDT 248
                      : ::  .   *    .  *  *****:  :: :                        .:. ::****.**. *  .
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                                                        MOTOR DOMAIN

T.THERMOPHILA_KIN13A  QTRKDGAEINKSLLALKECIRALDQG-----KNYTPFRGSKLTLVLKDSFTG---NCRTVMIGNISPCQSSSEHTLNTLR 774
T.THERMOPHILA_KIN13B  QRRVEGANINQSLLALKECIRAMDSG-----AQHVPFRGSKLTLVLRDSFLSKQSNSHIIMFACISPGSSSSDHTVNTLR 449
T.THERMOPHILA_KIN13C  QRRMEGAEINKSLLALKECIRAMDTG-----AAHVPFRASKLTLVLRDSFQSKSDKSKIVMIACISPGSSSSDHTVNTLR 496
H.SAPIENS_KIF2A       QTRLEGAEINKSLLALKECIRALGRN-----KPHTPFRASKLTQVLRDSFIGE--NSRTCMIATISPGMASCENTLNTLR 545
H.SAPIENS_KIF2B       KRQLEGAEINKSLLALKECILALGQN-----KPHTPFRASKLTLVLRDSFIGQ--NSSTCMIATISPGMTSCENTLNTLR 535
H.SAPIENS_MCAK        QTRMEGAEINKSLLALKECIRALGQN-----KAHTPFRESKLTQVLRDSFIGE--NSRTCMIATISPGISSCEYTLNTLR 580
M.MUSCULUS_KIF2A      QTRLEGAEINKSLLALKECIRALGRN-----KPHTPFRASKLTQVLRDSFIGE--NSRTCMIATISPGMASCENTLNTLR 544
M.MUSCULUS_KIF2B      KRQLEGAEINKSLLALKECIRALGKN-----KSHTPFRASKLTQVLRDSFIGQ--NSYTCMIATISPGMTSCENTLNTLR 535
M.MUSCULUS_MCAK       QTRMEGAEINKSLLALKECIRALGQN-----KAHTPFRESKLTQVLRDSFIGE--NSRTCMIAMISPGISSCEYTLNTLR 576
C.REINHARDTII_KIN13   QTRLEGAEINKSLLALKECIRALDSD-----ARHVPFRGSKLTAVLRDSFVGD--QARTVMIANISPCSSSVEHTLNTLR 453
G.INTESTINALIS_KIN13  QTRMEGAEINKSLLALKECIRAMDKSNDSKSGAHIPFRGSKLTMVLRDSFIG---NSQTVMIANISPNDKSCDNTLNTLR 507
L.MAJOR_KIN13.2       KTRREGAEINKSLLALKECIRAMSMR-----KRHIPFRGSKLTQILRESFVG---RCKTCVIAAISPCQGHCEDTLNTLR 347
T.BRUCEI_KIN13.2      RGRHEGAEINKSLLALKECIRAMSRN-----RRHIPFRASKLTQVLRESFIG---NCKTCFIATVSPLQRHCEDTLNTLR 320
                      : : :**:**:********* *:.         : *** **** :*::** .   ..   .:. :**     : *:****
                      ________________________________________________________________________________
                                                        MOTOR DOMAIN

                                      ___
                                   KEC DOMAIN

T.THERMOPHILA_KIN13A  YADRVKELKKPTNQDLSEQ-VNYNHKLEQ--------------------------------------------------- 802
T.THERMOPHILA_KIN13B  YADRLKESNGIKQDV-I--KI---------IEEQSKAKKKKQNYQSSQQQMASAPQAAAQKKKEKEKEENDSNKKNQNAP 517
T.THERMOPHILA_KIN13C  YADRLKENKPPVKGG-MP-RI----DAPQLIDEMPSYNINHNNIKSD-NQLNDQPSSQ---------------------- 547
H.SAPIENS_KIF2A       YANRVKELTVDPTA------------------------------------------------------------------ 559
H.SAPIENS_KIF2B       YANRVKKLNVDVRP------------------------------------------------------------------ 549
H.SAPIENS_MCAK        YADRVKELSPHSGP------------------------------------------------------------------ 594
M.MUSCULUS_KIF2A      YANRVKELTVNPAA------------------------------------------------------------------ 558
M.MUSCULUS_KIF2B      YANRVKELALEARP------------------------------------------------------------------ 549
M.MUSCULUS_MCAK       YADRVKELSPHSGP------------------------------------------------------------------ 590
C.REINHARDTII_KIN13   YADRVKELRKDKADRTPGG-VTPGDDAY---------------------------------------------------- 480
G.INTESTINALIS_KIN13  YADRVKELQHGKGGI-IKF-N-----VLKMG---------------------------------------------QN-- 533
L.MAJOR_KIN13.2       YADRIKELKGPANPHNGVKPIPC--KT----------------------------------------------------- 372
T.BRUCEI_KIN13.2      YANRIRDLKAPSDDGFSR-KISM--TC----------------------------------------------------- 344
                      **:*::.
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                      MOTOR DOMAIN

T.THERMOPHILA_KIN13A  ----------------------LMKSAQN--------SNFAYNLPQQPNNFPPYQPQTQAQQPRTNYNNFMAGDQMGNNN 852
T.THERMOPHILA_KIN13B  PVKNLKGENKNKEERQYDHTQYLMNNAKNKENMQSVDNIPSIGYQDKPS---------------------QQEK------ 570
T.THERMOPHILA_KIN13C  --KEQLSN-------RRNHSSNQMDDASVIFFYLLMLNYILFIYEIKPQ---------------------QQ-------- 589
H.SAPIENS_KIF2A       ----------------A-------------------------------------------------------GD------ 562
H.SAPIENS_KIF2B       ----------------YHR-----------------------------------------------------GH------ 554
H.SAPIENS_MCAK        ----------------S-------------------------------------------------------GE------ 597
M.MUSCULUS_KIF2A      ----------------A-------------------------------------------------------GD------ 561
M.MUSCULUS_KIF2B      ----------------YHH-----------------------------------------------------CV------ 554
M.MUSCULUS_MCAK       ----------------S-------------------------------------------------------GE------ 593
C.REINHARDTII_KIN13   -------------------------------------YAA-VARAAGPG---------------------QAAA------ 495
G.INTESTINALIS_KIN13  ------------------AADVILGTARDDEN--DVYKAGIVGVNAAPS---------------------QQAR------ 566
L.MAJOR_KIN13.2       -------------------------------------------------C---------------------GQP--I--- 377
T.BRUCEI_KIN13.2      -----------------------------------------------PNC---------------------NGP--V--- 351


T.THERMOPHILA_KIN13A  NNILSAHNNNAL------------NPNLNANNMYPGSQSEMFDIE--------PRQLNKTPQQQQQSFAGIKMNQQPQSQ 912
T.THERMOPHILA_KIN13B  -----------KLNAQQAKSSQIQ--------KI---------------------------------------------- 585
T.THERMOPHILA_KIN13C  -----------------------LPPKQNKTPLL---------------------------------------------- 600
H.SAPIENS_KIF2A       --------------------------------VR---------------------------------------------- 564
H.SAPIENS_KIF2B       ---------------------------------Y---------------------------------------------- 555
H.SAPIENS_MCAK        ---------------------------------Q---------------------------------------------- 598
M.MUSCULUS_KIF2A      --------------------------------VH---------------------------------------------- 563
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M.MUSCULUS_KIF2B      ---------------------------------S---------------------------------------------- 555
M.MUSCULUS_MCAK       ---------------------------------Q---------------------------------------------- 594
C.REINHARDTII_KIN13   -------------------------P-------APERERERADLQRERDRERASDRYPSPPRQQAGAFAGG--------- 534
G.INTESTINALIS_KIN13  -------------------------------------------------------------------------------- 566
L.MAJOR_KIN13.2       -------------------------------------------------------------------------------- 377
T.BRUCEI_KIN13.2      -------------------------------------------------------------------------------- 351


T.THERMOPHILA_KIN13A  QQYRPPSNNQ-LGYQ-----------NQMDQNTINSQTN----PINLNIEQI-ENWTA---------------------- 953
T.THERMOPHILA_KIN13B  ----PPIQQS-V-------------------------------------------------------------------- 592
T.THERMOPHILA_KIN13C  ----PPADKRIA-------------------------------------------------------------------- 608
H.SAPIENS_KIF2A       ----PIMHHP-P-------------------------------------------------------------------- 571
H.SAPIENS_KIF2B       ----PIGHEA-P-------------------------------------------------------------------- 562
H.SAPIENS_MCAK        ----LIQMET-E-------------------------------------------------------------------- 605
M.MUSCULUS_KIF2A      ----PIMHHP-P-------------------------------------------------------------------- 570
M.MUSCULUS_KIF2B      ----PPGHEV-P-------------------------------------------------------------------- 562
M.MUSCULUS_MCAK       ----PVQMET-E-------------------------------------------------------------------- 601
C.REINHARDTII_KIN13   --------------------------------------GGGGAGA----------------------------------- 541
G.INTESTINALIS_KIN13  ---VPPASQA-PITA-----------RQIQQNLPQPHYNPNYNPPNSKP-AFEPRVET---------------------- 608
L.MAJOR_KIN13.2       ---FIGDRHV-CKRQLVVCPHCRQDVD---KQELDTHMSE----CKESPMRC-QYCNERMLRSESVGHSRRCARAPIRCG 445
T.BRUCEI_KIN13.2      ---RPDASHT-CVRLSTRCPHCRQVVE---KHNLEGHIEE----CSEFPVRC-PRCNELLVRGDIPRHNRRCSRSLVRCP 419


T.THERMOPHILA_KIN13A  -------------------------------------------------------------------------------- 953
T.THERMOPHILA_KIN13B  -------QQIEQASTQNSTQQVVSSTSVSSSASALAQLHREKRDERPQTQQKRQSSIGKKNANQTDTSNQNLNNLLQQKI 665
T.THERMOPHILA_KIN13C  -------QKIEEERIEK--------------------------------------------------------------- 618
H.SAPIENS_KIF2A       -------NQIDDLETQW--------------------------------------------------------------- 581
H.SAPIENS_KIF2B       -------RMLKSHIGN---------------------------------------------------------------- 571
H.SAPIENS_MCAK        -------EMEAC---SN--------------------------------------------------------------- 612
M.MUSCULUS_KIF2A      -------SQIDDLETQW--------------------------------------------------------------- 580
M.MUSCULUS_KIF2B      -------LMIENDNTN---------------------------------------------------------------- 571
M.MUSCULUS_MCAK       -------VMEAS---SN--------------------------------------------------------------- 608
C.REINHARDTII_KIN13   -------------------------------------------------------------------------------- 541
G.INTESTINALIS_KIN13  -------------------------------------------------------------------------------- 608
L.MAJOR_KIN13.2       ACGATVPRQLIDR------------------------------------------------------------------- 458
T.BRUCEI_KIN13.2      LCTCHVMRCGLEK------------------------------------------------------------------- 432


T.THERMOPHILA_KIN13A  -------------------------------------------------------------------------------- 953
T.THERMOPHILA_KIN13B  LNTDASLA--TNHNHDHLSGVDQNKALSLKQLKQISQSNPVTTQNNQGQQIRINSAHPSNNNNSQNN---NTRDDNNNSF 740
T.THERMOPHILA_KIN13C  ---EKKLQQQQQQQAQQQQQHHMKRGQ----SSNLPSANKQTPTNQQQQQQK---------NNSQNNLSKNSSDDEGEQI 682
H.SAPIENS_KIF2A       G-VGSSPQRD---------------------------------------------------------------------- 590
H.SAPIENS_KIF2B       --SEMSLQRD---------------------------------------------------------------------- 579
H.SAPIENS_MCAK        G---AL-------------------------------------------------------------------------- 615
M.MUSCULUS_KIF2A      G-VGSSPQRD---------------------------------------------------------------------- 589
M.MUSCULUS_KIF2B      --SGKSLQRD---------------------------------------------------------------------- 579
M.MUSCULUS_MCAK       G---TS-------------------------------------------------------------------------- 611
C.REINHARDTII_KIN13   -------------------------------------------------------------------------------- 541
G.INTESTINALIS_KIN13  -------------------------------------------------------------------------------- 608
L.MAJOR_KIN13.2       -------------------------------------------------------------------------------- 458
T.BRUCEI_KIN13.2      -------------------------------------------------------------------------------- 432


T.THERMOPHILA_KIN13A  ---------------------------------------------------RNEEDL-QLI------------------- 962
T.THERMOPHILA_KIN13B  NQLPKKGHNNQQQKKTQQNMDNI-STI---NNKNNRDSSANHNSRHNSSSNNNNNQINNNNFNQNLNDKSLNDHILQKNK 816
T.THERMOPHILA_KIN13C  QQVNKGVK------------DDV-RCM---KET---------------LKMDKNNKVSNE-------------------- 711
H.SAPIENS_KIF2A       ---------------------DL-KLL---CE-------------------QNEEEVSPQ-------------------- 606
H.SAPIENS_KIF2B       ---------------------EFIKIP--YVQ-------------------SEEQKEIEE-------------------- 597
H.SAPIENS_MCAK        --------------------------IPGNLS-------------------KEEEELSSQ-------------------- 630
M.MUSCULUS_KIF2A      ---------------------DL-KLL---CE-------------------QNEEEVSPQ-------------------- 605
M.MUSCULUS_KIF2B      ---------------------EVIQIP--TVE-------------------KEEEKESDE-------------------- 597
M.MUSCULUS_MCAK       -----------------------------LTG-------------------NEEEELSSQ-------------------- 623
C.REINHARDTII_KIN13   ---------------------------------------------------DGEGSA-AAL------------------- 550
G.INTESTINALIS_KIN13  ---------------------------------------------------TDE----DDM------------------- 614
L.MAJOR_KIN13.2       --------------HAQQECAEA-KVK---CR-------------------YCGCVQSRQL------------------- 482
T.BRUCEI_KIN13.2      --------------HTLMDCGAK-LEK---CR-------------------YCGQGFPRHS------------------- 456


T.THERMOPHILA_KIN13A  --------------SQKHEQ-LISLILAE--------------------------------------------------- 976
T.THERMOPHILA_KIN13B  EVQENIEKAQQHQIEQKTKDLILQQIKEK--------------------------------------------------- 845
T.THERMOPHILA_KIN13C  --------------FFDFHE-KVNTILEE--------------------------------------------------- 725
H.SAPIENS_KIF2A       --------------LFTFHE-AVSQMVEM--------------------------------------------------- 620
H.SAPIENS_KIF2B       --------------VET-----------L--------------------------------------------------- 601
H.SAPIENS_MCAK        --------------MSSFNE-AMTQIREL--------------------------------------------------- 644
M.MUSCULUS_KIF2A      --------------LFTFHE-AVSQMVEM--------------------------------------------------- 619
M.MUSCULUS_KIF2B      --------------LTS--------------------------------------------------------------- 600
M.MUSCULUS_MCAK       --------------MSSFNE-AMTQIREL--------------------------------------------------- 637
C.REINHARDTII_KIN13   --------------AERHDE-LMDSILLE--------------------------------------------------- 564
G.INTESTINALIS_KIN13  --------------VRTHCD-LVDSIYEQ--------------------------------------------------- 628
L.MAJOR_KIN13.2       --------------LAAHEQ-NCDAAKVACPHCLQFMRKRRLDGHVATCVRNLSRAMHTP-------------------- 527
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T.BRUCEI_KIN13.2      --------------LKRHED-VCTMMKIACPYCLQYFRKVCVDAHASVCVRNPNCRRVSPSRIRDSGEEVWKITNGKEWR 521


T.THERMOPHILA_KIN13A  ------EEDV-------------------------------IASHRSHIDDMV--------------------------- 992
T.THERMOPHILA_KIN13B  ------QEDM-------------------------------FSSHMSAIKEDA--------------------------- 861
T.THERMOPHILA_KIN13C  ------QEEI-------------------------------FATHMAAIKEDA--------------------------- 741
H.SAPIENS_KIF2A       ------EEQV-------------------------------VEDHRAVFQESI--------------------------- 636
H.SAPIENS_KIF2B       ------PTLL-------------------------------GKDTTISGKGSS--------------------------- 617
H.SAPIENS_MCAK        ------EEKA-------------------------------MEELKEIIQQGP--------------------------- 660
M.MUSCULUS_KIF2A      ------EEQV-------------------------------VEDHRAVFQESI--------------------------- 635
M.MUSCULUS_KIF2B      -----------------------------------------KKEPAASWSRSN--------------------------- 612
M.MUSCULUS_MCAK       ------EERA-------------------------------LEELREIIQQGP--------------------------- 653
C.REINHARDTII_KIN13   ------EENL-------------------------------VAFHRAKLEEDM--------------------------- 580
G.INTESTINALIS_KIN13  ------EDLI-------------------------------VRAHRRQVDSMM--------------------------- 644
L.MAJOR_KIN13.2       -----RSTALNIIASTSMETSQTLASSSSSIGAQQSIPKSATAQTAASS---RASSSHNRNVAAEPAGGQVD----LVAA 595
T.BRUCEI_KIN13.2      QRPRMLRNQSLKQLEAISRTKSSVQ----------------------------------LREGRKPLGPLEDNFSLPALH 567


T.THERMOPHILA_KIN13A  ------------------------------------------ELTKQEMMLLHDV---DKPASD--VDVY---------- 1015
T.THERMOPHILA_KIN13B  ------------------------------------------NLLSLESGLLTDCQKDGFMDCD--IDSY---------- 887
T.THERMOPHILA_KIN13C  ------------------------------------------KLLTQESELISKVQGTGFIDYD--IDLY---------- 767
H.SAPIENS_KIF2A       ------------------------------------------RWLEDEKALLEMT---EEVDYD--VDSY---------- 659
H.SAPIENS_KIF2B       ------------------------------------------QWLE---NIQERA---GGVHHD--IDFC---------- 637
H.SAPIENS_MCAK        ------------------------------------------DWLE----LSEMT---EQPDYD--LETF---------- 679
M.MUSCULUS_KIF2A      ------------------------------------------RWIEDEKALLEMT---EEVDYD--VDSY---------- 658
M.MUSCULUS_KIF2B      ------------------------------------------QWWE---AIQETA---EGVNGD--VDFC---------- 632
M.MUSCULUS_MCAK       ------------------------------------------NWLE----LSEMT---DQPDYD--LETF---------- 672
C.REINHARDTII_KIN13   ------------------------------------------ETMRQEMALLQEV---DKPGSE--IDHY---------- 603
G.INTESTINALIS_KIN13  ------------------------------------------QLVKEEVALLHAI---ENDQVS--IDDW---------- 667
L.MAJOR_KIN13.2       DEGTGPLNFTRAHSSRRSSAQLASGVSLANQSQSNRAPGAGGRWNAGALGADEVS---AACDSD--CGSV---------- 660
T.BRUCEI_KIN13.2      APSSAPDRKHPPVTSAFTE------------------------------SLQSHP---NSEDDDADKEVCRTAPTISGEN 614
                                                                                     .


T.THERMOPHILA_KIN13A  ---------V------------------QNLDAILQHKS---EIINMLRQRLQT-----FRSHLKK-------------- 1046
T.THERMOPHILA_KIN13B  ---------V------------------KKFESIVSKKL---LMYNLLQQKMDT-----LK-KMRNEYNNKYSLNQINNN 931
T.THERMOPHILA_KIN13C  ---------V------------------KKLETVIKKKL---KMK-----------------HLQ--------------- 785
H.SAPIENS_KIF2A       ---------A------------------TQLEAILEQKI---DILTELRDKVKS-----FRAALQ--------------- 689
H.SAPIENS_KIF2B       ---------I------------------ARSLSILEQKI---DALTEIQKKLKL-----LLADLH--------------- 667
H.SAPIENS_MCAK        ---------V------------------NKAESALAQQA---KHFSALRDVIKA-----LRLAMQ--------------- 709
M.MUSCULUS_KIF2A      ---------A------------------TQLEAILEQKI---DILTELRDKVKS-----FRAALQ--------------- 688
M.MUSCULUS_KIF2B      ---------I------------------AQSLSVLEQKI---GVLTDIQKKLQS-----LREDLQ--------------- 662
M.MUSCULUS_MCAK       ---------V------------------NKAESALTQQAKQAKHFSALREVIKA-----LRLAMQ--------------- 705
C.REINHARDTII_KIN13   ---------V------------------EQMSALLNIKR---QGIQELQAKLDT-----FKAKLRE-------------- 634
G.INTESTINALIS_KIN13  ---------L------------------VKLSDILSRKE---EAITTLKGNLSA-----FKQALQK-------------- 698
L.MAJOR_KIN13.2       ---------VCPYSRYGCPVKVTRLNVAAHLKESMQQHL---ELVTTYADRVDEQNMQLRRLVIHE-------------- 714
T.BRUCEI_KIN13.2      SSRVGGEGCVCPYAAYGCLHTVCDSSLEKHMKDSVEMHL---QLVRDYAERVSEENNIL-RERVNE-------------- 676
                                                   .    :  :                         :.


T.THERMOPHILA_KIN13A  ------EELLSKKF-YEQRAQIMDVFDLNSNTINPNNDEMQLLDDLPD-LYDN 1091
T.THERMOPHILA_KIN13B  HHEKNQQQQQAKQIEDPNKKRQS---------FL-----------LKK-KIEN 963
T.THERMOPHILA_KIN13C  -----EEEEISSK--------------------------------VKD-TFYF 800
H.SAPIENS_KIF2A       -----EEEQASKQI-------------------N------------PKRPRAL 706
H.SAPIENS_KIF2B       -----VK------------------------------------------SKVE 673
H.SAPIENS_MCAK        -----LEEQASRQI-------------------S------------SK-KRPQ 725
M.MUSCULUS_KIF2A      -----EEEQASKQI-------------------N------------PKRPRAL 705
M.MUSCULUS_KIF2B      -----KK------------------------------------------SQVE 668
M.MUSCULUS_MCAK       -----LEEQASKQI-------------------N------------SK-KRHQ 721
C.REINHARDTII_KIN13   ------EEALSRTV-H---------------------------------KIRT 647
G.INTESTINALIS_KIN13  ------EEELSHSI-DLN-----------------------------K-ARKK 714
L.MAJOR_KIN13.2       ------TDTLSSRV-T-M-----------------------------E-RLDK 729
T.BRUCEI_KIN13.2      ------GTTKASKL---H-----------------------------E-LESV 690
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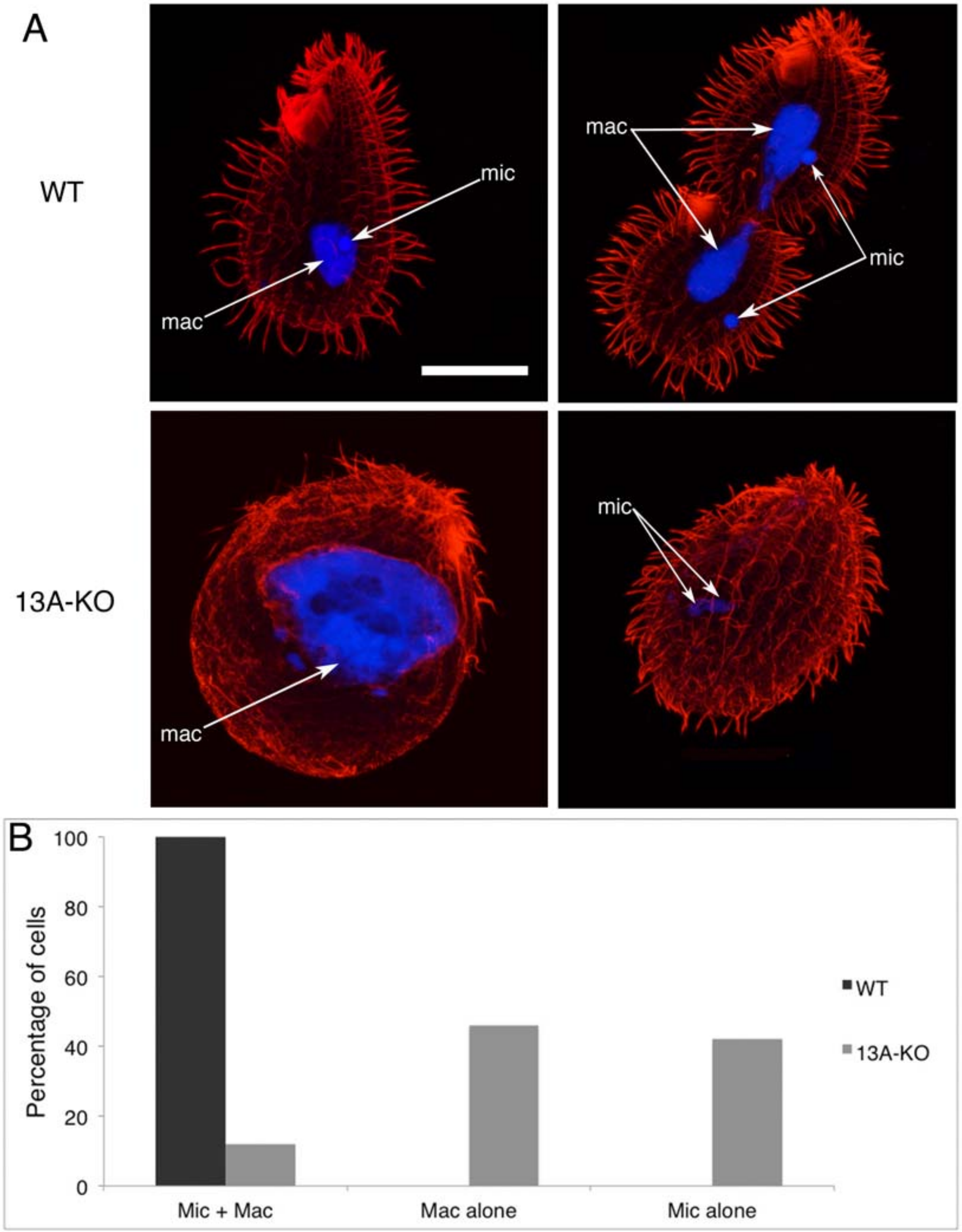
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Mic alone
WT
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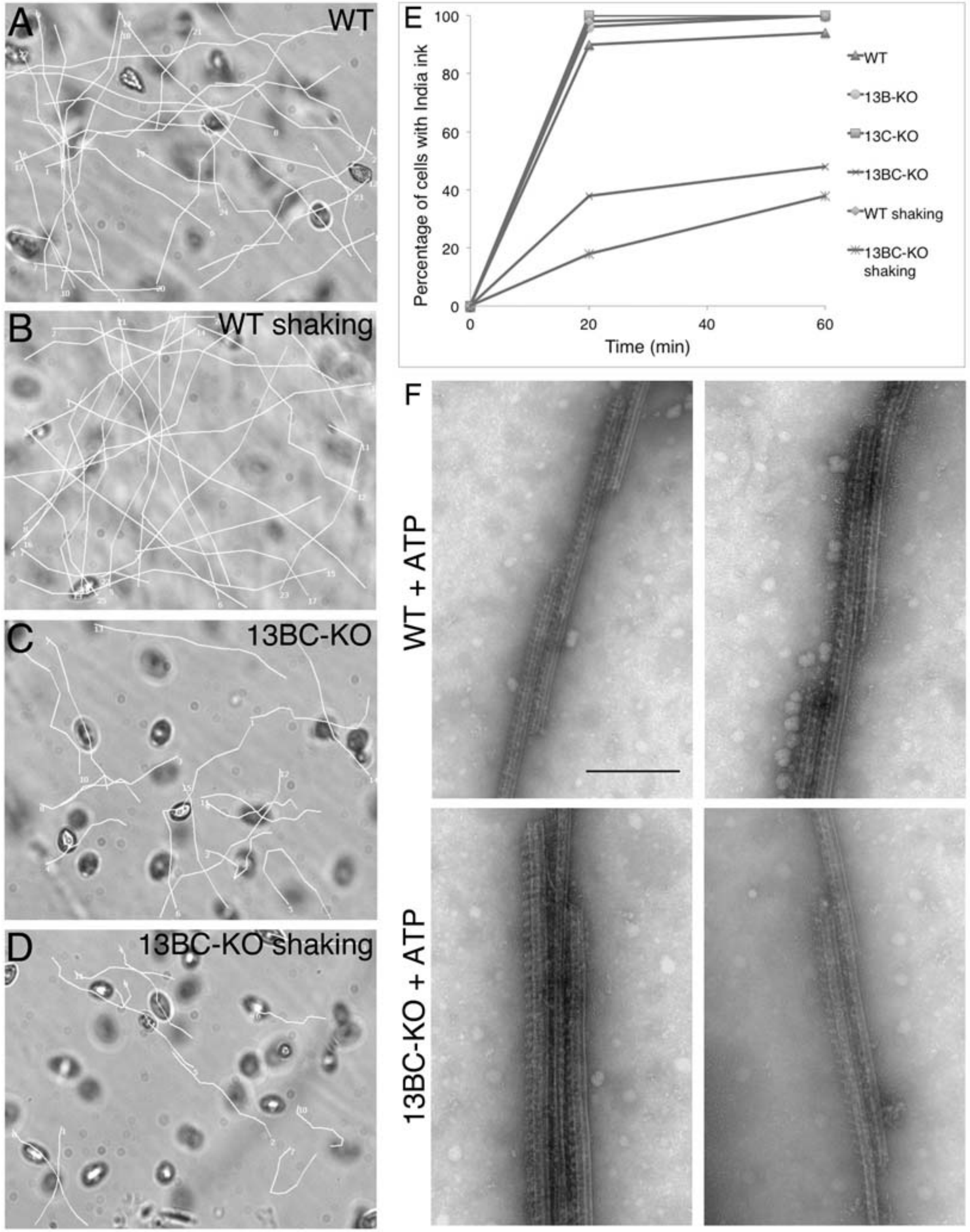
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0
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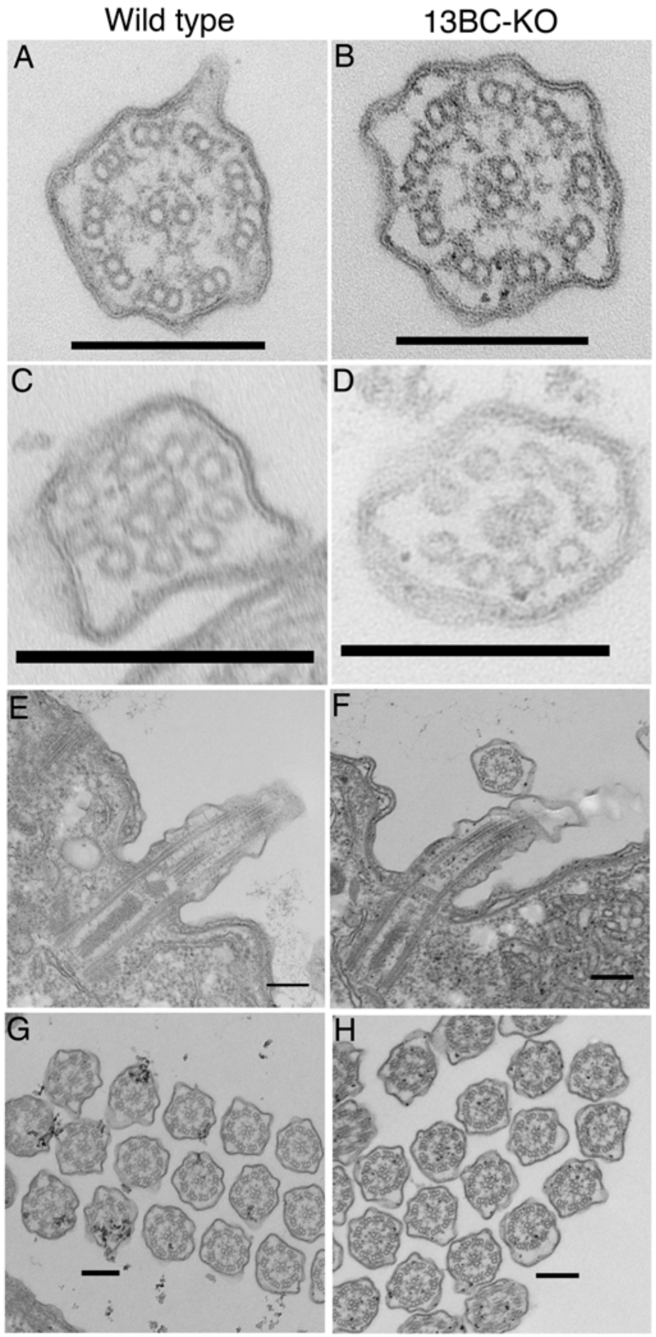
F
WT + ATP
13BC-KO + ATP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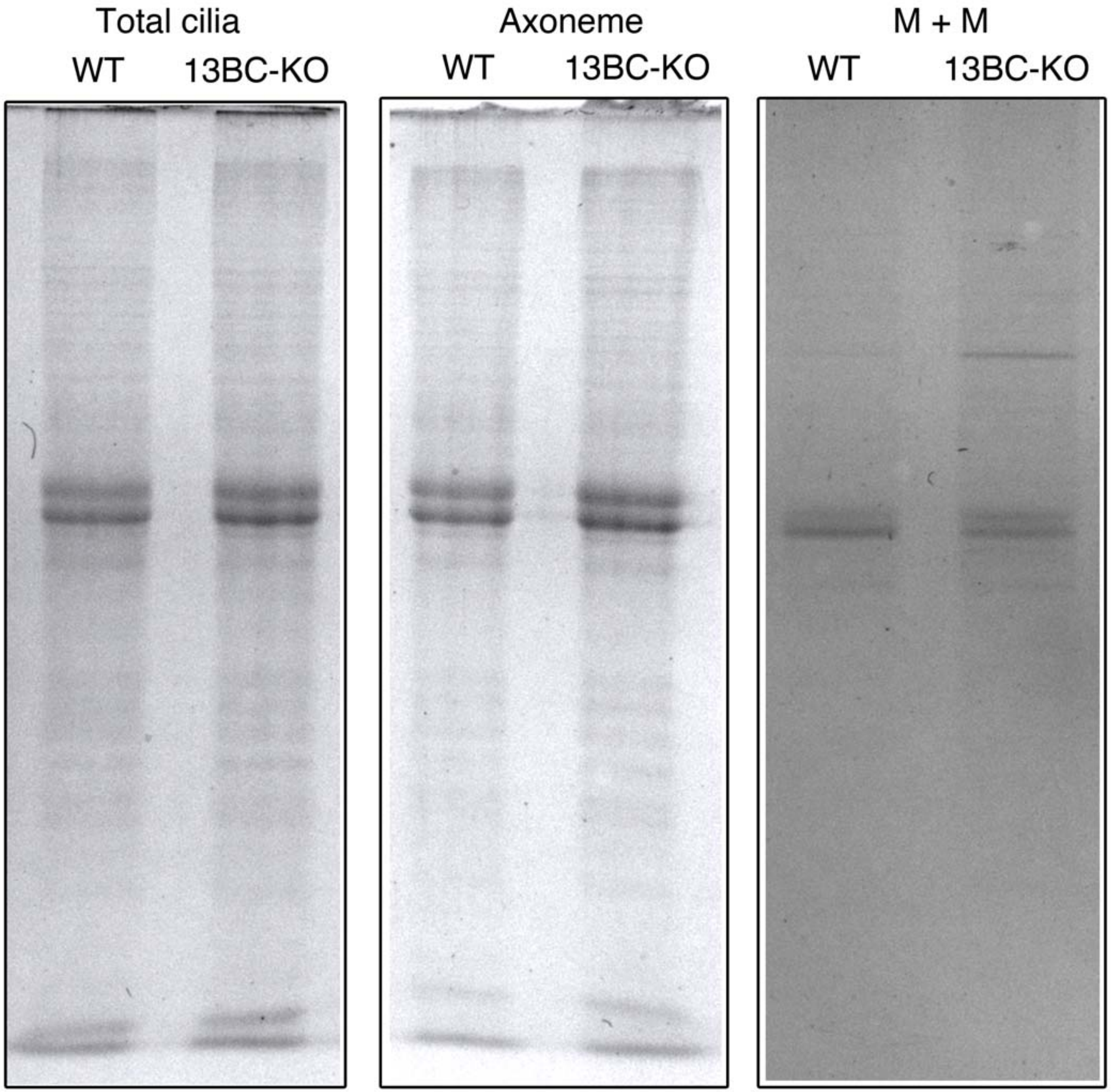
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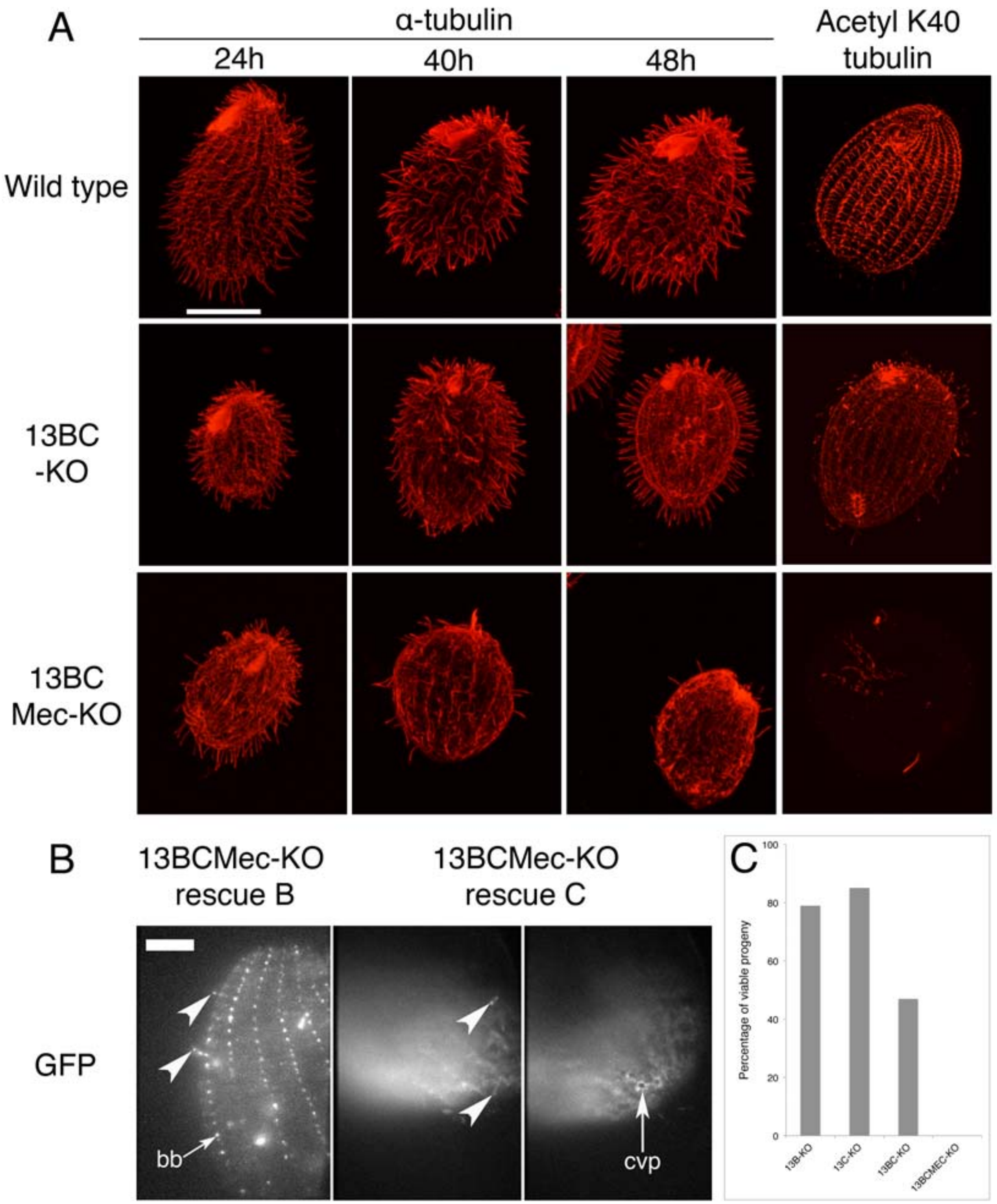
13BC-KO
Axoneme
WT
13BC-KO
M + M
WT
13BC-KO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40h
48h
Acetyl K40 tubulin
Wild type
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B
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GFP
bb
cvp
C
Percentage of viable progeny
100
80
60
40
20
0
13B-KO
13C-KO
13BC-KO
13BCMEC-KO