

## CellCognition: time-resolved phenotype annotation in high-throughput live cell imaging

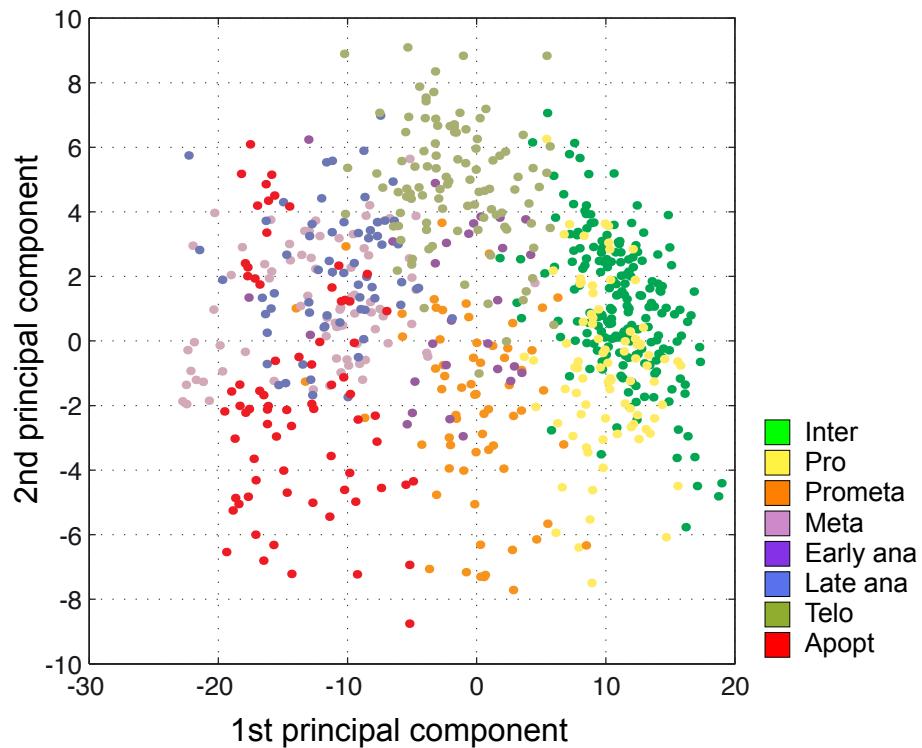
Michael Held, Michael H A Schmitz, Bernd Fischer, Thomas Walter, Beate Neumann, Michael H Olma, Matthias Peter, Jan Ellenberg & Daniel W Gerlich

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*Note: Supplementary Movies 1–16 and Supplementary Software are available on the Nature Methods website.*

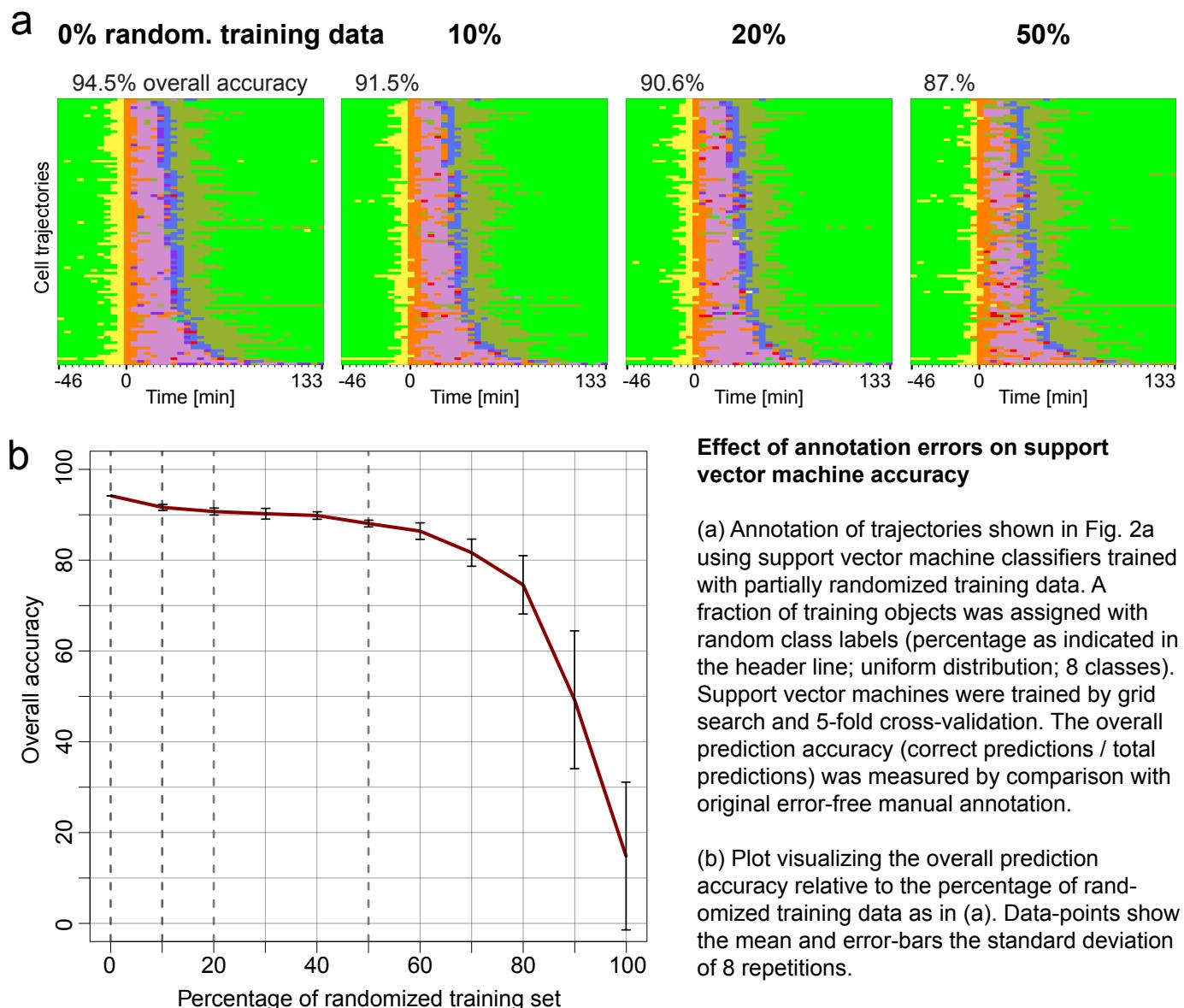
## Supplementary Figure 1



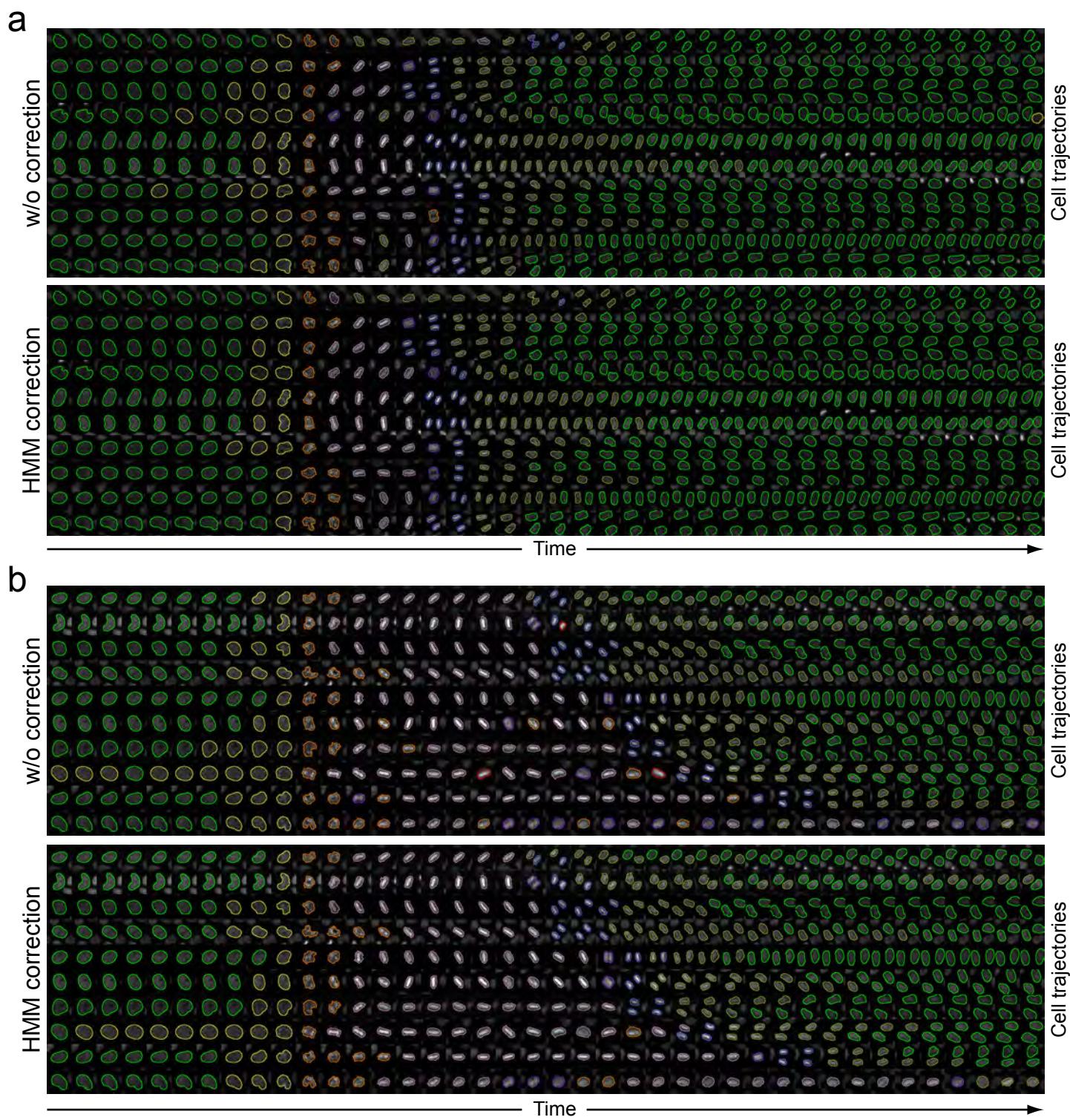
### Feature visualization in the subspace of the first two principal components

Data points visualize the first two principal components computed from 186 features and 689 manually annotated objects of the support vector machine classifier shown in Fig. 1d (color labels indicate morphology classes). Each object corresponds to a single H2B-labeled cell of the training set. Classes form overlapping clusters, which prevents perfect separation at this point.

## Supplementary Figure 2



## Supplementary Figure 3

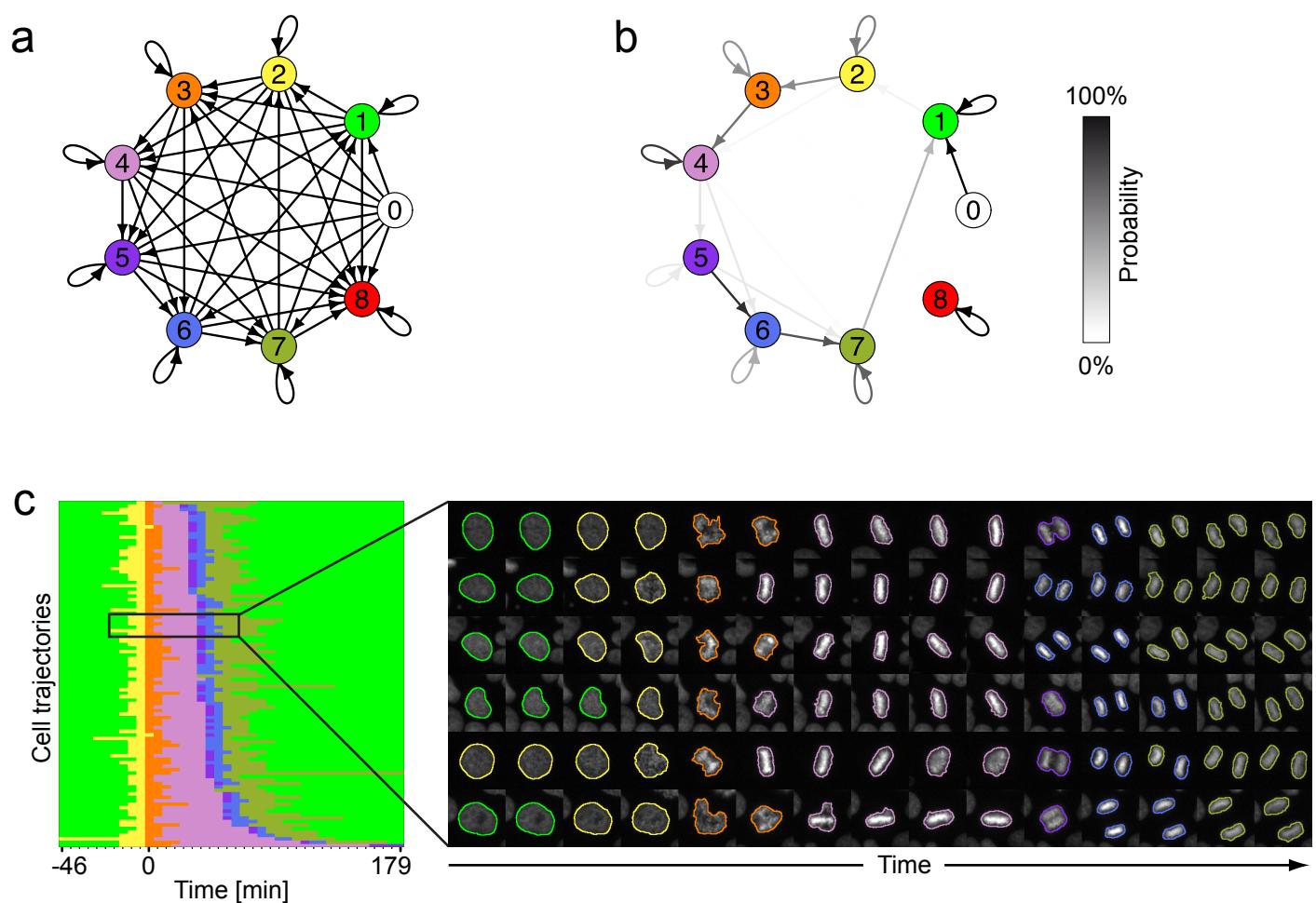


### Annotation of the fastest and slowest trajectories

(a) Trajectories of the 10% cells progressing fastest through mitosis, from the cells shown in Fig. 2. Contour colors indicate the class label predictions by the support vector machine (upper row; w/o correction; see Fig. 2a), and the hidden Markov model-corrected class labels (lower row; HMM correction; see Fig. 2f).

(b) Trajectories of the 10% cells progressing slowest through mitosis as in (a).

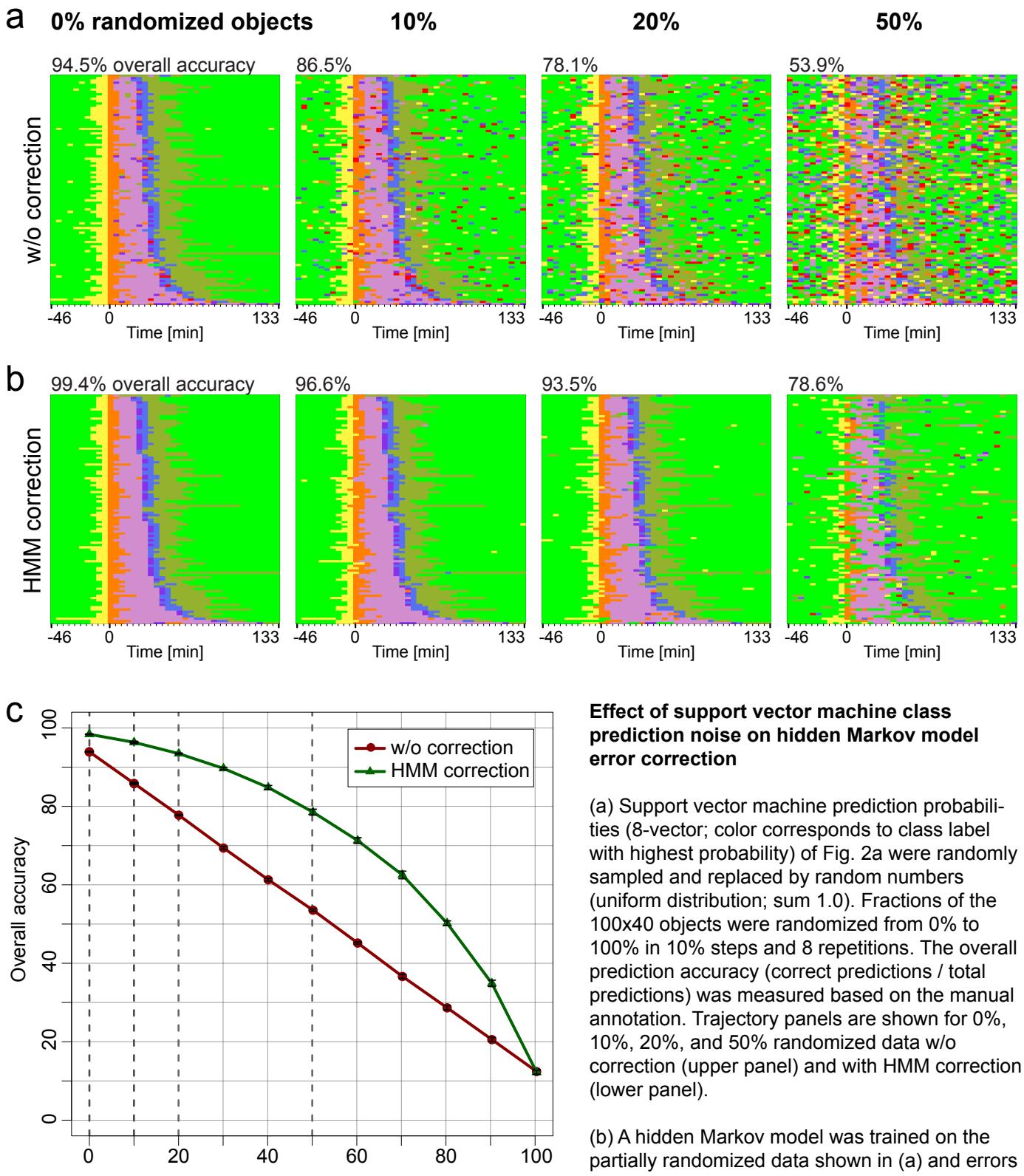
## Supplementary Figure 4



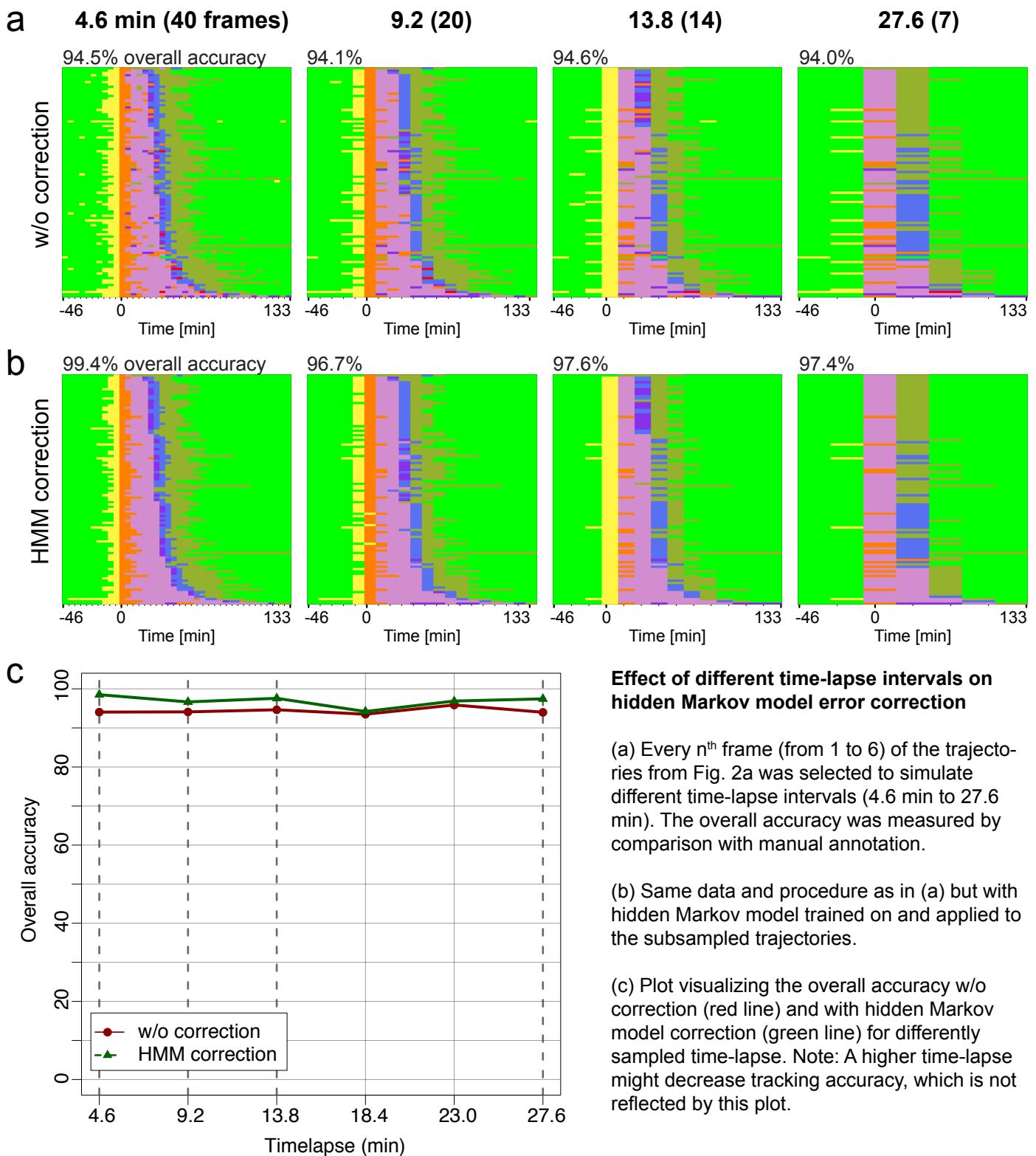
### Hidden Markov model error correction based on biological a priori knowledge

- (a) Class transitions were constrained to the forward direction of 3 consecutive frames, and apoptosis was defined as terminal state.
- (b) Learned stage transition probabilities for the constrained model based on the same data shown in Fig. 2a.
- (c) Error correction of the data shown in Fig. 2a using the constrained hidden Markov model.

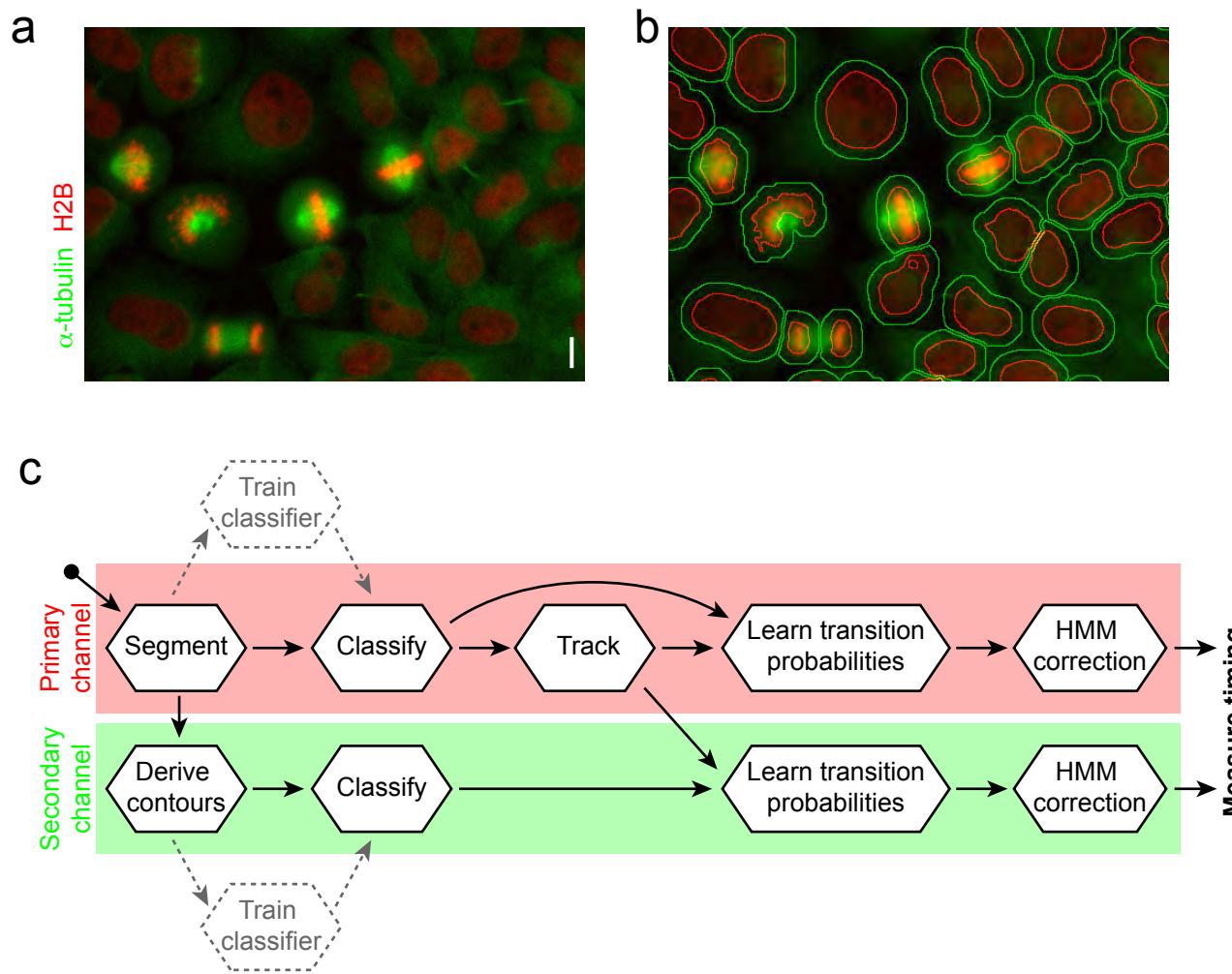
## Supplementary Figure 5



## Supplementary Figure 6



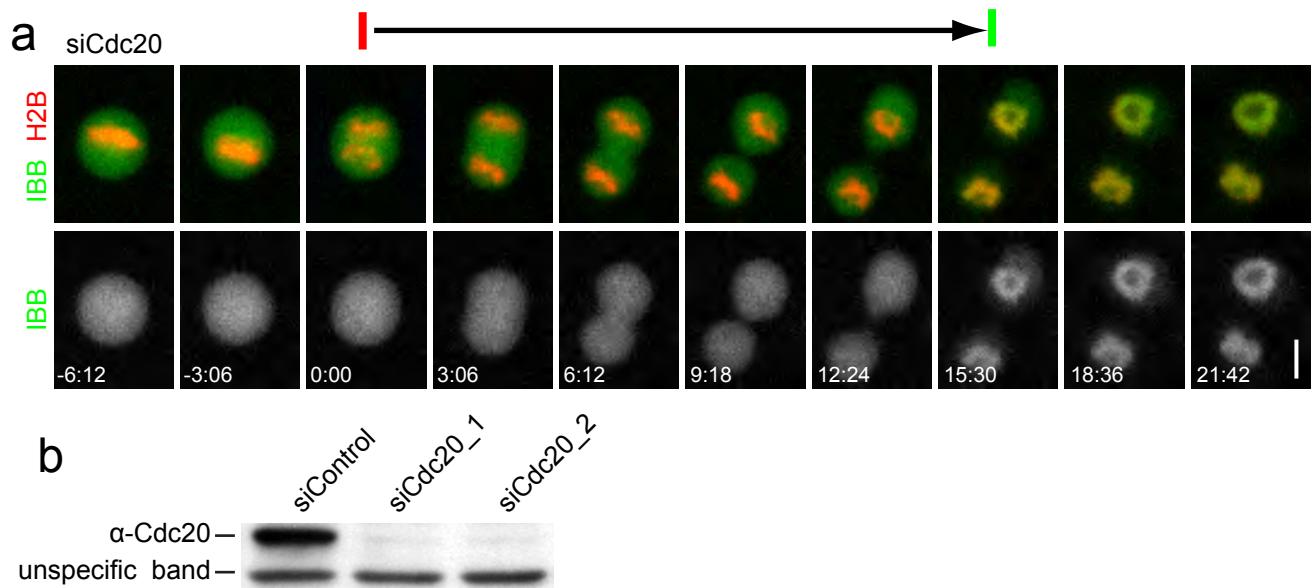
## Supplementary Figure 7



### Strategy for annotation of multi-channel assays.

- Single frame of a movie from a cell expressing H2B-mCherry and mEGFP- $\alpha$ -tubulin.
- Segmentation of secondary channel. Cells were first segmented by the H2B-mCherry (red contours), which was dilated to derive cytoplasmic regions (green contours).
- Workflow schematic for processing of two-channel experiments. The training of the classifier (dashed lines) applies only once per experiment, all other worksteps are automated.

## Supplementary Figure 8



### Cdc20 RNAi phenotype

(a) Mitotic exit timing in Cdc20 RNAi cell expressing H2B-mCherry and IBB-EGFP. The arrow indicates timing from anaphase onset (red bar) until onset of nuclear accumulation of IBB-EGFP (green bar). Cells were imaged as 2D time series with widefield epifluorescence 10x dry objective; time is in min:s. Bar: 10  $\mu$ m

(b) Validation of Cdc20 RNAi. Western Blotting of whole cell lysates 60 h after transfection of two different siRNA oligos targeting Cdc20, or a non-silencing siRNA oligo for negative control. The unspecific band detected by the anti-Cdc20 antibody served as a loading control.

**Suppl. Table 1.** Shape and texture features

Shape and size	circularity dist_max dist_min dist_ratio irregularity irregularity2 perimeter roisize		h4_variance h8_ASM h8_CON h8_COR h8_COV h8_DAV h8_ENT h8_IDM h8_PRO h8_SAV h8_SET h8_SHA h8_SVA h8_VAR h8_average h8_variance
Haralick <sup>1</sup> (32 gray levels, not normalized, distances 1,2,4 and 8 pixels rotation invariant)	h1_ASM h1_CON h1_COR h1_COV h1_DAV h1_ENT h1_IDM h1_PRO h1_SAV h1_SET h1_SHA h1_SVA h1_VAR h1_average h1_variance h2_ASM h2_CON h2_COR h2_COV h2_DAV h2_ENT h2_IDM h2_PRO h2_SAV h2_SET h2_SHA h2_SVA h2_VAR h2_average h2_variance h4_ASM h4_CON h4_COR h4_COV h4_DAV h4_ENT h4_IDM h4_PRO h4_SAV h4_SET h4_SHA h4_SVA h4_VAR h4_average	Haralick <sup>1</sup> (32 gray levels, normalized to min/max gray values per object, distances 1,2,4 and 8 pixels rotation invariant)	h1_2ASM h1_2CON h1_2COR h1_2COV h1_2DAV h1_2ENT h1_2IDM h1_2PRO h1_2SAV h1_2SET h1_2SHA h1_2SVA h1_2VAR h1_2average h1_2variance h2_2ASM h2_2CON h2_2COR h2_2COV h2_2DAV h2_2ENT h2_2IDM h2_2PRO h2_2SAV h2_2SET h2_2SHA h2_2SVA h2_2VAR h2_2average h2_2variance h4_2ASM h4_2CON h4_2COR h4_2COV h4_2DAV h4_2ENT

	h4_2IDM h4_2PRO h4_2SAV h4_2SET h4_2SHA h4_2SVA h4_2VAR h4_2average h4_2variance h8_2ASM h8_2CON h8_2COR h8_2COV h8_2DAV h8_2ENT h8_2IDM h8_2PRO h8_2SAV h8_2SET h8_2SHA h8_2SVA h8_2VAR h8_2average h8_2variance	ls1_DISP_sample_sd ls1_INTERIA_avg_value ls1_INTERIA_max_value ls1_INTERIA_sample_mean ls1_INTERIA_sample_sd ls1_IRGL_avg_value ls1_IRGL_max_value ls1_IRGL_sample_mean ls1_IRGL_sample_sd ls1_NCA_avg_value ls1_NCA_max_value ls1_NCA_sample_mean ls1_NCA_sample_sd ls1_TAREA_avg_value ls1_TAREA_max_value ls1_TAREA_sample_mean ls1_TAREA_sample_sd
Statistical Geometric Features <sup>2</sup>	ls0_CAREA_avg_value ls0_CAREA_max_value ls0_CAREA_sample_mean ls0_CAREA_sample_sd ls0_DISP_avg_value ls0_DISP_max_value ls0_DISP_sample_mean ls0_DISP_sample_sd ls0_INTERIA_avg_value ls0_INTERIA_max_value ls0_INTERIA_sample_mean ls0_INTERIA_sample_sd ls0_IRGL_avg_value ls0_IRGL_max_value ls0_IRGL_sample_mean ls0_IRGL_sample_sd ls0_NCA_avg_value ls0_NCA_max_value ls0_NCA_sample_mean ls0_NCA_sample_sd ls0_TAREA_avg_value ls0_TAREA_max_value ls0_TAREA_sample_mean ls0_TAREA_sample_sd ls1_CAREA_avg_value ls1_CAREA_max_value ls1_CAREA_sample_mean ls1_CAREA_sample_sd ls1_DISP_avg_value ls1_DISP_max_value ls1_DISP_sample_mean	n2_avg n2_stddev n2_wavg n2_wdist n2_wiavg  n_avg n_stddev n_wavg n_wdist n_wiavg

1. Haralick, R., Dinstein & Shanmugam in IEEE Transactions on Systems 1973).
2. Walker, R. & Jackway, P. in Pattern Recognition, 1996., Proceedings of the 13th International Conference on, Vol. 21996).

**Suppl. Table 2.** siRNA oligos used for RNAi screening

Gene HUGO Symbol	Full Gene Name	Entrez Gene ID	RefSeq Accession Number	Ambion siRNA ID	Sense siRNA Sequence	Antisense siRNA Sequence
1-Sep	septin 1	1731	NM_052838,	35578	GGAUGCAGAGAUGAAGGAAtt	UUCUUCAUCUGCAUCCTq
1-Sep	septin 1	1731	NM_052838,	35491	GGAAGAGGAGAUCCACAAUtt	GAUGUGGAUCUCUCUJUCCt
1-Sep	septin 1	1731	NM_052838,	35399	GGAGCAUUUUGAGCAGUAc	GUACUGCUAAUUGCUCCt
3-Sep	septin 3	55964	NM_019106.NM_145733.NM_145734,	38214	GGAGCUUGAAGUAAAUGGct	GCCAUUUACUUAAGCUCt
3-Sep	septin 3	55964	NM_019106.NM_145733.NM_145734,	38123	GGAGAAACGCAUCCCUGAAtt	UCAGGGAUUGCUCUUCUCCt
3-Sep	septin 3	55964	NM_019106.NM_145733.NM_145734,	133703	GGGCCAACCCUUUUUAGUtt	ACUAAAAGGGCUCUGGCCt
6-Sep	septin 6	23157	NM_015129.NM_145799.NM_145800.NN	136765	GGCUAAAGCUCACGAUCGUtt	ACGAUCGUGAGCUCUUAGCCt
6-Sep	septin 6	23157	NM_015129.NM_145799.NM_145800.NN	136764	GCAACGUGAGGCUAAAGCt	AGCUUJAGCCACAGUGCt
6-Sep	septin 6	23157	NM_015129.NM_145799.NM_145800.NN	136766	GCUCACGAUCGUAGCACAt	UGUGCUJAAACGAUCUGAGCt
8-Sep	septin 8	23176	XM_034872,	264717	CCUCUUCACUUCUAAUAGt	ACAUAGUGAGUAGGAGGt
8-Sep	septin 8	23176	XM_034872,	264716	CGCCAUCUUUUCUAAUtt	AUAUAGAAAAGUAUGGCGt
8-Sep	septin 8	23176	XM_034872,	264715	GGCAGAUUGUUCUACAACAt	UUGUJAGACAAACUUCCT
10-Sep	septin 10	151011	NM_144710.NM_178584,	215107	CCUUGACAGCAAGGUAAAAt	GUUACCUUUCGUCAAGGt
10-Sep	septin 10	151011	NM_144710.NM_178584,	37634	GGUGGAUGUGAAAAGUAAt	UUCAUGUUUCAACUCCACt
10-Sep	septin 10	151011	NM_144710.NM_178584,	37539	GGCUUAUAGUUAAGGGt	CCACCUUAAJACAUAAJAGCt
11-Sep	septin 11	55752	NM_018243,	125139	CCUGUACUAAAAGCCUAAUtt	AUUAGGCAUUAAGCAGGt
11-Sep	septin 11	55752	NM_018243,	125138	GGGUUUUCGGUAAAAGGCA	UGGUUUUAAACGCCACACt
11-Sep	septin 11	55752	NM_018243,	125137	CGUUAUAGGACACUUUUtt	AACAAAGUGCUCAUAAACGt
ANLN	anillin, actin binding protein (scraps homolog)	54443	NM_018685,	132620	GGAAAGCUACAUUCUGUCCt	GGAAAGCUACAUUCUGUCCt
ANLN	anillin, actin binding protein (scraps homolog)	54443	NM_018685,	132619	CCUGGUACCCGUUUGUtt	UAAAACAGGGUACCCAGGt
ANLN	anillin, actin binding protein (scraps homolog)	54443	NM_018685,	132621	GGGUUCACUAGAAUCGCAAAt	UUUCGCAUUCAGUGAACACt
ARHGAP17	Rho GTPase activating protein 17	55114	NM_018054.NM_001006634,	26221	GGAUCAAGACAAAAAAACUtt	AAGUUUUUUGUCUUGAUCCt
ARHGAP17	Rho GTPase activating protein 17	55114	NM_018054.NM_001006634,	26127	GGUGGAGAUUCACAUACAt	GAUGUJGGAAUCUCCACt
ARHGAP17	Rho GTPase activating protein 17	55114	NM_018054.NM_001006634,	26031	GGAGACACAAAAAACUGCCt	GGCAGUUUUUUGUCUCCt
AURKB	aurora kinase B	9212	NM_004217,	495	GGUGAUGGAGAAUAGCAGUtt	ACUGCUAAUUCUCAUCACt
AURKB	aurora kinase B	9212	NM_004217,	494	GGAGGAUCUACUUGAUUtt	AGAAUCAAGUAGAUCCt
AURKB	aurora kinase B	9212	NM_004217,	493	GGCAAGUJGGAAAGCAGUtt	ACACGUUJCCACAUUCGt
AURKC	aurora kinase C	6795	NM_003160.NM_001015878.NM_001015	111219	GGCAGAAAGUAGUACAAAt	UGUUCACUAAUUCUCCt
AURKC	aurora kinase C	6795	NM_003160.NM_001015878.NM_001015	379	GGAAAGCCAUCUUAUUGUGt	CACAAUGAAAUGGCUUCCt
AURKC	aurora kinase C	6795	NM_003160.NM_001015878.NM_001015	378	GGUAGACUGAGGAGGUUCCAt	UGGAAACCUCAACAUCCt
BIRC5	baculoviral IAP repeat-containing 5 (survivin)	332	NM_001168.NM_001012270.NM_001012	121296	GGCAGUGGCCUAAAUCUtt	AAGGAUJUAGGCCACUGCt
BIRC5	baculoviral IAP repeat-containing 5 (survivin)	332	NM_001168.NM_001012270.NM_001012	121295	GGCAUUCUACUAGUAAUtt	CCCAUUGACUUAAGGAGCt
BIRC5	baculoviral IAP repeat-containing 5 (survivin)	332	NM_001168.NM_001012270.NM_001012	121294	CCACUUCAGGGGUUUAUUCt	GAUAAAACCUGGAAGUGGt
BUB1	BUB1 budding uninhibited by benzimidazole	699	NM_004336,	510	GGCAGAAAGUAGAAGAAAGt	ACUUUUCUACGGUUUUCGt
BUB1	BUB1 budding uninhibited by benzimidazole	699	NM_004336,	509	GGUUAUUCUAGACACGCCt	AGGCGUGUCUGAAAUAACt
BUB1	BUB1 budding uninhibited by benzimidazole	699	NM_004336,	147346	CGAAGAGUAGUACGAAUtt	AAAUCGUGACUCUUCUGt
BUB1B	BUB1 budding uninhibited by benzimidazole	701	NM_001211,	90	GGGGGAAGGAGAGUAAUtt	UAUACUCUCCUUCCCACt
BUB1B	BUB1 budding uninhibited by benzimidazole	701	NM_001211,	89	GGCUUCAGAAAGUAAUAt	UUGUUAUUCUUCUGAAGCt
BUB1B	BUB1 budding uninhibited by benzimidazole	701	NM_001211,	88	GGGUUJGGGUUJJCACUJGt	CAAGUGAAACACCAAAUCt
BUB3	BUB3 budding uninhibited by benzimidazole	9184	NM_004725.NM_001007793,	137638	GCAGGGUUAUGUUAUAGCt	GCUUAUACAUACCCUGCt
BUB3	BUB3 budding uninhibited by benzimidazole	9184	NM_004725.NM_001007793,	137637	GGCUGAAAAGGUUAUACAt	GGUUAUACCUUUCAGGt
BUB3	BUB3 budding uninhibited by benzimidazole	9184	NM_004725.NM_001007793,	15258	GGUUAUACCCUUCUCAUGUtt	CACUGAGAGGGUUAUACt
CCNB1	cyclin B1	891	NM_031966,	118840	GCUGUACCAAAACCUUtt	UACAAAGGUUJUGGAUCAGCt
CCNB1	cyclin B1	891	NM_031966,	118839	GGCUAUUUJUGUUGAUACUtt	AGUAUCAACAAUAGGt
CCNB1	cyclin B1	891	NM_031966,	118838	GCAAACCUUCAGCUACUtt	CAGUAGCUGAAGGUUUCGt
CDC10	septin 7	989	NM_001788.NM_001011553,	10504	GGGAAGAUUCUUAUACAUtt	GAGUUAUAAAAGUACUUCCCt
CDC10	septin 7	989	NM_001788.NM_001011553,	10417	GGCUUUUCAUCAGAAUAt	UAAAUCAUAGAGAAGGACt
CDC10	septin 7	989	NM_001788.NM_001011553,	10323	GGUUUUGAAUUCACGCUUAt	UAAGCGUGAAUCAAAACt
CDC14A	CDC14 cell division cycle 14 homolog A (S. pombe)	8556	NM_033312.NM_033313.NM_003672,	105908	GGAAAUAGUGACACUACAt	GGUGUAGUGCCACAUUCCt
CDC14A	CDC14 cell division cycle 14 homolog A (S. pombe)	8556	NM_033312.NM_033313.NM_003672,	105907	GAUUUJGGGCCGCUACUtt	AGUCAGCGGUCCAAAACt
CDC14A	CDC14 cell division cycle 14 homolog A (S. pombe)	8556	NM_033312.NM_033313.NM_003672,	105906	GCACAGUAAAUAACCCACUtt	UAGGGGUUAUJACUGUGCt
CDC14B	CDC14 cell division cycle 14 homolog B (S. pombe)	8555	NM_033311.NM_03332.NM_003671,	45650	GAUJJUJGACACAUCAUtt	GAUJUGAGUGGUCCAAAACt
CDC14B	CDC14 cell division cycle 14 homolog B (S. pombe)	8555	NM_033311.NM_03332.NM_003671,	45559	GAACUUCUACCCAGAUUtt	AAAUCUGGUJAGGUACUAt
CDC14B	CDC14 cell division cycle 14 homolog B (S. pombe)	8555	NM_033311.NM_03332.NM_003671,	35174	GGUGUAGACUUCGGCCUACUtt	AGGCCGAAGGUCAUCACt
CDC16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	8881	NM_003903,	137341	GCCUAGUGAAACGGCUACUtt	GAUGACCGGUUJACUAGGt
CDC16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	8881	NM_003903,	137340	GGCGACUGGGAAAAGUACGCAAt	UGUGACAUUUCCCAGUGGt
CDC16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	8881	NM_003903,	137342	CCAAUACUACUAAACUACUtt	GCUAGUJUJAGGUUAUAGGt
CDC2	cell division cycle 2, G1 to S and G2 to M	983	NM_033379.NM_001786,	42819	GGAAUCUUCGUCAUCAAAAt	AUUUJGGAUGAGCAAGGUCCt
CDC2	cell division cycle 2, G1 to S and G2 to M	983	NM_033379.NM_001786,	1625	GGUUAUACUCAUCUUUtt	UCAAAGAUGAGAAUACt
CDC2	cell division cycle 2, G1 to S and G2 to M	983	NM_033379.NM_001786,	1440	GGCUAGUGGUAGCAGCAUtt	UCAUGGUACCCACUUGCCt
CDC20	CDC20 cell division cycle 20 homolog (S. cerevisiae)	991	NM_001255,	215139	CCUUGGGUAGGUAGGUUtt	AGAACUCCAAUUCACAGGt
CDC20	CDC20 cell division cycle 20 homolog (S. cerevisiae)	991	NM_001255,	145701	CCAGCUAGUUAUJUJGAGAt	CUUCCAAAUAUACUGCUGt
CDC20	CDC20 cell division cycle 20 homolog (S. cerevisiae)	991	NM_001255,	145700	CCUGCCGUUACAUUCUCCt	GAAGGAAGUUAACGGCAGGt
CDCA1	cell division cycle associated 1	83540	NM_031423.NM_145697,	131098	GGACCUUUCAGAUUAAUAGGt	CCUAAUJAUUCUGUAAGGt
CDCA1	cell division cycle associated 1	83540	NM_031423.NM_145697,	131097	GCACCGGGUACAUACGUAAt	UAUACGUUUUACGGCAUCt
CDCA1	cell division cycle associated 1	83540	NM_031423.NM_145697,	131099	CGCACAGUAAAUGAGGAAUtt	AAUCCUCAAAUACUGUGCGt
CDCA1	kinesin heavy chain member 2	3796	NM_004520,	118425	CGUAGAAAUCUAAUUCUUGUtt	CACAAUJAUAGGUUUCUACGt
CDCA8	cell division cycle associated 8	55143	NM_018101,	132285	GGCUAGCCGGCUUACACAt	GUGUJAGACGGCUUACCCt
CDCA8	cell division cycle associated 8	55143	NM_018101,	132284	GGUAGAGUAAAAGUAGUAt	CACUAUCAUUCUACUCCt
CDCA8	cell division cycle associated 8	55143	NM_018101,	132286	GGCUUJUJAGGUACACUtt	CACACUCAAAACAUAAGCCt
CENPE	centromere protein E, 312kDa	1062	NM_001813,	121339	GGCUACUAAUACAGGAAUAt	AAUUCUCCUGAUUUAUGACt
CENPE	centromere protein E, 312kDa	1062	NM_001813,	121337	CCAAUACUAGCAUUCUGCCt	UGGCAGAAUCGAUGAUUAGGt
CENPE	centromere protein E, 312kDa	1062	NM_001813,	10706	GGAAUUAAGGCGUAAAAGAt	UCUUUUJGAGGUUUAUUCt
CENPF	centromere protein F, 350/400ka (mitosin)	1063	NM_016343,	146738	GGUGACUUCAGUAGCAGUAt	UGAUCGACUJGGAGACCCt
CENPF	centromere protein F, 350/400ka (mitosin)	1063	NM_016343,	146737	CCAGACUAAUUAUJAGUtt	CAUCUAAUJAGUACUUGGt
CEP1	centrosomal protein 1	11064	NM_007018,	136173	GGCUAAUACUAAUAGGGAAAt	UUCCCUAAUAGGUUAUAGCt
CEP1	centrosomal protein 1	11064	NM_007018,	136172	GGAGUAGUAGAAUUAUACGt	CUGUAAUAAUACUACUCCt
CEP1	centrosomal protein 1	11064	NM_007018,	136174	GGCCACUAAUUAUUAUACAt	UGGAUAAAUAUJUAGUGGt
ch-TOG	cytoskeleton associated protein 5	9793	NM_014756.NM_001008938,	122705	GGUGUJUJAGGUACACCCt	UUUAGGUJUJAGGUACACCCt
ch-TOG	cytoskeleton associated protein 5	9793	NM_014756.NM_001008938,	122704	GGUGUJUJAGGUAGGUAGGt	ACACCUCUUAACACACCt
ch-TOG	cytoskeleton associated protein 5	9793	NM_014756.NM_001008938,	122703	GCAACCCACAUACUACCCt	CAUACCCACAUACUACCCt
CHC1	chromosome condensation 1	1104	NM_001269,	145718	GGAAACGACCUACUGGUAGt	UCACCAAGUGGUUCUUCt
CHC1	chromosome condensation 1	1104	NM_001269,	145717	CCGUGUGCUUAGCAACAGGt	CUUUCGUUAGACACACCGt
CHC1	chromosome condensation 1	1104	NM_001269,	145719	GCAUACAGCUUUAUAGUAt	GACUAAUAGACUGUJAGCt
CIT	citron (rho-interacting, serine/threonine kinase)	11113	NM_007174,	103737	GGAAUAAAAGGGGUCAUAt	AAUGACCCUUAUUAUACt
CIT	citron (rho-interacting, serine/threonine kinase)	11113	NM_007174,	103729	GGGAAUAAAAGGUAGCCUCUtt	AGAGGGCAUCUAAUACCCt
CIT	citron (rho-interacting, serine/threonine kinase)	11113	NM_007174,	103721	GGCUGAAUCUGUUCUCCAt	UGGAAGAACAGAUUCAGCt
CLASP1	cytoplasmic linker associated protein 1	23332	NM_015282,	136867	GCACAGACUUAACACAUAt	UUAGGUJUJAGGUACCCt

CLASP1	cytoplasmic linker associated protein 1	23332	NM_015282.	136866	CCAUGUUAGAUAAAUCUUGUtt	ACAAGUUUAUCUAAACAUAGCt
CLASP1	cytoplasmic linker associated protein 1	23332	NM_015282.	136868	CGACACAUAAAGCAUAAAAGtt	CUAAUACUGAUAGUGUCGtt
CSNK2B	casein kinase 2, beta polypeptide	1460	NM_001320.	9896	GGAACCCGUAGUUGGUUtt	AAAACCAUACAGGGUUCtq
CSNK2B	casein kinase 2, beta polypeptide	1460	NM_001320.	9806	GGAGACUUUJGGGUACUGUtt	GACAGUAACCAAAGCUCCt
CSNK2B	casein kinase 2, beta polypeptide	1460	NM_001320.	9710	GGCAGCCGAGAUGCUUUAUtt	AUAAAGCAUCUCGGCUGCCtq
DCTN1	dynactin 1 (p150, glued homolog, Drosophili	1639	NM_023019.NM_004082.	242562	CCACAUUAAGAUUACCGCAGtt	CUGCGUGAACUUAUUGUGGtt
DCTN1	dynactin 1 (p150, glued homolog, Drosophili	1639	NM_023019.NM_004082.	242561	GGAGAAAGAGGUUAGGAGGtt	CUCCUAAACUUCUUCUCCt
DCTN1	dynactin 1 (p150, glued homolog, Drosophili	1639	NM_023019.NM_004082.	242560	GGCAGAGGACCAAUAGUtt	AUCAUAGGUGCUCUCUGCCt
DCTN2	dynactin 2 (p50)	10540	NM_006400.	135759	GGUGCACCAGCUAUAGAAtt	UUCAUUAUAGCUGGUGCACt
DCTN2	dynactin 2 (p50)	10540	NM_006400.	135758	GGACAGGAAUAGUAUAGGtt	CCAGAUUCAUACUCGCCt
DCTN2	dynactin 2 (p50)	10540	NM_006400.	135757	GCGGAGUUCGAUGCGUUUGtt	CAAACCGCAUCAACUCCt
DLG7	discs, large homolog 7 (Drosophila)	9787	NM_014750.	138400	CGAAAAAGACCUUUGGUUtt	UGGAAUAGGCUUUUUUGGt
DLG7	discs, large homolog 7 (Drosophila)	9787	NM_014750.	138399	CGAAAAAGACCUUUGGUUtt	AACCAAGUGUCUAAUUCGtt
DLG7	discs, large homolog 7 (Drosophila)	9787	NM_014750.	138401	CGAGGAUUAUUAAGUGGtt	CCACUUAUAAUACUUCUGt
DNC1H	dynein, cytoplasmic, heavy polypeptide 1	1778	NM_001376.	118311	GCCCCAAAGUACAGACUUtt	AAAGUCUGUAACUJJUUGGt
DNC1H	dynein, cytoplasmic, heavy polypeptide 1	1778	NM_001376.	118310	GCAAAAUUUAUGAAAUCUCCtt	CGGAUUUCAUAAUUUUGCt
ECT2	epithelial cell transforming sequence 2 oncc	1894	NM_018098.	26257	CGUACUCCCGUAGUAGUtt	CAUCAUACAGGGAGACGtt
ECT2	epithelial cell transforming sequence 2 oncc	1894	NM_018098.	26165	GGUUUUGAUUCUCCGGAAUtt	GCAACUUAUAAUJUUGGt
ECT2	epithelial cell transforming sequence 2 oncc	1894	NM_018098.	26070	GGACAUAAAAGUGGCCUUUtt	AAAGCCACUUUAUUGCCt
ESPL1	extra spindle poles like 1 ( <i>S. cerevisiae</i> )	9700	NM_012291.	121653	CCAUAAAUAAGGAAAGUCCtt	GGACACUJJUUAUUAUUGGt
ESPL1	extra spindle poles like 1 ( <i>S. cerevisiae</i> )	9700	NM_012291.	121652	GCAGCUGACUGCUAAUCUtt	UAGCUUAGCAGCAGCUGCt
ESPL1	extra spindle poles like 1 ( <i>S. cerevisiae</i> )	9700	NM_012291.	121651	CGCUUGUAGGCGCAUCCGtt	UCAGGAGGCAUACAAGCt
FZR1	fuzzy/cell division cycle 20 related 1 (Drosop	51343	NM_016263.	241641	UUAAAAGCCUGAUUGUGAAtt	UUCACAUACAGGCAUUAAtg
FZR1	fuzzy/cell division cycle 20 related 1 (Drosop	51343	NM_016263.	241640	GCAAAACCCGUGUCCGACAAtt	UUUGUGCAACGGGUUUGCt
FZR1	fuzzy/cell division cycle 20 related 1 (Drosop	51343	NM_016263.	241639	CGACAGGCGAAAGGCCAAtt	UUGGCUUJUCCGGUJCUGACt
INCENP	inner centromere protein antigens 135/155k	3619	NM_020238.	28431	GGAGAGAAGAAGCAGAUUtt	AAUCUGCUUUCUUCUCCt
INCENP	inner centromere protein antigens 135/155k	3619	NM_020238.	145370	CGGAAGAAGAGCAGGUUtt	AAUCCGUUCUUCUCCGt
INCENP	inner centromere protein antigens 135/155k	3619	NM_020238.	145369	CGCAUGUUCUACCGAGAAtt	UUCUGGUGAACAUGCGt
INCENP	inner centromere protein antigens 135/155k	3619	NM_020238.	28244	GGACAUUUGGUUGGCCUUGAGt	CUAAGCCACACCAAGUCt
KEAP1	kelch-like ECH-associated protein 1	9817	NM_012289.NM_203500.	138235	CGAGUGGCGAUAUGACAAtt	UGGAUCAUUCGCCACUCGt
KEAP1	kelch-like ECH-associated protein 1	9817	NM_012289.NM_203500.	138234	GGACAGAGGUGGCGAUAGUtt	AUCAUUCGCCACUCUGCCt
KEAP1	kelch-like ECH-associated protein 1	9817	NM_012289.NM_203500.	138233	CGGGACAAACCGCCUUAAUtt	AUUAAGGCGGUUJUUGCCGt
KIF11	kinesin family member 11	3832	NM_004523.	118431	GGAGUGAUUAUAAAAGGUUtt	AACCUUUAUUAUACUCt
KIF11	kinesin family member 11	3832	NM_004523.	118430	GCUCAAGGAAAACAUACAct	GUGUAUJUUCUUCUUGAGCt
KIF11	kinesin family member 11	3832	NM_004523.	118429	CCAUUAAAUUUJGGCAGACGtt	GCUCUGCCAAUAAAUAUGGt
KIF2	kinesin heavy chain member 2	3796	NM_004520.	118424	GCCCCAAAGUAAAACAAAAGtt	CAAUUJUJUUAUJJUUGGt
KIF2	kinesin heavy chain member 2	3796	NM_004520.	118423	CCUGGAGAGCAUCUUUCAtt	UGAAAAGUGCUCUCCAGGt
KIF20A	kinesin family member 20A	10112	NM_005733.	118443	GGUAAAAGCJUAAAUCAGtt	CUGUAUJUJUAGCJUUAACt
KIF20A	kinesin family member 20A	10112	NM_005733.	118442	GCAGCAGGUGGUCAUCUGAGtt	CUCAGAUGGAGACUCUGCt
KIF20A	kinesin family member 20A	10112	NM_005733.	118441	CCGUCAUCAUCAGCUCUtt	AGAGCAGUCAUAGCAGGtt
KIF23	kinesin family member 23	9493	NM_138555.NM_004856.	118503	CCAUAAACAUUGAUUGUGCAtt	UGCAACAUACAUJUUAUGGt
KIF23	kinesin family member 23	9493	NM_138555.NM_004856.	118502	GGUUAUGGUCAUUAUAGAAtt	UUCUAAUAGGCAUACACt
KIF23	kinesin family member 23	9493	NM_138555.NM_004856.	118501	CGGAAUAGGAGACUACUAGtt	CUUUAUGGUCCAUUCUGGt
KIF23	kinesin family member 23	9493	NM_138555.NM_004856.	118446	GCAACUUGUUUJGGCAUAGtt	CAUACUACAAACAAUGGt
KIF2C	kinesin family member 2C	11004	NM_006845.	118445	GCUUCUUCUCCUJUACAUCCGtt	CGGAUGUAAGGGAGAAGCt
KIF2C	kinesin family member 2C	11004	NM_006845.	214569	CGAGCGUCCAGCAGACAAUtt	UAUUJUUCUGCUJUGCCt
KIF4A	kinesin family member 4A	24137	NM_012310.	118455	GGCAAGAAAAGUAAAAGUAGtt	CGGUUCAUJJUUAUJUUGGt
KIF4A	kinesin family member 4A	24137	NM_012310.	118454	GCAAGCGAAUAGAAAAAAAGtt	CAUUUUUCAUJUUCGUUGCt
KIF4A	kinesin family member 4A	24137	NM_012310.	118453	GGUAAAAGCCCAUACUCUtt	UAAGAGUAUJGGCAUUAACt
KIF5B	kinesin family member 5B	3799	NM_004521.	118428	CGUCAGUGGAGAAACCUUUAUtt	AUAAGGUUJUUCACACUGCt
KIF5B	kinesin family member 5B	3799	NM_004521.	118427	GCAACUCAUCAAGCAGCAAGtt	ACUUGCUCUJUGAGAUGUGt
KIF5B	kinesin family member 5B	3799	NM_004521.	118426	GCCUUUAGCAUJUUGAUUCGtt	CCGAUAAAUGCAUAAAGCt
KIFC1	kinesin family member C1	3833	NM_002263.	118527	CCUAAAUGCGAACUAAAAtt	UUUAGUUCUGCAUUAUAGGt
KIFC1	kinesin family member C1	3833	NM_002263.	118526	GGCAGACGACACAGCUCUtt	UUUGAGCUGUGGUGUCGCCt
KIFC1	kinesin family member C1	3833	NM_002263.	118525	CGACCAAAUUAUACCAACUtt	GAUGGUJUUAUJUGGUCCt
KNS2	kinesin 2 60/70kDa	3831	NM_005552.NM_182923.	118512	GCAUCUGGAGGUUUAUGAAUtt	AUUAUAAACUCCAGAUUGCt
KNS2	kinesin 2 60/70kDa	3831	NM_005552.NM_182923.	118511	GCACAAUUCUCAUUAUUCAAUtt	UUGUAAAAGGUUJUUGGt
KNS2	kinesin 2 60/70kDa	3831	NM_005552.NM_182923.	118510	GGUUAAGGAAGAAGCAGCAAtt	UGUGCUCAUUCUJUACAGGt
LATS1	LATS, large tumor suppressor, homolog 1 (0	9113	NM_004690.	567	GGAGGUJUJUACUCUCCACtt	GGUGGGAGGAGUACACUCt
LATS1	LATS, large tumor suppressor, homolog 1 (0	9113	NM_004690.	566	GGUUCUGAGAGGUAAAUAUAtt	UAAUUUJACUCUCAGAACt
LATS1	LATS, large tumor suppressor, homolog 1 (0	9113	NM_004690.	565	GGACAGAGGAGGUCAUAGUtt	AACUAUAGCCUUCUCUGCCt
LIMK1	LIM domain kinase 1	3984	NM_022314.NM_016735.	1413	GGACAGAGGGCUUACACUUCtt	GAAGUUAGGCCUUCUUGGt
LIMK1	LIM domain kinase 1	3984	NM_022314.NM_016735.	1318	GGUGACACCCGGUGAGACAtt	UGUCUCACGGUGUGACCCt
LIMK1	LIM domain kinase 1	3984	NM_022314.NM_016735.	1223	GGAUCAUAGGUAGGGCAUAtt	UACUGGCCACAUAGACt
LOC285643	LOC285643	285643	XM_209695.	118521	CGAACUGGAGUAAAAGUAGtt	CGUUAUGGUCCAUACUUCGt
LOC285643	LOC285643	285643	XM_209695.	118520	GGUACACCCACACCUUCAtt	UAAGAGUGGUCCUGUUAACt
LOC285643	LOC285643	285643	XM_209695.	118519	CCAACAGUUGGUCAUUAUCCtt	GAAUAAUGCCAACUGUUGGt
MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	8379	NM_00350.NM_001013836.NM_001013	121449	CCAAAGUUCGACUACAGCAAtt	CUCAUGGCAJUACACUGGt
MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	8379	NM_00350.NM_001013836.NM_001013	121448	CGGAUGGUAGAAAAGUAGtt	JCAUGUJUCAUCAACUCCGt
MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	8379	NM_00350.NM_001013836.NM_001013	121447	GGAUCCAGCGUAGUUGAGAAtt	CUUCACAAUUCGGCUGCAUCt
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	4085	NM_002358.	143483	GCGUGGCAUUAUACCAUCUtt	AGAUGGUUAUAGGCCACGt
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	4085	NM_002358.	11455	GGAGGAUCAUAGGAGGAAUAtt	UAUUJUUCUCAUGUACACt
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	4085	NM_002358.	11361	GGAGAAAACGGGUUCAUGUtt	CACUGAACGGGUUUAUACUCCt
MAP1B	microtubule-associated protein 1B	4131	NM_032010.NM_005909.	144102	GCUCAACACAUUCAGACUUtt	AAAGUCUAGAUUUJUGAGGt
MAP1B	microtubule-associated protein 1B	4131	NM_032010.NM_005909.	144101	GCCCAGUUCACCCGUUJUtt	AGAACAGGGGUUAACGGUCCt
MAP1B	microtubule-associated protein 1B	4131	NM_032010.NM_005909.	144100	CCCUUCUGUAGAACAGCAGUtt	GACUGCUUCAUCAAGAGGt
MAPRE1	microtubule-associated protein, RP/EB fami	22919	NM_012325.	136500	GCAGGUCAUCCACGUUAAAAtt	UUUCAACAUACGUUCCACUCCt
MAPRE1	microtubule-associated protein, RP/EB fami	22919	NM_012325.	136499	GCUAACGUAGAACACAGGtt	ACUGGUUCCUACGUUACGt
MAPRE1	microtubule-associated protein, RP/EB fami	22919	NM_012325.	136501	GGUCAACGUAGUJUAGAACUAtt	AAGUUUCAACAUACGUUGACt
MOBK1B	MOB1, Mps One Binder kinase activator-like	55233	NM_018221.	132366	GGCACACAAAGUUAUUAACtt	GUUAUACUJUUAUJUUGGt
MOBK1B	MOB1, Mps One Binder kinase activator-like	55233	NM_018221.	26356	GGAUCAUCAUCAGUAGAACtt	GUUCAUACUJUUAUACAGGt
MOBK1B	MOB1, Mps One Binder kinase activator-like	55233	NM_018221.	26450	GGGAGAGGAGUCAUUAUAAAtt	UUCUAAUACUUCUCUCCt
MOBK1A	MOB1, Mps One Binder kinase activator-like	92597	NM_173468.	148184	GGUUUJUUGGGGUUUAUUAAtt	UAAAUUUACCUACACCCt
MOBK1A	MOB1, Mps One Binder kinase activator-like	92597	NM_173468.	148183	CCAUAAUUCAUUAUUGGUAGGtt	CCUAGCAUUAAGAAUAGUUGGt
MOBK1A	MOB1, Mps One Binder kinase activator-like	92597	NM_173468.	148185	GGAUUGGUAAAACACUACUtt	UGUAGUJUUAUACCUACUCCt
MPP1	membrane protein, palmitoylated 1, 55kDa	4354	NM_002436.	121379	CCGAGGACAUGUACACCAAtt	UUGGUGUACAUUGCCUCGt
MPP1	membrane protein, palmitoylated 1, 55kDa	4354	NM_002436.	121381	GCACAGCUCGAGUJUJUUGAUtt	AUCAAAAACUCCGAGCUGUGt
MPP1	membrane protein, palmitoylated 1, 55kDa	4354	NM_002436.	121380	CCGGCUUUCUCUGCACUACAtt	UGUAGUGCAGGAAAGACCGt
MSF	septin 9	10801	NM_006640.	135963	CGCACGAUUAUJUGAGGAGAAtt	UUCUCUCAUUAUCUGUGCCt
MSF	septin 9	10801	NM_006640.	18321	GGAGGGAGGUCAACAUACAtt	GUUGAUUGUUGACCUACCCt
MSF	septin 9	10801	NM_006640.	18228	GGGCUUCUGAGUACAUACUtt	GAUGUGUAGACUAGGAACCCt
NEDD4	neural precursor cell expressed, developme	4734	NM_198400.NM_006154.	120779	GGGAUUCUUCUUGGUAGGUACAtt	UAUUAGUUCAAAAGAUUCUCCt
NEDD4	neural precursor cell expressed, developme	4734	NM_198400.NM_006154.	120778	GGACCACAUUAUUGGUAGGUACAtt	UGGUUUACAUAAAAGGUUGCCt
NEDD4	neural precursor cell expressed, developme	4734	NM_198400.NM_006154.	120777	GGAUACUUCUUGGUAGGUACAtt	GGUCCUUCACAUACGUACUCCt

NEDD5	septin 2	4735	NM_004404.NM_001008491.NM_001008	14802	GCGCUGUCUCAUUUAUUUUUtt	AAAAAAAAGAGACGCCtg
NEDD5	septin 2	4735	NM_004404.NM_001008491.NM_001008	14709	GCGAAUACACAACAAAGGUGt	CACCUUUGUUGUGUAUJUGCtt
NEDD5	septin 2	4735	NM_004404.NM_001008491.NM_001008	14614	GCGGGCACAUCAUUGUAAtt	UUAUCAAUGAUGUCGCCtg
PLCB2	phospholipase C, beta 2	5330	NM_004573.	15072	GGUUAAGAGAGAGAUUAAtt	UAAUACUCUCUCCUAAACCtc
PLCB2	phospholipase C, beta 2	5330	NM_004573.	14977	GGAGAUGGAGGUUUCUGGAUtt	AUCCAGAACCUCAUCUCCtt
PLCB2	phospholipase C, beta 2	5330	NM_004573.	14881	GGGCUCACUCAUUAUACUGGt	CCAGUAUAAGUAGUAGGCCtt
PLK1	polo-like kinase 1 (Drosophila)	5347	NM_005030.	42856	GGAGGUGUUCGCCGGGCAAGt	CUUGCCCGCAACACCUCtt
PLK1	polo-like kinase 1 (Drosophila)	5347	NM_005030.	1341	GGUUUUUAGAUUUCUCCCAHt	CUGGGACCAACUCAAACCCtt
PLK1	polo-like kinase 1 (Drosophila)	5347	NM_005030.	103548	GGUGGAUGUGGUCCAUtt	AAUGGACCACACAUCACCtt
PMF1	polyamine-modulated factor 1	11243	NM_007221.	253762	CCUCUGAGAACGGCUGAAAtt	UUUCAGCCGUUCAGAGGta
PMF1	polyamine-modulated factor 1	11243	NM_007221.	253761	GUGAGGAGACGCCAGCCtt	GGGCUUCCGGGUUCUCACTc
PMF1	polyamine-modulated factor 1	11243	NM_007221.	253760	UUUCAGGGUGUAGGUCCUtt	AGGAGCUUCAACCCUCCGAAAt
PNUTL1	septin 5	5413	NM_002688.NM_001009939.	12081	GCGCAUUGCAUAGAGAAGGUt	GACCUUCAUAGCAUGCCtt
PNUTL1	septin 5	5413	NM_002688.NM_001009939.	11993	GGGAGUCAAGCUGAAGGUCh	GAGCUUCAGCUGACUCCtt
PNUTL1	septin 5	5413	NM_002688.NM_001009939.	11898	GGCUUJUGACUCAACACUAtt	UGAGUGUGAGUCAAAGGtt
PNUTL2	septin 4	5414	NM_080415.NM_080416.NM_080417.NN	142770	GCUUGAUCCCCAUAGAUUCCt	GGAAUCAUAGGAUACAGCtt
PNUTL2	septin 4	5414	NM_080415.NM_080416.NM_080417.NN	14882	GGAUUUCUCAGGAAAUCGt	CGCAUUUCUGAGAAAUCtt
PNUTL2	septin 4	5414	NM_080415.NM_080416.NM_080417.NN	15073	GGAGAUGUCAACACAAAAtt	UAUUUUGUGUAGCAUCUCCtg
PRC1	protein regulator of cytokinesis 1	9055	NM_003981.NM_199413.NM_199414.	137453	GGGGUUAACAAAAGACUAGt	CUCAGUUUUUUGUAACCCtg
PRC1	protein regulator of cytokinesis 1	9055	NM_003981.NM_199413.NM_199414.	137452	CCAGCGGUUAACAAAAGACUtt	AGUUCUUUUAACCCGUGGtc
PRC1	protein regulator of cytokinesis 1	9055	NM_003981.NM_199413.NM_199414.	137454	CCAUUUAGUCUGGUCAAAtt	UUUGACCCAGACAAU AUGGtq
PTTG1	pituitary tumor-transforming 1	9232	NM_004219.	42068	GAGUUGUGUGUUAUUGUAtt	UACAAAUACACCAAACUCCtq
PTTG1	pituitary tumor-transforming 1	9232	NM_004219.	41990	GCGUCUGAACAGCAAGGGt	UCCCUUUGGUUUACAGACtt
PTTG1	pituitary tumor-transforming 1	9232	NM_004219.	41900	GAUCUCAAGUUUCAACACCCt	GGGUUGAAACUJUGAGAU Ctc
RABBA	RAB8A, member RAS oncogene family	4218	NM_005370.	3022	GGAAAGCACAAUAGAAGGt	UCCUCAUJJUGUGUUCUCCt
RABBA	RAB8A, member RAS oncogene family	4218	NM_005370.	2930	GGGAGUCAAAAAGACCCGt	CGGUGUGAUUJUGACUCCtg
RABBA	RAB8A, member RAS oncogene family	4218	NM_005370.	2836	GGCCAACAUCAUAGUGGAAtt	UCCACAUUUGAUUGUUGCCt
RABGAP1	RAB GTPase activating protein 1	23637	NM_012197.	147469	GGAAUUGUGAGACUUCUAGt	CUAAGAGUCUCACAAUCtt
RABGAP1	RAB GTPase activating protein 1	23637	NM_012197.	147468	CCCUUGGUCAUAGUAGGGt	CCCUACUAAUGGCACAGGGt
RABGAP1	RAB GTPase activating protein 1	23637	NM_012197.	147470	CGUGUAAGCCGAUACUUUtt	AAAGUAUCCGGCUUACAGCtt
RACGAP1	Rac GTPase activating protein 1	29127	NM_013277.	20374	GGCAACUUUUUJUGCUUCUtt	GAGAAGCAAAAAGUUGCCt
RACGAP1	Rac GTPase activating protein 1	29127	NM_013277.	20283	GGGUUUCUCCGUAAGGUtt	CCACUUUUUACCGGAAUCtt
RACGAP1	Rac GTPase activating protein 1	29127	NM_013277.	20189	GGACUUGAGGUUUCUCCgt	ACGAAAUCUCCUAGUCCtt
RASSF1	Ras association (RalGDS/AF-6) domain fan	11186	NM_007182.NM_170712.NM_170713.NN	137076	GGAAUUCUUAACAGACUCCt	AGCUCUGAUAAAGGUACUCCtq
RASSF1	Ras association (RalGDS/AF-6) domain fan	11186	NM_007182.NM_170712.NM_170713.NN	137075	CGGUUCUUACACAGGUUCt	GAAGCCUGUUAAGAACCCtq
RASSF1	Ras association (RalGDS/AF-6) domain fan	11186	NM_007182.NM_170712.NM_170713.NN	40417	GGUCUAGCGUAAAGCUGGUtt	CACCAUCUUCAGCUGAACCCt
Rif1	RAP1 interacting factor homolog (yeast)	55183	NM_018151.	223389	CCACAUUUUUJUCAGAACAGt	CUGUUCUGAAAAAAUJUGGtt
Rif1	RAP1 interacting factor homolog (yeast)	55183	NM_018151.	223388	CCUGAGUUUCGAAUUUAGGUt	ACCUAAUUCGAAACUCCtq
Rif1	RAP1 interacting factor homolog (yeast)	55183	NM_018151.	223387	GCACUJUJGGGUAGAUUCAUAtt	UAGAUUAACACCAAAAGUGCtc
ROCK2	Rho-associated, coiled-coil containing prote	9475	NM_004850.	596	GGAAAGACUACUUAAAACAGt	CUGGUUUUAGGUUACUUCtt
ROCK2	Rho-associated, coiled-coil containing prote	9475	NM_004850.	595	GGUGGUUUUJGGUAGGUAGGt	GCACUUCACAAAAGCACCtc
ROCK2	Rho-associated, coiled-coil containing prote	9475	NM_004850.	110867	GGCCACAAAGGACGACUAtt	UAGUCGUGCUUJUGUGGCCt
RSN	restin (Reed-Steinberg cell-expressed intern	6249	NM_022956.NM_198240.	241427	AUCAAAUJACCAAAAGGUAtt	AUACCUUUUJGGUUAUJGAUtc
RSN	restin (Reed-Steinberg cell-expressed intern	6249	NM_022956.NM_198240.	241426	CCUUCAGUUCGGGUUGUAtt	UUCAACCCGGAAACUGAGGt
RSN	restin (Reed-Steinberg cell-expressed intern	6249	NM_022956.NM_198240.	142518	GGUAAAUCGAAUUAAGGUAtt	UCUUCAUUUCCGAAUUAACtt
RSU1	Ras suppressor protein 1	6251	NM_152724.NM_012425.	143078	CCGAGAUAGUCAUAAAAtt	UAAAUAUAGCAUJUCUCCGtq
RSU1	Ras suppressor protein 1	6251	NM_152724.NM_012425.	108352	GGCCGUAGCAGGUUAGGUCCt	UCCGUCAACUGGUACUGGCCt
RSU1	Ras suppressor protein 1	6251	NM_152724.NM_012425.	3713	GGGUUCUACAUUUUJUGUAtt	AUJAAAAGUUGUAGCACCtc
SEC5L1	SEC5-like 1 (S. cerevisiae)	55770	NM_018303.	147719	GGUGCAAGUUUUJUCAGAAAAtt	UUUCUUUAAAACUCCtq
SEC5L1	SEC5-like 1 (S. cerevisiae)	55770	NM_018303.	147718	GGACUJUAGAAAGUCAUUCt	GAAUAGCAUJUUCUAGUCCt
SEC5L1	SEC5-like 1 (S. cerevisiae)	55770	NM_018303.	147717	GGAAACAAAGGAAUUCGGCCt	GGCGGAAUUCUCCJUUGUCCtq
SECBL1	SEC8-like 1 (S. cerevisiae)	60412	NM_021807.NM_001037126.	147808	GCUAAGCAUUCGUUAGAACt	GUUCAGGACAUCGUUUAUGCtq
SECBL1	SEC8-like 1 (S. cerevisiae)	60412	NM_021807.NM_001037126.	147807	GCCUACGAGAAAUGUAGGUtt	GGUCACAUUUCUCGUUAGGCCt
SECBL1	SEC8-like 1 (S. cerevisiae)	60412	NM_021807.NM_001037126.	29348	GGACUCUGUCAUUCUAGUAtt	UACUAGUAGACAGAGUCCtq
SMC2L1	SMC2 structural maintenance of chromosom	10592	NM_006444.	135817	GGCCGGAUUAACAAAAGGUAtt	UACUUGUUAUJGGCCGtq
SMC2L1	SMC2 structural maintenance of chromosom	10592	NM_006444.	135816	GGGGGUUAUJGGGUUGGUAtt	UCUACCCACAAUACACCtq
SMC2L1	SMC2 structural maintenance of chromosom	10592	NM_006444.	135818	GCUCUAAUAGCCAGAUUCCt	GAAACUCCGGCUUAAUAGAGCt
SMC4L1	SMC4 structural maintenance of chromosom	10051	NM_005496.NM_00102799.NM_001002	137983	GGCAAUUAGAUAGUAGGUCCt	AGCACAUUACAUUACUAAUUCtt
SMC4L1	SMC4 structural maintenance of chromosom	10051	NM_005496.NM_00102799.NM_001002	137982	GGCCAGACUAGAACACAGt	CAUCGUUAGCAGUCCGGCCt
SPAG5	sperm associated antigen 5	10615	NM_006461.	135834	GGCCCGUUUAAGUACCAUAtt	UUAUCAUAGCCGAGGGCtq
SPAG5	sperm associated antigen 5	10615	NM_006461.	135833	CCAUUCGUUAGUACCAUAtt	GAUGGUACAAAGGAGUAGGtt
SPAG5	sperm associated antigen 5	10615	NM_006461.	135835	CGAGUAGAGAUAGUJGUUAtt	UACCAACAUUJCACUUCGtq
STK3	serine/threonine kinase 3 (STE20 homolog)	6788	NM_006281.	792	GGAUAGUUUULCAAUAGGUtt	CCUAAUUGAAAACUAAUCttq
STK3	serine/threonine kinase 3 (STE20 homolog)	6788	NM_006281.	791	GGACAUJGAAAAGUCCAGt	CUGCCAAUJJGGUACUCCtt
STK3	serine/threonine kinase 3 (STE20 homolog)	6788	NM_006281.	793	GGGUUCUUAAGGAGUAGGUAtt	AUACACUUCUCAAGAACCCt
STK38	serine/threonine kinase 38	11329	NM_007271.	865	GGGUUUUUCUCCAUUAUJGt	GCACUUAUJGGGAGUAGGUCCt
STK38	serine/threonine kinase 38	11329	NM_007271.	864	GGAGAAACGACUCCGGAGAtt	UCUCCGGAGUUCGUUUCUCCt
STK38	serine/threonine kinase 38	11329	NM_007271.	863	GGCCUAAAAGGAGGUAGGAGAtt	UCUCCCAUUCUJUUGGAGCt
STK4	serine/threonine kinase 4	6789	NM_006282.	795	GGACAUJGAAAAGAAGGt	CCCUUJUUUCAJAGUUCtt
STK4	serine/threonine kinase 4	6789	NM_006282.	794	GGGACUJUAGUAAACCUUCAUAtt	AUGAGGUACACUJUGGUCCtq
STK4	serine/threonine kinase 4	6789	NM_006282.	796	GGGUCCUAUJGGCAGCGUAtt	UAACGCGUJUAGGACGCCt
STK6	serine/threonine kinase 6	6790	NM_03600.NM_198433.NM_198434.NN	427	GGCAACAGGUACUCCUCAUAtt	AUGAGGUACACUJUGGUCCtq
STK6	serine/threonine kinase 6	6790	NM_03600.NM_198433.NM_198434.NN	426	GGACUUCGGCAUAAAACAGt	CUGGUUUJGGCAGGUAGGUCCt
STK6	serine/threonine kinase 6	6790	NM_03600.NM_198433.NM_198434.NN	425	GGUCCAAAACGUUJGGUUCUCCt	CGAACACGUUJUUGGAGCt
STMN1	stathmin 1/oncoprotein 18	3925	NM_005563.NM_203399.NM_203401.	144044	GGCGUJUJUJUAGAGAACAGt	CUGUUCUJUAGAAACACCCt
STMN1	stathmin 1/oncoprotein 18	3925	NM_005563.NM_203399.NM_203401.	144043	GGCGACUAAUJGUUJGUUCAUAtt	UACAGAACAAUJAGUCAGCt
STMN1	stathmin 1/oncoprotein 18	3925	NM_005563.NM_203399.NM_203401.	144042	GGCCUCGGUCAAAAAGGUAtt	GAUUCUJUAGGUAGGGAGCtq
STMN3	stathmin-like 3	50861	NM_015894.	134696	CCUGUGUJUUAAGACAUAtt	CAUGUCUAAAACACACAGGtq
STMN3	stathmin-like 3	50861	NM_015894.	134695	GGGGCGGGGUAAAUCUCCAUAtt	AUGAGGAUAAUCCCGAGGCCt
STMN3	stathmin-like 3	50861	NM_015894.	134694	CGUUCGGGUJUUAUJGGGUUJGt	CAAACCCAAAACCGGAGGtq
TD-60	regulator of chromosome condensation 2	55920	NM_018715.	123152	CGUUCUJUUAUJGGGUUJGt	UAGGUJUAGGUUAGCAACCCt
TD-60	regulator of chromosome condensation 2	55920	NM_018715.	123151	GGGUCAAAAGUAGCAAAGGGt	GCCCCUUGCACUJUUGACCt
TPX2	TPX2, microtubule-associated protein homc	22974	NM_012112.	136426	GCCAAGGGUAGACAUACAGt	CAUGUCUJUAGGUUJGGCCt
TPX2	TPX2, microtubule-associated protein homc	22974	NM_012112.	136425	GGCCAAAACUCCUJUUGAGAtt	UCUAAAGGAGGUUUJGGCCtq
TPX2	TPX2, microtubule-associated protein homc	22974	NM_012112.	136427	CCUJGCCCCUACUAGAUUAtt	AAAUCUJUAGUAGGGCAGGtq
TUBG1	tubulin, gamma 1	7283	NM_001070.	120784	GAACCUUCGGCCAGUAGUAtt	UCAUACUGGCCGACAGGUCCt
TUBG1	tubulin, gamma 1	7283	NM_001070.	120193	CCUGUGCGGAGUACUAGCAUAtt	UUGUCUJUAGGUAGCCAGGt
TUBG1	tubulin, gamma 1	7283	NM_001070.	9227	GGGAGAAAAGAUCCAGUAGAGt	CUCAUGGUUJGGUUCUCCtq
TUBG2	tubulin, gamma 2	27175	NM_016437.	120877	CGACAGUAGGAUGUAGCAGUAtt	AACUGUCACUUCUCCACUCCt
TUBG2	tubulin, gamma 2	27175	NM_016437.	120570	GGCUUCACCUACUAGGACACt	GUUGCCAGUAGGGAGGAGCtq
TUBG2	tubulin, gamma 2	27175	NM_016437.	120876	CCGAGAAACGAGAUGGAUAtt	ACUCCAAUCUGGUUCUCCGt
ZW10	ZW10 homolog, centromere/kinetochore pro	9183	NM_004724.	137635	GCAGUUGGAAAAGACUACUAtt	UGAGUCUJUUCUCCACUCCtq
ZW10	ZW10 homolog, centromere/kinetochore pro	9183	NM_004724.	137634	GGUGUGCAUUAUGAUUAGCt	GCUAAUCUJUAGUAGCACCCt

ZW10	ZW10 homolog, centromere/kinetochore protein	9183	NM_004724.	137636	GCAAAUCGGAGAUUUUAtt	AAAAAUAUUCUCCGAUUUGCtc
ZYX	zyxin	7791	NM_003461.NM_001010972	115435	CCUCCCCAGCULCACCJAUGt	CAUAGGGUGAAGCUGGGAGGt
ZYX	zyxin	7791	NM_003461.NM_001010972	115434	GCAGUAUJGAAUJUUGGAGAUt	AUCUCCAAAUCAUACUGCtc
ZYX	zyxin	7791	NM_003461.NM_001010972	139068	CCCAACAUJGUCLUAAGGGAUt	AUCCCUAGACCAUJGUJGGGtc

**Supplementary Table 3. Support vector machine performance on four classes**

	<i>Inter</i>	<i>Pro</i>	<i>Meta</i>	<i>Ana</i>
<i>Precision (positive predictive value)</i>	97.9%	95.3%	98.7%	98.4%
<i>Sensitivity (recall)</i>	97.9%	96.5%	97.4%	98.4%

Performance of support vector machine prediction on four classes, similar to an analysis by Wang M., et al., *Context-based mixture model for cell phase identification in automated fluorescence microscopy*, BMC Bioinformatics (2007). Manually annotated objects for interphase, prophase, metaphase, and anaphase class of the same data shown in Fig. 1d were used for training. Precision and sensitivity of class predictions were calculated for each class individually, considering the respective class as positive, and the respective other classes as negative. The calculations were based on the amount of true-positive (tp), true-negative (tn), false-positive (fp), and false-negative (fn) predictions. Precision is defined as tp / (tp + fp), which sometimes is also referred to as *positive predictive value*. Sensitivity is defined as tp / (tp + fn), sometimes referred to as *recall*.

**Supplementary Table 4. Prediction performance with and without error correction**

	<i>Inter</i>	<i>Pro</i>	<i>Prometa</i>	<i>Meta</i>	<i>Early ana</i>	<i>Late ana</i>	<i>Telo</i>
<b>Precision (w/o HMM)</b>	99.8%	80.2%	84.6%	99.8%	62.7%	94.2%	82.9%
<b>Precision (HMM)</b>	100.0%	100.0%	98.0%	99.8%	93.1%	100.0%	96.4%
<b>Sensitivity (w/o HMM)</b>	95.5%	99.5%	97.0%	86.0%	75.0%	96.1%	97.5%
<b>Sensitivity (HMM)</b>	100.0%	100.0%	100.0%	95.7%	96.4%	99.3%	100.0%

Per class prediction performance compared with manual annotation of data without error correction (Fig. 2a) and with HMM error correction (Fig. 2f).

**Supplementary Table 5. Plasmid constructs for expression of fluorescent markers**

Plasmid name	Tag	Source plasmids	Vector backbone	Backbone cloning sites
pPDS1-mEGFP-IRES-puro2b	mEGFP <sup>32</sup>	pPDS1-YFP <sup>27</sup>	pIRES-puro2b	NdeI/BamHI
pIBB-mEGFP-IRES-puro2b	mEGFP <sup>32</sup>	pIBB-mEGFP <sup>33</sup>	pIRES-puro2b	EcoRI/NotI
pGalT-EGFP-IRES-puro2b	EGFP	pGalT-EGFP (MluI blunted/EcoRI) <sup>34</sup>	pIRES-puro2b	(NotI blunted/EcoRI)
pEGFP-PCNA-IRES-puro2b	EGFP	EGFP-PCNA <sup>35</sup>	pIRES-puro2b	NdeI/XbaI

**Supplementary Table 6. Cell lines stably expressing fluorescent markers**

Cell line name	Plasmid 1	Plasmid 2
H2B-mCherry <sup>36</sup>	pH2B-mCherry-IRES-neo3	-
H2B-mCherry and mEGFP-a-tubulin <sup>36</sup>	pH2B-mCherry-IRES-neo3	pmEGFP-a-tubulin-IRES-puro2b
H2B-mCherry and IBB-mEGFP	pH2B-mCherry-IRES-neo3	pIBB-mEGFP-IRES-puro2b
H2B-mCherry and GalT-GFP	pH2B-mCherry-IRES-neo3	pGalT-GFP-IRES-puro2b
H2B-mCherry and PDS1-mEGFP	pH2B-mCherry-IRES-neo3	pPDS1-mEGFP-IRES-puro2b
H2B-mCherry and EGFP-PCNA	pH2B-mCherry-IRES-neo3	pEGFP-PCNA-IRES-puro2b