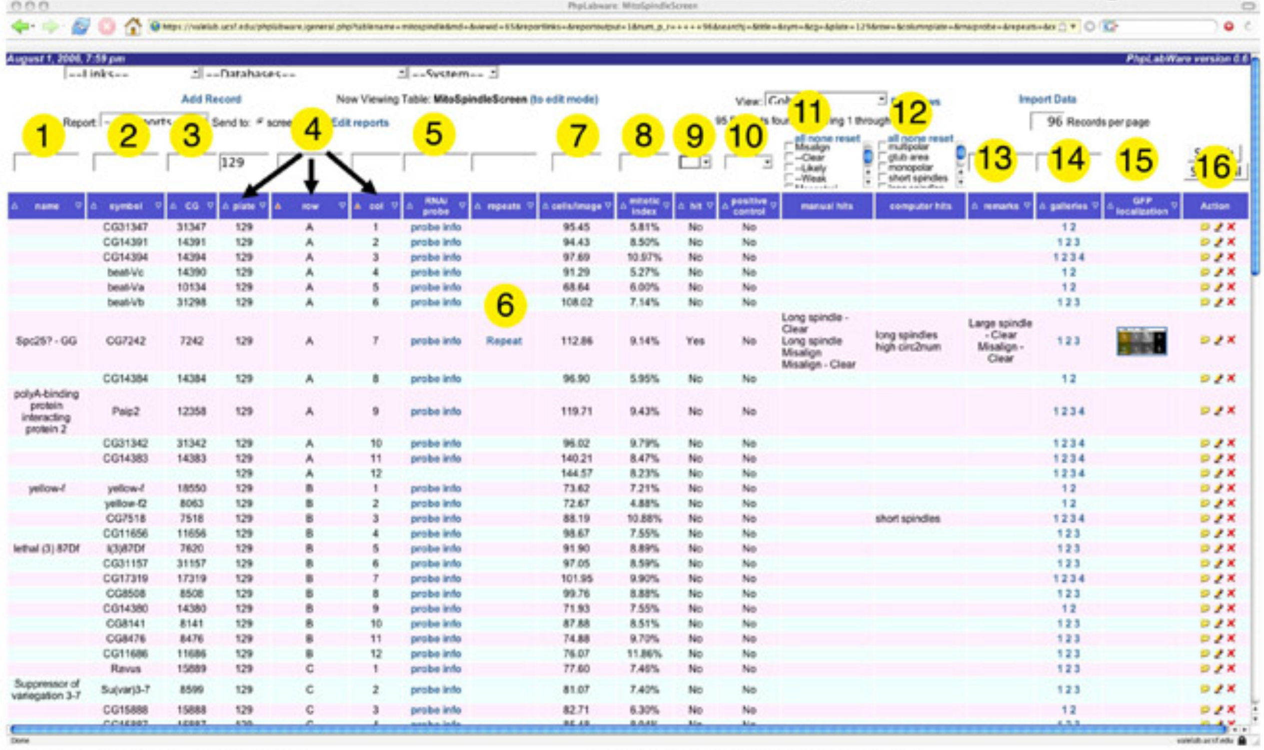
Supplemental Figure 2-1



name	symbol	CG	plate	row	col	RNAi probe	repeats	cells/image	mitotic index	hit	positive control	manual hits	computer hits	remarks	galleries	GFP localization	Action
	CG31347	31347	129	A	1	probe info		95.45	5.81%	No	No				1 2		
	CG14391	14391	129	A	2	probe info		94.43	8.50%	No	No				1 2 3		
	CG14394	14394	129	A	3	probe info		97.69	10.97%	No	No				1 2 3 4		
	beat-Vc	14390	129	A	4	probe info		91.29	5.27%	No	No				1 2		
	beat-Va	10134	129	A	5	probe info		68.64	6.00%	No	No				1 2		
	beat-Vb	31298	129	A	6	probe info		108.02	7.14%	No	No				1 2 3		
Spc25? - GG	CG7242	7242	129	A	7	probe info	Repeat	112.86	9.14%	Yes	No	Long spindle - Clear Long spindle Misalign Misalign - Clear	long spindles high circ2num	Large spindle - Clear Misalign - Clear	1 2 3		
	CG14384	14384	129	A	8	probe info		96.90	5.95%	No	No				1 2		
polyA-binding protein interacting protein 2	Paip2	12358	129	A	9	probe info		119.71	9.43%	No	No				1 2 3 4		
	CG31342	31342	129	A	10	probe info		96.02	9.79%	No	No				1 2 3 4		
	CG14383	14383	129	A	11	probe info		140.21	8.47%	No	No				1 2 3 4		
			129	A	12			144.57	8.23%	No	No				1 2 3 4		
yellow-f	yellow-f	18550	129	B	1	probe info		73.62	7.21%	No	No				1 2		
	yellow-f2	8063	129	B	2	probe info		72.67	4.88%	No	No				1 2		
	CG7518	7518	129	B	3	probe info		88.19	10.88%	No	No		short spindles		1 2 3 4		
	CG11656	11656	129	B	4	probe info		98.67	7.55%	No	No				1 2 3		
lethal (3) 87Df	l(3)87Df	7620	129	B	5	probe info		91.90	8.89%	No	No				1 2 3		
	CG31157	31157	129	B	6	probe info		97.05	8.59%	No	No				1 2 3		
	CG17319	17319	129	B	7	probe info		101.95	9.90%	No	No				1 2 3 4		
	CG8508	8508	129	B	8	probe info		99.76	8.88%	No	No				1 2 3		
	CG14380	14380	129	B	9	probe info		71.93	7.55%	No	No				1 2		
	CG8141	8141	129	B	10	probe info		87.88	8.51%	No	No				1 2 3		
	CG8476	8476	129	B	11	probe info		74.88	9.70%	No	No				1 2 3		
	CG11686	11686	129	B	12	probe info		76.07	11.86%	No	No				1 2 3		
	Ravus	15889	129	C	1	probe info		77.60	7.46%	No	No				1 2 3		
Suppressor of variegation 3-7	Su(var)3-7	8599	129	C	2	probe info		81.07	7.40%	No	No				1 2 3		
	CG15888	15888	129	C	3	probe info		82.71	6.30%	No	No				1 2		

1. Gene name from Flybase or
   based on Blast homology search
2. Symbol from Flybase
3. CG number
4. Well information (plate, row, column)
5. RNAi probe information link (see Suppl. fig 2-2)
6. Repeated RNAi link (see Suppl. fig 2-3)
7. Cell density (number/image) based on DAPI signals
8. Mitotic index based on phospho-Histone staining
9. Hit list (phenotype reproduced)
10. Positive contol list (known mitotic genes)
11. Phenotype scored manually (see Suppl. fig 2-4)
12. Phenotype revealed by computation
13. Phenotype & other remarks
14. Gallery link (see Suppl. fig 2-5)
15. GFP localization gallery link (see Suppl. fig 2-5)
16. Modification of information

Searches in the database can be carried out on any of the columns shown, and search statements in multiple columns are executed using a logical 'AND'. Data can be sorted on any column using the up- and down-arrows in the column titles. Searches in numeric fields can be implemented using a range (i.e. 30-40) or using multiple, comma-separated numbers (31,37,38). Hyperlinks link to the spindle galleries (column 14), information on the RNAi probe used (column 5) and repeats (column 6). The columns contain the following information:

(Link 5) Screenshot of the web page describing the RNAi reagents. Primer sequences for every gene tested are given. The hyperlink in the 'plate' field leads to an image of the gel run with dsRNA from that particular plate. Loading was with alternating rows (i.e., order is A1 B1 A2, etc..).

(Link 6) Selecting 'Repeat' in the main page starts a search for all instances in which this gene was tested in the screen.

(Link 11) Searches can be performed on a specific phenotypic description (in this case: Anastral - Clear), by selecting the phenotype and clicking the 'Search' button or pressing Enter.

(Link 14) Galleries (jpg version of the data used to perform the analysis) can be directly accessed from the web interface. Note that the image quality is reduced from the original images due to conversion to the jpg format.

(Link 15) Figures showing the localization of GFP-fusion proteins (if prepared).

[Spindle Screen] [Next]

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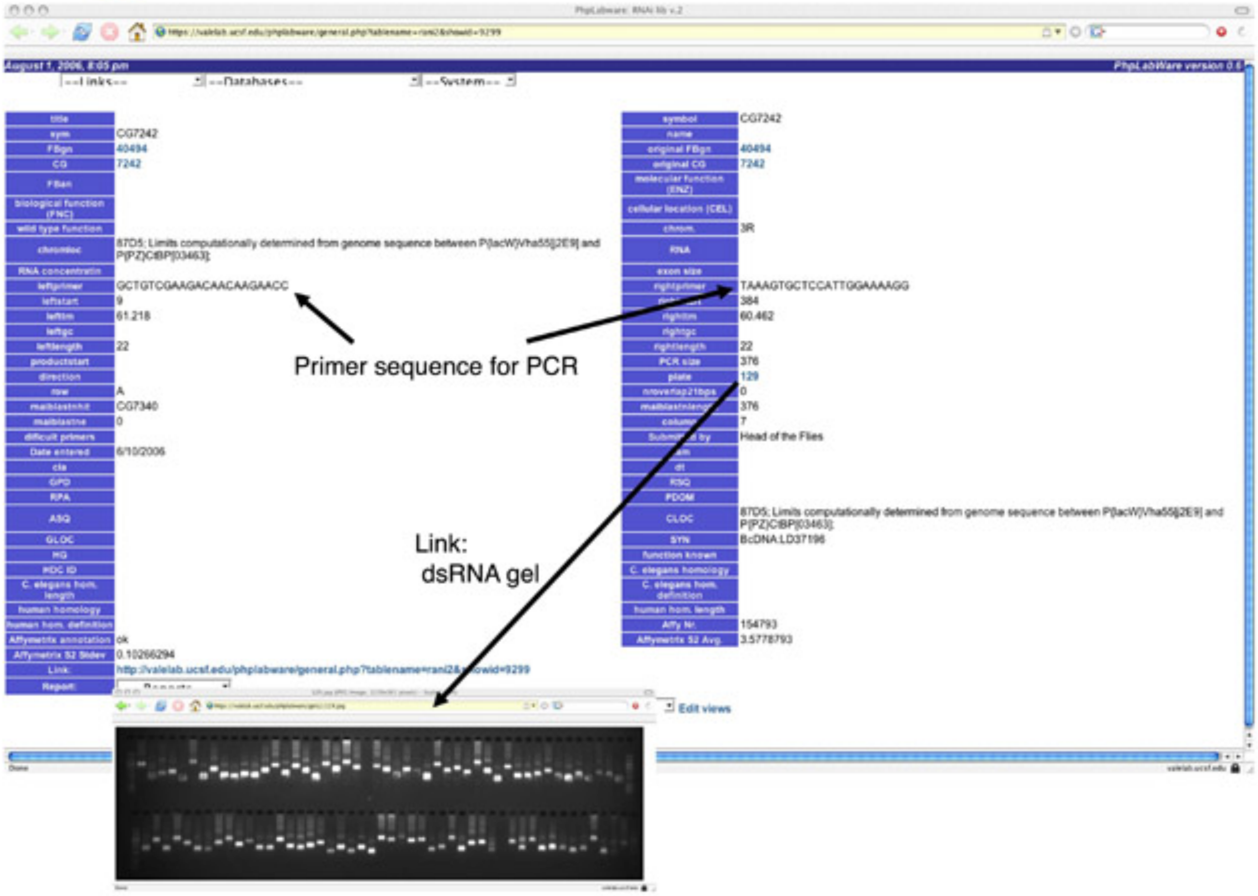
Supplemental Figure 2-2

Link 5 RNAi probe information



August 1, 2006, 8:05 pm

title	
sym	CG7242
FBgn	40494
CG	7242
FBan	
biological function (FNC)	
wild type function	
chromloc	87D5; Limits computationally determined from genome sequence between P{lacW}Vha55[j2E9] and P{PZ}CtBP[03463];
RNA concentratin	
leftprimer	GCTGTCGAAGACAACAAGAACC
leftstart	9
lefttm	61.218
leftgc	
leftlength	22
productstart	
direction	
row	A
malblastnhit	CG7340
malblastne	0
dificult primers	
Date entered	6/10/2006
cla	
GPD	
RPA	
ASQ	
GLOC	
HG	
HDC ID	
C. elegans hom. length	
human homology	
human hom. definition	
Affymetrix annotation	ok
Affymetrix S2 Stdev	0.10266294
Link:	http://valelab.ucsf.edu/phplabware/general.php?tablename=rani2&showid=9299
Report:	

symbol	CG7242
name	
original FBgn	40494
original CG	7242
molecular function (ENZ)	
cellular location (CEL)	
chrom.	3R
RNA	
exon size	
rightprimer	TAAAGTGCTCCATTGGAAAAGG
[illegible]	384
righttm	60.462
rightgc	
rightlength	22
PCR size	376
plate	129
nroverlap21bps	0
malblastnlength	376
column	7
Submitted by	Head of the Flies
[illegible]	
dt	
RSQ	
PDOM	
CLOC	87D5; Limits computationally determined from genome sequence between P{lacW}Vha55[j2E9] and P{PZ}CtBP[03463];
SYN	BcDNA:LD37196
function known	
C. elegans homology	
C. elegans hom. definition	
human hom. length	
Affy Nr.	154793
Affymetrix S2 Avg.	3.5778793

Primer sequence for PCR

Link:
dsRNA gel

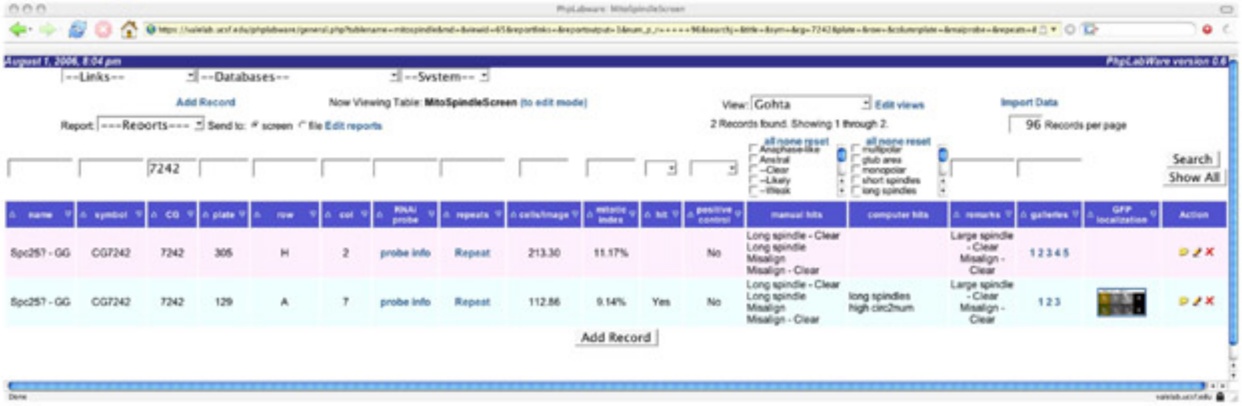
(Link 5) Screenshot of the web page describing the RNAi reagents. Primer sequences for every gene tested are given. The hyperlink in the 'plate' field leads to an image of the gel run with dsRNA from that particular plate. Loading was with alternating rows (i.e., order is A1 B1 A2, etc..).

[Previous] [Spindle Screen] [Next]

[Previous] [Spindle Screen] [Next]

Supplemental Figure 2-3

Link 6 Repeat RNAi



August 1, 2006, 8:04 pm

PhpLabWare version 0.6

Now Viewing Table: **MitoSpindleScreen** (to edit mode)

View: Gohta

2 Records found. Showing 1 through 2.

96 Records per page

name	symbol	CG	plate	row	col	RNAi probe	repeats	cells/image	mitotic index	hit	positive control	manual hits	computer hits	remarks	galleries	GFP localization	Action
Spc25? - GG	CG7242	7242	305	H	2	probe info	Repeat	213.30	11.17%		No	Long spindle - Clear Long spindle Misalign Misalign - Clear		Large spindle - Clear Misalign - Clear	1 2 3 4 5		
Spc25? - GG	CG7242	7242	129	A	7	probe info	Repeat	112.86	9.14%	Yes	No	Long spindle - Clear Long spindle Misalign Misalign - Clear	long spindles high circ2num	Large spindle - Clear Misalign - Clear	1 2 3		

Note: computational phenotype scoring is not done for repeat plates

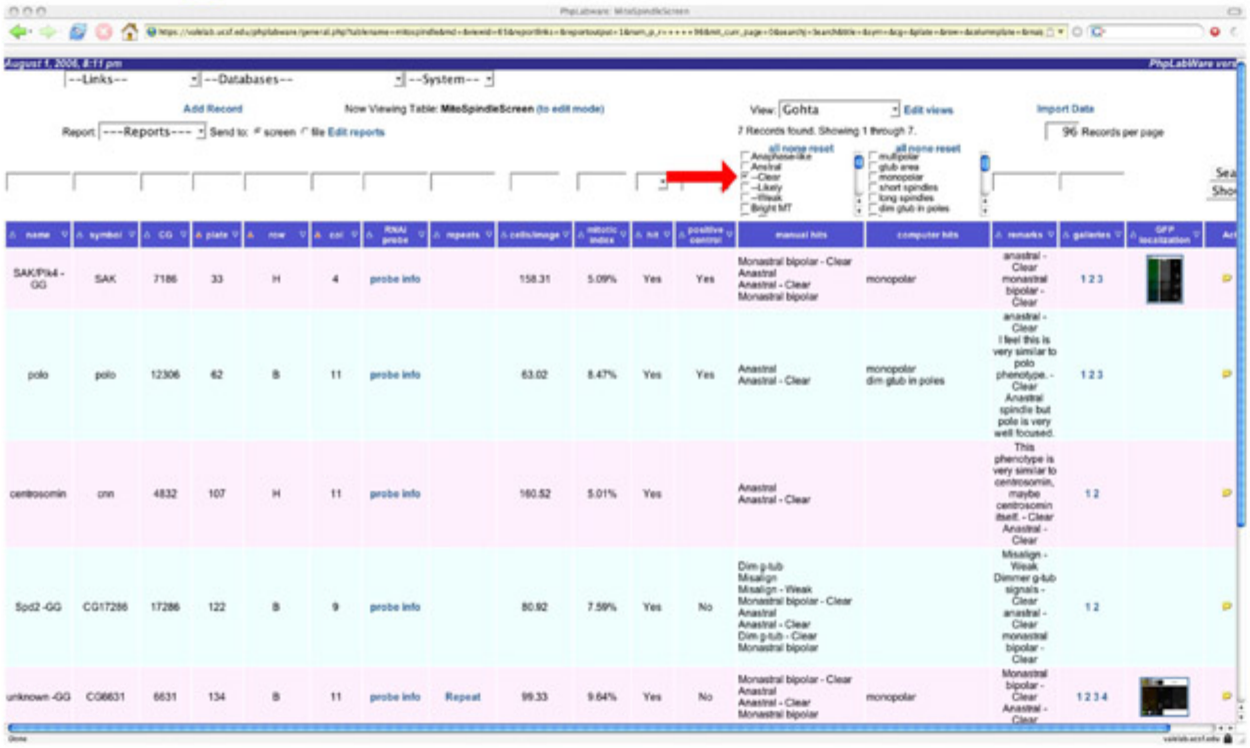
(Link 6) Selecting 'Repeat' in the main page starts a search for all instances in which this gene was tested in the screen.

[Previous] [Spindle Screen] [Next]

[Previous] [Spindle Screen] [Next]

Supplemental Figure 2-4

Search ⑪ e.g. “Anastral, Clear”



Now Viewing Table: **MitoSpindleScreen** (to edit mode)

View: Gohta

Report: ---Reports--- Send to: ● screen ○ file

7 Records found. Showing 1 through 7.

96 Records per page

all none reset
☐ Anaphase-like
☐ Anstral
☑ --Clear
☐ --Likely
☐ --Weak
☐ Bright MT

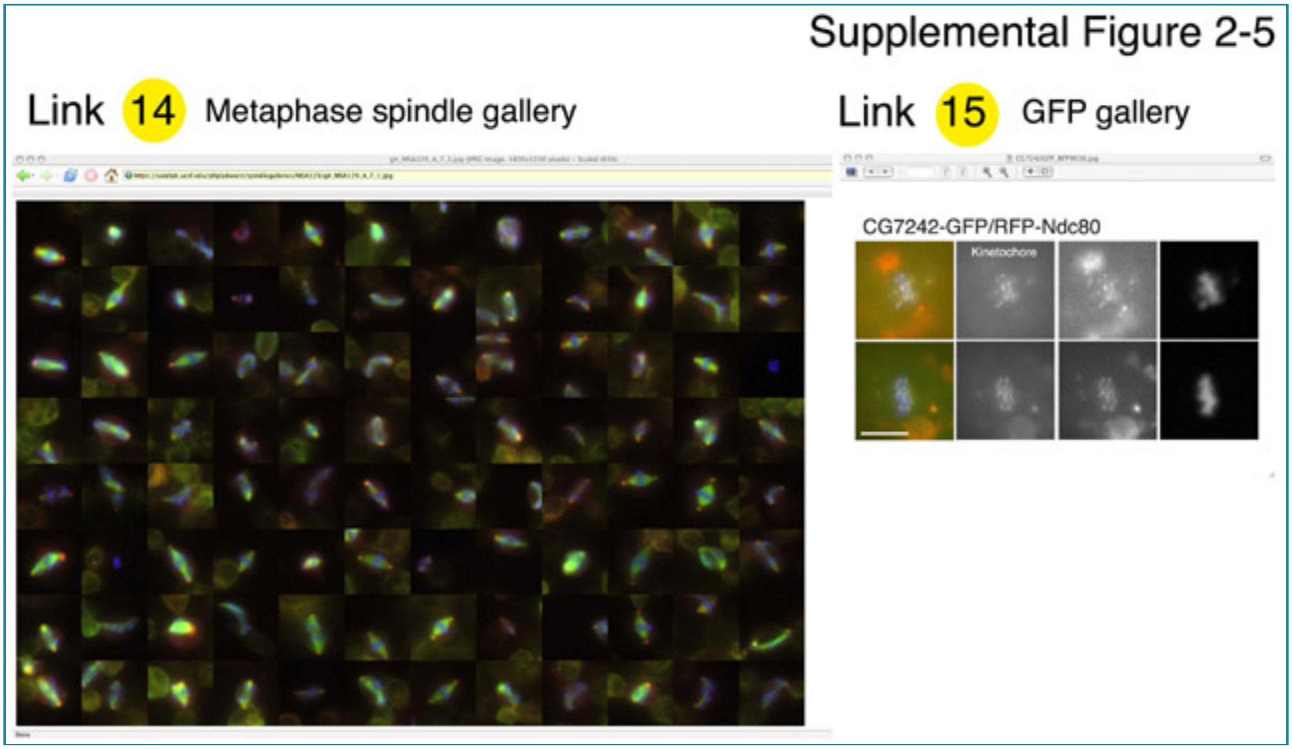
all none reset
☐ multipolar
☐ gtub area
☐ monopolar
☐ short spindles
☐ long spindles
☐ dim gtub in poles

name	symbol	CG	plate	row	col	RNAi probe	repeats	cells/image	mitotic index	hit	positive control	manual hits	computer hits	remarks	galleries	GFP localization
SAK/Plk4 - GG	SAK	7186	33	H	4	probe info		158.31	5.09%	Yes	Yes	Monastral bipolar - Clear Anastral Anastral - Clear Monastral bipolar	monopolar	anastral - Clear monastral bipolar - Clear	1 2 3	
polo	polo	12306	62	B	11	probe info		63.02	8.47%	Yes	Yes	Anastral Anastral - Clear	monopolar dim gtub in poles	anastral - Clear I feel this is very similar to polo phenotype. - Clear Anastral spindle but pole is very well focused.	1 2 3	
centrosomin	cnn	4832	107	H	11	probe info		160.52	5.01%	Yes		Anastral Anastral - Clear		This phenotype is very similar to centrosomin, maybe centrosomin itself. - Clear Anastral - Clear	1 2	
Spd2 -GG	CG17286	17286	122	B	9	probe info		80.92	7.59%	Yes	No	Dim g-tub Misalign Misalign - Weak Monastral bipolar - Clear Anastral Anastral - Clear Dim g-tub - Clear Monastral bipolar		Misalign - Weak Dimmer g-tub signals - Clear anastral - Clear monastral bipolar - Clear	1 2	
unknown -GG	CG6631	6631	134	B	11	probe info	Repeat	99.33	9.64%	Yes	No	Monastral bipolar - Clear Anastral Anastral - Clear Monastral bipolar	monopolar	Monastral bipolar - Clear Anastral - Clear	1 2 3 4	

(Link 11) Searches can be performed on a specific phenotypic description (in this case: Anastral - Clear), by selecting the phenotype and clicking the 'Search' button or pressing Enter.

[Previous] [Spindle Screen] [Next]

[Previous] [Spindle Screen]



(Link 14) Galleries (jpg version of the data used to perform the analysis) can be directly accessed from the web interface. Note that the image quality is reduced from the original images due to conversion to the jpg format.

(Link 15) Figures showing the localization of GFP-fusion proteins (if prepared).

[Previous] [Spindle Screen]