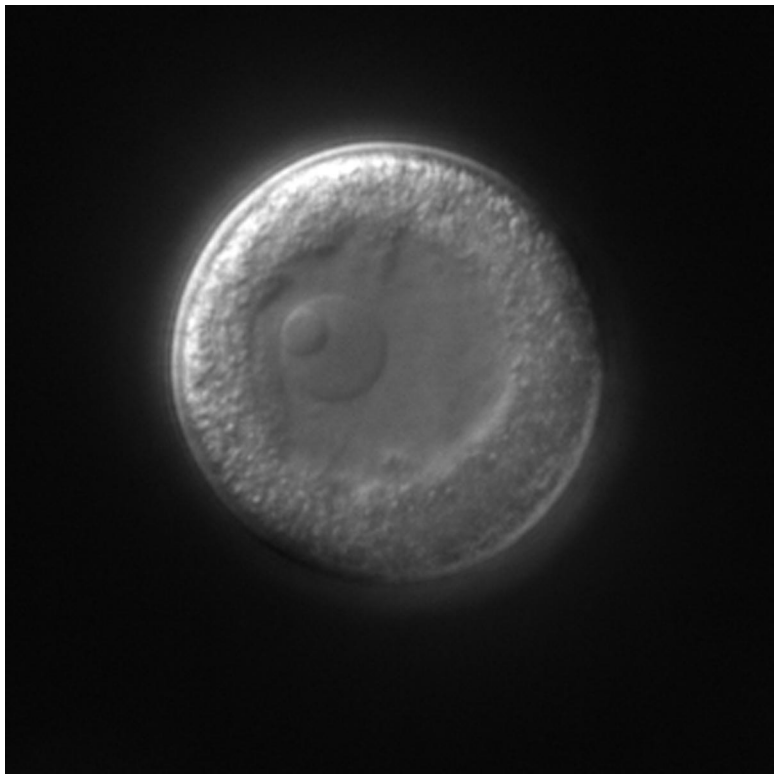
Supporting Information

Alliegro and Alliegro 10.1073/pnas.0802293105



Movie S1. Time-lapse sequence showing correlation between the position of the nucleolinus and the first meiotic spindle. The nucleolinus persists in the activated oocyte cytoplasm after the nuclear envelope and nucleolus dissipate. Its placement before its own subsequent dissolution reliably predicts the position of the meiosis I spindle pole, as originally suggested by Allen (1, 2). Coupled with the *in situ* localization of cnRNA65 in the oocyte nucleus and its later association with centrosomes (Fig. 3 *A–D*), the video sequence suggests a relationship between centrosomes (i.e., the spindle pole), and structures present in the oocyte nucleus before its breakdown. Images were captured 15 sec apart from 4:45 to 37:25 postactivation with KCl. Compare with Fig. 3*E* to identify nucleolus (arrow) and nucleolinus (arrowhead).

Movie S1 (MOV)

Table S1. Summary of database matches for 39 cnRNA clones

Clone	Similarity	E-value, e^{-x}
(A) BAC clones, uncharacterized DNA, or chromosomal sequences		
13	Human BAC clone	35
20	Human chromosome 6 DNA	25
26	Mouse chromosome 3 DNA	57
43	Rat hypothetical protein	31
75/177	Mouse BAC clone	25
103	*Candida* chromosome M DNA	25
114	Mouse chromosome 11 DNA	25
120	*Oryzias* chromosome 6 DNA	23
153	Rat BAC clone	30
174/270/311	Mouse chromosome 13 DNA	27
208	*Xenopus* clone	28
217	Mouse chromosome 5	62
218	Human BAC	60
221	*Caenorhabditis* cosmid	36
238	Mouse chromosome 13	27
279	Mouse BAC	35
286	Mouse chromosome 19 BAC	25
291	Human chromosome 8	23
305	Human chromosome 8	35
(B) Nucleic acid metabolism, gene expression, genome structure and maintenance		
15	*Branchiostoma* kinesin LC-like protein and CR1 RTP	40
48	Mouse chromosome 5; *Entamoeba* U_1 snRNP	43; 22
65	Sea urchin RNA polymerase; zebrafish DNA	30; 60
86/123/186	*V. mercenaria* clam microsatellite DNA	22
93	Zebrafish linkage group 18; *Oryzias* LINE-like RE	41; 33
118	Human chromosome 11 sequence; human RNA pol II	125; 67
142	Pufferfish GYPSY-like RTP	74
145	*Plasmodium* hypothetical, similar to exoribonuclease	110
154	*V. mercenaria* microsatellite DNA	24
171	*Xenopus* cDNA clone; pufferfish RTP	39; 24
179/210	Mouse chromosome 13; similar to rat ott RNA binding	31; 21
219	Zebrafish DNA clone; *Crassostrea* microsatellite	24; 20
226	Pig microsatellite DNA	26
227	Mouse cation channel; fish/pig microsatellite	31; 29
248	Human *MUC4* gene intronic tandem repeats	80
249	Mouse mucin 2; *Caenorhabditis* zinc finger protein	30; 20
(C) Unrelated characterized molecules		
35	Bacterial mannanase	37
115	Human dentin sialoprotein	25
273	*Venerupis* clam mitochondrial DNA cytochrome *c*	20
313	*Caenorhabditis* ced-1 receptor family	27

Best matches are listed with taxonomic source and approximate E-values. In some cases, a second-best match is shown but only if informational (i.e., not indicating another uncharacterized clone, or a similar molecule from another species, etc.). The results are divided into three categories: BAC clones and other uncharacterized DNA or chromosomal sequences; molecules related to nucleic acid metabolism, gene expression, or genome structure, and maintenance; and characterized molecules with no apparent relationship to either of the first two categories. Databases accessed for similarity searches and the algorithms used are detailed in *Materials and Methods.* RTP, retrotransposon; RE, retroelement.

Table S2. PCR screen for enrichment in centrosomes

Clone	Insert size, bp	Primer 1	Primer 2	Product size, bp	Ooplasm	Centrosome
3	963	AAGCAACAGCCTTCCGTCTTG	TCTCCGTCTGACTTTTGAACGC	148	-	++
10/212	543	GTTGATGAAGGGTTATCTGACG	TGGCTATTCTTGGCATTGC	413	-	+++
11	638	CTGAAAGTTCCGTGAGACCTGC	ACGCAAGGGATTGAGGCTTC	541	-	+++
15	692	GCTGTAGTTAGCGGCGTTTCAC	TGTCGGTATGTGTGTCCAGGAGAG	372	-	+++
35	669	CGCAGAAGCCATTTCCGTTAC	TTTTGGTGGGGGACACATCGTC	282	-	+
41/164	780	CGGTGAATGTAACTATGCCTTGG	ACGGAGAACGGTGGGTAATGCTAC	242	+	+++
46	958	GGATGCGATGGAATCAGTGC	GCTTATGGTCTCCTTTTTCGTCTG	469	-	+++
65	749	CCATTGGAAGCCTCAAATAACG	AAAGTGACGAGACCGACTGACTGG	293	+	+++
68/205	581	CCGATGTCTCTGTTGASCG	TCATTGGGCAGGGAAAAC	162	-	-
102	831	TGCTGCGACCGAGATTTGAACC	AAGCGATAGATGTCCAATAGGGTG	219	-	++
113	751	TGCTCTCCACACGAAATCGC	TCGCCATCCTGTTGAAAGGG	260	-	++
131	695	GGGACGAACTTGCGTTTTAGTGAC	TCCAGCGACTGTATCATTGGC	582	-	++
137	602	TGTTTCTCGTAAGAGGCTCACTGTG	TTCTCCCAATCCGAATGAACG	398	-	+
142	1536	GCAAAAATCTTGGATGTGCCAC	GCCCTGGTCTTTACTCAATCGC	553	+	+++
170	698	CTCCTTGGATAGTTGGATACAGCAC	CATTGAACGACGGGAAGATGC	427	-	++
183	639	TCCAACACATTCATACTCCCCAC	CCCTTGATTTATTCTTGTCCACGC	546	-	+++
184	870	TAGGATTTCCAGGTCGGGTAGG	CAACTGCGTCAAACAACCAGC	415	-	+++
185	638	TCACCCAAGAGCCAAATAATGC	ATGACCGCACACACTCCAAGGTTG	248	-	+
194	671	CATTCTAAGGCGTTTCATCCAGG	GCATCATCATCGGCTCTGAGTG	513	+	+++
195	859	CAGAACCAGGGAAACTGTTAGAGG	CAGGAGGTATTGTCGTATCTTGTGC	501	-	+++
200/300	1057	TTTACCCATTAGAGCAAGTCCCC	CAAAAAACCGTCACCAGAATCG	194	+	++
228	685	TGGCTCAAGCAGCAGCAATG	TGAATCTTCCTTCTGTTTCCCCAC	166	+	+
234	678	GGCGATGTATTTCGTAATCCCAG	GAACTGCGTTGGCATTGTTTTG	253	-	+
239	665	GTTGCCTTACTAATACAATCGCCG	TTATCGTGAGACACCAGTCCCC	467	-	+++
240	643	TCTTCTCGTCATAGCGGTTGTCTC	GGGACCATTGGGTTCTCAGTTTG	202	-	-
243	726	ACACCTTTATGAGCGTCAGCGG	TGATAGATGTCGGGGTTTGGC	219	-	-
246	632	GTGGGTCAATCAGTGTATCAGCAG	AGTCAGTATTACGGCAGTGGGTTC	155	-	-
264/59	456	TCAGCATTGTAAACTCTGTGTGGC	AAAAGCGGCACGAATCTGC	139	-	+
273	675	CATAAGCCAAAACACAAGGGGAC	TCGGGAAACTCGGACTCTTCTG	305	++	+++
276	467	GCAATGCGATGTAACCTTCACC	GCTTAGGGCTATGGATGTTGGC	218	-	++
278	633	GCACCTTGTTTATTGGGGTCTG	TTCTAAGAGCGTATGTGATGGACG	347	-	-
288	826	TTGGCGAGAGCACAATGTTTG	AAGGCGTAAGGTTGAATGGTAGG	277	-	-
290	750	TCCCATAGCAGCCCAAAACAC	AAGGAAGCCAACGAAGCATTG	191	+	++
299	401	GGGAGGTCCAGGTTCAAATCTC	TTTCATTGGGTTTTACGCCG	214	++	+++
312	805	TTTTTTTCTAAGGGGGGGGTC	TTCTCTGCGACTGGACATTGC	220	-	-
314	594	TACACGCATTTAGGGACGCAC	CTGGTTGGTGATTGCTCTTTGTC	301	-	+
PABP		CGAGCGTCTTGAGCAAATGG	CAAAGCCGAAACCCTTAGAACG	482	++++	-
RR		GAACCATTATTGGCTGACAACCC	CACAGTGAAGACCCTCATCTCTGC	604	++++	-
18S rRNA		TGTTAGCCCAAAACCAATCCG	GCCGAGACACTCAATCAAGAGC	553	++++	++++

Primer pairs are shown in 5′ to 3′ direction. Last two columns indicate relative strength of amplified product signal from whole oocyte template and centrosomal template. Key: −, no signal detected; +, weak signal detected; ++, moderate signal; +++, strong signal. These designations can be evaluated by comparing this table with corresponding gel lanes in Fig. 1. Note that signal strength was estimated visually in agarose gels and depends on PCR product size, due to stoichiometric incorporation of ethidium bromide, so signal strength is underestimated for small products relative to larger.

Other Supporting Information Files

Dataset S1 (XLS)