

SUPPLEMENTAL FIGURE LEGENDS

Supp. Fig. 1. Conservation of CCR4 and CAF1 homologs. Shown is the percent similarity and identity of the *Xenopus* CCR4 and CAF1 proteins to their cognate proteins in the indicated species. The percent similarity and identity designated is across the whole protein.

Supp. Fig. 2. Quantification of deadenylation by CCR4 and CAF1. (*Top*) The blot shown is the same as in figure 3b. Lanes 1 and 3 show the ³²P RNA without a poly(A) before and after injection into oocytes, respectively. Lanes 2 and 4 show the ³²P RNA with a poly(A) tail before and after injection into oocytes, respectively. Lanes 5-10 indicate poly(A) tail length of the ³²P RNA when tethered to the indicated MS2 fusion protein. The portion of adenylated and deadenylated RNA is indicated and was determined arbitrarily. (*Bottom*) A graph shows the ratio of deadenylated to adenylated product.

Supp. Fig. 3. XICAF1 required the 7-methyl GpppG cap for translational repression. (A) The relative translation of firefly luciferase activity for the indicated reporter mRNAs. The luciferase mRNAs used contained a 7-methyl GpppG cap, a ApppG cap or a 7-methyl GpppG cap and stemloop in the 5'UTR. All of the reporter RNAs contained a poly(A) tail of 39 adenosines. Normalization and error bars were determined as in Fig 1b. (B) The relative translation of firefly luciferase activity in response to each protein is shown. The luciferase mRNAs used contained a ApppG cap and no poly(A) tail. Normalization and error bars were determined as in Fig 1b.

| X. laevis CCR4a | | | X. laevis CCR4b | | |
|------------------------|------------|--------------|------------------------|------------|--------------|
| | % Identity | % Similarity | | % Identity | % Similarity |
| <i>H. sapiens</i> | 95% | 96% | <i>H. sapiens</i> | 88% | 96% |
| <i>M. musculus</i> | 98% | 98% | <i>M. musculus</i> | 87% | 95% |
| <i>D. melanogaster</i> | 56% | 72% | <i>D. melanogaster</i> | 57% | 73% |
| <i>S. pombe</i> | 38% | 55% | <i>S. pombe</i> | 38% | 56% |

| X. laevis CAF1a | | | X. laevis CAF1b | | |
|------------------------|------------|--------------|------------------------|------------|--------------|
| | % Identity | % Similarity | | % Identity | % Similarity |
| <i>H. sapiens</i> | 97% | 98% | <i>H. sapiens</i> | 91% | 95% |
| <i>M. musculus</i> | 97% | 98% | <i>M. musculus</i> | 91% | 95% |
| <i>D. melanogaster</i> | 73% | 88% | <i>D. melanogaster</i> | 73% | 88% |
| <i>S. pombe</i> | 54% | 69% | <i>S. pombe</i> | 50% | 67% |



