Table 1 H1 content and DNA length of the various monomers

Class of monomers	% Monomer (relative proportion)	H1 content	% H1⁰/total H1	DNA length in base pairs at Mean	Halfwidth
1	35	No	—	148 ± 3	140-166
2	10	No	—	183 ± 3	169-202
3	15	$H1^0$	99	177 ± 3	166-200
4	40	H1-1, H1-2, $H1^0$	20	180 ± 3	167-204
Native chromatin		H1-1, H1-2, $H1^0$	35	—	—

$H1^0$/total H1 was determined by densitometry after scanning the protein electrophoresis gel (Fig. 1). DNA length, obtained by densitometry scanning of the DNA electrophoresis gel (Fig. 1), is expressed in base pairs at the maximum absorbance and at the halfwidth of the peak.
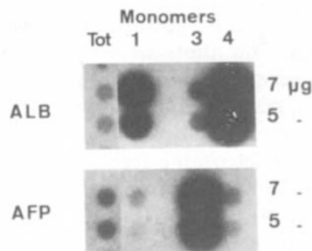

Fig. 2 Albumin and α-fetoprotein sequences among the various monomers. Purified DNAs isolated from the different monomers were hybridized to AFP1 and pmalb2 probes.
Methods. Plasmids were amplified in *Escherichia coli* (HB101) in rich medium containing 25 g ml⁻¹ ampicillin and recovered by lysis of the cells with alkali[18]. They were purified by centrifugation to equilibrium in a caesium chloride/ethidium bromide density gradient and purified as described elsewhere[18]. The probes were excised by *Hind*III digestion[18]. They were further purified by electroelution in water after electrophoresis in 1% agarose gel in 89 mM Tris buffer *p*H 8.0, 89 mM boric acid, 2 mM EDTA and 0.025 g ml⁻¹ ethidium bromide. They were then purified by chromatography on ELUTIP (Cera Labo) and precipitated with 2 vol. ethanol. The purity and the amount of DNA were estimated from the ultraviolet absorption spectra. Probes were labelled by nick-translation[18] with ³²P-dCTP and ³²P-dTTP to a specific activity of 2.2-2.5×10⁸ c.p.m. per g DNA. The DNA from the various monomer fractions was dissolved in 10 mM Tris-HCl *p*H 8.0, 1 mM EDTA and denatured by heating to 100°C for 10 min. After chilling the samples on ice, an equal volume of 1 M NaOH was added and the solution was incubated at room temperature for 20 min. The DNA samples were then neutralized by adding 0.5 vol. of a solution of 1 M NaCl, 0.3 M sodium citrate, 0.5 M Tris-HCl *p*H 8.0 and 1 M HCl[18]. They were spotted directly onto nitrocellulose paper (BA 83, 0.25 μm, Schleicher & Schuell) which had been treated previously with H₂O and equilibrated with 20× SSC buffer (1×SSC buffer is 0.15 M NaCl, 0.015 M trisodium citrate) using a vacuum minifold apparatus (Schleicher & Schuell). The nitrocellulose filters were dried under a lamp and baked for 2 h at 80 °C. They were then prehybridized for 24 h at 42 °C and hybridized for 65 h at 42 °C using the technique described by Thomas[20]. The blots were exposed to X-ray film for 3 days at −70 °C using a Kodak intensifying screen. Total monomers (Tot) were prepared by two successive centrifugations on a 5-30% sucrose gradient for 21 h at 110,000*g* followed by treatment with RNase and proteinase K and purification by phenol and chloroform[18]. Equal amounts of the different DNA samples on the filters were spotted (5 and 7 μg).

other fractions tested (class 1 and 4 monomers). During maturation, the repression of the AFP gene[8,9] occurs concomitantly with the increase in $H1^0$ content[3,4]. We show here that coding sequences for the AFP gene are preferentially associated with nucleosomes bearing $H1^0$. This result reinforces the hypothesis that $H1^0$ may be involved at the level of gene expression during development.

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Corrigendum

A bacterial repressor protein or a yeast transcriptional terminator can block upstream activation of a yeast gene

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THE fourth paragraph in the Discussion section of this article (p. 615) contained several inaccuracies resulting from the use of upper-case Greek alpha, which looks the same as the upper-case letter *A*. The paragraph should read:

There is evidence that other yeast genes can be repressed by negative regulatory factors bound between the upstream activator sequence and the TATA region. For example, it is likely that *MATα1* transcription is repressed in diploid yeast by binding of a negative regulatory factor (which is dependent on the expression of *MATA1* and *MATα2*) to a site between the *MATα1* upstream activator sequence and its TATA region[16]. *STE6* transcription is repressed by the *MATα2* product, which binds to a specific site in the *STE6* promoter, probably located between the upstream activator sequence and the TATA region (A. Johnson, K. Wilson and I. Herskowitz, personal communication). The repression of *MATα1* and *STE6* is at least 50 times greater than the 10-fold repression we observe for *lexA* operator-containing derivatives of the *GAL1* promoter. We do not understand why these yeast promoters are repressed so efficiently relative to the *lexA* operator-containing *GAL1* promoter.