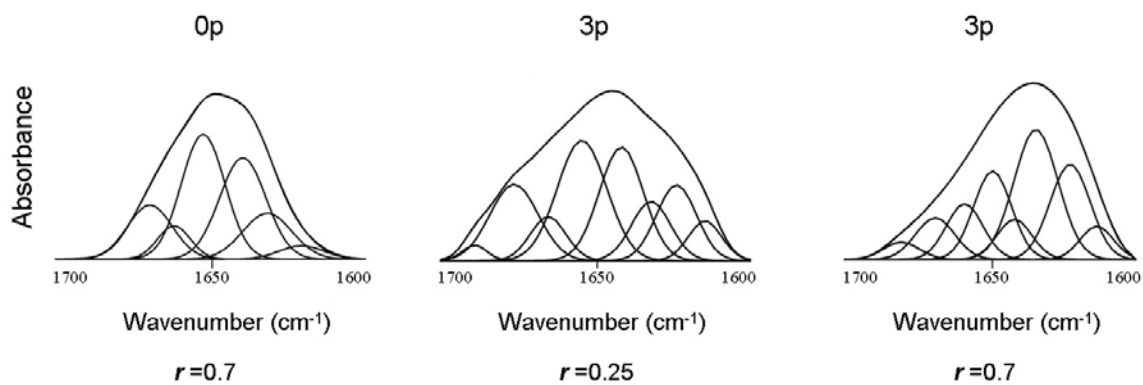


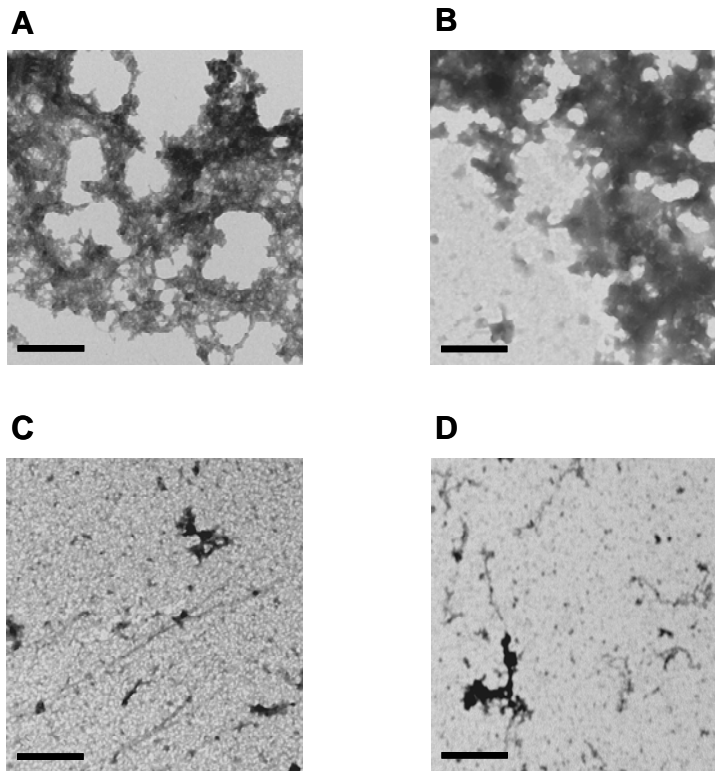
## SUPPLEMENTARY INFORMATION.

## Supplementary Figure 1



Supplementary Figure 1. Amide I decomposition of DNA-bound unphosphorylated (0p) and triphosphorylated (3p) CH1e at different protein/DNA ratio ( $r$ ) (w/w). The spectra were measured in D<sub>2</sub>O. The buffer was 10 mM HEPES plus 140 mM NaCl, pH 7.0, at 20 °C. The protein concentration was 5 mg/ml.

## Supplementary Figure 2



Supplementary Figure 2. Electron microscopy of complexes of CH1° with DNA. The DNA was pUC19. The protein/DNA ratio (w/w) was 0.1. The complexes were formed by direct mixing in 0.14 M NaCl, 10 mM HEPES, pH 7.0. Samples at a DNA concentration of 2  $\mu\text{g}/\text{ml}$  were adsorbed for 3 min and stained with 0.5% uranyl acetate. Images were obtained with a Jeol JEM-1400 electron microscope. (A) Unphosphorylated CH1°; (B) Triphosphorylated CH1°; (C) Monophosphorylated CH1° (CH1°/p140); (D) Diphosphorylated CH1° (CH1°/p140p152). The bar represents 200 nm.

Supplementary Table I

Percentages (%) of secondary structure of the DNA-bound carboxy-terminal domain of histone H1e						
Assignment	0p		3p			
	<i>r</i> =0.7		<i>r</i> =0.25		<i>r</i> =0.7	
	D <sub>2</sub> O		D <sub>2</sub> O		D <sub>2</sub> O	
	Band (cm <sup>-1</sup> )	%	Band (cm <sup>-1</sup> )	%	Band (cm <sup>-1</sup> )	%
Turns			1688	2	1682	3
Turns	1670	15	1676	16	1670	8
Turns	1663	6	1665	7	1660	10
$\alpha$ -helix	1653	33	1654	25	1651	17
Random coil/flexible regions	1641	28	1642	21	1644	7
$\beta$ -sheet	1633	14	1632	10	1636	29
Low frequency $\beta$ -sheet	1622	4	1624	13	1625	20
Low frequency $\beta$ -sheet			1615	6	1616	6

Band position (cm<sup>-1</sup>) and percentage area (%) and assignment of the components were obtained after curve fitting of the amide I band in D<sub>2</sub>O in 140 mM NaCl. The values were rounded off to the nearest integer.  
(0p) unphosphorylated domain, (3p) triphosphorylated domain.

Supplementary Table II

Percentages (%) of secondary structure by FTIR of the unphosphorylated (CH1<sup>o</sup>) and the triphosphorylated (CH1<sup>o</sup>3p) carboxy-terminal domain of histone H1<sup>o</sup> in aqueous solution and in the presence of Ficoll 70

Assignment	Buffer*				Ficoll <sup>†</sup>			
	CH1 <sup>o</sup> ‡		CH1 <sup>o</sup> 3p		CH1 <sup>o</sup> ‡		CH1 <sup>o</sup> 3p	
	Band	%	Band	%	Band	%	Band	%
	(cm <sup>-1</sup> )		(cm <sup>-1</sup> )		(cm <sup>-1</sup> )		(cm <sup>-1</sup> )	
Turns							1682	6
Turns	1676	3	1674	10	1685	1	1671	16
Turns	1661	31	1661	12	1667	26	1663	9
$\alpha$ -helix					1655	15	1655	15
Random coil/flexible regions	1642	52	1642	57	1644	23	1645	26
$\beta$ -sheet					1635	14	1635	12
$\beta$ -sheet	1630	9	1628	10	1626	13	1627	14
Low frequency $\beta$ -sheet	1617	5	1617	11	1616	8	1616	2

Band position (cm<sup>-1</sup>) and percentage area (%) and assignment of the components were obtained after curve fitting of the amide I band in D<sub>2</sub>O in 140 mM NaCl. The values were rounded off to the nearest integer.

\* Buffer: 10mM HEPES, 140 mM NaCl, pH 7.0, in D<sub>2</sub>O.

† The concentration of Ficoll 70 was 30%.

‡ The values were taken from Roque et al. (4)

Supplementary Table III

Percentages (%) of secondary structure of the DNA-bound carboxy-terminal domain of histone H1<sup>o</sup> mutated (T→A) at one, two or three positions

Assignment	Mutated positions													
	118		140		152		118/140		118/152		140/152		118/140/152	
	Band (cm <sup>-1</sup> )	%	Band (cm <sup>-1</sup> )	%	Band (cm <sup>-1</sup> )	%	Band (cm <sup>-1</sup> )	%	Band (cm <sup>-1</sup> )	%	Band (cm <sup>-1</sup> )	%	Band (cm <sup>-1</sup> )	%
Turns	1685	3					1678	12	1685	2	1685	1	1678	2
Turns	1674	4	1673	15	1674	10	1667	14	1674	9	1674	8	1668	12
Turns	1664	17	1660	19	1661	23	1660	5	1663	16	1659	19	1660	14
$\alpha$ -helix	1653	23	1653	27	1650	22	1651	26	1653	20	1652	28	1650	24
Random coil/flexible regions	1643	29	1644	20	1640	18	1641	16	1642	25	1644	20	1639	23
$\beta$ -sheet	1631	13	1632	15	1630	15	1630	18	1633	11	1632	16	1629	16
Low frequency $\beta$ -sheet			1624	3			1620	6	1624	11	1620	8		
Low frequency $\beta$ -sheet	1619	11	1615	1	1619	12	1613	3	1615	6			1615	10

Band position (cm<sup>-1</sup>) and percentage area (%) and assignment of the components were obtained after curve fitting of the amide I band in D<sub>2</sub>O in 140 mM NaCl. The values were rounded off to the nearest integer. The protein/DNA ratio was 0.5 (w/w).

Supplementary Table IV

**Percentages (%) of secondary structure of the DNA-bound carboxy-terminal domain of histone H1<sup>o</sup> phosphorylated on one or two positions at  $r=0.7$**

Assignment	1p(118)		1p(140)		1p(152)		2p(118/140)		2p(118/152)		2p(140/152)	
	Band (cm <sup>-1</sup> )	%	Band (cm <sup>-1</sup> )	%	Band (cm <sup>-1</sup> )	%	Band (cm <sup>-1</sup> )	%	Band (cm <sup>-1</sup> )	%	Band (cm <sup>-1</sup> )	%
Turns			1682	2	1681	3	1682	8	1682	3		
Turns	1670	9	1672	11	1671	5	1672	8	1672	11	1675	13
Turns	1660	20	1662	11	1662	19	1661	22	1661	17	1662	17
$\alpha$ -helix	1653	11	1654	22	1650	19	1650	11	1654	9	1652	17
Random coil/flexible regions	1643	31	1640	32	1643	25	1642	25	1643	33	1641	24
$\beta$ -sheet	1632	21	1630	10	1631	22	1630	19	1631	17	1630	17
Low frequency $\beta$ -sheet	1620	7	1622	9	1624	4	1622	3	1623	5	1622	6
Low frequency $\beta$ -sheet			1614	3	1614	3	1614	4	1615	5	1615	6

Band position (cm<sup>-1</sup>) and percentage area (%) and assignment of the components were obtained after curve fitting of the amide I band in D<sub>2</sub>O in 140 mM NaCl. The values were rounded off to the nearest integer. The numbers in parenthesis indicate the phosphorylated positions.