Table S4

			Codon Frequency			
Amino Acid	**Codon**	**Codon GC content**	**Within DNA-guided nucleosomes, relative to within *trans* factor-guided nucleosomes**	**Within DNA-guided nucleosomes**	**Within trans factor-guided nucleosomes**	**Within all regions**
A	GCG	1.000	0.361	0.019	0.052	0.019
A	GCT	0.667	0.857	0.537	0.626	0.537
A	GCA	0.667	1.309	0.348	0.266	0.340
A	GCC	1.000	1.705	0.097	0.057	0.104
C	TGT	0.333	0.672	0.465	0.693	0.535
C	TGC	0.667	1.742	0.535	0.307	0.465
D	GAT	0.333	0.923	0.801	0.868	0.805
D	GAC	0.667	1.510	0.199	0.132	0.195
E	GAA	0.333	0.951	0.801	0.842	0.811
E	GAG	0.667	1.261	0.199	0.158	0.189
F	TTC	0.333	0.942	0.313	0.332	0.311
F	TTT	0.000	1.029	0.687	0.668	0.689
G	GGA	0.667	0.737	0.434	0.588	0.438
G	GGT	0.667	1.082	0.391	0.361	0.398
G	GGC	1.000	3.255	0.117	0.036	0.112
G	GGG	1.000	3.997	0.059	0.015	0.053
H	CAT	0.333	0.929	0.667	0.718	0.695
H	CAC	0.667	1.181	0.333	0.282	0.305
I	ATA	0.000	0.725	0.333	0.460	0.346
I	ATT	0.000	1.224	0.509	0.416	0.509
I	ATC	0.333	1.268	0.158	0.124	0.146
K	AAA	0.000	0.957	0.696	0.727	0.707
K	AAG	0.333	1.114	0.304	0.273	0.293
L	CTC	0.667	0.835	0.095	0.114	0.072
L	TTA	0.000	0.864	0.388	0.449	0.414
L	CTT	0.333	0.878	0.212	0.241	0.217
L	CTA	0.333	1.396	0.100	0.072	0.107
L	TTG	0.333	1.600	0.174	0.108	0.159
L	CTG	0.667	1.991	0.031	0.016	0.031

Table S4. Biases in synonymous codon usage are encoded within distinct nucleosomal regions. DNA-guided and *trans*-factor guided nucleosomes are defined as in Supplemental Fig. S19. We examined nucleosomes from the log-phase dataset (light MNase digest), and from the set "B" *in vitro* experiment (performed with 4:10 histone:DNA, light MNase digest). Codons were considered as lying within a nucleosome, according to criteria described in Supplemental Table S3. Each group of synonymous codons was analyzed separately. The most GC-rich codon(s) within each group of synonymous codon is highlighted in red. For each codon, we calculated the ratio of its frequency in sequences that lie within DNA-guided nucleosomes, to its corresponding frequency within sequences that lie within *trans* factor-guided nucleosomes. Codons enriched in DNA-guided nucleosomes have the corresponding value > 1, and are highlighted in red. It quantifies the impact of accommodating DNA-guided nucleosomes on synonymous codon usage. The underlying codon usage for 13 out of 18 amino acids was biased towards GC-rich codons within coding regions that overlap with DNA-guided nucleosomes. Two amino acids (methionine and tryptophan) only have one corresponding codon each, and were excluded from this analysis.

Table S4 (contd.)

			Codon Frequency			
Amino Acid	**Codon**	**Codon GC content**	**Within DNA-guided nucleosomes, relative to within *trans* factor-guided nucleosomes**	**Within DNA-guided nucleosomes**	**Within trans factor-guided nucleosomes**	**Within all regions**
N	AAT	0.000	0.917	0.722	0.787	0.739
N	AAC	0.333	1.308	0.278	0.213	0.261
P	CCC	1.000	0.520	0.096	0.184	0.090
P	CCA	0.667	0.738	0.320	0.433	0.335
P	CCG	1.000	1.014	0.012	0.012	0.015
P	CCT	0.667	1.543	0.572	0.371	0.560
Q	CAA	0.333	0.894	0.234	0.261	0.225
Q	TAA	0.000	0.950	0.522	0.550	0.556
Q	TAG	0.333	1.120	0.192	0.172	0.172
Q	CAG	0.667	3.055	0.052	0.017	0.047
R	AGA	0.333	0.902	0.719	0.797	0.729
R	CGT	0.667	0.982	0.093	0.094	0.108
R	CGA	0.667	0.985	0.015	0.016	0.017
R	CGC	1.000	1.798	0.036	0.020	0.036
R	AGG	0.667	1.864	0.135	0.072	0.108
R	CGG	1.000	4.550	0.003	0.001	0.002
S	TCG	0.667	0.452	0.022	0.049	0.024
S	AGT	0.333	0.808	0.194	0.240	0.210
S	TCA	0.333	0.992	0.267	0.269	0.250
S	TCT	0.333	1.075	0.319	0.297	0.313
S	AGC	0.667	1.362	0.146	0.107	0.149
S	TCC	0.667	1.363	0.053	0.039	0.054
T	ACA	0.333	0.745	0.354	0.475	0.376
T	ACT	0.333	1.120	0.488	0.436	0.496
T	ACC	0.667	1.711	0.136	0.079	0.105
T	ACG	0.667	2.320	0.022	0.010	0.022
V	GTG	0.667	0.843	0.087	0.103	0.084
V	GTT	0.333	0.909	0.500	0.550	0.495
V	GTA	0.333	1.130	0.281	0.249	0.297
V	GTC	0.667	1.348	0.132	0.098	0.124
Y	TAT	0.000	0.845	0.667	0.789	0.695
Y	TAC	0.333	1.579	0.333	0.211	0.305
M	ATG	0.333	1.000	1.000	1.000	1.000
W	TGG	0.667	1.000	1.000	1.000	1.000