Dependence of the conclusion on modelling parameters.

The calculated values for the diameters and packing densities of chromatin fibres are based on simple assumptions derived from the 'pure' models, assuming fibres of infinite length. Given this caveat we would not necessarily expect a precise fit to all experimental data points. Nevertheless the trends observed are robust and different constraints and quantitative differences in the parameters do not affect the principal conclusions, i.e. that the values for the crossed-linker and helical ribbon models intersect and that the fit to the experimental data depends on linker length.

The assumptions used for modelling the 30 nm fibre are that the length of the linker DNA increases by 3.4 nm for every 10 bp increment and that each increment imparts a twist deficit. The simplest model is that this deficit is constant for all increments and is equivalent to 17° (see main text) but other models can be envisaged where the twist deficit is variable and is less for certain 10 bp increments or that the twist deficit remains constant but is a different, but close, value. The figure compares the predicted diameters and packing density for a constant twist deficit of 17°/increment (a, b as in Figure 2) and for a variable twist deficit (c,d). The qualitative conclusions are unaffected by this change. Additionally the dimensions of compact chromatin fibres solution may differ slightly (by ~7% in diameter) from those of the fixed samples used in the above comparison (Robinson et al 2006). Again such differences do not affect the correspondence observed between the measured and predicted values. Note that interdigitation of a 2-start helix, as envisaged by Sen et al. (1986) is not excluded by the analysis.

Reference:

Sen D, Mitra S, Crothers DM (1986) Higher order structure of chromatin: evidence from photochemically detected linear dichroism. *Biochemistry* **25**: 3441-3447.