SUPPLEMENTARY INFORMATION

Study of Cytochrome *c*–DNA Interaction - Evaluation of Binding Sites on the Redox Protein

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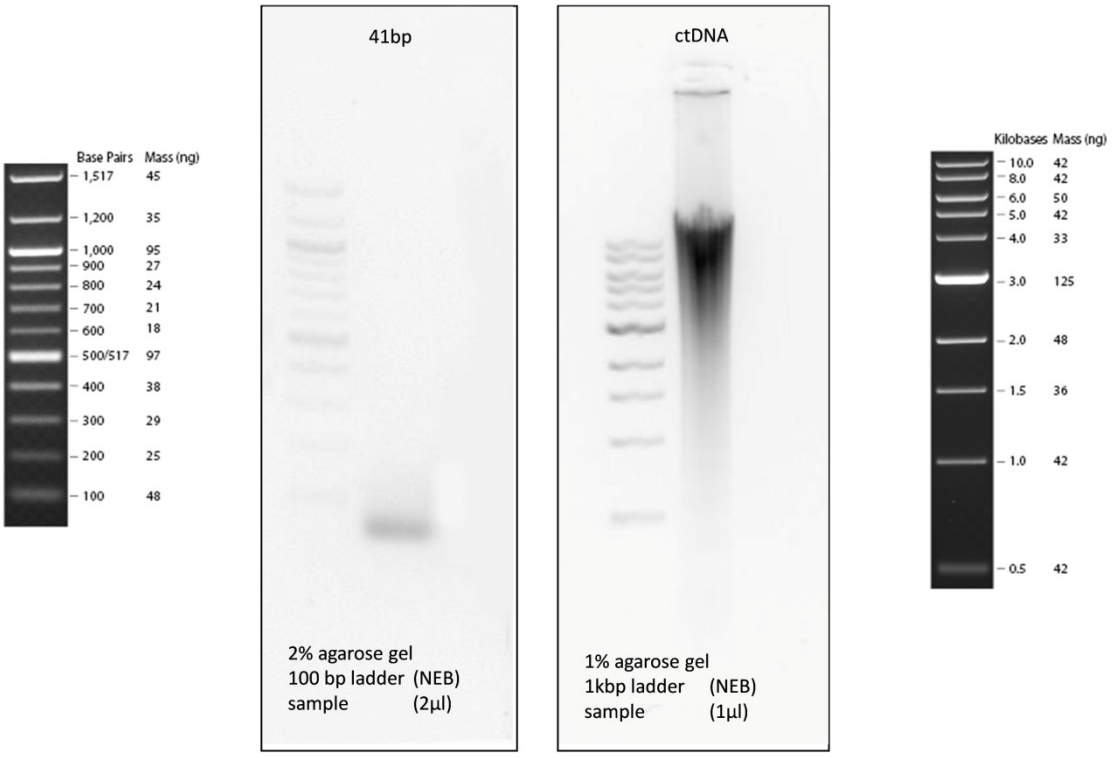

Figure S1. Agarose gel electrophoresis, 2 % agarose for oligonucleotides, 1 % for ctDNA. We used ctDNA and double stranded (ds) oligonucleotides (41- and 80 bps) diluted in 0.5 mM KPi, pH 5.0. GE revels that ctDNA is severely degraded into fragments of 10000- to 500 bps. The 80 bp oligonucleotides run slightly above the 41 bp oligonucleotides and closer to the 100 bp mark. This indicates that both oligonucleotide samples are hybridized and of the expected size.

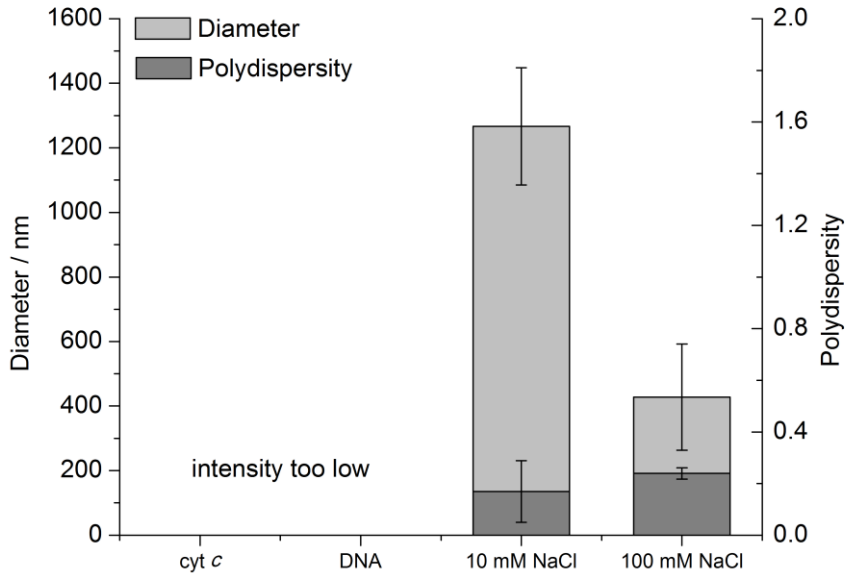

Figure S2. DLS measurements of cyt *c*-DNA samples containing 18 µM cyt *c* and 3 µM DNA in 20 mM KPi at pH 5.0, after 60 min incubation at RT and in the presence of 10 mM and 100 mM NaCl. The red column shows the average particle size, the blue column shows the polydispersity.

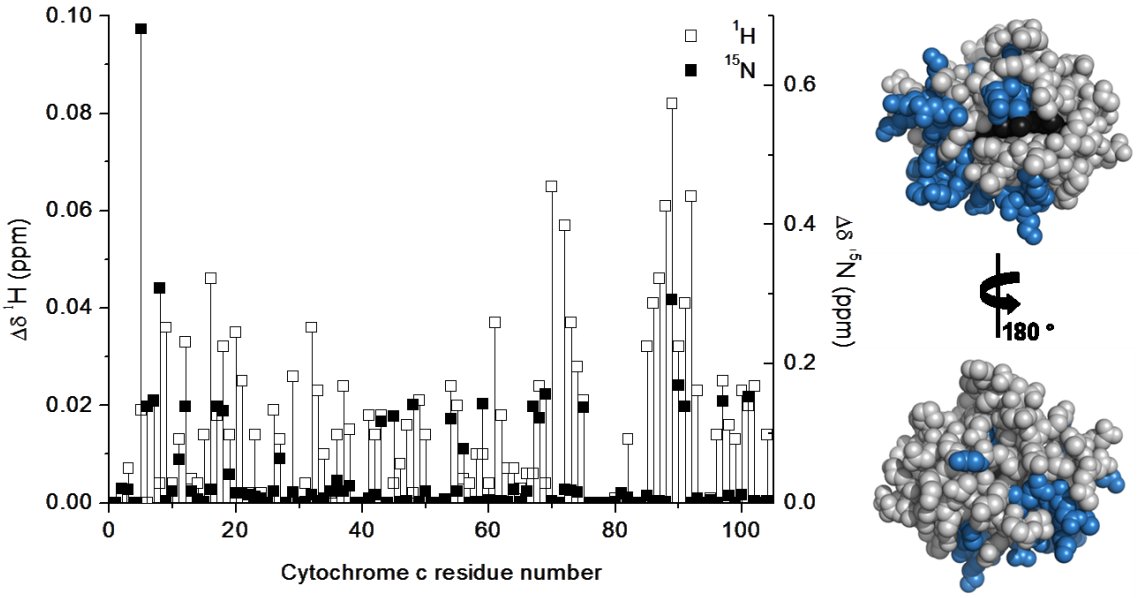

Figure S3. Plot of csps recorded from cyt *c* backbone amides at pH 6.0 with 6 µM DNA (20 mM KPi + 30 mM NaCl, 30°C). AAs residues are numbered from 1 to 104. Blanks correspond to proline residues 30, 44, 71 and 76 and unassigned G84. Below: Space filling representation of cyt *c* showing its secondary structure (light grey), the heme group (dark grey) and residues with a significant csp ($\Delta\delta$ ^{1}H $\geq$ 0.03 or ^{15}N $\geq$ 0.15 ppm) (blue).