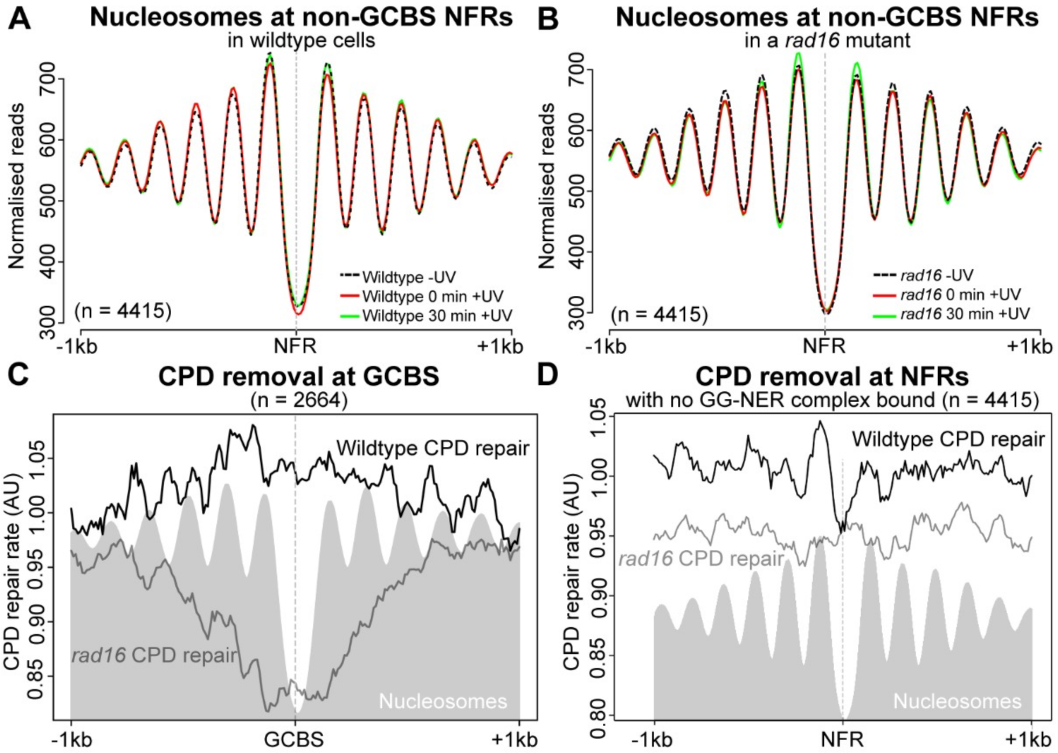

Figure S9 – UV-induced nucleosome remodeling and repair require chromatin binding of the GG-NER complex and are not common features of NFRs. The NFR positions (n = 4415) that do *not* overlap with an Abf1 binding sites or Abf1 consensus motif (as described in Figure S1), were used to plot the nucleosome data as composite plots in (A) wild type and (B) *rad16* deleted GG-NER defective cells. On the x-axis the NFR position and 1 kbp regions up- and downstream are displayed, while the y-axis depicts the normalised reads to indicate the nucleosome occupancy at these genomic locations. C) Relative repair rates from wild type and GG-NER deficient cells were plotted at GCBS's to show the effect on repair as described previously. The nucleosome landscape is presented as the grey shaded area, showing the repair rates in the context of nucleosome positions. The GCBS positions, including 1 kbp on either side are presented here. The CPD repair rates are expressed as arbitrary units. D) As described in C, but now using a set of genome-wide NFRs (n = 4415) to which *no* GG-NER complex is bound. Nucleosome and repair data of wild type and *RAD16* deleted cells was plotted at these genomic features.