3D-DIP-Chip: a microarray-based method to measure genomic DNA damage

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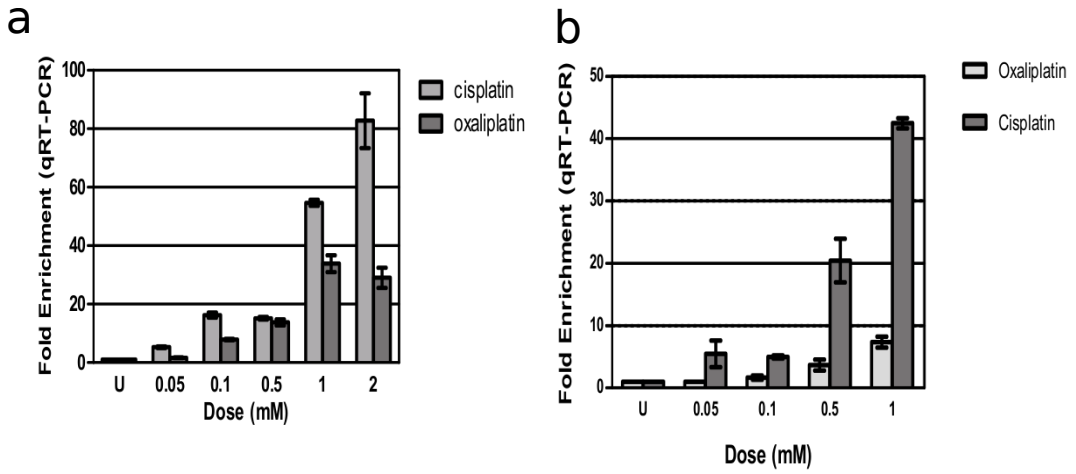
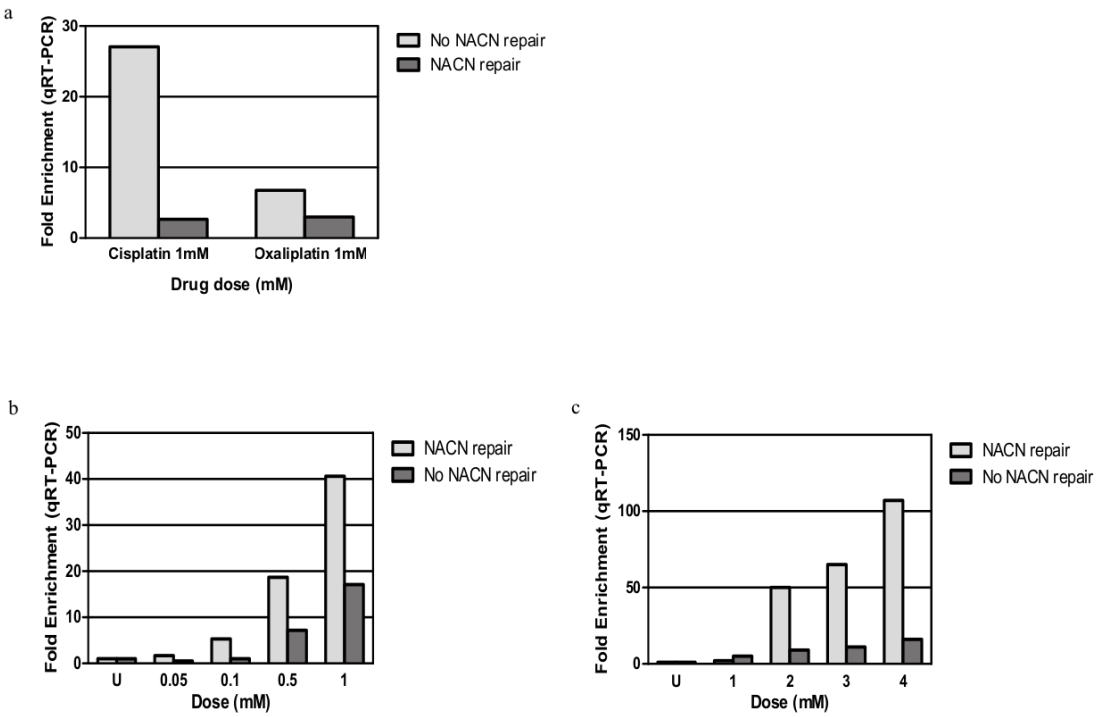
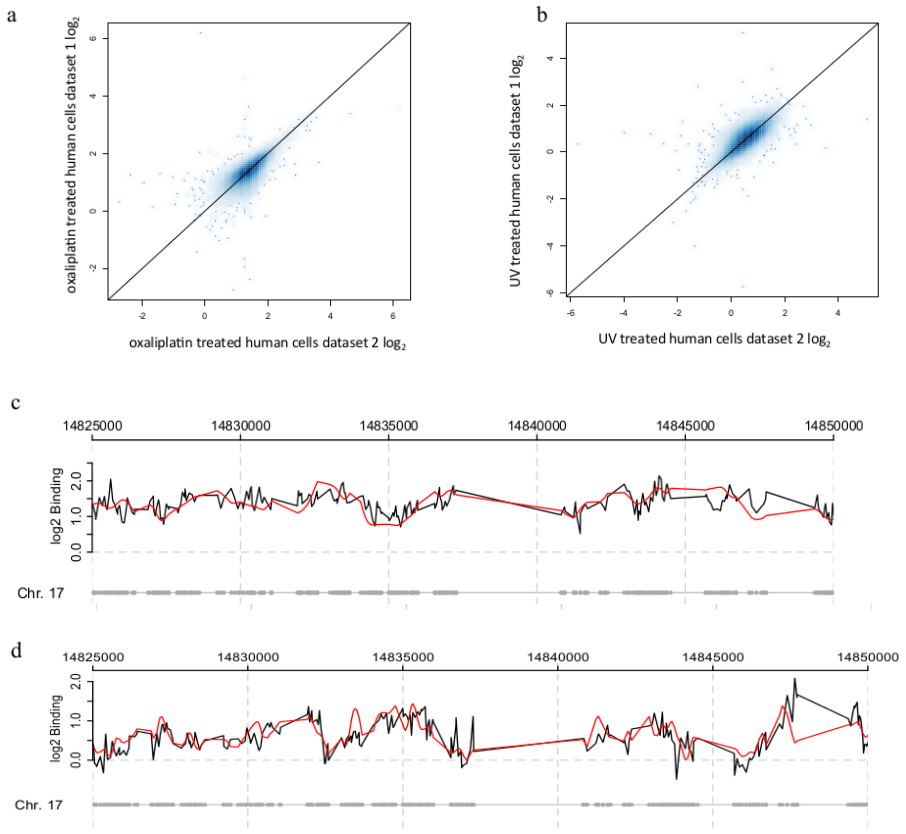
Supplementary Information



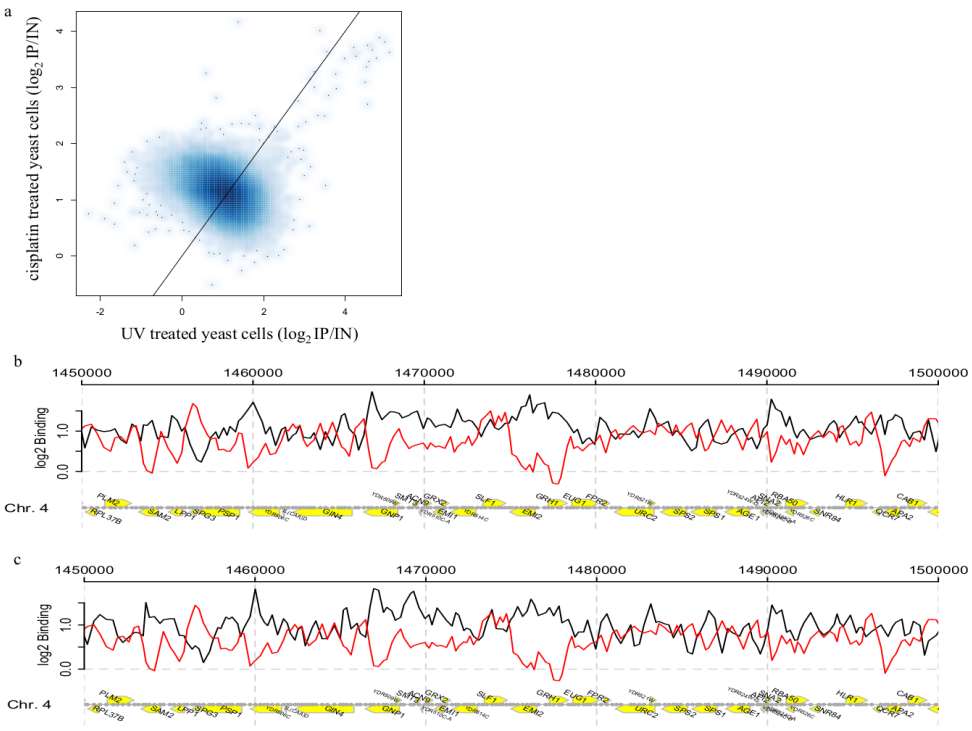
Supplementary Figure S1: DNA immunoprecipitation capturing cisplatin and oxaliplatin-induced DNA damage using CP9/19 antibody. a. Data from a dose titration DIP study of cisplatin and oxaliplatin treated yeast cells. **b**. Data for DIP of cisplatin and oxaliplatin treated human dermal fibroblasts. Fold enrichment of treated samples relative to untreated (U) are shown and data presented are means of 3 repeat studies. In each case the error bars represent +/- standard error of the mean.



Supplementary Figure S2: Studies demonstrating effectiveness of sodium cyanide (NaCN) in removing platinum adducts from platinum-treated human DNA samples. a. DIP studies demonstrate no enrichment of platinum treated samples for DNA samples that have been treated with NaCN pre-DIP. The same DNA samples not treated with NaCN demonstrate good enrichment for platinum damage. **b**. Cisplatin and oxaliplatin treated samples underwent DIP and qRT-PCR enrichment was compared between samples treated with or without NaCN following DIP. Improved qRT-PCR enrichment following NaCN treatment is shown for both cisplatin (**b**) and oxaliplatin (**c**).



Supplementary Figure S3: DNA microarray data for normal dermal fibroblast cells treated *in vivo* with oxaliplatin or UV. a and **b**. Scatter plots displaying the association between biological repeat oxaliplatin and UV treated microarray datasets, respectively. Log2 IP/IN values are presented as 'heat plots' whereby darker blue regions represent a greater density of data. These datasets demonstrate a linear relationship with the majority of values lying along or around the line of $x = y$ (Spearman's rank correlation values of 0.74 and 0.77 respectively). **c** and **d**. Selected regions of genome plots where log2 IP/IN ratios are plotted for a section of chromosome 17 showing the genomic distribution of oxaliplatin and UV induced DNA damage respectively (black lines) along with the associated predicted damage profile (red lines) in this region (Spearmans' rank correlation values of 0.40 and 0.51 for the whole genome). The grey dots along the genome plots show microarray probe positions.



Supplementary Figure S4: Data comparing cisplatin with UV-induced DNA damage in yeast cells *in vivo*.a. Scatter plot of cisplatin induced DNA damage against UV induced DNA damage. Log2 IP/IN values are presented as 'heat plots' whereby darker blue regions represent a greater density of data. The cisplatin dataset represents the mean values of 2 biological repeat samples, whilst the UV treated dataset represents the mean values of 4 biological repeat samples. Spearmans rank correlation between the two sets of data is -0.3. **b** and **c**. Selected regions of genome plots where log2 IP/IN ratios are plotted for a section of chromosome 17 showing the genomic distribution of cisplatin and UV induced DNA damage respectively (black lines) along with the associated predicted damage profile (red lines) in this region (Spearmans' rank correlation values of 0.61 and 0.51 for the whole genome). The grey dots along the genome plots show microarray probe positions. The yellow boxes show ORF positions.