

Supplemental Figure 1 Intra-chromosomal distribution of 8-oxoG of each individual.

Bar plot of 8-oxoG score is shown on the right of the ideogram. Four charts are corresponding to the results of volunteers A-D (left to right, respectively). The chromosome length is shown on the y-axis and the total 8-oxoG score from ten chromosomes is shown on the x-axis (max = 20 points, see Methods). The vertical lines on the right of the ideogram indicate 8-oxoG mapped regions, and bar of frequency per region was plotted in the center of the corresponding region.

Supplemental Figure 2 Genome-wide distribution of 8-oxoG of each individual.

(a) Bar plots of 8-oxoG frequency. The genome length (excluding the Y chromosome) is shown on the x-axis and the averaged 8-oxoG score per one megabase is shown on the y-axis. The averaged 8-oxoG score was calculated as follows, total 8-oxoG score in each detected region was divided with the length of corresponding region. The Kruskal-Wallis test was used initially to test for overall equality of medians in each data group. (b) Results of Spearman's rank correlation test between each individual.

Supplemental Figure 3 Genome-wide distribution pattern of 8-oxoG and SNP spectra.

Positions at which 8-oxoG was detected are indicated as vertical lines on the left of the ideogram. The total 8-oxoG score for each region was graded from zero to five and indicated as filled circles. The SNP frequency for each base substitution was calculated with a 200Kb window and in 50Kb steps and frequencies are represented by a bar plot. The substitution spectra are indicated by two letters on the top of each graph. For example, AG indicates that A and G were recorded in a single position, but does not supply the substitution direction. The numbers after the two letters are the chromosome number.

Supplemental Table 1

- (a) Total 8-oxoG scores for individual chromosomes.
- (b) Number and width of detected regions in each individual.
- (c) Frequency of commonly detected region in four individuals.

Supplemental Table 2 Comparison of sex averaged recombination rate in regions with a high density of 8-oxoG (G) vs. recombination rate in regions without a high density of

8-oxoG (N).

Supplementary Table 3 *P*-values obtained with the Mann-Whitney U-test for the SNP frequency in regions with a high density of 8-oxoG vs. SNP frequency in regions without a high density of 8-oxoG.

Supplemental Table 4 *P*-values obtained with the Mann-Whitney U-test for the SNP frequency in regions with a high density of 8-oxoG vs. SNP frequency in regions without a high density of 8-oxoG (SNP data from shotgun sequencing).