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# Supplementary Materials for

## Maintenance of genome sequence integrity in long- and short-lived rodent species

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**The PDF file includes:**

Figs. S1 to S4
Legends for tables S1 to S4

**Other Supplementary Material for this manuscript includes the following:**

Tables S1 to S4
Supporting files 1 and 2

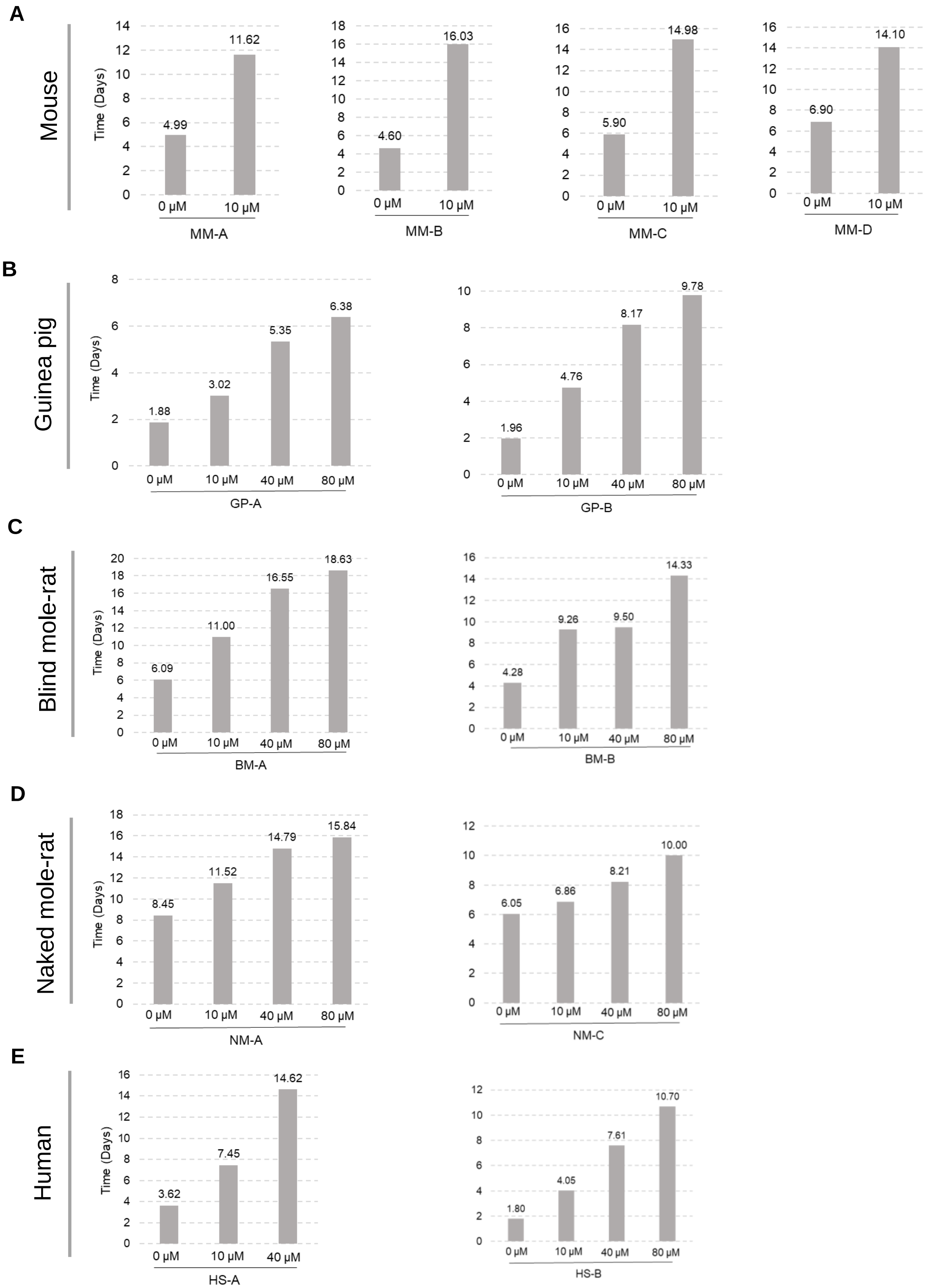


**Fig. S1. Estimation time of two passage doublings of lung fibroblasts with and without bleomycin treatment in different species**. (A-E) the time was taken for cells reaching two population doublings of every subject in each species.

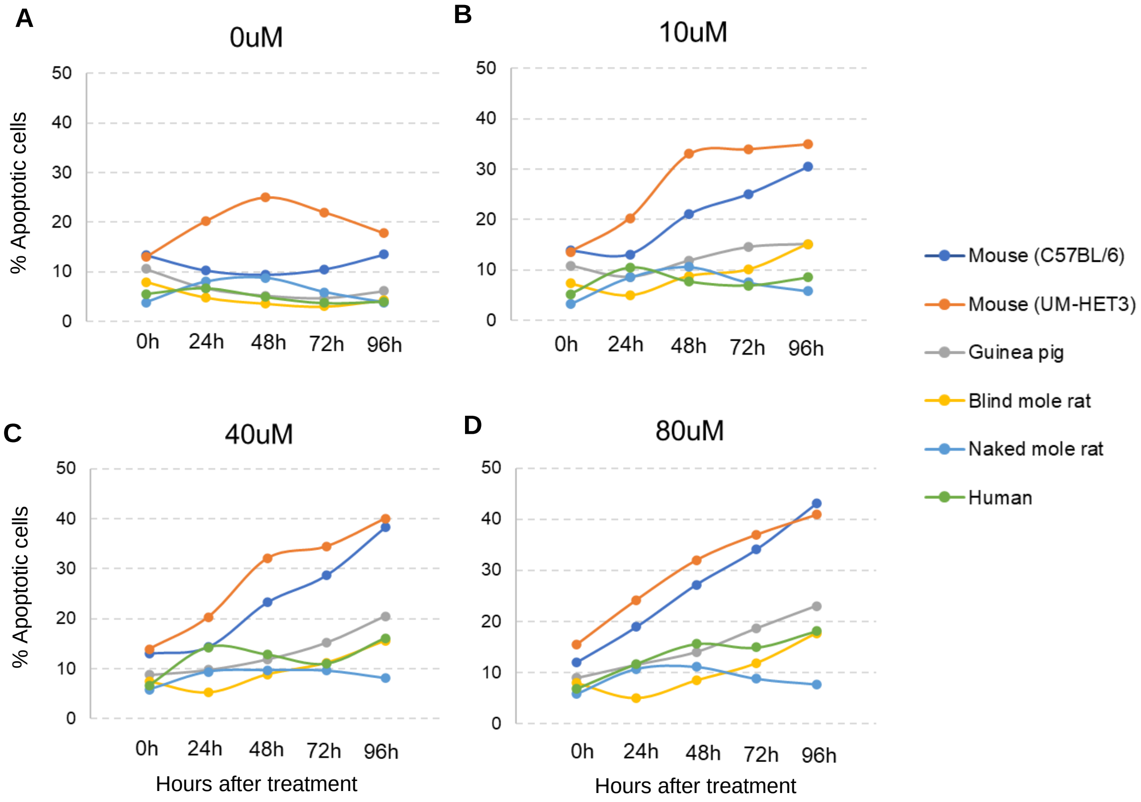
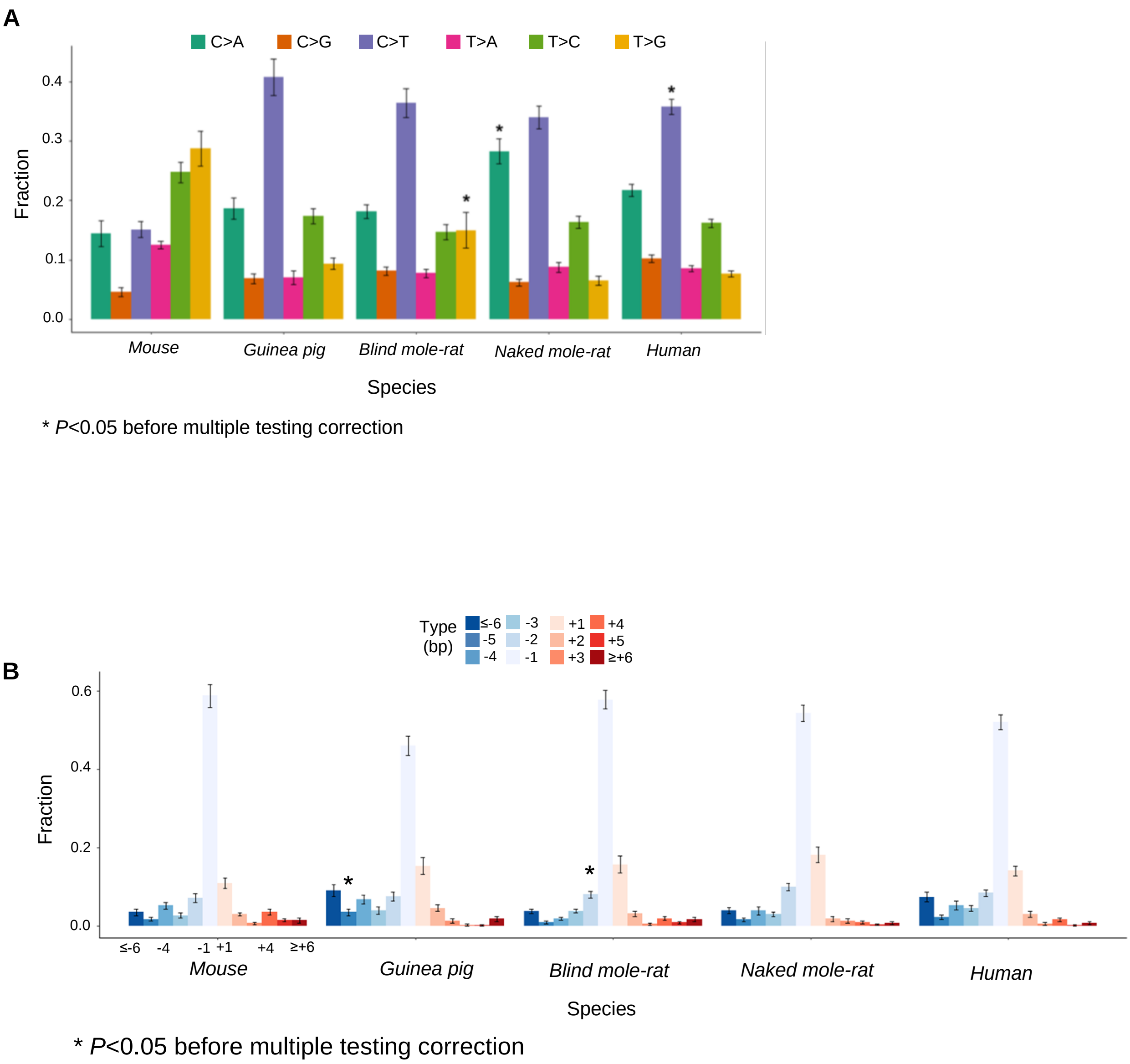


**Fig. S2. Fractions of apoptotic cells in each species after bleomycin treatment of different doses.** Fractions of apoptotic cells were estimated using the Guava Annexin Red Kit (Luminex) and Guava easyCyte flow cytometers (Millipore) after 0, 24, 48, 72 and 96 hours of bleomycin treatment of different doses. (A) Controls, (B) 10 µM, (C) 40 µM and (D) 80 µM bleomycin treatment.



* *P*<0.05 before multiple testing correction

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**Fig. S3. Mutational spectra of somatic mutations after bleomycin treatment.** Mutational spectra of somatic (A) SNVs and (B) INDELs in all cells of each species after bleomycin treatment. The "*" indicate increase of fraction of mutation type comparing to those without treatment, i.e., **Figs. 2A** and **D**, with P<0.05 before multiple testing correction. However, after correcting for multiple testing using FDR, no significant difference was found.

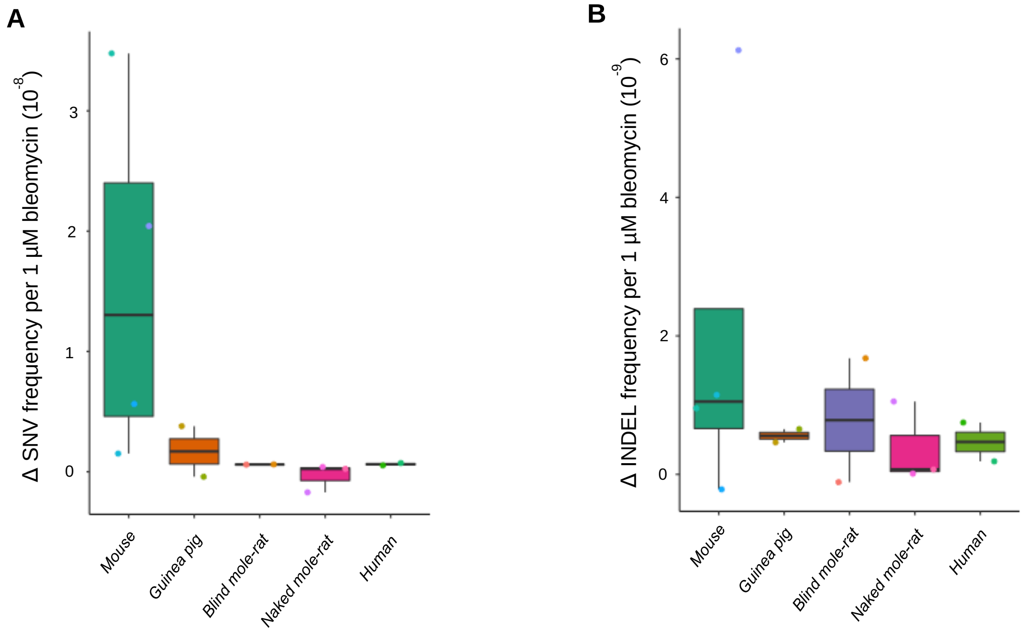

**Fig. S4. Change in mutation frequency per bleomycin dose for each subject.** Changes in (A) SNV and (B) INDEL frequency per 1 µM bleomycin. Each dot presents result of one subject, which was estimated using all the untreated and bleomycin-treated cells of the subject with linear regression. Boxplot elements are defined as: center line indicates median, box limits indicate upper and lower quartiles, whiskers indicate 1.5× interquartile range, and points indicate all data points.

**Table S1. (separate file)**
Reference genomes used in this study.

**Table S2. (separate file)**
Real-time PCR primers used for the locus-dropout test.

**Table S3. (separate file)**
Sequencing summary of all samples.

**Table S4. (separate file)**
Summary of somatic mutation calling and frequency estimation.