

# **The influence of carbon sources on the expression of the *recA* gene and genotoxicity detection by an *Acinetobacter* bioreporter**

**Bo Jiang<sup>a, b</sup>, Yizhi Song<sup>a, b</sup>, Dayi Zhang<sup>c, d</sup>, Wei E Huang<sup>e</sup>, Xu Zhang<sup>a, b</sup>, Guanghe Li<sup>a, b</sup>**

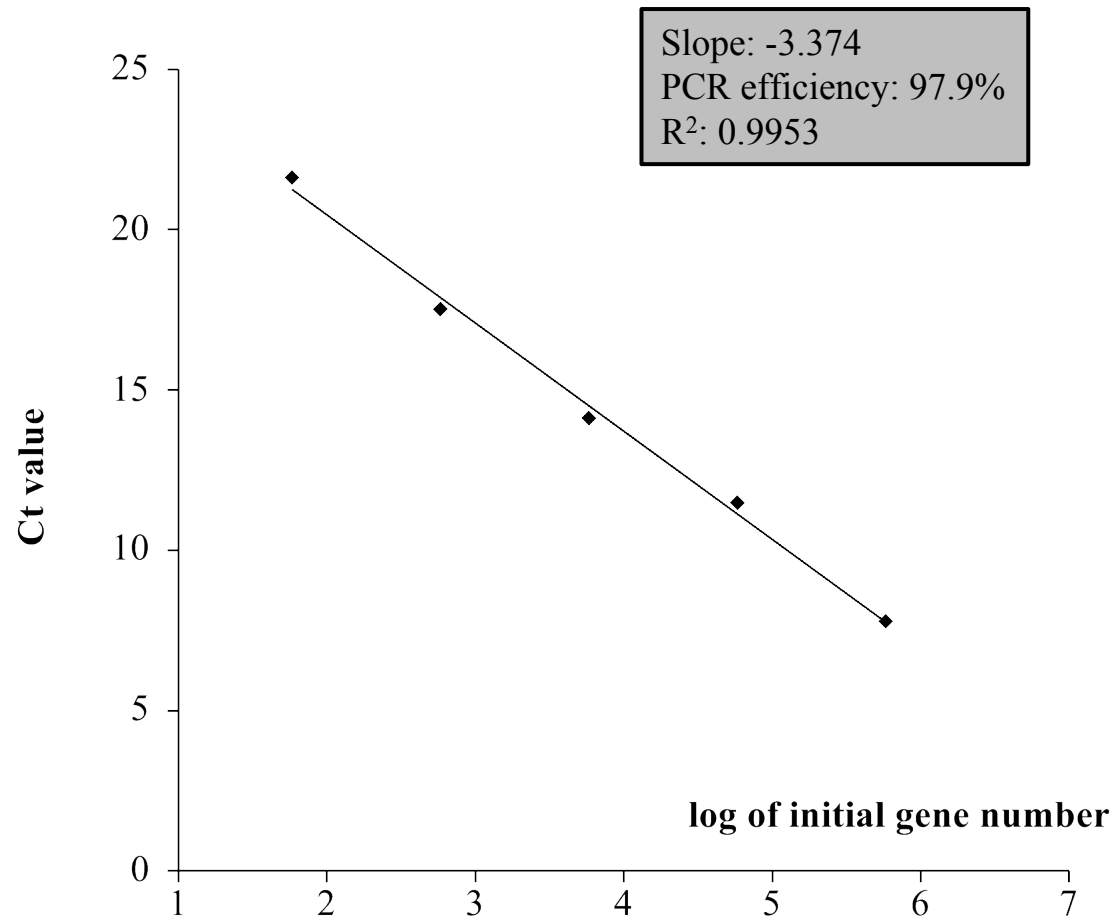
*<sup>a</sup> School of Environment, Tsinghua University, Beijing, 100084, PR China*

*<sup>b</sup> State Key Joint Laboratory of Environmental Simulation and Pollution Control, Beijing, 100084, PR China*

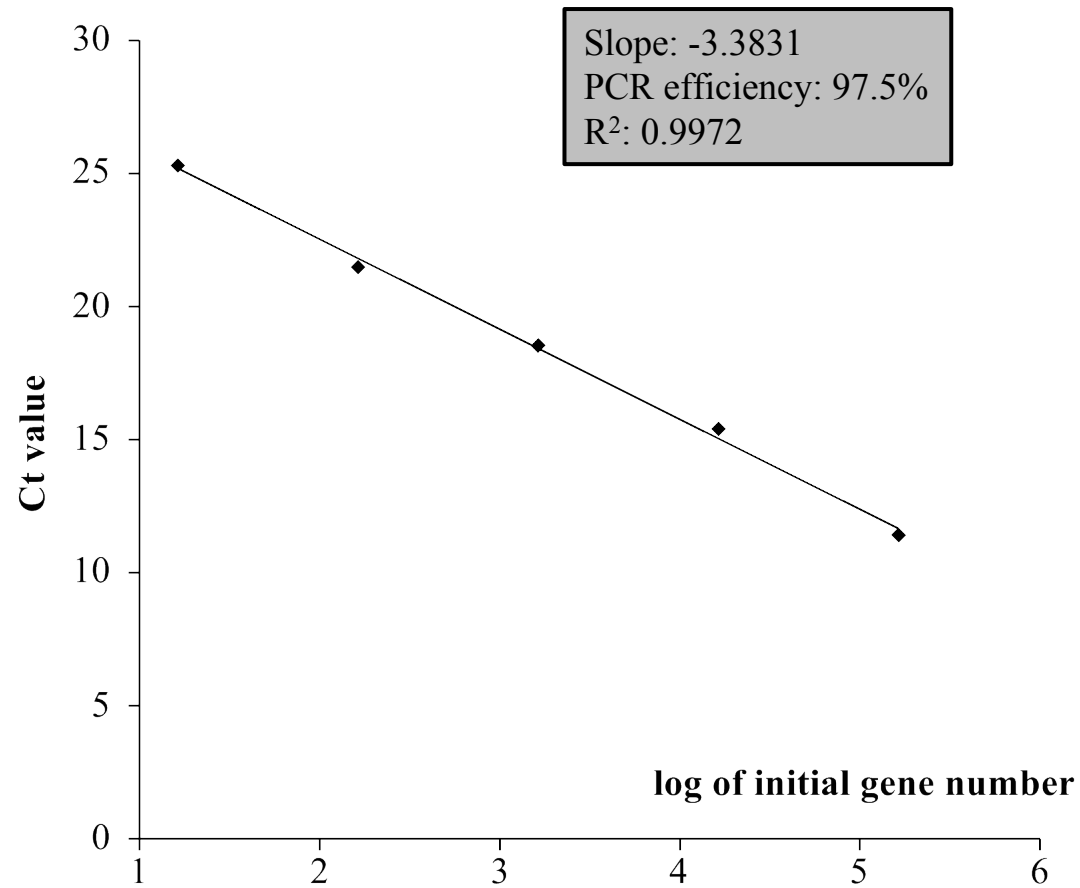
*<sup>c</sup> Kroto Research Institute, University of Sheffield, Sheffield, S3 7HQ, UK*

*<sup>d</sup> Lancaster Environment Centre, Lancaster University, Lancaster, LA1 4YQ, United Kingdom*

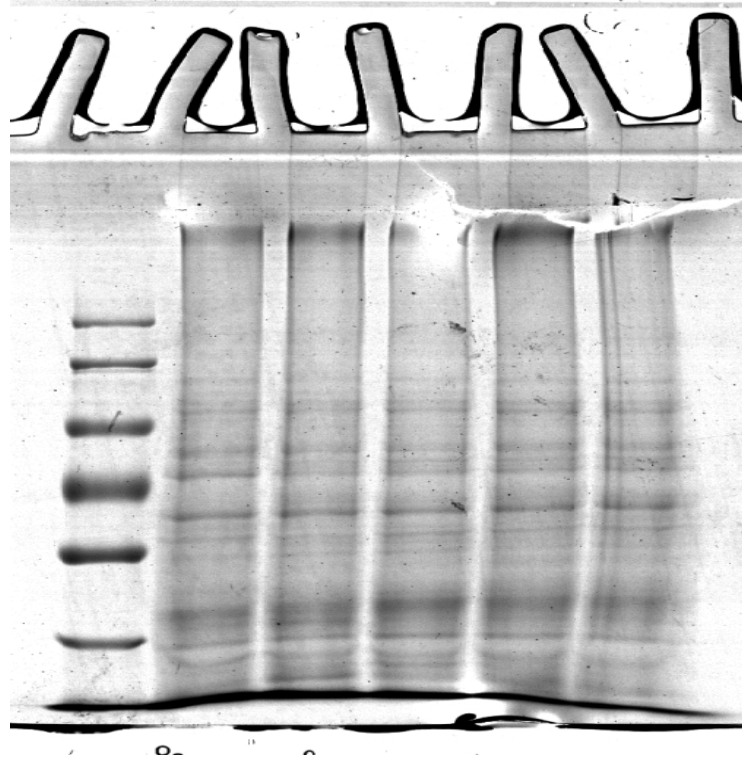
(A)



(B)

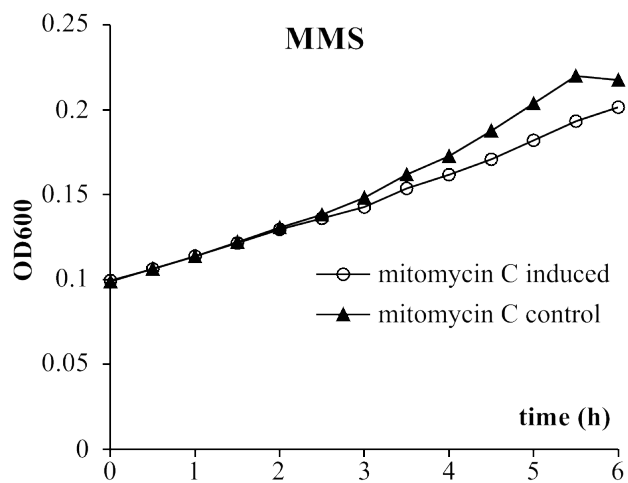
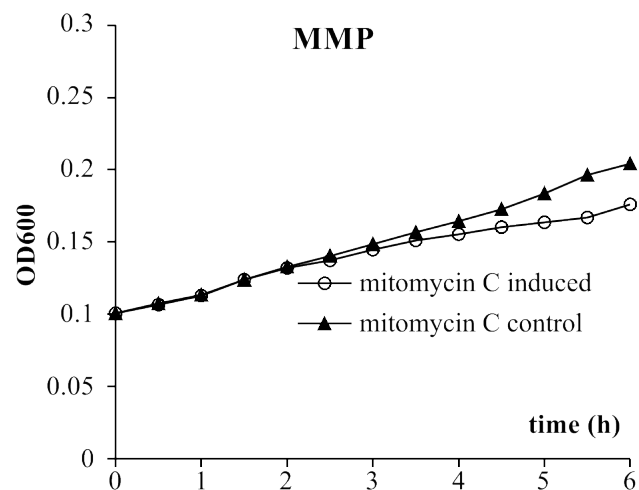
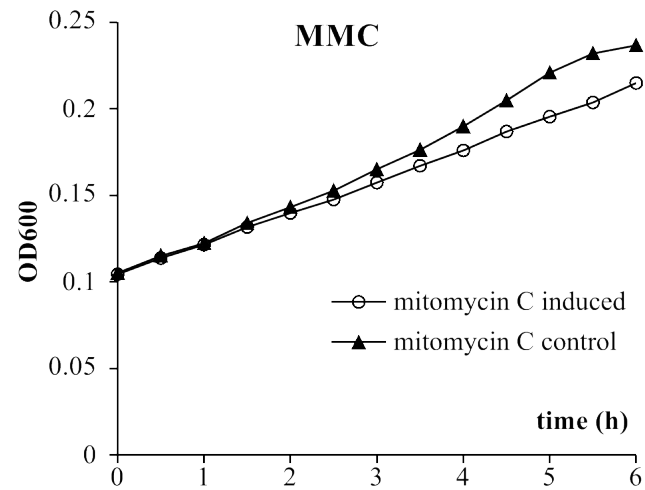
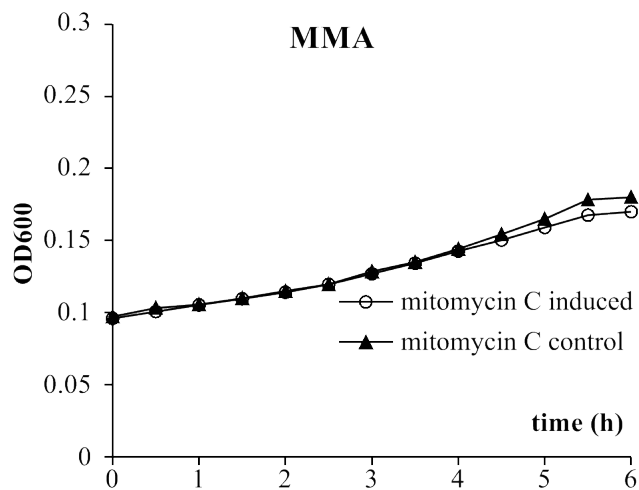
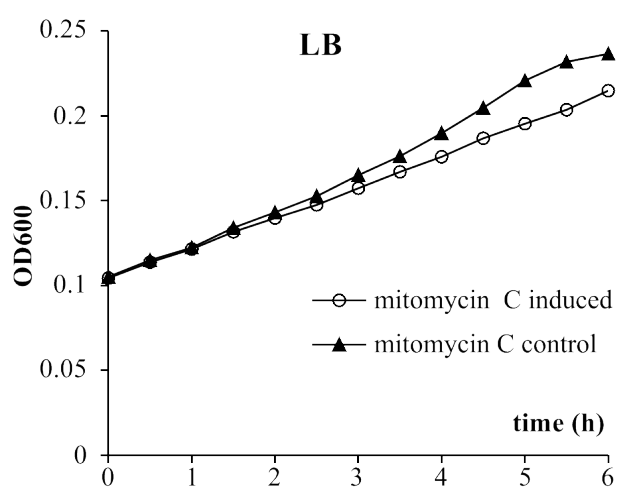


**Figure S1.** Calibration curve using 16S rRNA (A) and *recA* (B) as template. Error bars were the standard derivations of all replicates.

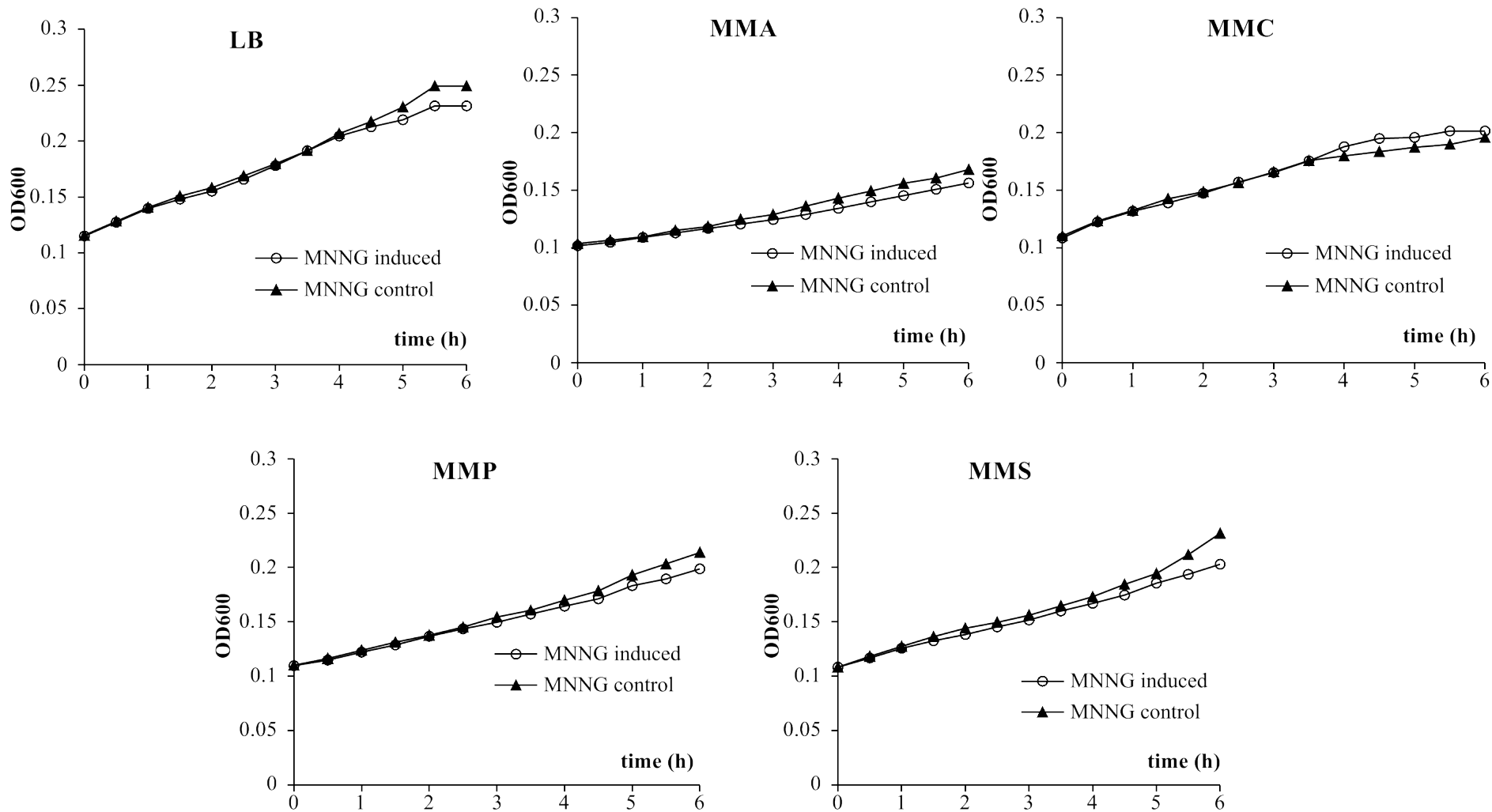


**Figure S2.** SDS-PAGE gel image of proteins extracted after bioreporters exposed (3 h) to mitomycin C in different carbon sources. Samples from left to right were marker, LB, MMA, MMC, MMP and MMS, respectively.

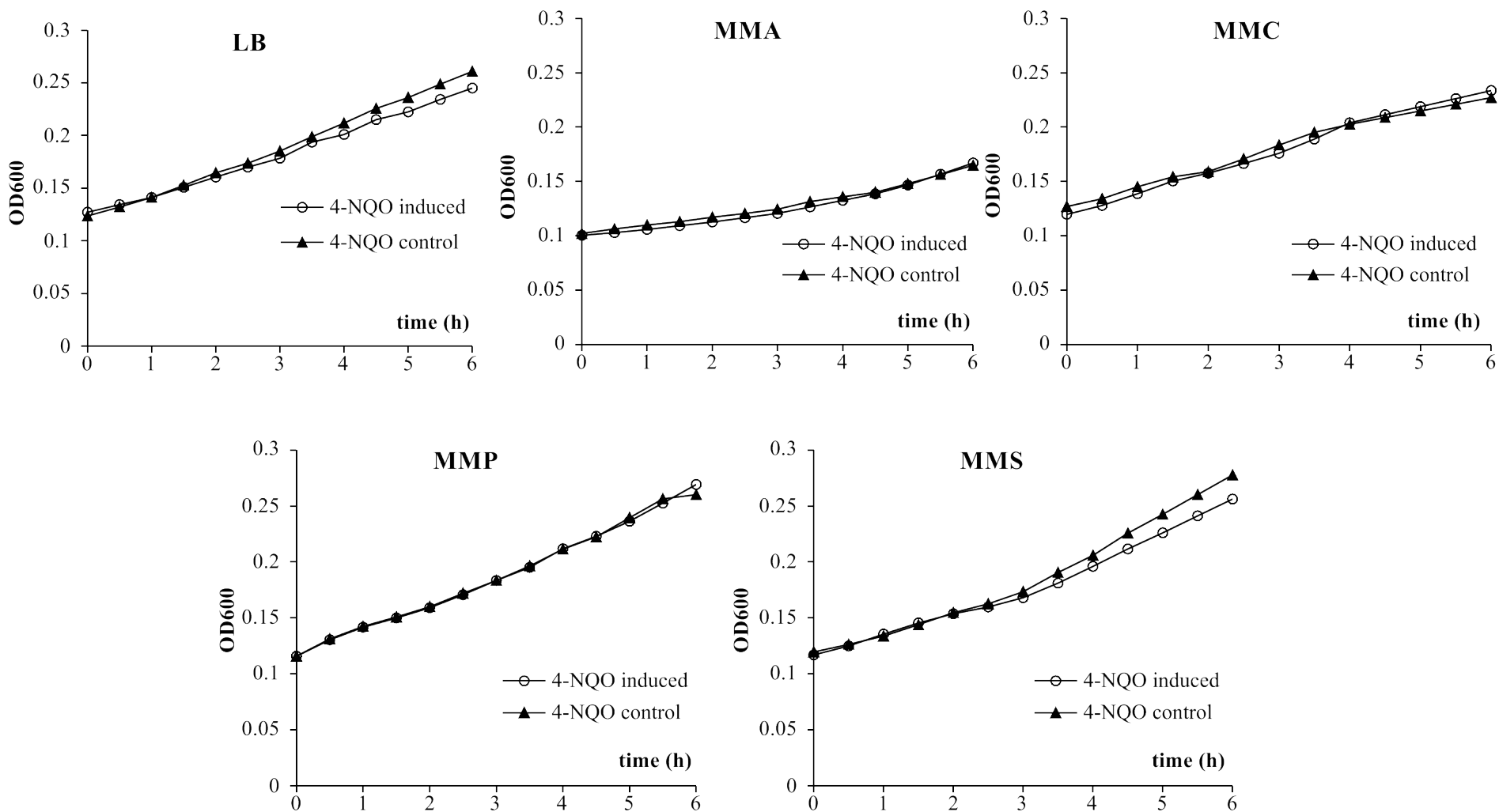
(A)



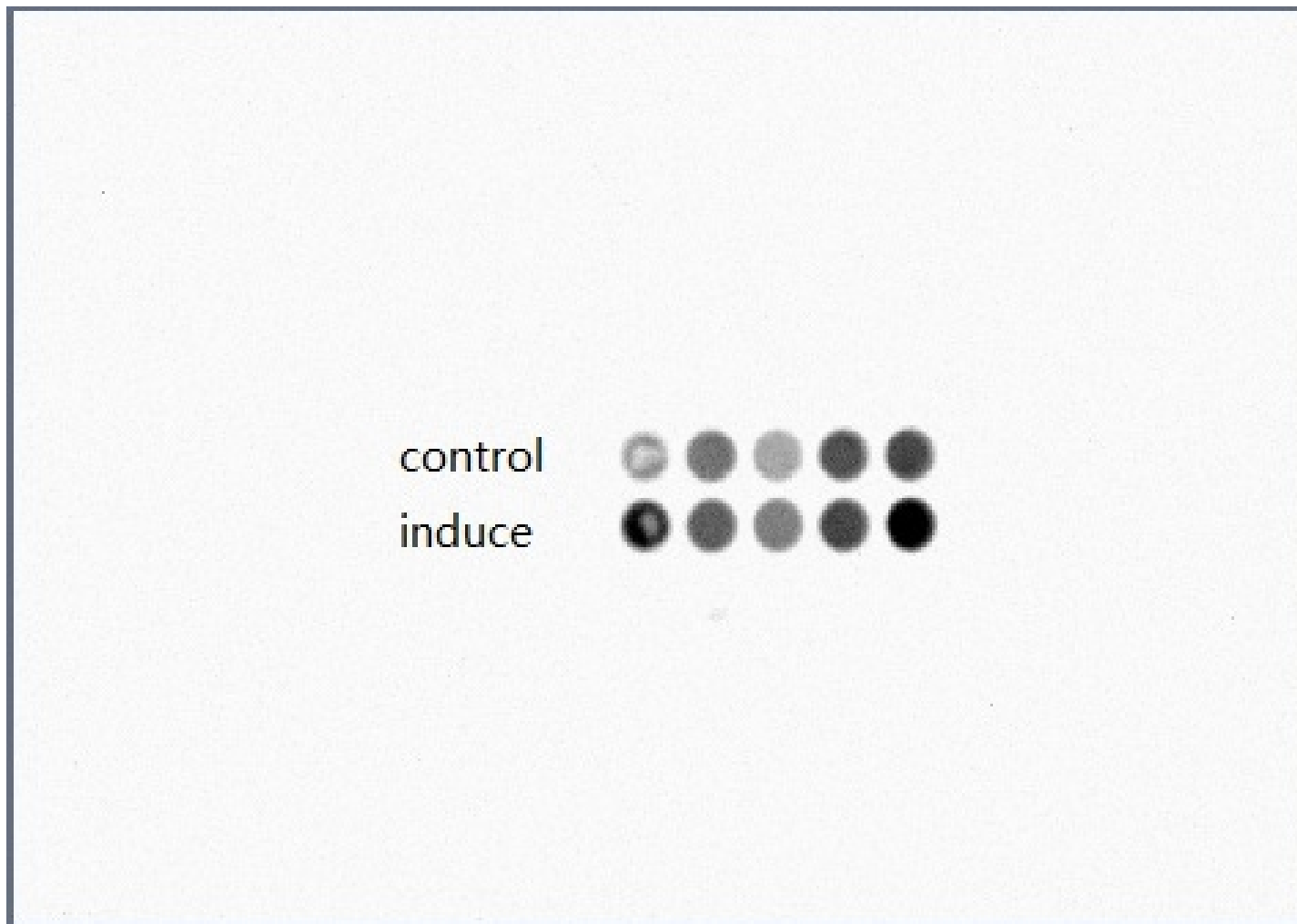
(B)



(C)



**Figure S3.** The time curve of OD<sub>600</sub> values of the ADP1 genotoxicity bioreporter in the five carbon sources under different genotoxins treatments-(A) mitomycin C (0.6  $\mu$ M), (B) MNNG (6.8  $\mu$ M), and (C) 4-NQO (5.3  $\mu$ M). Error bars were the standard derivations of all replicates.



**Figure S4.** The visualized bioluminescence taken by Versa Doc (Biorad) of induced (1  $\mu$ M of mitomycin C) and negative control samples, in which the carbon source from left to right was LB, MMA, MMC, MMP and MMS..