

21 **Table S1**22 **Basic physical and chemical properties of soil.**

| Soil physicochemical parameters | Value |
|---------------------------------------|-----------------------------|
| pH | 7.25 |
| specific conductance | 120.5 $\mu\text{S cm}^{-1}$ |
| cation exchange capacity | 7.21 cmol kg^{-1} |
| organic matter | 14.2 g kg^{-1} |
| percentage of saturated water content | 41% |
| thallium concentration in soil | not detected |
| Soil particle size proportions | |
| Sand | 35.25% |
| Silt | 53.03% |
| Clay | 11.72% |

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24 **Table S2**25 **Thallium concentration in soil.**

| Nominal soil thallium concentrations (mg kg^{-1}) | Soil thallium concentration measurements (mg kg^{-1}) |
|---|---|
| 0 | not detected |
| 2.5 | 2.2 ± 1.4 |
| 20 | 16.7 ± 2.1 |
| 60 | 55.6 ± 4.5 |

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27 **Table S3**28 **Microwave digestion heating program.**

| Order number | Temperature/ $^{\circ}\text{C}$ | Warming time/min | Holding time/min |
|--------------|----------------------------------|------------------|------------------|
| 1 | indoor temperature ~ 120 | 6 | 3 |
| 2 | 120 \sim 150 | 8 | 10 |
| 3 | 150 \sim 180 | 8 | 30 |

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31 **Table S4**32 **Sequences of primers used for real-time qPCR.**

| Gene | Accession number | Primer | Amplification efficiency |
|----------------|------------------|--|--------------------------|
| <i>β-actin</i> | GU177854 | F: TCCATCGTCCACAGAAAG R: AAATGTCCTCCGCAAGCT | 99.4% |
| <i>Hsp70</i> | GU177858 | F: CCAAGGACAACAACCTGCTC R: CGGCGTTCTTCACCATTTC | 100% |
| <i>MT</i> | AJ236886 | F: TGAAAAGTGAGTGCTTGCCG R: CACAGCACCCCTTCTTGCAT | 99.3% |
| <i>ANN</i> | GU177859 | F: TTTCTTCCGCCTGCTTTG R: ACCGACCTACCACCGACA | 98.3% |

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35 **Table S5**36 **The data supporting this article**

| Biomarker | Exposure concentration (mg kg ⁻¹) | Day 7 | Day 28 | Day 56 |
|--|---|-------------|-------------|-------------|
| SOD Activity (U mg ⁻¹ prot) | 0 | 139.18±6.47 | 155.92±5.2 | 148.48±6.58 |
| | 2.5 | 150.01±3.37 | 154.04±4.27 | 130.4±7.09 |
| | 20 | 161.27±7.43 | 137.17±5.14 | 118.92±5.88 |
| | 60 | 179.2±3.59 | 112.02±8.44 | 122.56±8.54 |
| CAT Activity (U mg ⁻¹ prot) | 0 | 10.61±0.45 | 10.58±0.53 | 10.1±0.67 |
| | 2.5 | 12.06±0.81 | 9.28±0.66 | 9.77±0.59 |
| | 20 | 14.26±1.14 | 11.22±0.58 | 7.12±0.56 |
| | 60 | 13.09±0.81 | 7.83±0.72 | 6.92±0.64 |
| GST Activity (U mg ⁻¹ prot) | 0 | 40.55±1.41 | 45.3±2.5 | 46.23±1.63 |
| | 2.5 | 45.13±2.86 | 46.02±2.62 | 41.35±2.27 |
| | 20 | 55.36±1.26 | 37.55±2.44 | 33.86±2.08 |
| | 60 | 65.95±4.06 | 37.92±1.29 | 28.92±1.91 |
| MDA Content (nmol mg ⁻¹ prot) | 0 | 1.3±0.06 | 1.49±0.05 | 1.54±0.11 |
| | 2.5 | 1.44±0.1 | 1.71±0.1 | 1.88±0.08 |
| | 20 | 1.38±0.07 | 1.83±0.08 | 2.34±0.23 |
| | 60 | 1.47±0.08 | 2.12±0.21 | 2.71±0.23 |
| 8-OHdG Content (ng L ⁻¹) | 0 | 22.33±0.86 | 21.93±0.86 | 19.54±0.41 |
| | 2.5 | 23.92±1.33 | 23.82±1.01 | 20.21±0.81 |
| | 20 | 27.06±1.93 | 28.66±1.29 | 25.73±1.17 |
| | 60 | 26.06±0.5 | 32.27±0.82 | 26.85±1.1 |
| Relative expression level of <i>Hsp70</i> gene | 0 | 1.04±0.07 | 1.1±0.04 | 1.05±0.06 |
| | 2.5 | 1.23±0.07 | 1.34±0.07 | 1.34±0.07 |
| | 20 | 1.46±0.05 | 1.74±0.07 | 1.93±0.08 |
| | 60 | 1.73±0.08 | 1.93±0.08 | 2.42±0.19 |
| Relative expression level of <i>MT</i> gene | 0 | 0.98±0.05 | 1.05±0.08 | 1±0.07 |
| | 2.5 | 1.29±0.11 | 1.18±0.05 | 1.22±0.11 |
| | 20 | 1.31±0.08 | 1.5±0.07 | 1.52±0.05 |
| | 60 | 1.59±0.1 | 1.72±0.09 | 1.92±0.08 |
| Relative expression level of <i>ANN</i> gene | 0 | 1.11±0.06 | 1.39±0.08 | 1.08±0.09 |
| | 2.5 | 1.28±0.09 | 1.12±0.07 | 0.73±0.03 |
| | 20 | 1.32±0.03 | 0.89±0.06 | 0.53±0.03 |
| | 60 | 1.08±0.07 | 0.65±0.05 | 0.39±0.02 |

38 **Text S1**

39 The 0.5 g of soil was placed in the digestive tube, then 5 mL of concentrated HNO₃,
40 3 ml of hydrofluoric acid, and 3 ml of hydrogen peroxide were added and rinsed
41 according to the heating procedure (Table S3). The rinsing solution was cooled to room
42 temperature and transferred to a 25 mL volumetric flask, and the solution was diluted
43 with 1% nitric acid and then passed through a 0.45 μm membrane to be measured.
44 Thallium (Tl) standards were obtained from Tanmo Technology Company (Jiangsu,
45 China). Graphite furnace atomic absorption spectrophotometry (Thermo Fisher
46 Scientific, ICE 3500) was used for the analysis. Tl content in soil was expressed as μg
47 g⁻¹ (wet weight). Tl recovery was determined by adding a known amount of Tl standard
48 to the samples and the average recovery was 104.17 ± 0.11%.

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50 **Text S2**

51 **Methods for the determination of biomarkers of oxidative stress**

52 **1. Homogenizing solution preparation**

53 Earthworm samples were mixed with a PBS buffer solution containing KH₂PO₄
54 and K₂HPO₄ (0.1 mol L⁻¹, pH = 7.4) in a ratio of 1:9 (weight : volume). The resulting
55 mixture was homogenized using a mechanical homogenizer while being cooled under
56 ice-water bath conditions. The homogenate was then centrifuged at 4,000 rpm for 10
57 minutes. The supernatant was collected for biomarker analysis.

58 **2. Calculation of protein content**

59 Protein determination was performed by Caulmers Brilliant Blue method. In brief,
60 when the -NH³⁺ group of protein molecule encounters the brownish-red Caulmers
61 Brilliant Blue colorant, the anion on the Caulmers Brilliant Blue dye combines with the
62 protein -NH³⁺ to make the solution turn blue, and the protein content can be calculated
63 by measuring the absorbance.¹ The assay was carried out according to the instructions
64 of TP Kit (Catalog No. A045-2) from Nanjing Jiancheng Bioengineering Institute
65 (Nanjing, China). Briefly, 0.05 mL of homogenized supernatant was taken, added to
66 the working solution, mixed, and allowed to stand for 10 min, and the absorbance value
67 was measured at 595 nm. The protein content was calculated following the instructions
68 from the manufacturer.

69 **3. Superoxide dismutase (SOD)**

70 SOD activity was measured using the WST-1 method, which generates a water-
71 soluble dye by reacting WST-1 with superoxide anion. The assay was carried out

72 according to instructions provided by the SOD Assay Kit (catalog no. A001-3) from
73 Nanjing Jiancheng Bioengineering Institute (Nanjing, China). UV absorbance readings
74 at 450 nm were taken with a UV-2600 spectrophotometer (Shimadzu, Kyoto, Japan),
75 and the SOD activity of each sample was subsequently calculated.

76 **4. Catalase (CAT)**

77 CAT was measured by the ammonium molybdate method. Briefly, the
78 decomposition of H₂O₂ by CAT can be rapidly stopped by adding ammonium
79 molybdate. The remaining H₂O₂ then reacts with the ammonium molybdate to form a
80 yellowish complex, which is measured at 405 nm to calculate the activity of CAT.² The
81 CAT activity of each sample was determined according to the instructions of the CAT
82 Assay Kit (Catalog No. A007-1-1) from Nanjing Jiancheng Bioengineering Institute
83 (Nanjing, China). UV absorbance was measured at 405 nm using a UV-2600
84 spectrophotometer (Shimadzu, Kyoto, Japan). CAT activity was calculated according
85 to the formula provided by the manufacturer.

86 **5. Glutathione S-transferase (GST)**

87 The activity of GST was performed using the instructions of the GST Assay Kit
88 (Catalog No. A004-1-1) from Nanjing Jiancheng Bioengineering Institute (Nanjing,
89 China). Briefly, 0.1 mL of homogenate supernatant was taken and mixed with the
90 working solution. The mixture was then centrifuged, and the supernatant was collected
91 as the supernatant of the color development reaction. Subsequently, 2 mL of the color
92 reaction supernatant was taken and reacted with the application solution. The
93 absorbance at 412 nm was measured to calculate the GST activity of each sample.

94 **6. Malondialdehyde (MDA)**

95 MDA was determined by the TBA method. The method utilizes the fact that MDA
96 in the degradation products of lipid peroxidation can condense with thiobarbituric acid
97 (TBA) to form a red product with a maximum absorption peak at 532 nm.³ The assay
98 was performed according to the instructions of the MDA Kit (Catalog No. A003-1)
99 from Nanjing Jiancheng Bioengineering Institute (Nanjing, China). Briefly, 0.2 mL of
100 homogenized supernatant was introduced into the working solution, thoroughly mixed,
101 and subsequently subjected to a 40-minute heating at 95°C in a water bath. Following
102 this, the sample was cooled using running water and centrifuged at a speed of 3,500 to
103 4,000 revolutions per minute for 10 minutes. The extracted supernatant is measured at
104 a wavelength of 532 nanometers. The MDA content was calculated following the
105 instructions of the manufacturer.

106 7. 8-hydroxy-2'-deoxyguanosine (8-OHdG)

107 8-OHdG content was tested by kit procedure. First, the tissue homogenate was
108 added to the purified antibodies of 8-OHdG. After thoroughly washing and drying the
109 plate, horseradish peroxidase (HRP)-conjugated 8-OHdG antibody reagent was added.
110 After washing and drying, 3,3',5,5'-tetramethyl benzidine (TMB) was added to develop
111 color at 37 °C for 25 min. The color depth of the solution was positively correlated with
112 the 8-OHdG content. Finally, 1 M sulfuric acid was added to stop the reaction. The OD
113 value was determined to be 450 nm.

114

115 Text S3

116 The BRI index calculation method

117 The Biomarker Response Index (BRI) is calculated comprehensively through three
118 steps, summarizing four Biological Health Statuses (BHS). Firstly, the alteration level
119 (AL) for each biomarker is calculated using equation (1):

$$120 \quad AL = (BR_t - BR_c) / BR_c \quad (1)$$

121 where BR_t and BR_c refer to biomarker responses of exposure and control
122 treatments, respectively.

123 Secondly, weights are assigned based on the mechanism of action of each
124 biomarker. For biomarkers such as SOD, CAT, and GST, which do not directly reflect
125 toxicity, a weight of 1.0 is assigned. Biomarkers related to specific adverse effects, such
126 as MDA, are assigned a weight of 1.2, and 8-OHdG, which is associated with oxidative
127 DNA damage, is given a weight of 1.5. Biomarkers related to genetic damage, such as
128 Hsp70, MT, and ANN, are assigned a weight of 1.0.

129 Thirdly, the Biomarker Response Index (BRI) is calculated by integrating the
130 values using equation (2).

$$131 \quad BRI = \sum(S_n \times W_n) / \sum W_n \quad (2)$$

132 In this context, S_n represents the score of each biomarker, while W_n denotes the
133 corresponding weight.

134 Ultimately, the BRI value is classified into four Biological Health Status (BHS)
135 levels according to the categorization by Hagger *et al.*,⁴ ranging from 1.0 to 2.5 (severe
136 alterations), 2.51 to 2.75 (major alterations), 2.76 to 3.00 (moderate alterations), and
137 3.01 to 4.00. Due to the broad range of the last interval, it is further subdivided into 3.01
138 to 3.75 (minor alterations) and 3.76 to 4.00 (normal response with no change).

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140 **References**

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