**Table.** S**1:** Primers sequences used in qRT-PCR analysis

|  |  |
| --- | --- |
| **Gene** | **Forward and reverse Primer sequence (5’ – 3’)** |
| ***SODA*** | *TGGATGGGTGTGGCTAGCTTT*  *AGTATGCATGCTCCCAGACAT* |
| ***SODB*** | *TACTACGGCCTCACGACTCC*  *CGGGTTGCCGTTGTTGTAGG* |
| ***CAT1*** | *AACTCCGCCTACTGGACCAC*  *ACGTTCAGGTATGCGTTCCC* |
| ***CAT2*** | *ACCGCAACGTCGACAACTTC*  *TTGACGGGGAGCATCAGGTA* |
| ***APX*** | *GAGGTCTGGCTTTGAGGGAC*  *TCAGCAGAGTTTTGTCACTTGGA* |
| ***GR*** | *GAGCTACGACTACGACCTCTTC*  *CACGTATCACGCACGTCCC* |
| ***GST1*** | *TCCAAGTACCTGGCTGGAGA*  *CGGGTAAGCGTCGAACAGAG* |
| ***GST6*** | *AGCATCTCGTCAGAAACCCGT*  *TCGACCTCGTCCGTCTTGTA* |
| ***Actin*** | *CCCTAGCATAGTTGGTCGCC*  *CTCGATGGGGTACTTGAGCG* |

**Table S2.** Effect of CdO and nano-CdO treatments at 100 mg/l and 1000 mg/l on morphometric parameters and cadmium accumulation in roots and shoots of one-week-old barley seedlings.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Treatment** | **Root length, cm** | **Root fresh weight, mg** | **Root dry weight, mg** | **Shoot length, cm** | **Shoot fresh weight, mg** | **Shoot dry weight, mg** | **Cd content in root, mg/g** | **Cd content in shot, mg/g** |
| **Control** | 6.6±0.5 | 39.3±4.5 | 4.1±0.5 | 11.1±1.1 | 95.8±7.5 | 9.2±0.7 | 0.00043 ±0.0001 | 0.00024  ±0.0001 |
| **100 mg/l CdO** | 5.7±0.5 | 35.7±3.9 | 3.2±0.4\* | 8.9±0.7\* | 80.7±7.1 | 8.3±0.7 | 3.028  ±0.105\* | 0.043  ±0.004\* |
| **100 mg/l nano-CdO** | 4.1±0.5\* | 35.0±3.7 | 3.3±0.3\* | 7.7±0.6\* | 82.4±6.2 | 8.0±0.6 | 3.842  ±0.113\* | 0.190  ±0.004 |
| **1000 mg/l CdO** | 4.0±1.1\* | 26.8±3.0\* | 2.4±0.3\* | 6.9±0.8\* | 70.2±7.2\* | 6.9±0.7\* | 20.455 ±1.207\* | 0.599  ±0.011\* |
| **1000 mg/l nano-CdO** | 3.8±0.3\* | 23.2±3.2\* | 2.2±0.3\* | 6.8±0.7\* | 70.7±7.1\* | 6.8±0.7\* | 25.020 ±1.070\* | 0.648  ±0.022\* |

Asterix (\*) indicates statistically significant differences from the control at p<0.05