Supplementary data (S1)

ROS-related gene expression profiling in MTFs after cisplatin treatment.

The gene expression of *Srxn1, Fmo2, Nqo1, Fth1, Gstp1, Scd1, Gpx3, Ptgs2, Prnp, ldh1, Apoe, Cyba, Gpx1, Gclc, Gpx7, Hmox1, Gss, Sod2, Txnrd1, Ccs, Psmb5, Gpx5, Nfb, Txn1, Prdx3, Hspa1a, Gpx4, Ctsb, Txnip, Prdx5, Prdx1, Gclm, Sqstm1, Lpo, Ehd2, Mpo, Gstk1, Gpx6, Prdx2, Cygb, Sod3, Park7, Txnrd2, Sod1, Aox1, Serpinb1b, Cat, Fancc, Ift172, Prdx4, Duox1, Nox4, ll19, Slc38a1, Dnm2, Gpx2, Txnrd3,* and *Als2* in cisplatin-treated MTFs were higher than in control. The expression levels of *Ercc2, Crcc6,* and *Recql4* were lower in cisplatin-treated MTFs than in control. Gene expression levels are presented as $\log_2$ value compared to the control value ($\log_2 O$). Quantitative analysis of each protein level. Data are shown using the mean and the standard error of the mean (n = 3). Statistical significance was set at $P < 0.05$.