Supplementary methods- Quantitative RT-PCR

For gene expression measurement in U2OS cells, equal amount of total RNAs were used for reverse-transcription using the Transcriptor First Strand cDNA synthesis kit (Roche). The following TaqMan® probes from the universal probe library (Roche) were used: NQO1 (#87), GCLM (#18), HMOX1 (#25), TXN (#50), TXRD1 (#64), GSTP1 (#56), GCLC (#25), AKR1B10 (#25), AKR1C1 (#49) and GAPDH (#25). Quantitative real-time PCR (qRT-PCR) was performed on the Lightcycler® 480 system (Roche) as follows: one cycle of initial denaturation (95°C for 4 minutes), 45 cycles of amplification (95°C for 10 sec and 60°C for 30 sec), and a cooling period.

The following primers were synthesized by Integrated DNA Technologies:
NQO1: ATGTATGACAAAGGACCCTTCC and TCCCTTGCAGAGAGTACATGG
HMOX1: AACTTTCAGAAGGGCCAGGT and CTGGGCTCTCCTTGTTGC
GCLC: GGATGATGCTAATGAGTCTGACC and TCTACTCTCCATCCAATGTCTGAG
GCLM: GACAAAACACAGTTGGAACAGC and CAGTCAAATCTGGTGGCATC
GSTP1: TCCCTCATCTACACCAACTATGAG and GGTCTTGCCTCCCTGGTT
TXN: TCAAATGCATGCCAACATTC and GGTGGCTTCAAGCTTTTCCT
TXRD1: TTGGAATCCACCCTGTCTGT and CATCCACACTGGGGCTTAAC
AKR1B10: AAAGCAACGTTCTTGGATGC and TGGAAGTGGCTGAAATTGG
AKR1C1: CATGCCTGTCCTGGGATTT and AGAATCAATATGGCGGAAGC
GAPDH: CTGACTTCAACAGCGACACC and TGCTGTAGCCAAATTCGTTGT

To measure gene expression in T98G cells, total RNAs were extracted and cDNAs were generated using the SureScript® III First Strand Synthesis System (Invitrogen). Real-time PCR was performed using Brilliant II SYBR® Green QPCR Master Mix (Agilent Technologies) on a MX3005P system (Stratagene) using the following parameters: 15 min initial denaturation and hotstart enzyme activation, 40 cycles of amplification (95°C for 10 sec and 60°C for 30 sec) followed by melting curve measurement.

Primers were synthesized by Sigma. The sequences of the primers are as follows:
NQO1: GCAGACCTTGTGATATTCCAGT and GTCATACATGGCAGCGTAAGTG
HMOX1: GCCAGCAACAAAGTGCAAGATTC and CACCAGAAAGCTGAGTGTAAGGAC
GCLC: CTGGATGATGCTAATGAGTCTGA and CTACTCTCCATCCAATGTCTGA
GCLM: CTAGACAAAACACAGTTGGAACA and ATGCAGTCAAATCTGGTGGCAT
TXN: AAGTCAAATGCATGCCAACATTC and AATGGTGGCTTCAAGCTTTTCCT
AKR1B10: GAAAAGCAACGTTCTTGGATGCCT and ATCTGGAAGTGGCTGAAATTGGA
AKR1C1: CTACAATGAGCAGCGCATCAGAC and GTCAAATATCGCACATTTCTGTTTAG
GAPDH: GTCTCCTCTGACTTCAACAGCGAC and CCAAATTCGTTGTCATACCAGGAA

Experiments were performed in triplicates at least twice. NQO1, GCLM and AKR1B10 were measured at least 3 times. Data presented are relative mRNA levels normalized to that of GAPDH, with the value in the control group set as 1. Error bars represent the standard deviations.