

Aging-associated effects of a long-term dietary modulation of four trace elements in mice

– Figures and Tables Supporting Information –

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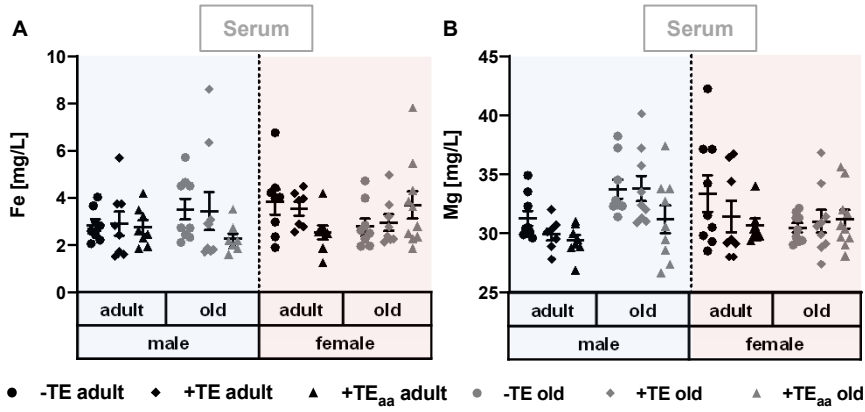
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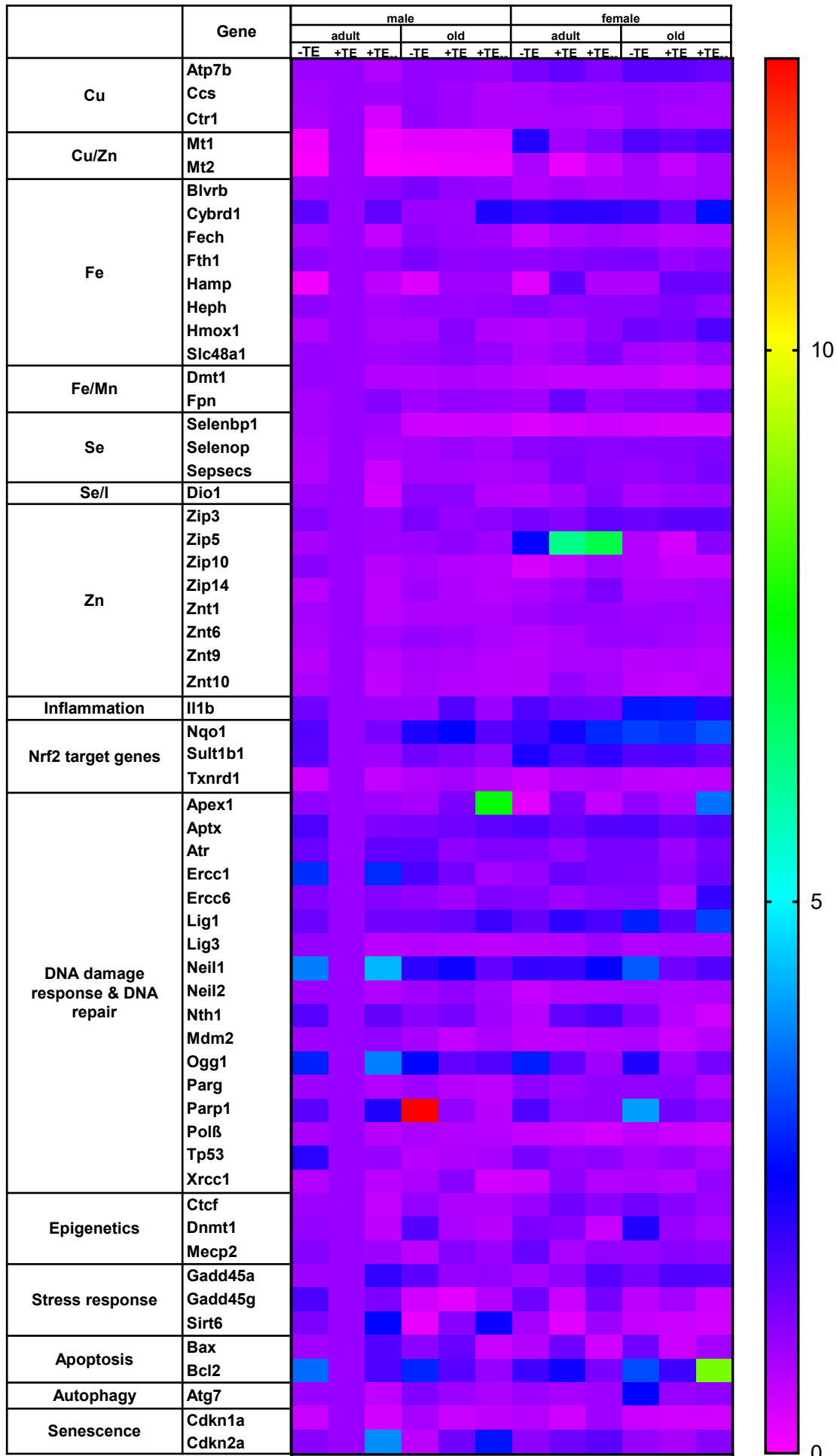
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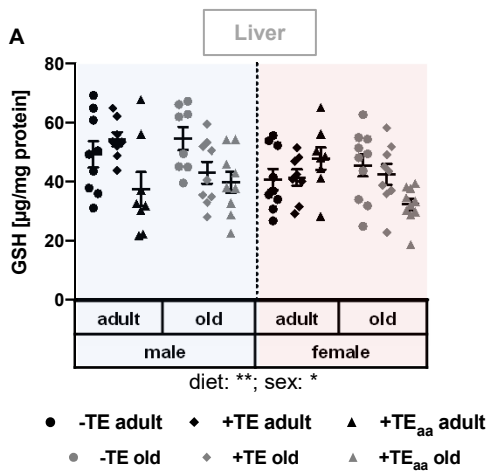
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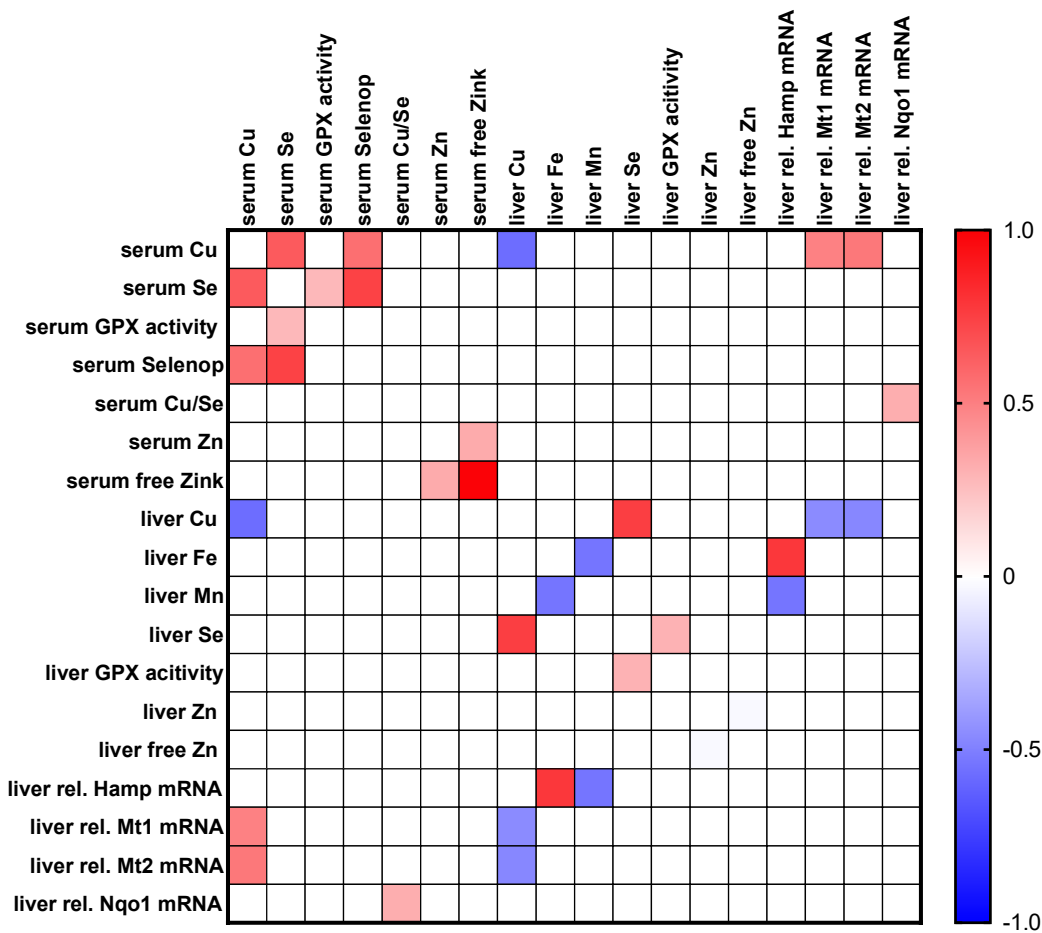
Supplementary Information Figure 1. Changes in murine serum element concentrations. Murine serum element concentrations were determined adult (30 weeks) and old (66 weeks) male and female C57BL/6Jrj mice ($n = 8-10$) receiving a -TE, +TE, or +TE_{aa} diet for 26 weeks. Total serum Fe (A) and Mn (B) concentrations were analysed by ICP-MS/MS. Statistical testing based on Three-Way ANOVA and Bonferroni's post-test with * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.



Supplementary Figure 2. Quantitative Real Time-PCR array screening of TE-, DNA damage response-, and DNA repair-related gene expression in murine liver. Relative expression level of selected genes related to TE homeostasis, DNA damage response, DNA repair mechanisms, stress response, epigenetics, cell death, as well as senescence in the liver of adult (30 weeks) and old (66 weeks) male and female C57BL/6Jrj mice (n = 8-10) receiving a -TE, +TE, or +TE_{aa} diet for 26 weeks. Expression levels were normalised to a composite factor based on the house keeper genes Hprt and Rpl13a. Finally, variances are expressed as fold changes compared to +TE male adults (mean +TE male adult = 1).



Supplementary Information Figure 3. Changes in further analysed markers indicative for redox status in murine liver. Gsh level were analysed in liver tissue of adult (30 weeks) and old (66 weeks) male and female C57BL/6Jrj mice (n = 8-10) receiving a -TE, +TE, or +TE_{aa} diet for 26 weeks. GSH levels were quantified by HPLC-qTOF. Statistical testing based on Three-Way ANOVA and Bonferroni's post-test with * p < 0.05, ** p < 0.01, *** p < 0.001.



Supplementary Information Figure 4. Heatmap among selected serum and hepatic TE concentrations and biomarkers, TE-related genes and redox markers in liver based on Spearman's correlation. Serum and hepatic TE concentrations of Cu, Fe, Mn, Se, and Zn were analysed via ICP-MS/MS and on the basis of TE levels Cu/Se ratio was calculated. While Selenop concentrations were determined using, an affinity-HPLC-ICP-MS/MS, GPX activity was evaluated by a NADPH-consuming glutathione reductase coupled assay. Additionally, free Zn concentrations in liver and serum were analysed using a fluorescent probe, whereas relative mRNA expression of Hamp, Mt1, Mt2, and Nqo1 were determined by qRT-PCR analysis. Hepatic transcription levels were normalised to a composite factor based on the house keeper genes Hprt and Rpl13a. Finally, variances are expressed as fold changes compared to +TE male adults (mean +TE male adult = 1). Correlation coefficients vary between - 1 (blue) and 1 (red), indicated by colored changes.

Parameter	Unit	Male												Statistics						
		Adult				Old				Female				Diet	Sex	Age	Diet x sex	Diet x age	Sex x age	Diet x sex x age
		-TE	+TE	+TE _{aa}	-TE	+TE	+TE _{aa}	-TE	+TE	+TE _{aa}	-TE	+TE	+TE _{aa}							
Polβ protein		1.13 ± 0.77	3.82 ± 3.00	1.37 ± 0.50	1.46 ± 0.43	1.40 ± 0.68	1.35 ± 0.84	1.38 ± 0.19	3.32 ± 3.1	2.37 ± 1.72	1.19 ± 0.31	2.07 ± 1.01	1.19 ± 0.32	0.009	0.704	0.027	0.836	0.120	0.877	0.405
rel. Apex1 mRNA		1.11 ± 1.06	1 ± 0.54	0.96 ± 0.78	0.87 ± 0.5	1.28 ± 0.64	7.55 ± 14.55	0.29 ± 0.03	1.29 ± 0.88	0.6 ± 0.04	1.09 ± 1.24	0.82 ± 0.29	3.64 ± 5.01	0.085	0.204	0.018	0.840	0.023	0.741	0.139
rel. Aptx mRNA		1.76 ± 0.87	1 ± 0.28	1.28 ± 0.52	1.34 ± 0.26	1.42 ± 0.46	1.58 ± 0.99	1.71 ± 0.59	1.46 ± 0.34	1.68 ± 0.38	1.74 ± 0.29	1.49 ± 0.2	1.67 ± 0.37	0.099	0.048	0.611	0.945	0.277	0.712	0.246
rel. Atg7 mRNA		1 ± 0.38	1 ± 0.21	0.63 ± 0.26	1.24 ± 0.19	0.98 ± 0.47	0.84 ± 0.48	1 ± 0.33	0.86 ± 0.22	0.93 ± 0.24	2.51 ± 2.49	1.01 ± 0.31	1.09 ± 0.42	0.031	0.170	0.067	0.336	0.157	0.278	0.267
rel. Atr mRNA		1.49 ± 0.66	1 ± 0.39	1.56 ± 0.24	1.55 ± 0.55	1.12 ± 0.38	1.26 ± 0.88	1.26 ± 0.57	1.05 ± 0.51	1.3 ± 0.23	1.32 ± 0.5	0.99 ± 0.3	1.35 ± 0.57	0.018	0.303	0.924	0.763	0.765	0.797	0.619
rel. Bax mRNA		0.94 ± 0.55	1 ± 0.39	1.69 ± 1.1	1.13 ± 0.51	1.5 ± 0.63	0.55 ± 0.16	0.74 ± 0.38	1.42 ± 0.77	0.46 ± 0.14	1.41 ± 1.07	0.51 ± 0.12	0.9 ± 0.66	0.468	0.115	0.771	0.366	0.063	0.448	<0.001
rel. Bcl2 mRNA		3.57 ± 1.37	1 ± 0.53	1.76 ± 0.77	2.88 ± 0.7	1.66 ± 0.69	1.05 ± 0.46	1.89 ± 0.61	2.36 ± 1.85	1.3 ± 0.42	3.27 ± 1.8	1.92 ± 0.5	8.77 ± 9.38	0.172	0.065	0.063	0.036	0.088	0.027	0.019
rel. Cdkn1a mRNA		0.56 ± 0.24	1 ± 0.62	0.44 ± 0.4	0.86 ± 0.9	0.55 ± 0.53	0.65 ± 0.66	0.72 ± 0.64	0.48 ± 0.31	0.94 ± 1.06	0.53 ± 0.46	0.47 ± 0.18	0.46 ± 0.23	0.236	0.473	0.334	0.244	0.533	0.927	0.196
rel. Cdkn2a mRNA		1.17 ± 0.67	1 ± 0.8	3.93 ± 4.4	0.66 ± 0.34	1.41 ± 1.42	2.7 ± 1.66	1.12 ± 0.72	1.42 ± 1.28	1.62 ± 0.84	1.04 ± 0.45	0.85 ± 0.59	1.17 ± 1.24	0.008	0.089	0.242	0.062	0.755	0.994	0.514
rel. Ctcf mRNA		0.97 ± 0.19	1 ± 0.28	0.61 ± 0.26	1.08 ± 0.32	0.8 ± 0.14	0.81 ± 0.32	1 ± 0.26	1.42 ± 0.74	1.15 ± 0.34	1.41 ± 0.76	1.17 ± 0.33	0.98 ± 0.23	0.064	0.001	0.436	0.664	0.189	0.769	0.154
rel. Dnmt1 mRNA		1.08 ± 0.47	1 ± 0.43	0.64 ± 0.6	1.67 ± 1.24	0.84 ± 0.55	0.69 ± 0.33	1.27 ± 0.66	1.17 ± 0.93	0.54 ± 0.32	2.19 ± 1.61	1.03 ± 0.58	0.84 ± 0.33	<0.001	0.189	0.086	0.848	0.100	0.703	0.914
rel. Ercc1 mRNA		2.97 ± 2.61	1 ± 0.34	2.92 ± 3.82	1.78 ± 0.53	1.35 ± 0.31	0.92 ± 0.38	1.05 ± 0.28	1.48 ± 0.49	1.3 ± 0.48	1.28 ± 0.64	1.1 ± 0.13	1.46 ± 0.58	0.351	0.083	0.132	0.230	0.497	0.129	0.152
rel. Ercc6 mRNA		1.23 ± 0.37	1 ± 0.27	1.21 ± 0.44	1.09 ± 0.35	0.92 ± 0.35	1.26 ± 0.55	1.2 ± 0.41	0.97 ± 0.36	1.14 ± 0.43	1.18 ± 0.26	0.73 ± 0.22	2 ± 2.18	0.012	0.558	0.475	0.790	0.609	0.940	0.805
rel. Gadd45a mRNA		0.97 ± 0.58	1 ± 0.39	2.03 ± 1.72	1.59 ± 0.78	1.03 ± 0.5	1.05 ± 0.44	0.87 ± 0.52	1.11 ± 0.5	1.66 ± 0.6	1.37 ± 0.5	1.7 ± 0.53	1.67 ± 0.79	0.078	0.471	0.450	0.377	0.028	0.152	0.360
rel. Gadd45g mRNA		1.75 ± 1.38	1 ± 0.79	1.28 ± 1.17	0.46 ± 0.31	0.28 ± 0.06	0.74 ± 0.53	1.44 ± 1.23	0.55 ± 0.26	1.36 ± 0.83	0.66 ± 0.36	0.92 ± 0.59	0.52 ± 0.28	0.180	0.953	<0.001	0.919	0.144	0.216	0.274
rel. Lig1 mRNA		1.46 ± 0.54	1 ± 0.27	1.39 ± 0.48	1.42 ± 0.5	1.5 ± 0.47	1.92 ± 1.4	1.52 ± 0.81	2.07 ± 0.34	1.78 ± 0.56	2.81 ± 0.85	1.61 ± 0.21	3.17 ± 1.89	0.099	<0.001	0.888	0.145	0.291	0.047	
rel. Lig3 mRNA		1.05 ± 0.71	1 ± 0.35	0.68 ± 0.31	0.72 ± 0.23	0.68 ± 0.11	0.64 ± 0.19	0.71 ± 0.31	0.74 ± 0.13	0.98 ± 0.27	0.74 ± 0.22	0.82 ± 0.22	0.82 ± 0.17	0.254	0.512	0.243	0.012	0.367	0.092	0.090
rel. Mdm2 mRNA		0.96 ± 0.38	1 ± 0.19	1.07 ± 0.21	0.86 ± 0.16	0.61 ± 0.27	0.85 ± 0.45	0.62 ± 0.32	0.64 ± 0.31	0.74 ± 0.18	0.78 ± 0.24	0.54 ± 0.11	0.74 ± 0.3	0.135	<0.001	0.079	0.997	0.190	0.039	0.972
rel. Mecp2 mRNA		1.19 ± 0.23	1 ± 0.13	0.97 ± 0.39	0.66 ± 0.27	1.21 ± 0.36	1.01 ± 0.45	1.51 ± 0.46	0.84 ± 0.36	1.06 ± 0.32	1.05 ± 0.26	1.16 ± 0.67	1.1 ± 0.55	0.809	0.204	0.472	0.119	0.003	0.744	0.969
rel. Neil1 mRNA		3.77 ± 3.8	1 ± 0.83	4.34 ± 1.85	2.07 ± 1.14	2.41 ± 1.52	1.53 ± 0.75	2 ± 1.19	1.97 ± 0.43	2.47 ± 0.97	3.42 ± 1.68	1.4 ± 0.45	1.7 ± 0.74	0.038	0.323	0.168	0.637	0.050	0.147	0.014
rel. Neil2 mRNA		0.99 ± 0.85	1 ± 0.36	0.76 ± 0.39	0.95 ± 0.54	1.09 ± 0.72	0.91 ± 0.53	0.56 ± 0.45	0.73 ± 0.48	0.76 ± 0.33	0.83 ± 0.55	0.76 ± 0.38	0.79 ± 0.61	0.809	0.071	0.449	0.675	0.981	0.854	0.703
rel. Nth1 mRNA		1.65 ± 0.84	1 ± 0.4	1.52 ± 0.98	1.17 ± 0.57	1.34 ± 0.6	0.95 ± 0.5	0.71 ± 0.15	1.55 ± 1.23	1.79 ± 1.65	1.23 ± 1.03	0.72 ± 0.12	0.49 ± 0.26	0.986	0.332	0.051	0.661	0.117	0.444	0.062
rel. Ogg1 mRNA		2.84 ± 3.19	1 ± 0.84	3.8 ± 3.4	2.56 ± 2.52	1.55 ± 1.24	1.7 ± 1.46	2.8 ± 2.3	1.56 ± 0.56	0.92 ± 0.41	2.19 ± 1.41	0.97 ± 0.55	1.33 ± 0.68	0.049	0.153	0.308	0.228	0.727	0.688	0.178
rel. Parg mRNA		0.97 ± 0.2	1 ± 0.33	0.75 ± 0.43	0.94 ± 0.39	0.71 ± 0.18	0.65 ± 0.38	1.09 ± 0.51	0.95 ± 0.36	1.11 ± 0.17	1.07 ± 0.42	1.12 ± 0.31	0.78 ± 0.23	0.102	0.019	0.199	0.821	0.542	0.588	0.183
rel. Parp1 mRNA		1.63 ± 0.61	1 ± 0.37	2.22 ± 1.24	12.65 ± 10.24	1.06 ± 0.44	0.69 ± 0.16	1.74 ± 0.87	1.08 ± 0.02	1.1 ± 0.6	4.09 ± 3.66	1.37 ± 0.4	1.14 ± 0.2	0.002	0.037	0.007	0.179	0.004	0.078	0.066
rel. Polβ mRNA		0.88 ± 0.19	1 ± 0.23	0.69 ± 0.42	0.83 ± 0.29	0.76 ± 0.32	0.72 ± 0.31	0.61 ± 0.15	0.57 ± 0.1	0.45 ± 0.12	0.66 ± 0.11	0.52 ± 0.07	0.48 ± 0.23	0.025	<0.001	0.437	0.625	0.339	0.338	0.762
rel. Sirt6 mRNA		1.27 ± 1.58	1 ± 0.78	2.55 ± 1.59	0.23 ± 0.08	1.18 ± 0.95	2.41 ± 3.07	0.91 ± 0.53	0.31 ± 0.09	0.97 ± 0.42	0.57 ± 0.48	0.52 ± 0.07	0.47 ± 0.33	0.020	0.004	0.325	0.034	0.417	0.821	0.713
rel. Tp53 mRNA		2.11 ± 3.2	1 ± 0.37	1.01 ± 0.28	0.71 ± 0.29	0.79 ± 0.29	0.86 ± 0.44	1.34 ± 0.69	1.05 ± 0.42	1.12 ± 0.08	0.9 ± 0.21	1.03 ± 0.1	0.84 ± 0.25	0.255	0.015	0.038	0.283	0.695	0.658	0.403
rel. Xrcc1 mRNA		0.74 ± 0.43	1 ± 1.01	0.67 ± 0.31	0.83 ± 0.34	1.15 ± 0.52	0.43 ± 0.24	0.51 ± 0.1	1.11 ± 0.78	0.74 ± 0.44	0.8 ± 0.61	0.7 ± 0.11	1.04 ± 0.57	0.123	0.910	0.798	0.152	0.576	0.803	0.172

Supplementary Information Table 2. Oligonucleotide sequences (5'→3')

Gen, encoded protein	RefSeq-ID	Sequence 5'→3'	Modified melting temperature
Apex1, apurinic/aprimidinic endonuclease 1	NM_009687.2	CCCTCCAGATCAGAAAACCTC AGGCAGCTCTTCAGTTGAG	melting temperature 55°C
Aptx, aprataxin	NM_025545.4	CTGCGCTTCCGATTGGGCTA GTCACCTCTGCCGGCTTCCTG	
Atg7, autophagy related 7	NM_001253717.1	CAAGTTGCAGTTGCCCCCT GGGCAGACCAGCAGAGTAC	
Atp7b, ATPase, Cu ⁺⁺ transporting, beta polypeptide	NM_007511.2	CAGATGTCAAAGGCTCCCAATTCAG CCAATGACGATCCACACCACC	
Atr, ataxia telangiectasia and Rad3 related	NM_019864.1	CCGTCTCTGGAGCGGCATAC GGCAAGGAGCACTTGGGAGT	
Bax, BCL2-associated X protein	NM_007527.3	CGGGTGGCAGCTGACATGTTT CCAGCCACCCTGGTCTTGAT	
Bcl2, B cell leukemia/lymphoma 2	NM_009741.5	GGTGGGTGATGTGTGGAG CGCATGCTGGGGCCATATAGTT	
Blvrb, biliverdin reductase B	NM_144923	TGGCAACGACCTCAGTCCCA GTAGGAAGGCCGAGGTGCAG	
Ccs, copper chaperone for superoxide dismutase	NM_016892.3	GATGTGATTGCGCCAGCCT CACAGCCAACCTCTTCCCA	
Cdkn1a, cyclin-dependent kinase inhibitor 1A (P21)	NM_001111099.2	GACAGTGAGCAGTTGCGCC CTCAGACACCAGAGTGCAAGAC	melting temperature 55°C
Cdkn2a, cyclin dependent kinase inhibitor 2A	NM_009877.2	GGGTTTTCTTGGTGAAGTTGCTG TTGCCATCATCATCACTGGT	melting temperature 55°C
Ctcf, CCCTC-binding factor	NM_181322.3	CTGCAGCCACTGCGACAAGA GCCATCTGGACCAGCACAGTT	
Ctr1, solute carrier family 31, member 1	NM_175090.4	ACCATGCCACCTCACCACCA GCTCCAGCCATTTCTCCAGGT	
Cybrd1, cytochrome b reductase 1	NM_028593.2	CAGGGCATCGCCATCATCTGT GGTACTCAAACACAGCCACCAC	
Dio1, deiodinase, iodothyronine, type I	NM_007860.3	GGGATTTCAITCAAGGCAGCAGG TGTGGAGGGCAAAGTCATCTACGA	
Dmt1, solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	NM_001146161.1	CTCAGCCATCGCCATCAATCTC TTCCGCAAGCCATATTTGCCA	
Dnmt1, DNA methyltransferase (cytosine-5) 1	NM_001199432.1	GGAGTCACACACCGTTCCCG CACACTCGGGCCTTTGGT	
Ercc1, excision repair cross-complementing rodent repair deficiency, complementation group 1	NM_007948.2	GAACTTCGCCCTTCGTGTGC CAGGGTGCAGTCAGCCAAGA	
Ercc6, excision repair cross-complementing rodent repair deficiency, complementation group 6	NM_001081221.2	GGGACCACCACCATAGCGTCT GTTGGCACCGGTCAAGTTCA	
Fech, ferrochelatase	NM_007998.4	TCCAGAGGAGAAGAGGAGGAG GTACTGGACCAACCTTGGACTG	
Fpn, ferroportin, solute carrier family 40 (iron-regulated transporter), member 1	NM_016917.2	CTGGTGGTTTCAAGATGTCCGT AGCAGACAGTAAGGACCCATCCA	
Fth1, ferritin heavy polypeptide 1	NM_010239.2	CGCCGAAGACTACCACAGGA TTCTTCAGAGCCATCATCTCGG	
Gadd45a, growth arrest and DNA-damage-inducible 45 alpha	NM_007836.1	AGAAGACCCGAAAGGATGGACAC CACGGATGAGGGTGAAATGGAT	melting temperature 55°C
Gadd45g, growth arrest and DNA-damage-inducible 45 gamma	NM_011817.2	CGGGAAAGCACTGCACGAAC CACATTGTCAAGGTCCACATTAG	
Hamp, hepcidin antimicrobial peptide	NM_032541.1	AAGCAGGGCAGACATTGGCA TGCAACAGATAACCACACTGGGA	
Heph, hephaestin	NM_010417.2	CTCTTGCTCCATGGACCCAC ATCTGGGCCACTTCTCGCT	
Hmox1, heme oxygenase (decycling) 1	NM_010442.1	CCTGGTGCAGATACTGCC GAAGCTGAGAGTGAGGACCCA	
Hprt1, hypoxanthine guanine phosphoribosyl transferase	NM_013556.2	GCAGTCCCAGCGTCTGTG GGCTCCCATCTCCTTCAT	
Il1b, interleukin 1 beta	NM_008361.3	TTGAAGAAGAGCCATCCTCTGTG TTGTTCACTCGGAGCCTGTAGTG	
Lig1, ligase I	NM_001083188.2	CACCCCCAAAGTCCAGAAGCC GGGGGAGCTGCAGTTGAAGAC	
Lig3, ligase III	NM_010716.3	CCTCGGAAGTTCTCGGCTTTT CCGGAACTCTCTAGCAGACA	
Mdm2, transformed mouse 3T3 cell double minute 2	NM_001288586.2	CAGAGACGCCCTGCATCAG GAGAGCTCGTGCCTTCGTC	
Mecp2, methyl CpG binding protein 2	NM_010788.4	TCCATTATCCGTGACCGGGGA GGTCCAAGGAGGTGTCTCCCA	
Mt1, metallothionein 1	NM_013602.3	CTCCTGCAAGAAGAGCTGCTG GCACAGCAGTGCACCTTGTG	
Mt2, metallothionein 2	NM_008630.2	TCCTGTGCCTCCGATGGATC TTGCAGATGCAGCCCTGGGA	
Neil1, nei endonuclease VIII-like 1	NM_028347.3	GCTTGCCCTTTGCTTCGTAGA CACAGATGGCCGGTCAAAG	
Neil2, nei endonuclease like 2	NM_201610.2	CCCAGTGATTGAGCCACCTG GAACCGAGAGAGGGGATGGA	
Nqo1, NAD(P)H dehydrogenase, quinone 1	NM_008706.4	ATGTACGACAACGGTCTTTCCAG GATGCCACTCTGAATCGGCCA	
Nth1, nth (endonuclease III)-like 1	NM_008743.2	GATCGCTCGGAAGGTGTAG GTTCTGGGGCTCCCAACGG	
Ogg1, 8-oxoguanine DNA-glycosylase 1	NM_010957.4	GTGACTACGGCTGGCATCC AGGCTTGGTTGGCGAAGG	10 cycles melting temperature 55°C, followed by 45 cycles melting temperature 56°C
Parg, poly (ADP-ribose) glycohydrolase	NM_011960.3	CACACGACCCAGAACTTGA GTTGGCCCTCTGCTTCTCA	
Parp1, poly (ADP-ribose) polymerase family, member 1	NM_007415.3	GGCAGCCTGATGTTGAGGTG GCTACTCCGCTAAAAGTCCAC	melting temperature 55°C
Polb, polymerase beta	NM_011130.2	GCGCAGAGTCGAGTGGAGAC CCTTCTCGCTGGAAAGCTGG	
Rpl13a, ribosomal protein L13a	NM_009438.5	GTTCCGGCTGAAGCCTACCA TTCCGTAACCTCAAGATCTGCT	
Selenbp1, selenium binding protein 1	NM_009150.3	CAGGTATCCACAGGTTGCCCA ACGTAGATGCCGGAGGAGATGAG	
Selenop, selenoprotein P	NM_001042613.1	CTCATCTATGACAGATGTGGCCGT AAGACTCGTGAGATTGCAGTTCC	
Sepsecs, Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	NM_172490	TCTAGAGCAGGGCAAGTGTCCA AGCAACCAAAGCAGAGGCCA	
Sirt6, sirtuin 6	NM_181586.4	ACGCGGATAAGGGCAAGTG CTCCACACCTTGCCTTC	melting temperature 55°C
Slc48a1, Slc48a1, solute carrier family 48 (heme transporter), member 1	NM_026353.4	ATTGGCCATCACCCAGCATCAG CTGATGTCGCCAAAGTCAGCC	
Sult1b1, sulfotransferase family 1B, member 1	NM_019878.3	CTGCCACAGCAATGATGGA GCATCAAATTGCTCAGITTTGGGTC	
Trp53, transformation related protein 53	NM_001127233.1	CACAGTCGGATATCAGCCTCG CATGCAGTGAGGTGATGGCA	

Gen, encoded protein	RefSeq-ID	Sequence 5'→3'	Modified melting temperature
Txnrd1, thioredoxin reductase 1	NM_001042523.1	AGCAGCTAAGGAGGCAGCCA TTTCCAGCCATAGTTGCGCGAG	
Xrcc1, X-ray repair complementing defective repair in chinese hamster cells 1	NM_009532.5	CAGAGGCTGACCTGCCAATCC GTGATGACGAACTGGACCCGC	
Zip3, solute carrier family 39 (zinc transporter), member 3 (Slc39a3)	NM_134135	CTGGGGTACGCCGTTCTG GGGACGTGCTCTGTGTCCTT	
Zip5, solute carrier family 39 (metal ion transporter), member 5 (Slc39a5)	NM_028051	GGGCAGCCTCATGTTTACCA CCACATCAGCCGTCAGGAA	
Zip10, solute carrier family 39 (zinc transporter), member 10 (Slc39a10)	NM_172653	TGGCTTACATAGGAATGCTCATAGG TGCGAAGATCCAGAGTGTGATG	
Zip14, solute carrier family 39, member 14	NM_144808	GAGCCAACTGATAATCCATTGCT GTCAACGGCCACATTTTCAA	
Znt1, ZnT1, solute carrier family 30, member 1 (Slc30a1)	NM_009579	CACGACTTACCCATTGCTCAAG CTTTCACCAAGTGTGATATCGATT	
Znt6, solute carrier family 30 (zinc transporter), member 6 (Slc30a6)	NM_144798	TCCCAGGACTCAGCAGTATCTT GCCCCAGCAAGATCAATCAG	
Znt9, solute carrier family 30 (zinc transporter), member 9 (Slc30a9)	NM_178651	GGAAGCCTTGAAGCTCTTGCCA GGAACGTGGCTTTGTGTTTCCC	
Znt10, solute carrier family 30, member 10 (Slc30a10)	NM_001033286	ACTGGCAGTGCTACATTGACCC CAGCTGGCTCATCAGCTCTTC	