

SUPPLEMENTARY TABLE S2. GENE EXPRESSION PROFILE OF OXIDATIVE STRESS-RELATED GENES IN NAI-TREATED NOD.H2^{h4} AND CBA/J THYROCYTES

RefSeq	Symbol	Description	Fold change (+Nai/-Nai)	
			CBA/J	NOD.H2 ^{h4}
NM_009654	Alb	Albumin	-2.43 ^c	-3.31 ^b
NM_028717	Als2	Amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	-1.42	-1.19
NM_009676	Aox1	Aldehyde oxidase 1	-1.34	1.37
NM_007462	Apc	Adenomatosis polyposis coli	1.04	1.02
NM_009696	ApoE	Apolipoprotein E	1.80	1.34
NM_019864	Atr	Ataxia telangiectasia and rad3 related	1.09	1.24
NM_009804	Cat	Catalase	1.42	1.14
NM_013653	Ccl5	Chemokine (C-C motif) ligand 5	2.26	1.17
NM_016892	Ccs	Copper chaperone for superoxide dismutase	1.38	-1.18
NM_007798	Ctsb	Cathepsin B	1.23	-1.27
NM_007806	Cyba	Cytochrome b-245, alpha polypeptide	1.29	1.08
NM_030206	Cygb	Cytoglobin	1.47	-2.19
NM_001039520	Dnm2	Dynamamin 2	-1.01	-1.82
NM_001099297	Duox1	Dual oxidase 1	1.48	-1.17
NM_153068	Ehd2	EH-domain containing 2	1.28	-1.77
NM_007946	Epx	Eosinophil peroxidase	-1.91 ^b	-1.07 ^b
NM_007949	Ercc2	Excision repair cross-complementing rodent repair deficiency, complementation group 2	-1.11	-1.60
NM_001081221	Ercc6	Excision repair cross-complementing rodent repair deficiency, complementation group 6	1.25	-1.18
NM_007985	Fancc	Fanconi anemia, complementation group C	-1.09	-1.20
NM_018881	Fmo2	Flavin containing monooxygenase 2	2.07	-1.13
NM_010239	Fth1	Ferritin heavy chain 1	2.05	-1.02
NM_010295	Gclc	Glutamate-cysteine ligase, catalytic subunit	1.47	1.22
NM_008129	Gclm	Glutamate-cysteine ligase, modifier subunit	1.69	1.28
NM_008160	Gpx1	Glutathione peroxidase 1	1.76	-1.07
NM_030677	Gpx2	Glutathione peroxidase 2	3.14	2.55
NM_008161	Gpx3	Glutathione peroxidase 3	1.64	-1.56
NM_008162	Gpx4	Glutathione peroxidase 4	2.03	-1.04
NM_010343	Gpx5	Glutathione peroxidase 5	-1.07 ^b	2.34 ^b
NM_145451	Gpx6	Glutathione peroxidase 6	1.74 ^b	2.57 ^b
NM_024198	Gpx7	Glutathione peroxidase 7	2.64	-1.04
NM_010344	Gsr	Glutathione reductase	1.69	-1.06
NM_008180	Gss	Glutathione synthetase	1.48	-1.05
NM_029555	Gstk1	Glutathione S-transferase kappa 1	1.72	1.12
NM_013541	Gstp1	Glutathione S-transferase, pi 1	1.81	1.08
NM_010442	Hmox1	Heme oxygenase (decycling) 1	1.99	1.20
NM_010479	Hspa1a	Heat shock protein 1A	1.96	1.02
NM_010497	Idh1	Isocitrate dehydrogenase 1 (NADP+), soluble	1.86	1.05
NM_026298	Ift172	Intraflagellar transport 172 homolog (Chlamydomonas)	1.03	-1.33
NM_001009940	Il19	Interleukin 19	-1.03 ^b	1.02 ^b
NM_016971	Il22	Interleukin 22	2.16 ^b	-1.22
NM_008473	Krt1	Keratin 1	1.09 ^a	-3.64 ^b
NM_080420	Lpo	Lactoperoxidase	1.02 ^a	2.57 ^b
NM_013593	Mb	Myoglobin	2.01	-1.49
NM_010824	Mpo	Myeloperoxidase	3.20	-1.40
NM_010876	Ncf1	Neutrophil cytosolic factor 1	1.28	-1.77
NM_010877	Ncf2	Neutrophil cytosolic factor 2	2.96	-1.03
NM_022414	Ngb	Neuroglobin	1.38	-1.94
NM_010927	Nos2	Nitric oxide synthase 2, inducible	-1.05 ^a	-5.40 ^a
NM_172203	Nox1	NADPH oxidase 1	2.30 ^b	1.26 ^b
NM_015760	Nox4	NADPH oxidase 4	1.92	-1.54
NM_172204	Noxa1	NADPH oxidase activator 1	4.11 ^a	2.97 ^a
NM_027988	Noxo1	NADPH oxidase organizer 1	1.42	2.09
NM_008706	Nqo1	NAD(P)H dehydrogenase, quinone 1	2.89	2.37
NM_020569	Park7	Parkinson disease (autosomal recessive, early onset) 7	2.49	-1.03
NM_011034	Prdx1	Peroxiredoxin 1	2.97	1.12
NM_011563	Prdx2	Peroxiredoxin 2	2.43	-1.03
NM_007452	Prdx3	Peroxiredoxin 3	1.82	1.02

(continued)

SUPPLEMENTARY TABLE S2. (CONTINUED)

RefSeq	Symbol	Description	Fold change (+ NaI/- NaI)	
			CBA/J	NOD.H2 ^{h4}
NM_016764	Prdx4	Peroxiredoxin 4	1.91	-1.16
NM_012021	Prdx5	Peroxiredoxin 5	2.27	-1.03
NM_007453	Prdx6	Peroxiredoxin 6	1.91	-1.17
NM_011170	Prnp	Prion protein	1.48	-1.21
NM_011186	Psmb5	Proteasome (prosome, macropain) subunit, beta type 5	2.18	1.04
NM_008969	Ptgs1	Prostaglandin-endoperoxide synthase 1	1.42	-1.31
NM_011198	Ptgs2	Prostaglandin-endoperoxide synthase 2	1.37	-1.30
NM_009020	Rag2	Recombination activating gene 2	1.08	1.91
NM_058214	Recq4	RecQ protein-like 4	1.53	-1.55
NM_009127	Scd1	Stearoyl-Coenzyme A desaturase 1	1.92	-1.12
NM_173052	Serpinb1b	Serine (or cysteine) peptidase inhibitor, clade B, member 1b	2.87	1.08
NM_134086	Slc38a1	Solute carrier family 38, member 1	1.19	-1.39
NM_011434	Sod1	Superoxide dismutase 1, soluble	3.57	1.02
NM_013671	Sod2	Superoxide dismutase 2, mitochondrial	1.38	-1.35
NM_011435	Sod3	Superoxide dismutase 3, extracellular	1.20	-1.56
NM_011018	Sqstm1	Sequestosome 1	1.18	1.20
NM_029688	Srxn1	Sulfiredoxin 1 homolog (S. cerevisiae)	1.22	1.04
NM_009417	Tpo	Thyroid peroxidase	5.77	1.65
NM_011660	Txn1	Thioredoxin 1	2.13	1.40
NM_023719	Txnip	Thioredoxin interacting protein	2.62	1.40
NM_015762	Txnrd1	Thioredoxin reductase 1	1.63	-1.26
NM_013711	Txnrd2	Thioredoxin reductase 2	1.93	-1.09
NM_153162	Txnrd3	Thioredoxin reductase 3	1.41	-1.21
NM_011671	Ucp2	Uncoupling protein 2 (mitochondrial, proton carrier)	2.01	-1.24
NM_009464	Ucp3	Uncoupling protein 3 (mitochondrial, proton carrier)	2.15	-1.67
NM_011701	Vim	Vimentin	1.88	-1.21
NM_011728	Xpa	Xeroderma pigmentosum, complementation group A	1.51	-1.00
NM_007393	Actb	Actin, beta	-1.10	-1.36
NM_009735	B2m	Beta-2 microglobulin	-1.19	1.31
NM_008084	Gapdh	Glyceraldehyde-3-phosphate dehydrogenase	1.27	-1.16
NM_010368	Gusb	Glucuronidase, beta	1.03	1.21
NM_008302	Hsp90ab1	Heat shock protein 90 alpha (cytosolic), class B member 1	1.00	-1.00

For certain indicated genes expression analysis was not made possible due to: (a) nonspecific amplification of the product as indicated by the melting curve analysis; (b) a high threshold cycle (30–35 cycles) in both control and test samples; and (c) an undetermined threshold cycle i.e. greater than the defined cutoff (35 cycles) in both control and test samples.