

## Supplementary Data

SUPPLEMENTARY TABLE S1. GENE EXPRESSION PROFILE OF APOPTOSIS-RELATED GENES  
IN IODIDE-TREATED NOD.H2<sup>h4</sup> AND CBA/J THYROCYTES

RefSeq	Symbol	Description	Fold change (+NaI/-NaI)	
			CBA/J	NOD.H2 <sup>h4</sup>
NM_009594	Abl1	C-abl oncogene 1, nonreceptor tyrosine kinase	-2.07	-1.47
NM_012019	Aifm1	Apoptosis-inducing factor, mitochondrion-associated 1	1.49	1.07
NM_009652	Akt1	Thymoma viral proto-oncogene 1	-1.69	-1.70
NM_009673	Anxa5	Annexin A5	-1.18	1.23
NM_009684	Apaf1	Apoptotic peptidase activating factor 1	-1.82	-1.29
NM_007466	Api5	Apoptosis inhibitor 5	-1.38	-1.04
NM_030693	Atf5	Activating transcription factor 5	-2.26	-1.84
NM_007522	Bad	BCL2-associated agonist of cell death	1.18	1.10
NM_009736	Bag1	Bcl2-associated athanogene 1	1.18	-1.01
NM_013863	Bag3	Bcl2-associated athanogene 3	-1.11	-1.16
NM_007523	Bak1	BCL2-antagonist/killer 1	-1.33	-1.14
NM_007527	Bax	Bcl2-associated X protein	-1.28	1.03
NM_009740	Bcl10	B-cell leukemia/lymphoma 10	-1.55	-1.18
NM_009741	Bcl2	B-cell leukemia/lymphoma 2	-1.57	1.72
NM_009742	Bcl2a1a	B-cell leukemia/lymphoma 2 related protein A1a	-1.29 <sup>a</sup>	1.12
NM_009743	Bcl2l1	Bcl2-like 1	-1.61	-1.20
NM_013479	Bcl2l10	Bcl2-like 10	-2.15	-1.51
NM_009754	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	-1.37	1.15
NM_007537	Bcl2l2	Bcl2-like 2	-1.73	-1.38
NM_007544	Bid	BH3 interacting domain death agonist	-1.49	1.31
NM_007465	Birc2	Baculoviral IAP repeat-containing 2	-1.39	1.27
NM_007464	Birc3	Baculoviral IAP repeat-containing 3	-1.46	1.47
NM_009689	Birc5	Baculoviral IAP repeat-containing 5	1.43	1.36
NM_016787	Bnip2	BCL2/adenovirus E1B interacting protein 2	-1.27	-1.03
NM_009760	Bnip3	BCL2/adenovirus E1B interacting protein 3	-1.16	1.27
NM_009761	Bnip3l	BCL2/adenovirus E1B interacting protein 3-like	-1.38	1.15
NM_016778	Bok	BCL2-related ovarian killer protein	-4.06	-527.93
NM_130859	Card10	Caspase recruitment domain family, member 10	-3.80	-1.07
NM_009807	Casp1	Caspase 1	-1.50	-1.16
NM_009808	Casp12	Caspase 12	-1.29	1.05
NM_009809	Casp14	Caspase 14	1.69	-2.19 <sup>a</sup>
NM_007610	Casp2	Caspase 2	-1.18	-1.08
NM_009810	Casp3	Caspase 3	-1.55	-1.21
NM_007609	Casp4	Caspase 4, apoptosis-related cysteine peptidase	-1.23	1.27
NM_009811	Casp6	Caspase 6	-1.20	1.33
NM_007611	Casp7	Caspase 7	-1.22	1.03
NM_009812	Casp8	Caspase 8	-1.33	1.45
NM_015733	Casp9	Caspase 9	-2.47	1.01
NM_011611	Cd40	CD40 antigen	1.12	1.99
NM_011616	Cd40lg	CD40 ligand	-3.68 <sup>c</sup>	-1.92 <sup>c</sup>
NM_011617	Cd70	CD70 antigen	-1.58 <sup>b</sup>	-1.18
NM_009805	Cflar	CASP8 and FADD-like apoptosis regulator	-1.68	-1.25
NM_007702	Cidea	Cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	1.19	1.76
NM_009894	Cideb	Cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	1.07	1.19
NM_009950	Cradd	CASP2 and RIPK1 domain containing adaptor with death domain	-1.43	1.24
NM_010015	Dad1	Defender against cell death 1	1.31	1.41
NM_029653	Dapk1	Death associated protein kinase 1	-1.69	-1.00
NM_010044	Dffa	DNA fragmentation factor, alpha subunit	-1.74	-1.07
NM_007859	Dffb	DNA fragmentation factor, beta subunit	-2.13	1.61
NM_023232	Diablo	Diablo homolog (Drosophila)	-1.03	1.16
NM_010175	Fadd	Fas (TNFRSF6)-associated via death domain	-1.81	-1.08

(continued)

SUPPLEMENTARY TABLE S1. (CONTINUED)

RefSeq	Symbol	Description	Fold change (+NaI/-NaI)	
			CBA/J	NOD.H2 <sup>b4</sup>
NM_007987	Fas	Fas (TNF receptor superfamily member 6)	-1.61	1.09
NM_010177	FasL	Fas ligand (TNF superfamily, member 6)	-1.44 <sup>b</sup>	-1.92 <sup>c</sup>
NM_007836	Gadd45a	Growth arrest and DNA-damage-inducible 45 alpha	-1.57	1.09
NM_010513	Igf1r	Insulin-like growth factor I receptor	-1.74	-1.17
NM_010548	Il10	Interleukin 10	-2.67	-1.83
NM_010712	Lhx4	LIM homeobox protein 4	-3.68 <sup>c</sup>	-3.48
NM_010736	Ltbr	Lymphotoxin B receptor	-1.94	-1.27
NM_011949	Mapk1	Mitogen-activated protein kinase 1	-1.35	1.03
NM_008562	Mcl1	Myeloid cell leukemia sequence 1	-1.83	-1.46
NM_008670	Naip1	NLR family, apoptosis inhibitory protein 1	-17.00 <sup>b</sup>	-1.67
NM_010872	Naip2	NLR family, apoptosis inhibitory protein 2	1.27	1.02
NM_008689	Nfkb1	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1, p105	-1.55	1.02
NM_080637	Nme5	Nonmetastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	-1.43	1.79
NM_172729	Nod1	Nucleotide-binding oligomerization domain containing 1	-1.22	-1.08
NM_030152	Nol3	Nucleolar protein 3 (apoptosis repressor with CARD domain)	1.19	1.04
NM_011130	Polb	Polymerase (DNA directed), beta	-1.16	1.02
NM_011563	Prdx2	Peroxiredoxin 2	1.08	1.20
NM_023258	Pycard	PYD and CARD domain containing	1.02	1.31
NM_009068	Ripk1	Receptor (TNFRSF)-interacting serine-threonine kinase 1	-2.11	-1.09
NM_013693	Tnf	Tumor necrosis factor	1.23	-1.18
NM_020275	Tnfrsf10b	Tumor necrosis factor receptor superfamily, member 10b	-1.59	1.14
NM_008764	Tnfrsf11b	Tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	-1.76	-1.26
NM_011609	Tnfrsf1a	Tumor necrosis factor receptor superfamily, member 1a	-1.34	-1.24
NM_009425	Tnfsf10	Tumor necrosis factor (ligand) superfamily, member 10	2.36	1.22
NM_011614	Tnfsf12	Tumor necrosis factor (ligand) superfamily, member 12	-1.22	1.08
NM_009421	Traf1	Tnf receptor-associated factor 1	1.34	1.10
NM_009422	Traf2	Tnf receptor-associated factor 2	-1.43	1.18
NM_011632	Traf3	Tnf receptor-associated factor 3	-1.63	-1.20
NM_011640	Trp53	Transformation related protein 53	-1.26	1.12
NM_173378	Trp53bp2	Transformation related protein 53 binding protein 2	-1.51	1.04
NM_011641	Trp63	Transformation related protein 63	-1.62	1.57
NM_011642	Trp73	Transformation related protein 73	-2.10 <sup>a</sup>	1.06
NM_009688	Xiap	X-linked inhibitor of apoptosis	-1.62	-1.16
NM_007393	Actb	Actin, beta	-1.22	-1.36
NM_009735	B2m	Beta-2 microglobulin	1.56	1.41
NM_008084	Gapdh	Glyceraldehyde-3-phosphate dehydrogenase	1.03	-1.33
NM_010368	Gusb	Glucuronidase, beta	-1.14	1.12
NM_008302	Hsp90ab1	Heat shock protein 90 alpha (cytosolic), class B member 1	-1.15	1.14

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, that is, greater than the defined cutoff (35 cycles) in both control and test samples.