

## SUPPLEMENTARY INFORMATION

Figure S1. Sequence logos created from AREs in different species. The differences may reflect species diversity in response to oxidants. Sequence logo visualizes contributions of individual positions and individual nucleotides to the overall ARE motif. Generated by the WebLogo program (<http://weblogo.berkeley.edu>). The height of each letter is proportional to its frequency, and the height of the entire stack is adjusted to signify the ‘information content’ (measured in bits) of the sequences at that position. The logo displays both significant residues and subtle sequence patterns.

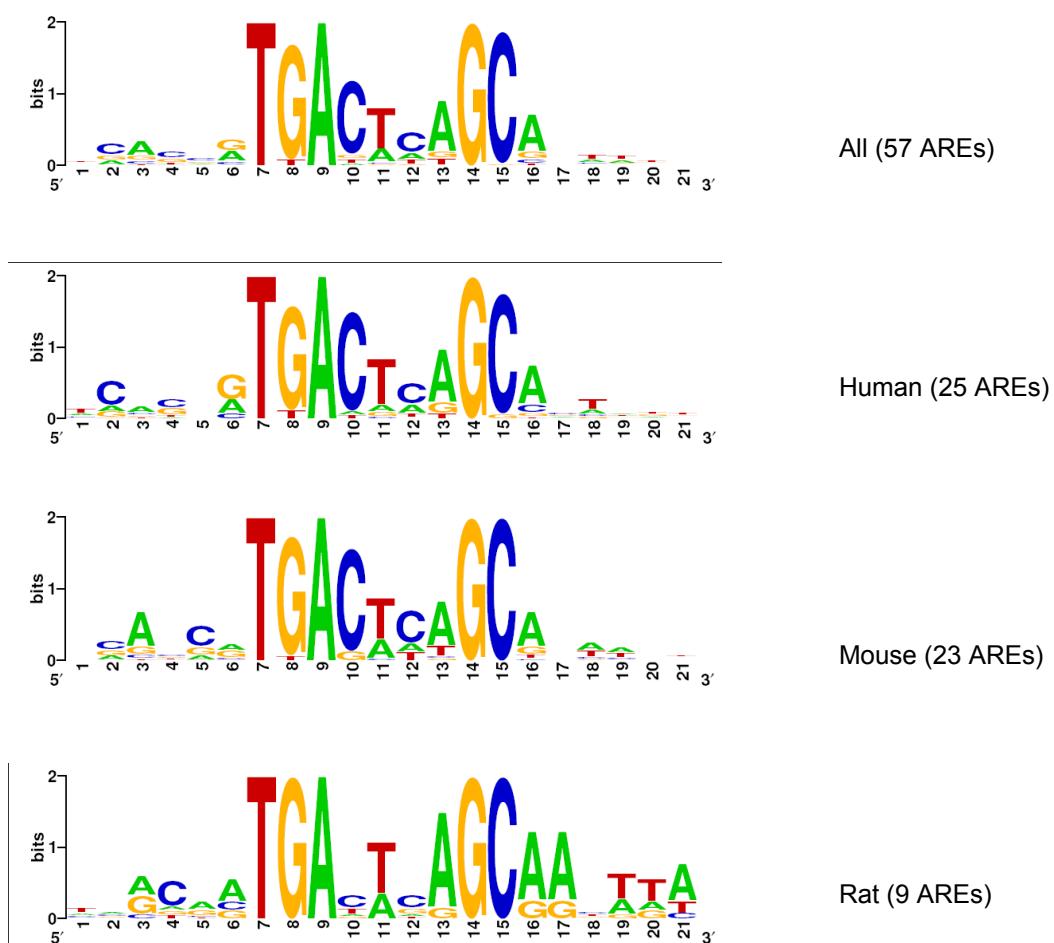


Table S1. A set of known antioxidant response elements (AREs, also known as NRF2 binding sites). They were validated by experimental methods, such as deletion/mutagenesis (DM), reporter gene assay (RGA), nuclease protection assay (NPA), electrophoretic mobility shift assay (EMSA), and chromatin immunoprecipitation (CHIP). The PWM scores were calculated using formulae described by Wasserman and Sandelin (1). References refer to the publications describing the functional validation of AREs (listed at the end of supplement).

Species	Gene	Sequence	PWM score	validation	References
	<b>ARE consensus</b>	<b>RTKAYnnnGCR</b>			(2)
human	<i>ABCC1</i>	TCTGTGTGACTCAGCTTGGAA	12.9	NPA, EMSA, RGA	(3)
human	<i>AKR1C1</i>	TCAGGGTGACTCAGCAGCTTG	20.2	DM, EMSA, RGA, CHIP	(4)
human	<i>ETS1</i>	AGCGGGTGACCAAGCCCTCAA	8.8	DM, EMSA, RGA	(5)
human	<i>FTH1</i>	CCTCCATGACAAAGCACTTT	17.3	DM, EMSA, RGA, CHIP	(6)
human	<i>FTH1</i>	CCACCGTGACTCAGCACTCCG	19.6	DM, EMSA, RGA, CHIP	(6)
human	<i>FTL</i>	TCAGCATGACTCAGCAGTCGC	20.0	DM, RGA	(7)
human	<i>GCLC</i>	TCCCCGTGACTCAGCGTTTG	18.9	DM, EMSA, RGA	(8, 9)
human	<i>GCLM</i>	TAACGGTTACGAAGCACTTTC	12.2	DM, EMSA, RGA	(2, 10)
human	<i>GCLM</i>	AGACAATGACTAACGAGAAAT	17.6	DM, EMSA, RGA	(2, 10)
human	<i>GNAT2</i>	AGCCTGTGACTGGGCCGGGGC	6.4	DM, EMSA, RGA, CHIP	(11)
human	<i>GPX2</i>	CCAGGATGACTTAGCAAAAC	17.9	DM, EMSA, RGA, CHIP	(12)
human	<i>GSTP1</i>	GCGCCGTGACTCAGCACTGGG	18.8	DM, EMSA, RGA	(13)
human	<i>HBB   HBE1</i>	TCATCATGACTCAGCATTGCT	18.6	NPA, EMSA, CHIP	(14, 15)
human	<i>HMBS</i>	CTCCAGTGACTCAGCACAGGT	15.4	DM, EMSA, RGA	(16)
human	<i>NQO1</i>	TCACAGTGACTCAGCAGAACATC	21.3	DM, EMSA, RGA	(17)
human	<i>NQO2</i>	AGGTGGTGATGTTGCATCACA	6.7	DM, EMSA, RGA, CHIP	(18)
human	<i>S100A6</i>	GACACGTGACTCGGCAAGGGG	12.0	DM, EMSA, RGA	(19)
human	<i>SAT</i>	CCGCTATGACTAACGCGCTAGT	15.5	DM, NPA, EMSA, RGA	(20)
human	<i>SPTA1</i>	ACTGGGTGACTCAGCAGTTT	18.9	DM, NPA, EMSA, RGA	(21)
human	<i>TBXAS1</i>	AAGGAATGAATCAGCAACTTT	13.8	DM, EMSA, RGA, CHIP	(22)
human	<i>TXN</i>	TCACCGTTACTCAGCACTTG	19.3	DM, EMSA, RGA	(23)
human	<i>TXNRD1</i>	TCATTCTGACTCTGGCAGTTA	8.0	DM, EMSA, RGA	(24)
human	<i>TXNRD1</i>	TCAGAATGACAAAGCAGAAAT	17.4	DM, EMSA, RGA	(24)
human	<i>UGT1A6</i>	GAAAGCTGACACGGCCATAGT	10.7	DM, EMSA, RGA	(25)
human	<i>UGT1A6</i>	TCTGTCTGACTTGGAAAAAT	12.1	DM, EMSA, RGA	(25)
mouse	<i>Abcc2</i>	CTGGGATGACATAGCATTGAT	11.5	DM, EMSA, RGA	(26)
mouse	<i>Akr1b3</i>	GGAGCATGACCCAGCAGAAGG	15.5	DM, EMSA, RGA	(27)
mouse	<i>Fth1</i>	CCTCCATGACAAAGCACTTT	17.3	DM, EMSA, RGA	(28, 29)
mouse	<i>Fth1</i>	CCACCGTGACTCAGCATTCTG	20.5	DM, EMSA, RGA	(28, 29)
mouse	<i>Ft11</i>	TCAGCGTGACTCAGCAGAACT	20.7	DM, EMSA, RGA	(28, 30)
mouse	<i>Gclc</i>	TCACCGTGACTCAGCACTCTG	21.6	DM, EMSA, RGA	(31)
mouse	<i>Gclm</i>	AGACAATGACTAACGAGAAAC	16.9	DM, EMSA, RGA	(31)
mouse	<i>Gsta1</i>	TGGAAATGACATTGCTAATGG	7.7	DM, EMSA, RGA	(30)
mouse	<i>Gsta1</i>	TAATGGTGACAAAGCAACTTT	16.2	DM, EMSA, RGA	(30)
mouse	<i>Gsta3</i>	CAGGCATGACATTGCATTTT	12.9	DM, EMSA, RGA	(32)
mouse	<i>Gstpl</i>	ACGTGTTGAGTCAGCATCCGG	8.6	DM, NPA, EMSA, RGA	(33)

mouse	<i>Hmox1</i>	AGAGGGTGACTCAGCAAAATC	19.3	DM, RGA	(34)
mouse	<i>Hmox1</i>	CAACCATGACACAGCATAAAA	17.7	DM, RGA	(34)
mouse	<i>Hmox1</i>	GGACCTTGACTCAGCAGAAAA	16.6	DM, NPA, RGA	(35)
mouse	<i>Hmox1</i>	GGACCGTGACTCAGCGTCACA	15.0	DM, NPA, RGA	(35)
mouse	<i>Hmox1</i>	GAACCATGACTCAGCGAAAAC	17.7	DM, NPA, RGA	(35)
mouse	<i>Mafg</i>	TCATGCTGACTCAGCGGATCG	15.3	EMSA, RGA, CHIP	(36)
mouse	<i>Mt1</i>	GGCGCGTGACTATGCGTGGGC	8.3	DM, RGA	(37)
mouse	<i>Nfe2l2</i>	CCCACCTGACTCCGCCATGCC	8.6	DM, EMSA, RGA, CHIP	(38)
mouse	<i>Nqo1</i>	TCACAGTGAGTCGGCAAATT	16.4	DM, EMSA, RGA, CHIP	(39)
mouse	<i>Pparg</i>	TCATTGTGACATAGCACTTAT	16.2	DM, EMSA	(40)
mouse	<i>Slc7a11</i>	CCAACATTACTCAGCTTTTT	14.1	DM, RGA	(41)
mouse	<i>Trp53</i>	GAATCCTGACTCTGCAAGTCC	12.8	DM, EMSA, RGA	(42)
rat	<i>Adra2b</i>	GAGCGATGACTCAGCAGTTA	18.6	DM, NPA, EMSA, RGA	(43)
rat	<i>Akr7a3</i>	ATGCCCTGAGTGAGCGAGTGA	6.5	DM, RGA	(44)
rat	<i>Akr7a3</i>	TGGAAATGATTTCAGCAGTTA	13.6	DM, RGA	(44)
rat	<i>Ggt1</i>	CCACAATGACACAGCAAGAAA	18.0	DM, EMSA, RGA, CHIP	(45)
rat	<i>Gsta2</i>	TAATGGTGACAAAGCAACTTT	16.2	DM, EMSA, RGA	(46)
rat	<i>Gsta5</i>	CACGGCTGACAGAGCGATGGA	8.9	DM, EMSA, RGA	(47)
rat	<i>Gstp1</i>	TCACTATGATTTCAGCAACAAA	15.7	DM, NPA, EMSA, RGA	(48, 49)
rat	<i>Nqo1</i>	TCACAGTGACTTGGCAAATC	17.1	DM, EMSA, RGA	(49)
rat	<i>Tbxas1</i>	AGGCAATGAATCAGCAACTTT	14.4	DM, EMSA, RGA	(50)

Table S2. A list of human genes that have positionally conserved AREs (phylogenetic footprints) in upstream 5-kb regions. The conserved AREs were discovered by examining multiple sequence alignment of the upstream 5-kb regions from orthologous human, mouse and rat genes. An ARE is considered to be “highly conserved” (or HC) if all sequences in the alignment have PWM scores that are above the threshold (defined as the minimum PWM score among all known AREs in Table S1), otherwise, the binding site is “conserved” (or C) if any of mouse or rat sequence has a PWM lower than the threshold. The numbers in the corresponding columns refer to the number of AREs in that gene that are considered conserved or highly conserved.

Symbol	Conservation			Gene description
	HC	C	ARE gene	
<i>AKR1B1</i>	1	0	yes	aldo-keto reductase family 1, member B1 (aldose reductase)
<i>ETS1</i>	1	0	yes	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)
<i>FTH1</i>	2	1	yes	ferritin, heavy polypeptide 1
<i>FTL</i>	1	1	yes	ferritin, light polypeptide
<i>GCLC</i>	1	1	yes	glutamate-cysteine ligase, catalytic subunit
<i>GCLM</i>	1	0	yes	glutamate-cysteine ligase, modifier subunit
<i>GSTP1</i>	1	1	yes	glutathione S-transferase pi
<i>HMBS</i>	1	0	yes	hydroxymethylbilane synthase
<i>HMOX1</i>	1	2	yes	heme oxygenase (decycling) 1
<i>MAFG</i>	2	0	yes	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)
<i>NOS2A</i>	1	0	yes	nitric oxide synthase 2A (inducible, hepatocytes)
<i>NQO1</i>	1	0	yes	NAD(P)H dehydrogenase, quinone 1
<i>SPTA1</i>	1	0	yes	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)
<i>TXN</i>	1	0	yes	thioredoxin
<i>TXNRD1</i>	1	1	yes	thioredoxin reductase 1
<i>ABCB8</i>	1	1		ATP-binding cassette, sub-family B (MDR/TAP), member 8
<i>ABCF3</i>	1	2		ATP-binding cassette, sub-family F (GCN20), member 3
<i>ABCG5</i>	1	0		ATP-binding cassette, sub-family G (WHITE), member 5 (sterolin 1)
<i>ACOT8</i>	1	0		acyl-CoA thioesterase 8
<i>ADRM1</i>	1	0		adhesion regulating molecule 1
<i>AGER</i>	1	1		advanced glycosylation end product-specific receptor
<i>AGPAT1</i>	1	2		1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)
<i>AKT3</i>	1	1		v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)
<i>ALDH3A1</i>	1	0		aldehyde dehydrogenase 3 family, member A1
<i>ALG8</i>	1	0		asparagine-linked glycosylation 8 homolog (S. cerevisiae, alpha-1,3-glucosyltransferase)
<i>AMH</i>	1	1		anti-Mullerian hormone
<i>AMIGO3</i>	2	1		adhesion molecule with Ig-like domain 3
<i>ANKRD1</i>	1	1		ankyrin repeat domain 1 (cardiac muscle)
<i>APEXI</i>	1	0		APEX nuclelease (multifunctional DNA repair enzyme) 1
<i>APH1A</i>	1	0		anterior pharynx defective 1 homolog A (C. elegans)
<i>ARF5</i>	2	0		ADP-ribosylation factor 5
<i>ASPA</i>	2	0		aspartoacylase (Canavan disease)
<i>ATP1A3</i>	1	0		ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, alpha 3 polypeptide
<i>ATP1B1</i>	2	2		ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 1 polypeptide
<i>ATP1B4</i>	2	3		ATPase, (Na <sup>+</sup> )/K <sup>+</sup> transporting, beta 4 polypeptide
<i>ATP5I</i>	1	0		ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit E

<i>ATP6V0D1</i>	1	1	ATPase, H <sup>+</sup> transporting, lysosomal 38kDa, V0 subunit d1
<i>BAIAP2L1</i>	1	0	BAI1-associated protein 2-like 1
<i>BARHL2</i>	2	2	BarH-like 2 (Drosophila)
<i>BAT4</i>	1	0	HLA-B associated transcript 4
<i>BCAP29</i>	1	0	B-cell receptor-associated protein 29
<i>BCAP31</i>	2	1	B-cell receptor-associated protein 31
<i>BCL10</i>	1	0	B-cell CLL/lymphoma 10
<i>BGN</i>	1	1	biglycan
<i>BSCL2</i>	2	1	Bernardinelli-Seip congenital lipodystrophy 2 (seipin)
<i>BZW2</i>	1	0	basic leucine zipper and W2 domains 2
<i>CACNAIF</i>	1	0	calcium channel, voltage-dependent, alpha 1F subunit
<i>CACNA2D3</i>	1	0	calcium channel, voltage-dependent, alpha 2/delta 3 subunit
<i>CACNG2</i>	2	0	calcium channel, voltage-dependent, gamma subunit 2
<i>CALCR</i>	0	1	calcitonin receptor
<i>CAPN6</i>	1	1	calpain 6
<i>CART1</i>	1	2	cartilage paired-class homeoprotein 1
<i>CAT</i>	0	1	catalase
<i>CBX3</i>	1	2	chromobox homolog 3 (HP1 gamma homolog, Drosophila)
<i>CCDC51</i>	1	1	coiled-coil domain containing 51
<i>CD276</i>	1	1	CD276 molecule
<i>CD4</i>	1	1	CD4 molecule
<i>CD68</i>	2	0	CD68 molecule
<i>CD69</i>	1	0	CD69 molecule
<i>CDC42SE1</i>	2	0	CDC42 small effector 1
<i>CDH8</i>	1	1	cadherin 8, type 2
<i>CDK5</i>	1	0	cyclin-dependent kinase 5
<i>CDON</i>	1	0	Cdon homolog (mouse)
<i>CFB</i>	2	0	complement factor B
<i>CHMP5</i>	3	0	chromatin modifying protein 5
<i>CHP</i>	1	1	calcium binding protein P22
<i>CHRM2</i>	1	2	cholinergic receptor, muscarinic 2
<i>CHRNA4</i>	1	0	cholinergic receptor, nicotinic, alpha 4
<i>CHRNBI</i>	1	2	cholinergic receptor, nicotinic, beta 1 (muscle)
<i>CIRBP</i>	2	0	cold inducible RNA binding protein
<i>CITED2</i>	1	0	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
<i>CLCF1</i>	3	0	cardiotrophin-like cytokine factor 1
<i>CLN3</i>	1	3	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)
<i>CNIH2</i>	1	0	cornichon homolog 2 (Drosophila)
<i>CNKSР3</i>	1	1	CNKSР family member 3
<i>CNOT6</i>	1	1	CCR4-NOT transcription complex, subunit 6
<i>CNTF</i>	2	0	ciliary neurotrophic factor
<i>CNTN6</i>	1	0	contactin 6
<i>CNTNAP1</i>	1	0	contactin associated protein 1
<i>COL11A2</i>	1	0	collagen, type XI, alpha 2
<i>CPA2</i>	1	0	carboxypeptidase A2 (pancreatic)
<i>CPB1</i>	1	0	carboxypeptidase B1 (tissue)
<i>CPB2</i>	1	0	carboxypeptidase B2 (plasma, carboxypeptidase U)
<i>CRAT</i>	1	1	carnitine acetyltransferase
<i>CRBN</i>	1	0	cereblon
<i>CREBL1</i>	1	2	cAMP responsive element binding protein-like 1
<i>CRY2</i>	1	2	cryptochrome 2 (photolyase-like)
<i>CRYBA2</i>	3	1	crystallin, beta A2
<i>CSAD</i>	1	2	cysteine sulfenic acid decarboxylase
<i>CSF3</i>	1	0	colony stimulating factor 3 (granulocyte)

<i>CTGF</i>	1	1	connective tissue growth factor
<i>CUTA</i>	1	3	cutA divalent cation tolerance homolog (E. coli)
<i>CXCL10</i>	1	0	chemokine (C-X-C motif) ligand 10
<i>CXCR3</i>	1	0	chemokine (C-X-C motif) receptor 3
<i>CYP3A5</i>	0	1	cytochrome P450, family 3, subfamily A, polypeptide 5
<i>DALRD3</i>	2	2	DALR anticodon binding domain containing 3
<i>DBH</i>	1	0	dopamine beta-hydroxylase (dopamine beta-monooxygenase)
<i>DCAKD</i>	1	1	dephospho-CoA kinase domain containing
<i>DDIT4L</i>	1	0	DNA-damage-inducible transcript 4-like
<i>DDX25</i>	1	0	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25
<i>DGAT1</i>	1	0	diacylglycerol O-acyltransferase homolog 1 (mouse)
<i>DGKG</i>	1	0	diacylglycerol kinase, gamma 90kDa
<i>DHRS3</i>	1	2	dehydrogenase/reductase (SDR family) member 3
<i>DIO2</i>	1	0	deiodinase, iodothyronine, type II
<i>DIXDC1</i>	1	0	DIX domain containing 1
<i>DLL1</i>	2	0	delta-like 1 ( <i>Drosophila</i> )
<i>DNAJC14</i>	1	2	DnaJ (Hsp40) homolog, subfamily C, member 14
<i>DNAJC4</i>	1	0	DnaJ (Hsp40) homolog, subfamily C, member 4
<i>DNAL4</i>	1	0	dynein, axonemal, light chain 4
<i>DPYSL3</i>	1	0	dihydropyrimidinase-like 3
<i>DRG1</i>	1	0	developmentally regulated GTP binding protein 1
<i>DUSP1</i>	1	0	dual specificity phosphatase 1
<i>DYNC1HI</i>	1	0	dynein, cytoplasmic 1, heavy chain 1
<i>ECE2</i>	3	0	endothelin converting enzyme 2
<i>EFCBP1</i>	1	1	EF-hand calcium binding protein 1
<i>EGR4</i>	1	0	early growth response 4
<i>EHD4</i>	1	0	EH-domain containing 4
<i>EHMT2</i>	1	0	euchromatic histone-lysine N-methyltransferase 2
<i>EIF4A1</i>	3	1	eukaryotic translation initiation factor 4A, isoform 1
<i>EIF4E</i>	1	0	eukaryotic translation initiation factor 4E
<i>EMPI</i>	1	2	epithelial membrane protein 1
<i>EPHX1</i>	0	2	epoxide hydrolase 1, microsomal (xenobiotic)
<i>ETFB</i>	1	0	electron-transfer-flavoprotein, beta polypeptide
<i>F10</i>	1	0	coagulation factor X
<i>F3</i>	1	0	coagulation factor III (thromboplastin, tissue factor)
<i>FABP3</i>	1	0	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)
<i>FABP4</i>	1	0	fatty acid binding protein 4, adipocyte
<i>FAP</i>	0	1	fibroblast activation protein, alpha
<i>FASLG</i>	1	0	Fas ligand (TNF superfamily, member 6)
<i>FDXR</i>	1	0	ferredoxin reductase
<i>FGB</i>	1	0	fibrinogen beta chain
<i>FGF14</i>	1	1	fibroblast growth factor 14
<i>FGF9</i>	1	2	fibroblast growth factor 9 (glia-activating factor)
<i>FGR</i>	2	1	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog
<i>FKBP14</i>	1	1	FK506 binding protein 14, 22 kDa
<i>FKRP</i>	1	1	fukutin related protein
<i>FMOD</i>	1	4	fibromodulin
<i>FOSL1</i>	0	1	FOS-like antigen 1
<i>FOXA2</i>	1	0	forkhead box A2
<i>FTSJ3</i>	1	0	FtsJ homolog 3 (E. coli)
<i>FUT11</i>	1	1	fucosyltransferase 11 (alpha (1,3) fucosyltransferase)
<i>GAD2</i>	1	0	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)
<i>GALR3</i>	1	0	galanin receptor 3
<i>GAP43</i>	0	1	growth associated protein 43
<i>GCAT</i>	1	1	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A

			ligase)
<i>GDI1</i>	1	1	GDP dissociation inhibitor 1
<i>GGN</i>	2	0	gametogenitin
<i>GGPS1</i>	1	0	geranylgeranyl diphosphate synthase 1
<i>GIPC2</i>	1	2	GIPC PDZ domain containing family, member 2
<i>GLTSCR2</i>	1	0	glioma tumor suppressor candidate region gene 2
<i>GMDS</i>	1	1	GDP-mannose 4,6-dehydratase
<i>GORASP1</i>	1	0	golgi reassembly stacking protein 1, 65kDa
<i>GP1BB</i>	1	2	glycoprotein Ib (platelet), beta polypeptide
<i>GP5</i>	1	0	glycoprotein V (platelet)
<i>GPBARI</i>	1	0	G protein-coupled bile acid receptor 1
<i>GPD1</i>	1	0	glycerol-3-phosphate dehydrogenase 1 (soluble)
<i>GPR3</i>	1	0	G protein-coupled receptor 3
<i>GPR88</i>	1	0	G protein-coupled receptor 88
<i>GPSN2</i>	1	0	glycoprotein, synaptic 2
<i>GRIA2</i>	1	2	glutamate receptor, ionotropic, AMPA 2
<i>GRIK2</i>	1	0	glutamate receptor, ionotropic, kainate 2
<i>GRPR</i>	3	2	gastrin-releasing peptide receptor
<i>GSK3B</i>	3	1	glycogen synthase kinase 3 beta
<i>GTF2A1</i>	1	0	general transcription factor IIA, 1, 19/37kDa
<i>GTPBP3</i>	1	0	GTP binding protein 3 (mitochondrial)
<i>GYLTL1B</i>	1	0	glycosyltransferase-like 1B
<i>HABP2</i>	1	1	hyaluronan binding protein 2
<i>HAL</i>	0	1	histidine ammonia-lyase
<i>HAPLN1</i>	1	1	hyaluronan and proteoglycan link protein 1
<i>HAS1</i>	1	0	hyaluronan synthase 1
<i>HERPUD1</i>	0	1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
<i>HGF</i>	1	0	hepatocyte growth factor (hepapoietin A; scatter factor)
<i>HK3</i>	1	0	hexokinase 3 (white cell)
<i>HOXA1</i>	1	3	homeobox A1
<i>HOXA2</i>	1	1	homeobox A2
<i>HRSP12</i>	1	0	heat-responsive protein 12
<i>HSD17B8</i>	1	2	hydroxysteroid (17-beta) dehydrogenase 8
<i>HSPA5</i>	0	2	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
<i>ICMT</i>	1	0	isoprenylcysteine carboxyl methyltransferase
<i>IDH3A</i>	1	0	isocitrate dehydrogenase 3 (NAD <sup>+</sup> ) alpha
<i>IGF1</i>	1	0	insulin-like growth factor 1 (somatomedin C)
<i>IGSF4</i>	1	3	immunoglobulin superfamily, member 4
<i>IL11</i>	4	0	interleukin 11
<i>IL1RN</i>	1	1	interleukin 1 receptor antagonist
<i>IL2RA</i>	1	1	interleukin 2 receptor, alpha
<i>IL6</i>	1	0	interleukin 6 (interferon, beta 2)
<i>INHA</i>	2	0	inhibin, alpha
<i>IRF7</i>	1	0	interferon regulatory factor 7
<i>ITGA1</i>	1	1	integrin, alpha 1
<i>ITM2B</i>	1	1	integral membrane protein 2B
<i>ITPKC</i>	2	2	inositol 1,4,5-trisphosphate 3-kinase C
<i>KCNE4</i>	2	0	potassium voltage-gated channel, Isk-related family, member 4
<i>KCNK4</i>	1	0	potassium channel, subfamily K, member 4
<i>KIF5A</i>	2	0	kinesin family member 5A
<i>KLC4</i>	1	0	kinesin light chain 4
<i>KLF4</i>	1	1	Krueppel-like factor 4 (gut)
<i>KLF5</i>	1	1	Krueppel-like factor 5 (intestinal)
<i>KLK1</i>	1	0	kallikrein 1, renal/pancreas/salivary
<i>KPNA2</i>	1	0	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)

<i>KRT13</i>	3	4	keratin 13
<i>KRT16</i>	1	1	keratin 16 (focal non-epidermolytic palmoplantar keratoderma)
<i>KRT27</i>	1	0	keratin 27
<i>KRT31</i>	1	0	keratin 31
<i>KRT8</i>	1	0	keratin 8
<i>LHX1</i>	1	0	LIM homeobox 1
<i>LIAS</i>	1	0	lipoic acid synthetase
<i>LIF</i>	1	1	leukemia inhibitory factor (cholinergic differentiation factor)
<i>LIG1</i>	1	0	ligase I, DNA, ATP-dependent
<i>LIM2</i>	1	0	lens intrinsic membrane protein 2, 19kDa
<i>LOXL1</i>	2	0	lysyl oxidase-like 1
<i>LPPR2</i>	1	0	lipid phosphate phosphatase-related protein type 2
<i>LSAMP</i>	2	1	limbic system-associated membrane protein
<i>LSG1</i>	1	1	large subunit GTPase 1 homolog (S. cerevisiae)
<i>LTA</i>	1	0	lymphotoxin alpha (TNF superfamily, member 1)
<i>LZTR2</i>	1	0	leucine zipper transcription regulator 2
<i>MAP2K7</i>	1	2	mitogen-activated protein kinase kinase 7
<i>MAPK12</i>	2	2	mitogen-activated protein kinase 12
<i>MAPKAPK3</i>	1	0	mitogen-activated protein kinase-activated protein kinase 3
<i>MDK</i>	1	2	midkine (neurite growth-promoting factor 2)
<i>MEF2D</i>	1	0	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D)
<i>MMP9</i>	0	3	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)
<i>MRC2</i>	1	0	mannose receptor, C type 2
<i>MRPL34</i>	1	0	mitochondrial ribosomal protein L34
<i>MTP18</i>	1	0	mitochondrial protein 18 kDa
<i>MYBBP1A</i>	1	1	MYB binding protein (P160) 1a
<i>MYO1C</i>	1	0	myosin IC
<i>NAPIL2</i>	1	0	nucleosome assembly protein 1-like 2
<i>NDRG2</i>	2	0	NDRG family member 2
<i>NDRG4</i>	1	0	NDRG family member 4
<i>NDUFS2</i>	1	3	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)
<i>NEDD8</i>	1	0	neural precursor cell expressed, developmentally down-regulated 8
<i>NEDD9</i>	2	1	neural precursor cell expressed, developmentally down-regulated 9
<i>NEFH</i>	1	2	neurofilament, heavy polypeptide 200kDa
<i>NEUROD2</i>	1	0	neurogenic differentiation 2
<i>NHNI</i>	1	0	conserved nuclear protein NHN1
<i>NIF3L1</i>	1	0	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)
<i>NME3</i>	1	3	non-metastatic cells 3, protein expressed in
<i>NOTCH4</i>	1	0	Notch homolog 4 (Drosophila)
<i>NPAS4</i>	1	0	neuronal PAS domain protein 4
<i>NPTX2</i>	1	1	neuronal pentraxin II
<i>NR2F2</i>	1	2	nuclear receptor subfamily 2, group F, member 2
<i>NR4A3</i>	1	4	nuclear receptor subfamily 4, group A, member 3
<i>NUP62</i>	1	1	nucleoporin 62kDa
<i>OGG1</i>	1	0	8-oxoguanine DNA glycosylase
<i>OMG</i>	1	1	oligodendrocyte myelin glycoprotein
<i>ONECUT1</i>	1	2	one cut domain, family member 1
<i>OR51E2</i>	1	0	olfactory receptor, family 51, subfamily E, member 2
<i>P2RXL1</i>	1	1	purinergic receptor P2X-like 1, orphan receptor
<i>PACSI</i>	1	0	phosphofuran acidic cluster sorting protein 1
<i>PADI4</i>	1	0	peptidyl arginine deiminase, type IV
<i>PAFAH1B1</i>	2	1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa

<i>PALMD</i>	1	0	palmdelphin
<i>PARD6A</i>	1	3	par-6 partitioning defective 6 homolog alpha (C.elegans)
<i>PAWR</i>	1	1	PRKC, apoptosis, WT1, regulator
<i>PBX2</i>	1	0	pre-B-cell leukemia transcription factor 2
<i>PCDH7</i>	1	0	BH-protocadherin (brain-heart)
<i>PCSK2</i>	1	0	proprotein convertase subtilisin/kexin type 2
<i>PCYT2</i>	2	2	phosphate cytidylyltransferase 2, ethanolamine
<i>PDE3B</i>	1	1	phosphodiesterase 3B, cGMP-inhibited
<i>PDE4A</i>	1	0	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)
<i>PDLIM5</i>	1	2	PDZ and LIM domain 5
<i>PELO</i>	1	1	pelota homolog (Drosophila)
<i>PER1</i>	1	1	period homolog 1 (Drosophila)
<i>PFDN6</i>	1	1	prefoldin subunit 6
<i>PFNI</i>	1	1	profilin 1
<i>PGC</i>	1	0	progastricsin (pepsinogen C)
<i>PGGT1B</i>	1	0	protein geranylgeranyltransferase type I, beta subunit
<i>PHF7</i>	2	1	PHD finger protein 7
<i>PHKA1</i>	1	0	phosphorylase kinase, alpha 1 (muscle)
<i>PIK3R3</i>	2	4	phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)
<i>PIM1</i>	3	0	pim-1 oncogene
<i>PIP5K1B</i>	1	0	phosphatidylinositol-4-phosphate 5-kinase, type I, beta
<i>PLCZ1</i>	1	1	phospholipase C, zeta 1
<i>PLEKHH3</i>	1	0	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3
<i>PLIN</i>	1	1	perilipin
<i>PLP2</i>	1	0	proteolipid protein 2 (colonic epithelium-enriched)
<i>POLRIC</i>	1	0	polymerase (RNA) I polypeptide C, 30kDa
<i>POUFI1</i>	1	0	POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1)
<i>PPARGC1A</i>	1	0	peroxisome proliferative activated receptor, gamma, coactivator 1, alpha
<i>PPIB</i>	1	1	peptidylprolyl isomerase B (cyclophilin B)
<i>PPP1CA</i>	1	2	protein phosphatase 1, catalytic subunit, alpha isoform
<i>PPP1R2</i>	2	2	protein phosphatase 1, regulatory (inhibitor) subunit 2
<i>PPP2R2B</i>	1	0	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform
<i>PPT2</i>	1	1	palmitoyl-protein thioesterase 2
<i>PRDX1</i>	1	0	peroxiredoxin 1
<i>PRKAG1</i>	1	0	protein kinase, AMP-activated, gamma 1 non-catalytic subunit
<i>PRKCDBP</i>	1	0	protein kinase C, delta binding protein
<i>PRR3</i>	1	0	proline rich 3
<i>PSENEN</i>	1	2	presenilin enhancer 2 homolog (C. elegans)
<i>PSMA46</i>	1	0	proteasome (prosome, macropain) subunit, alpha type, 6
<i>PSMA7</i>	1	1	proteasome (prosome, macropain) subunit, alpha type, 7
<i>PSMB6</i>	1	0	proteasome (prosome, macropain) subunit, beta type, 6
<i>PSMB8</i>	1	1	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)
<i>PSMC2</i>	1	0	proteasome (prosome, macropain) 26S subunit, ATPase, 2
<i>PSMC3IP</i>	2	1	PSMC3 interacting protein
<i>PSMC5</i>	2	1	proteasome (prosome, macropain) 26S subunit, ATPase, 5
<i>PSPH</i>	1	1	phosphoserine phosphatase
<i>PTGER1</i>	1	1	prostaglandin E receptor 1 (subtype EP1), 42kDa
<i>PTPRF</i>	1	0	protein tyrosine phosphatase, receptor type, F
<i>PTPRR</i>	1	0	protein tyrosine phosphatase, receptor type, R
<i>PXI9</i>	1	2	px19-like protein

<i>QDPR</i>	1	3	quinoid dihydropteridine reductase
<i>RAB3D</i>	1	0	RAB3D, member RAS oncogene family
<i>RBBP7</i>	1	0	retinoblastoma binding protein 7
<i>REEP6</i>	2	0	receptor accessory protein 6
<i>RFFL</i>	1	0	ring finger and FYVE-like domain containing 1
<i>RGS19</i>	1	0	regulator of G-protein signalling 19
<i>RHO</i>	2	0	rhodopsin (opsin 2, rod pigment) (retinitis pigmentosa 4, autosomal dominant)
<i>RIC8B</i>	1	1	resistance to inhibitors of cholinesterase 8 homolog B ( <i>C. elegans</i> )
<i>RING1</i>	2	1	ring finger protein 1
<i>RP11-</i>			
<i>217H1.1</i>	1	1	implantation-associated protein
<i>RP11-35N6.1</i>	1	2	plasticity related gene 3
<i>RP21</i>	1	1	ribonuclease P 21kDa subunit
<i>RPS18</i>	1	2	ribosomal protein S18
<i>RSHL1</i>	1	0	radial spokehead-like 1
<i>RTN3</i>	1	0	reticulon 3
<i>RTN4RL1</i>	1	0	reticulon 4 receptor-like 1
<i>RXRB</i>	2	1	retinoid X receptor, beta
<i>SCGN</i>	1	0	secretagogin, EF-hand calcium binding protein
<i>SDHD</i>	1	1	succinate dehydrogenase complex, subunit D, integral membrane protein
<i>SEC13L1</i>	1	1	SEC13-like 1 ( <i>S. cerevisiae</i> )
<i>SEMA4A</i>	1	0	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A
<i>SERINC2</i>	1	1	serine incorporator 2
<i>SERPINE1</i>	0	1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
<i>SERPINII</i>	1	2	serpin peptidase inhibitor, clade I (neuroserpin), member 1
<i>SF3B4</i>	1	3	splicing factor 3b, subunit 4, 49kDa
<i>SHC1</i>	1	1	SHC (Src homology 2 domain containing) transforming protein 1
<i>SHMT2</i>	1	0	serine hydroxymethyltransferase 2 (mitochondrial)
<i>SIPA1</i>	1	1	signal-induced proliferation-associated gene 1
<i>SIRT2</i>	1	0	sirtuin (silent mating type information regulation 2 homolog) 2 ( <i>S. cerevisiae</i> )
<i>SLC12A5</i>	1	0	solute carrier family 12, (potassium-chloride transporter) member 5
<i>SLC17A6</i>	1	1	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6
<i>SLC18A1</i>	1	1	solute carrier family 18 (vesicular monoamine), member 1
<i>SLC2A1</i>	1	1	solute carrier family 2 (facilitated glucose transporter), member 1
<i>SLC2A5</i>	1	0	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
<i>SLC35B1</i>	1	1	solute carrier family 35, member B1
<i>SLC5A1</i>	1	1	solute carrier family 5 (sodium/glucose cotransporter), member 1
<i>SLC6A5</i>	1	2	solute carrier family 6 (neurotransmitter transporter, glycine), member 5
<i>SNAPC2</i>	2	1	small nuclear RNA activating complex, polypeptide 2, 45kDa
<i>SNX1</i>	1	0	sorting nexin 1
<i>SNX15</i>	1	0	sorting nexin 15
<i>SOAT2</i>	1	1	sterol O-acyltransferase 2
<i>SOCS3</i>	2	1	suppressor of cytokine signaling 3
<i>SOD1</i>	0	1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
<i>SORBS3</i>	1	0	sorbin and SH3 domain containing 3
<i>SOST</i>	1	1	sclerosteosis

<i>SP7</i>	1	1	Sp7 transcription factor
<i>SPHK1</i>	1	3	sphingosine kinase 1
<i>SPTLC2</i>	1	2	serine palmitoyltransferase, long chain base subunit 2
<i>SQSTM1</i>	2	1	sequestosome 1
<i>SRPK3</i>	1	1	SFRS protein kinase 3
<i>SRPR</i>	1	0	signal recognition particle receptor (docking protein)
<i>SSBP3</i>	1	0	single stranded DNA binding protein 3
<i>SSRP1</i>	1	0	structure specific recognition protein 1
<i>ST3GAL1</i>	1	0	ST3 beta-galactoside alpha-2,3-sialyltransferase 1
<i>ST8SIA5</i>	1	2	ST8 alpha-N-acetyl-neuraminate alpha-2,8-sialyltransferase 5
<i>STK19</i>	2	2	serine/threonine kinase 19
<i>STK40</i>	1	0	serine/threonine kinase 40
<i>STMN2</i>	2	4	stathmin-like 2
<i>STOML2</i>	1	0	stomatin (EPB72)-like 2
<i>SUOX</i>	2	1	sulfite oxidase
<i>SURF1</i>	1	0	surfeit 1
<i>TAGLN</i>	1	1	transgelin
<i>TAGLN2</i>	1	1	transgelin 2
<i>TAPBP</i>	2	3	TAP binding protein (tapasin)
<i>TAT</i>	1	0	tyrosine aminotransferase
<i>TBP</i>	1	0	TATA box binding protein
<i>TFPI2</i>	1	1	tissue factor pathway inhibitor 2
<i>TG</i>	1	0	thyroglobulin
<i>TH</i>	1	4	tyrosine hydroxylase
<i>THOC6</i>	1	2	THO complex 6 homolog (Drosophila)
<i>TIMM8A</i>	1	0	translocase of inner mitochondrial membrane 8 homolog A (yeast)
<i>TIMP2</i>	1	0	TIMP metallopeptidase inhibitor 2
<i>TM7SF2</i>	1	0	transmembrane 7 superfamily member 2
<i>TMEM69</i>	1	0	transmembrane protein 69
<i>TNF</i>	2	0	tumor necrosis factor (TNF superfamily, member 2)
<i>TNFAIP1</i>	1	0	tumor necrosis factor, alpha-induced protein 1 (endothelial)
<i>TNNC1</i>	1	0	troponin C type 1 (slow)
<i>TNR</i>	2	0	tenascin R (restrictin, janusin)
<i>TOB1</i>	1	2	transducer of ERBB2, 1
<i>TP53</i>	1	0	tumor protein p53 (Li-Fraumeni syndrome)
<i>TPP1</i>	3	3	tripeptidyl peptidase I
<i>TRAPP3</i>	1	1	trafficking protein particle complex 3
<i>TRIM44</i>	1	0	tripartite motif-containing 44
<i>TSC22D3</i>	1	2	TSC22 domain family, member 3
<i>TSPAN31</i>	1	0	tetraspanin 31
<i>TSSK3</i>	1	0	testis-specific serine kinase 3
<i>TTC9C</i>	2	0	tetratricopeptide repeat domain 9C
<i>TUBB3</i>	1	3	tubulin, beta 3
<i>TYRO3</i>	1	1	TYRO3 protein tyrosine kinase
<i>UCHL1</i>	1	0	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
<i>UGP2</i>	1	1	UDP-glucose pyrophosphorylase 2
<i>UTS2</i>	1	1	urotensin 2
<i>VATI</i>	1	0	vesicle amine transport protein 1 homolog (T californica)
<i>VAX1</i>	2	0	ventral anterior homeobox 1
<i>VCP</i>	2	1	valosin-containing protein
<i>VEPH1</i>	1	1	ventricular zone expressed PH domain homolog 1 (zebrafish)
<i>VGF</i>	1	2	VGF nerve growth factor inducible
<i>VIM</i>	1	1	vimentin
<i>VISA</i>	1	0	virus-induced signaling adapter
<i>WBP11</i>	1	0	WW domain binding protein 11
<i>WDR46</i>	2	1	WD repeat domain 46

<i>WDR79</i>	1	0	WD repeat domain 79
<i>WNK4</i>	2	2	WNK lysine deficient protein kinase 4
<i>XK</i>	1	1	X-linked Kx blood group (McLeod syndrome)
<i>ZBTB22</i>	2	4	zinc finger and BTB domain containing 22
<i>ZDHC23</i>	1	1	zinc finger, DHHC-type containing 23
<i>ZDHC9</i>	1	1	zinc finger, DHHC-type containing 9
<i>ZFAND2A</i>	1	0	zinc finger, AN1-type domain 2A
<i>ZIC1</i>	3	0	Zic family member 1 (odd-paired homolog, Drosophila)
<i>ZMYND10</i>	1	3	zinc finger, MYND-type containing 10
<i>ZPBP2</i>	1	1	zona pellucida binding protein 2

Table S3. Human NRF2-dependent genes derived from microarray gene expression profiles using *Nrf2*-knockout mice (51-53) and human neuroblastoma cells (54) treated with oxidative stress and *Nrf2*-activating chemicals (see Table 2). First, four sets of up-regulated genes were intersected based on HomologeneID; Then, for each unique HomologeneID, the human GeneID was fetched and included in this list of potential human NRF2-dependent genes.

HomologeneID	GeneID	Symbol	reference
7	90	<i>ACVR1</i>	Cho_2005
37333	131	<i>ADH7</i>	Cho_2005
5255	11318	<i>ADM</i>	Cho_2005
3740	9590	<i>AKAP12</i>	Cho_2005
84774	57016	<i>AKR1B10</i>	Cho_2005
7410	23600	<i>AMACR</i>	Cho_2005
563	301	<i>ANXA1</i>	Cho_2005
68165	316	<i>AOXI</i>	Cho_2005
32434	54518	<i>APBB1IP</i>	Cho_2005
1243	339	<i>APOBEC1</i>	Cho_2005
30951	348	<i>APOE</i>	Cho_2005
68051	358	<i>AQPI</i>	Cho_2005
20318	397	<i>ARHGDI</i> B	Cho_2005
1265	467	<i>ATF3</i>	Cho_2005
30952	472	<i>ATM</i>	Cho_2005
7583	558	<i>AXL</i>	Cho_2005
7242	581	<i>BAX</i>	Cho_2005
20320	586	<i>BCAT1</i>	Cho_2005
569	593	<i>BCKDHA</i>	Cho_2005
20411	660	<i>BMX</i>	Cho_2005
418	713	<i>C1QB</i>	Cho_2005
37257	779	<i>CACNA1S</i>	Cho_2005
1320	799	<i>CALCR</i>	Cho_2005
37523	822	<i>CAPG</i>	Cho_2005
2736	8573	<i>CASK</i>	Cho_2005
37337	886	<i>CCKAR</i>	Cho_2005
4568	6354	<i>CCL7</i>	Cho_2005
20344	1230	<i>CCR1</i>	Cho_2005
537	1231	<i>CCR2</i>	Cho_2005
586	916	<i>CD3E</i>	Cho_2005
3622	1013	<i>CDH15</i>	Cho_2005

55465	1080	<i>CFTR</i>	Cho_2005
7666	27141	<i>CIDEB</i>	Cho_2005
4433	10370	<i>CITED2</i>	Cho_2005
7844	338339	<i>CLEC4D</i>	Cho_2005
22809	26253	<i>CLEC4E</i>	Cho_2005
73874	1277	<i>COL1A1</i>	Cho_2005
55433	1281	<i>COL3A1</i>	Cho_2005
1390	1284	<i>COL4A2</i>	Cho_2005
1391	1291	<i>COL6A1</i>	Cho_2005
37917	1293	<i>COL6A3</i>	Cho_2005
31199	8804	<i>CREG1</i>	Cho_2005
7042	1407	<i>CRYI</i>	Cho_2005
601	1441	<i>CSF3R</i>	Cho_2005
37551	1510	<i>CTSE</i>	Cho_2005
20867	1520	<i>CTSS</i>	Cho_2005
7733	84694	<i>CX62</i>	Cho_2005
48431	10563	<i>CXCL13</i>	Cho_2005
48156	6374	<i>CXCL5</i>	Cho_2005
84711	6372	<i>CXCL6</i>	Cho_2005
85917	1548	<i>CYP2A6</i>	Cho_2005
85917	1549	<i>CYP2A7</i>	Cho_2005
73894	1555	<i>CYP2B6</i>	Cho_2005
1444	1629	<i>DBT</i>	Cho_2005
621	1734	<i>DIO2</i>	Cho_2005
4104	28514	<i>DLL1</i>	Cho_2005
21193	10294	<i>DNAJA2</i>	Cho_2005
55957	3337	<i>DNAJB1</i>	Cho_2005
31239	1850	<i>DUSP8</i>	Cho_2005
1476	1906	<i>EDN1</i>	Cho_2005
5976	8890	<i>EIF2B4</i>	Cho_2005
9438	51705	<i>EMCN</i>	Cho_2005
3766	9982	<i>FGFBP1</i>	Cho_2005
3842	2268	<i>FGR</i>	Cho_2005
3040	2322	<i>FLT3</i>	Cho_2005
3844	2353	<i>FOS</i>	Cho_2005
3967	8061	<i>FOSL1</i>	Cho_2005
7762	3170	<i>FOXA2</i>	Cho_2005
74395	2358	<i>FPRL1</i>	Cho_2005
48065	2444	<i>FRK</i>	Cho_2005
37906	2539	<i>G6PD</i>	Cho_2005
37268	2548	<i>GAA</i>	Cho_2005
637	2618	<i>GART</i>	Cho_2005
1148	2729	<i>GCLC</i>	Cho_2005
3576	9518	<i>GDF15</i>	Cho_2005
68439	9945	<i>GFPT2</i>	Cho_2005
639	2677	<i>GGCX</i>	Cho_2005

68450	2678	<i>GGT1</i>	Cho_2005
68450	2679	<i>GGT2</i>	Cho_2005
20084	2779	<i>GNAT1</i>	Cho_2005
30972	2812	<i>GP1BB</i>	Cho_2005
144	2815	<i>GP9</i>	Cho_2005
145	2821	<i>GPI</i>	Cho_2005
20226	2890	<i>GRIA1</i>	Cho_2005
21098	2925	<i>GRPR</i>	Cho_2005
37355	2940	<i>GSTA3</i>	Cho_2005
74378	221357	<i>GSTA5</i>	Cho_2005
84561	2944	<i>GSTM1</i>	Cho_2005
84565	2949	<i>GSTM5</i>	Cho_2005
20235	2952	<i>GSTT1</i>	Cho_2005
1171	3091	<i>HIF1A</i>	Cho_2005
49956	3178	<i>HNRPAL1</i>	Cho_2005
68095	3248	<i>HPGD</i>	Cho_2005
20498	3249	<i>HPN</i>	Cho_2005
74557	3305	<i>HSPA1L</i>	Cho_2005
21322	10808	<i>HSPH1</i>	Cho_2005
8097	29851	<i>ICOS</i>	Cho_2005
499	3485	<i>IGFBP2</i>	Cho_2005
56489	3488	<i>IGFBP5</i>	Cho_2005
7784	3566	<i>IL4R</i>	Cho_2005
502	3569	<i>IL6</i>	Cho_2005
40119	3621	<i>ING1</i>	Cho_2005
1654	3625	<i>INHBB</i>	Cho_2005
4436	10379	<i>ISGF3G</i>	Cho_2005
179	3691	<i>ITGB4</i>	Cho_2005
1679	3725	<i>JUN</i>	Cho_2005
1691	3775	<i>KCNK1</i>	Cho_2005
187	3815	<i>KIT</i>	Cho_2005
7209	22914	<i>KLRK1</i>	Cho_2005
69533	92483	<i>LDHAL6B</i>	Cho_2005
55647	3945	<i>LDHB</i>	Cho_2005
4068	3975	<i>LHX1</i>	Cho_2005
40761	11025	<i>LILRB3</i>	Cho_2005
1252	653193	<i>LOC653193</i>	Cho_2005
1741	4015	<i>LOX</i>	Cho_2005
1750	4046	<i>LSP1</i>	Cho_2005
22477	1241	<i>LTB4R</i>	Cho_2005
1759	4063	<i>LY9</i>	Cho_2005
55649	4067	<i>LYN</i>	Cho_2005
37322	4125	<i>MAN2B1</i>	Cho_2005
4928	8685	<i>MARCO</i>	Cho_2005
20540	4199	<i>ME1</i>	Cho_2005
21040	4323	<i>MMP14</i>	Cho_2005

3659	4318	<i>MMP9</i>	Cho_2005
48388	4502	<i>MT2A</i>	Cho_2005
21321	10797	<i>MTHFD2</i>	Cho_2005
525	4689	<i>NCF4</i>	Cho_2005
8384	10787	<i>NCKAP1</i>	Cho_2005
4491	4778	<i>NFE2</i>	Cho_2005
2412	4780	<i>NFE2L2</i>	Cho_2005
1884	4856	<i>NOV</i>	Cho_2005
695	1728	<i>NQO1</i>	Cho_2005
21165	10062	<i>NR1H3</i>	Cho_2005
1895	4907	<i>NT5E</i>	Cho_2005
239	5184	<i>PEPD</i>	Cho_2005
48457	10857	<i>PGRMC1</i>	Cho_2005
5133	11142	<i>PKIG</i>	Cho_2005
37650	5315	<i>PKM2</i>	Cho_2005
3725	7941	<i>PLA2G7</i>	Cho_2005
717	5327	<i>PLAT</i>	Cho_2005
13245	5371	<i>PML</i>	Cho_2005
257	5373	<i>PMM2</i>	Cho_2005
4538	5425	<i>POLD2</i>	Cho_2005
68058	5444	<i>PON1</i>	Cho_2005
7899	5468	<i>PPARG</i>	Cho_2005
2038	5531	<i>PPP4C</i>	Cho_2005
925	639	<i>PRDMI</i>	Cho_2005
55679	5578	<i>PRKCA</i>	Cho_2005
84384	5583	<i>PRKCH</i>	Cho_2005
3116	9265	<i>PSCD3</i>	Cho_2005
5272	11344	<i>PTK9L</i>	Cho_2005
3941	5784	<i>PTPN14</i>	Cho_2005
2129	5793	<i>PTPRG</i>	Cho_2005
2130	5795	<i>PTPRJ</i>	Cho_2005
20902	9545	<i>RAB3D</i>	Cho_2005
38182	10567	<i>RABAC1</i>	Cho_2005
55702	5931	<i>RBBP7</i>	Cho_2005
7511	3516	<i>RBPSUH</i>	Cho_2005
4735	10636	<i>RGS14</i>	Cho_2005
56380	389	<i>RHOC</i>	Cho_2005
4146	7844	<i>RNF103</i>	Cho_2005
2225	6279	<i>S100A8</i>	Cho_2005
55706	6332	<i>SCN7A</i>	Cho_2005
539	6402	<i>SELL</i>	Cho_2005
20417	866	<i>SERPINA6</i>	Cho_2005
68070	5054	<i>SERPINE1</i>	Cho_2005
3715	6492	<i>SIM1</i>	Cho_2005
75059	51763	<i>SKIP</i>	Cho_2005
73884	6556	<i>SLC11A1</i>	Cho_2005

20283	6558	<i>SLC12A2</i>	Cho_2005
20655	6509	<i>SLC1A4</i>	Cho_2005
74302	6515	<i>SLC2A3</i>	Cho_2005
2291	6533	<i>SLC6A6</i>	Cho_2005
2941	9021	<i>SOCs3</i>	Cho_2005
22631	55553	<i>SOX6</i>	Cho_2005
43881	11171	<i>STRAP</i>	Cho_2005
37559	2054	<i>STX2</i>	Cho_2005
2856	8803	<i>SUCLA2</i>	Cho_2005
2398	6876	<i>TAGLN</i>	Cho_2005
7563	83439	<i>TCF7L1</i>	Cho_2005
6131	113419	<i>TEX261</i>	Cho_2005
540	7040	<i>TGFB1</i>	Cho_2005
37294	7045	<i>TGFBI</i>	Cho_2005
4580	7070	<i>THY1</i>	Cho_2005
68154	7086	<i>TKT</i>	Cho_2005
21223	10333	<i>TLR6</i>	Cho_2005
4582	7128	<i>TNFAIP3</i>	Cho_2005
2365	6737	<i>TRIM21</i>	Cho_2005
55733	7296	<i>TXNRD1</i>	Cho_2005
7594	7414	<i>VCL</i>	Cho_2005
32130	8876	<i>VNN1</i>	Cho_2005
2542	7447	<i>VSNL1</i>	Cho_2005
3401	7508	<i>XPC</i>	Cho_2005
875	122622	<i>ADSSL1</i>	Lee_2003
73889	216	<i>ALDH1A1</i>	Lee_2003
55480	217	<i>ALDH2</i>	Lee_2003
29	383	<i>ARG1</i>	Lee_2003
1266	468	<i>ATF4</i>	Lee_2003
7249	712	<i>C1QA</i>	Lee_2003
32020	714	<i>C1QC</i>	Lee_2003
55514	847	<i>CAT</i>	Lee_2003
3807	1051	<i>CEBPB</i>	Lee_2003
3817	1436	<i>CSF1R</i>	Lee_2003
2251	6376	<i>CX3CL1</i>	Lee_2003
68035	1545	<i>CYP1B1</i>	Lee_2003
94	2052	<i>EPHX1</i>	Lee_2003
55623	2098	<i>ESD</i>	Lee_2003
49234	2123	<i>EVI2A</i>	Lee_2003
74295	2495	<i>FTH1</i>	Lee_2003
1557	2730	<i>GCLM</i>	Lee_2003
31075	3162	<i>HMOX1</i>	Lee_2003
515	3479	<i>IGF1</i>	Lee_2003
20092	3689	<i>ITGB2</i>	Lee_2003
4922	7805	<i>LAPTM5</i>	Lee_2003
3055	3929	<i>LBP</i>	Lee_2003

80174	3936	<i>LCPI</i>	Lee_2003
37277	3988	<i>LIPA</i>	Lee_2003
200	4023	<i>LPL</i>	Lee_2003
20952	4036	<i>LRP2</i>	Lee_2003
40820	22949	<i>LTB4DH</i>	Lee_2003
37278	4069	<i>LYZ</i>	Lee_2003
20547	4321	<i>MMP12</i>	Lee_2003
1837	4488	<i>MSX2</i>	Lee_2003
1876	4803	<i>NGFB</i>	Lee_2003
32055	5154	<i>PDGFA</i>	Lee_2003
21685	5052	<i>PRDX1</i>	Lee_2003
3606	9588	<i>PRDX6</i>	Lee_2003
31000	5743	<i>PTGS2</i>	Lee_2003
74538	6319	<i>SCD</i>	Lee_2003
68520	6513	<i>SLC2A1</i>	Lee_2003
5050	6536	<i>SLC6A9</i>	Lee_2003
392	6647	<i>SOD1</i>	Lee_2003
32722	140809	<i>SRXN1</i>	Lee_2003
4916	6888	<i>TALDO1</i>	Lee_2003
2429	7037	<i>TFRC</i>	Lee_2003
7574	7050	<i>TGIF</i>	Lee_2003
315	7253	<i>TSHR</i>	Lee_2003
55732	7295	<i>TXN</i>	Lee_2003
5171	7546	<i>ZIC2</i>	Lee_2003
55742	7547	<i>ZIC3</i>	Lee_2003
536	178	<i>AGL</i>	Li_2002
81636	8644	<i>AKR1C3</i>	Li_2002
8528	25842	<i>ASF1A</i>	Li_2002
2614	8312	<i>AXINI</i>	Li_2002
8182	23527	<i>CENTB2</i>	Li_2002
31055	1122	<i>CHML</i>	Li_2002
7273	1268	<i>CNR1</i>	Li_2002
9081	23336	<i>DMN</i>	Li_2002
48437	8445	<i>DYRK2</i>	Li_2002
5117	11117	<i>EMILIN1</i>	Li_2002
37265	2073	<i>ERCC5</i>	Li_2002
20372	2274	<i>FHL2</i>	Li_2002
20373	2296	<i>FOXC1</i>	Li_2002
1449	1647	<i>GADD45A</i>	Li_2002
20477	2817	<i>GPC1</i>	Li_2002
531	2936	<i>GSR</i>	Li_2002
658	2947	<i>GSTM3</i>	Li_2002
40973	9709	<i>HERPUD1</i>	Li_2002
3908	3309	<i>HSPA5</i>	Li_2002
10196	55818	<i>JMJD1A</i>	Li_2002
8184	9817	<i>KEAP1</i>	Li_2002

48159	6416	<i>MAP2K4</i>	Li_2002
4301	10299	<i>MARCH6</i>	Li_2002
3442	9112	<i>MTA1</i>	Li_2002
4712	10608	<i>MXD4</i>	Li_2002
55941	4628	<i>MYH10</i>	Li_2002
23228	65009	<i>NDRG4</i>	Li_2002
40755	4744	<i>NEFH</i>	Li_2002
68442	9972	<i>NUP153</i>	Li_2002
8612	10439	<i>OLFM1</i>	Li_2002
75052	23022	<i>PALLD</i>	Li_2002
1943	5100	<i>PCDH8</i>	Li_2002
270	5830	<i>PEX5</i>	Li_2002
11059	9444	<i>QKI</i>	Li_2002
10875	5911	<i>RAP2A</i>	Li_2002
22840	9770	<i>RASSF2</i>	Li_2002
12315	112611	<i>RWDD2</i>	Li_2002
2591	7857	<i>SCG2</i>	Li_2002
4911	6645	<i>SNTB2</i>	Li_2002
8846	399979	<i>SNX19</i>	Li_2002
31202	8878	<i>SQSTM1</i>	Li_2002
23120	23208	<i>SYT11</i>	Li_2002
38056	10043	<i>TOM1</i>	Li_2002
20720	7474	<i>WNT5A</i>	Li_2002
5027	678	<i>ZFP36L2</i>	Li_2002
21400	7738	<i>ZNF184</i>	Li_2002
18698	25888	<i>ZNF473</i>	Li_2002
37524	873	<i>CBR1</i>	Thimmulappa_2002
618	1644	<i>DDC</i>	Thimmulappa_2002
32155	4189	<i>DNAJB9</i>	Thimmulappa_2002
68216	2028	<i>ENPEP</i>	Thimmulappa_2002
37457	957	<i>ENTPD5</i>	Thimmulappa_2002
40748	65108	<i>MARCKSL1</i>	Thimmulappa_2002
231	4942	<i>OAT</i>	Thimmulappa_2002
32763	5763	<i>PTMS</i>	Thimmulappa_2002
2520	7358	<i>UGDH</i>	Thimmulappa_2002

Table S4. We examined the surface plasmon resonance (SPR) binding data from Yamamoto et al (55) and compared their functional data to our predictions by computationally evaluating the sequences they have tested for binding. This tested if our statistical PWM model was compatible with their functional data. We calculated PWM scores for their tested sequences and found that all of their strong binding Group IV sequences have high PWM scores, and they are much higher than that of Group I or II weak binding sequences (see below). It suggests that our PWM model has power to select ARE sequences that bind to the MafG:Nrf2 heterodimer.

Line in Table 4*	Sequence name	sequence	PWM+	SPR assay	Yamamoto prediction	Our prediction\$
1	Human $\beta$ -globin LCR HS-4	<b>GGCTGACTCA</b> ctc	<b>11.3</b>	<b>IV</b>	<b>IV</b>	<b>binding</b>
2	Human $\beta$ -globin LCR HS-2	<b>TGCTGAGTC</b> AtgA	<b>16.9</b>		<b>IV</b>	<b>binding</b>
3	Mouse $\beta$ -globin LCR HS-2	<b>TGCTGAGTC</b> Atgc	<b>17.8</b>		<b>IV</b>	<b>binding</b>
4	Human porphobilinogen deaminase	<b>TGCTGAGTC</b> Actg	<b>17.8</b>		<b>IV</b>	<b>binding</b>
5	Human thromboxane synthase	<b>TGCTGAtTC</b> Attc	<b>13.2</b>		<b>IV</b>	<b>binding</b>
6	Human NQO1	<b>TGCTGAGTC</b> Actg	<b>17.8</b>	<b>IV</b>	<b>IV</b>	<b>binding</b>
7	Rat GST-P	<b>TGCTGAaTC</b> Atag	<b>13.2</b>		<b>IV</b>	<b>binding</b>
8	Mouse A170	<b>TGCTGAGTC</b> Atag	<b>17</b>		<b>IV</b>	<b>binding</b>
9	Mouse heme oxygenase-1	<b>TGCTGtGTC</b> Attg	<b>16.1</b>		<b>IV</b>	<b>binding</b>
10	Human GCLC	<b>cGCTGAGTC</b> Acgg	<b>16.5</b>		<b>IV</b>	<b>binding</b>
11	Human GCLM	<b>TGCTtAGTC</b> Attg	<b>16</b>		<b>IV</b>	<b>binding</b>
12	Rat, Mouse GST-Ya	<b>TGCTttGTC</b> AccA	<b>13.5</b>	<b>IV</b>	<b>IV</b>	<b>binding</b>
13	Mouse crystalline $\gamma$ F	TGCcaACaCAGCA	3.7		I	no-binding
14	Rat crystallin $\gamma$ D	TGCcaACgCAGCA	2.1		I	no-binding
15	Chicken crystallin $\alpha$ A	TGCTGACCacGtt	-1.6		II	no-binding
16	Chicken $\delta$ 1 crystallin	TGCTGAtcCtGCA	5.7		II	no-binding
17	Mouse type II collagen	gGCTctGTatGCg	1.3		I	no-binding
18	Mouse insulin	gGCTGAagCtGCA	5.8		II	no-binding
19	Human rhodopsin	<b>TGCTGAtTC</b> AGCc	<b>12.2</b>	<b>III</b>	<b>III</b>	<b>binding</b>

\*Table 4 in Yamamoto et al. + Our PWM calculation \$ Our binding prediction

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