Synergy and antagonism of two distinct, but confused, Nrf1 factors in integral regulation of the nuclear-to-mitochondrial respiratory and antioxidant transcription networks

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Abstract: There is hitherto no literature available for explaining two distinct, but confused Nrf1 transcription factors, because they shared the same abbreviations from nuclear factor erythroid 2-related factor 1 (also called Nfe2l1) and nuclear respiratory factor (originally designated α-Pal). Thus, we have here identified that Nfe2l1NRF1 and α-PalNRF1 exert synergistic and antagonistic roles in integrative regulation of the nuclear-to-mitochondrial respiratory and antioxidant transcription profiles. In mouse embryonic fibroblasts (MEFs), knockout of Nfe2l1−/− leads to substantial decreases in expression levels of α-PalNRF1 and Nfe2l2, together with TFAM (mitochondrial transcription factor A) and other target genes. Similar inhibitory results were determined in Nfe2l2−/− MEFs, with an exception that GSTa1 and Aldh1a1 were distinguishably up-regulated in Nfe2l1−/− MEFs. Such synergistic contributions of Nfe2l1 and Nfe2l2 to the positive regulation of α-PalNRF1 and TFAM were validated in Keap1−/− MEFs. However, human α-PalNRF1 expression was unaltered by hNfe2l1α−/−, hNfe2l2α−/−ΔTA or even hNfe2l1α−−siNrf2, albeit TFAM was activated by Nfe2l1 but inhibited by Nfe2l2; such an antagonism occurred in HepG2 cells. Conversely, almost all of mouse Nfe2l1, Nfe2l2 and co-target genes were down-expressed in α-PalNRF1−/− MEFs. On the contrary, up-regulation of human Nfe2l1, Nfe2l2 and relevant reporter genes took place after silencing of α-PalNRF1, but their down-regulation occurred upon ectopic expression of α-PalNRF1. Furthermore, Pitx2 (pituitary homeobox 2) was also identified as a direct upstream regulator of Nfe2l1 and TFAM, besides α-PalNRF1. Overall, these across-talks amongst Nfe2l1, Nfe2l2 and α-PalNRF1, along with Pitx2, are integrated from the endoplasmic reticulum to the nuclear-to-mitochondrial communication for targeting TFAM, in order to finely tune the cellular respiratory and antioxidant gene transcription networks, albeit they differ between the mouse and the human.

Keywords: Nfe2l1/Nrf1, Nfe2l2/Nrf2, α-PalNRF1, TFAM, Pitx2, cap‘n’collar (CNC), antioxidant response element (ARE), nuclear-to-mitochondrial respiratory system, and ER-nuclear-mitochondrial (ENUM) communication

Running title: Two distinct Nrf1 factors responsible for cellular antioxidant and respiration.

1. Introduction

In all life forms, distinct types of cells are the most basic unit of their biological structures and functions, because they are bounded by the membrane lipid bilayers and hence protected from extracellular oxidizing environments. Of note, eukaryotic cells are evolutionarily compartmentalized by endomembrane systems, as a unique trait that distinguishes from prokaryotic cells (1), in order to give rise to distinct functionally-specialized organelles, such as the endoplasmic reticulum (ER), mitochondria and nucleus in eukaryotic cells (2). Such great benefits can allow for cellular respiration, redox metabolism and biochemical reactions to take place in tempo-spatial order during diverse physio-pathological life processes. This is owing to the facts that such versatile organelles participate in a large number of cellular functions. Amongst them, the mitochondrion is known as a central site of cellular respiration, redox metabolism and biosynthesis, in order to meet a host of energy and growth demands (3,4).

Of particular concern is the mitochondrial origin from aerobic α-proteobacterium, which was firstly surmised to be engulped by a primordial anaerobic eukaryote (i.e., the endosymbiotic hypothesis (5)) or originally merged with its archaeal host to give rise to the first eukaryotic cell (i.e., the standpoint of comparative genomics (6,7)). Thereby, this
organelle has its own genetic system with the bacteria-like features, including a compact circular mtDNA genome (from maternal inheritance), along with a simple transcription system that yields multigenic RNA transcripts, and a translational apparatus with similar antibiotic sensitivities to prokaryotic cells. During subsequent endosymbiotic evolution, most of mitochondrial original genes have been lost or transferred to the nucleus in the eukaryotic cells, so that only 37 genes are retained in mammalian mitochondria (3,5). In this genome, only 13 mitochondrial genes encode proteins as essential subunits of the respiratory chain, whilst the remaining 24 genes encode specific tRNA and rRNA required for its protein translation within the mitochondrial matrix (8,9). Such a small complement of mitochondrial genes exists over the entire evolutionary process to strike a balance between the host and its endosymbionts (10,11). However, mitochondrial genetic system only possesses a semi-autonomous nature, such that its mtDNA replication, subsequent transcription and translation are subjected to the predominant control by several nuclear gene-encoding factors (9,11-13), such as mitochondrial transcription factor A (TFAM), B1 (TFB1M) and B2 (TFB2M) (14-17)). Transcriptional expression of these three factors are regulated by nuclear respiratory factor-1 (NRF-1) (18-20). Herein, NRF-1 is also referred to as α-PalNRF1, because it was originally designated α-Pal from its binding to the palindromic consensus site (5′-TGCGATGCGCA-3′) essential for the transcription of elf2α gene (21-23), which controls the general protein translation. Besides, mitochondrial structure and function, as well as its biogenesis, are monitored dominantly by nuclear genome-encoded proteins (17,24,25). Notably, all the other (except the aforementioned 13) subunits of the mitochondrial respiratory chain and oxidative phosphorylation are transcriptionally controlled by nuclear respiratory factors NRF-1 (i.e., α-PalNRF1) and NRF-2 (also called GA-binding protein and abbreviated GABPNRF2, with no homology with α-PalNRF1) binding to distinct consensus sites within these nuclear-encoding respiratory gene promoters (26,27).

Apart from mitochondria, the eukaryotic endomembrane system including the ER and nucleus has been posited to originate from the bacterial-like out membrane vesicles (OMVs) released by the endosymbiont mitochondrial ancestor within the cytosol of its archaeal host at eukaryote origin (1,6). The OMV-based model accounts for i) the functional homology of the ER and mitochondrial intermembrane space with dynamic topological exchanges of Ca^{2+} storage and the disulfide relay system required for redox signaling; ii) the cooperative contributions of the ER and mitochondria to eukaryotic lipid synthesis, as opposed to occurring at the plasma membrane as in all prokaryotes; iii) the distinction in lipid compositions of between the endomembrane system and the plasma membrane, which originated from the fact that bacterial-like lipids replaced the archaeal lipids from the inside in the first place; and that iv) the nuclear envelope is not homologous to the plasma membrane of putative archaeal host, just due to the formation of newly-enveloped nucleus from the ER in eukaryotic cells with open mitosis (6). Recently, functional and proteomic studies have revealed the remarkable complexity of mitochondrial protein machineries with diverse functions, such as protein translocation, oxidative respiration, metabolite transport, protein quality control and the control of membrane architecture, that also interact with each other in dynamic networks (28). These protein networks form distinct membrane contact sites, for example, with the ER, that are key for the integrity of mitochondria with eukaryotic cellular functions in bioenergetic synthesis, oxidative metabolism and redox signalling. The ER–mitochondria connections can also, in turn, determine mitochondrial fusion-fission dynamics. Furtherly, the mitochondrial dynamics and inheritance during cell division and development are also tightly regulated through evolutionary conserved mechanisms(29), such that they are properly segregated and partitioned as a functional set of the organelles to each of daughter cells during cell division, oogenesis, fertilization and subsequent development, as well as to ensure the integrity of its mtDNA during genetic selection of functional genomes. Contrarily, defects in these processes can lead to cell and tissue pathologies, including cancer and other degenerative diseases (29,30). However, whether putative ER-nuclear-mitochondrial (ENUM) communication is involved in mitochondrial regulation remains elusive.

Aside from only 13 mitochondrially-encoded per se proteins (9), all other thousands of the host nucleus-encoded
mitochondrial proteins for its biogenesis, structure and functions in the cellular respiration, oxidative phosphorylation, energy metabolism and redox balance are subjected to their temporospatial precision expression (10,28). Of note, a considerable number of the nucleus-encoded mitochondrial proteins are transcriptionally regulated by α-Pal\textsuperscript{NRF1} and GABP\textsuperscript{NRF2} (26,27), and also translationally monitored by α-Pal\textsuperscript{NRF1}-targeted elf2α (21-23). Particularly, another portion of those nucleus-encoded proteins localized within and around the outer and inner mitochondrial membranes are allowed for biosynthesis in proximity to the ribosome-budded ER, because the ER is central to biosynthesis of secretory and membrane proteins, their proper folding and processing into maturation by quality controls (31,32), before being transferred to the mitochondria and anchored within double mitochondrial membranes. Moreover, the mitochondrial intermembrane space is evolutionarily homologous to the most oxidizing ER lumen, with a lowest GSH/GSSG ratio of 1:1~3:1, than those in the relative reducing mitochondrial matrix and nuclear environments (with a higher GSH/GSSG ratio of ~100:1) (33-35). The reducing nucleus is also segregated by the ER-connected envelope membranes from the relative oxidizing cytoplasm (GSH/GSSH = 30:1~50:1)(33), in which mitochondria is a major source of reactive oxygen species (ROS) produced during cellular respiration (36). However, whether the ER-derived redox signalling mechanism contributes to the nuclear-to-mitochondrial respiratory and antioxidant transcription networks remains unknown.

Amongst the putative ER-derived redox signalling machineries, the most critical antioxidant arm is mediated by the membrane-bound nuclear factor erythroid-2 p45-related factor 1 (Nrf1, also called Nfe2l1) (37,38). The abbreviation is almost identical with nuclear respiratory factor-1 (NRF-1, also called α-Pal\textsuperscript{NRF1}), leading to the confused interpretation of relevant works, the most typical of which was published by L’Honore, et al (with no precision corrections, compared with its original version online in Developmental Cell (39)). As a matter of fact, Nfe2l1 (i.e. Nfe2l1\textsuperscript{NRF1}) is significantly distinctive from α-Pal\textsuperscript{NRF1}, because the former Nrf1 belongs to the cap’n’collar (CNC) basic region-lucine zipper (bZIP) family that regulate distinct subsets of antioxidant/electrophile response element (ARE/EpRE, 5’-TGAC/GnnnGC-3’) driven cytoprotective genes (37,40). Besides, this conserved CNC-bZIP family also includes α-Pal\textsuperscript{NRF2} that is negatively regulated by Kelch-like ECH-associated protein 1 (Keap1, which is an adaptor subunit of Cullin 3-based E3 ubiquitin ligase and also is a key sensor for oxidative and electrophilic stresses) (40). However, hitherto no literature is available for explaining two distinct, but confused Nrf1 transcription factors, albeit they shared the same abbreviations. Herein, we have identified that Nfe2l1\textsuperscript{Nrf1} and α-Pal\textsuperscript{NRF1} exert both synergistic and antagonistic roles in integrative regulation of the nuclear to mitochondrial respiratory and antioxidant transcription profiles. Knockout of Nfe2l1\textsuperscript{Nrf1} in mouse embryonic fibroblasts (MEFs) causes substantial decreases in expression levels of α-Pal\textsuperscript{NRF1} and Nfe2l2\textsuperscript{Nrf2}, along with TFAM and other target genes. Similar results were obtained from Nfe2l2\textsuperscript{Nrf2} MEFs, but rather GSTa1 and Aldh1a1 were significantly up-regulated. Such synergistic contributions of Nfe2l1 and Nfe2l2 to the positive regulation of α-Pal\textsuperscript{NRF1} and TFAM were also validated in Keap1\textsuperscript{−/−} MEFs. By contrast, human α-Pal\textsuperscript{NRF1} expression was almost unaltered by hNfe2l1\textsuperscript{−/−} or hNfe2l2\textsuperscript{−/−}MEFs, albeit its target TFAM was activated by Nfe2l1, along with antagonism against Nfe2l2 in HepG2 cells. Conversely, almost all of mouse Nfe2l1, Nfe2l2 and co-target genes were down-expressed in α-Pal\textsuperscript{NRF1/−} MEFs. Further investigation revealed that human Nfe2l1, Nfe2l2 and relevant reporter genes were down-regulated by ectopic expression of α-Pal\textsuperscript{NRF1}, but such inhibitory effects were reversed by silencing of α-Pal\textsuperscript{NRF1}. Moreover, Pitx2 (pituitary homebox 2) was also identified as a direct upstream regulator of Nfe2l1 and TFAM, besides α-Pal\textsuperscript{NRF1}. Collectively, these across-talks between Nfe2l1, Nfe2l2 and α-Pal\textsuperscript{NRF1}, together with Pitx2, are integrated from the ER-derived signalling to the nuclear-to-mitochondrial communications for their mitochondrial target TFAM, in order to finely tune distinct cellular respiratory and antioxidant gene transcription networks responsible for maintaining their subcellularly-compartmentalized organelle homeostasis, albeit they differ between the mouse and human.

2. Results
2.1 Knockout of Nfe2l1<sup>−/−</sup> in MEFs leads to substantial decreases of Nfe2l2, α-Pal<sup>NRF1</sup>, TFAM and other target genes.

Here, whether knockout of Nfe2l1 has an effect on the constitutive expression of Nfe2l2 and target genes in MEFs was firstly examined by real-time quantitative PCR (RT-qPCR) and Western blotting. As anticipated, loss of Nfe2l1 in mice resulted in substantial decreases in both mRNA and protein levels of Nfe2l2 expressed constitutively in Nfe2l1<sup>−/−</sup> MEFs (Figure 1, A-C). Meanwhile, an according decreases in basal expression of five of the examined ARE-driven genes HO-1 (heme oxygenase 1, HMOX1), GCLM (glutamate-cysteine ligase modifier subunit), MT-1 (metallothionein 1), GSTp (glutathione S-transferase pi 1) and SOD1 (superoxide dismutase 1) were determined in Nfe2l1<sup>−/−</sup> MEFs (Figure 1A). By contrast, significant increases in the basal expression of GSTa1 (glutathione S-transferase, alpha 1 (Ya)) and Aldh1a1 (aldehyde dehydrogenase family 1, subfamily A1) were also obtained from Nfe2l1<sup>−/−</sup> in MEFs (Figure 1 A), even though they were considered as Nfe2l2-target genes [41-43]. Western blotting of Nfe2l1<sup>−/−</sup> MEFs revealed obvious decreases in the protein abundances of HO-1, GCLM, and SOD1, as accompanied by a striking increase in Aldh1a1 protein levels (Figure 1C). In addition, it should also be noted that Nfe2l1α and its derivates were completely deleted in Nfe2l1<sup>−/−</sup> MEFs, but the residual shorter isoforms ΔN, β, γ and δ were detected by Western blotting with the antibodies against amino acids 291-741 of Nfe2l1<sup>−/−</sup> (Figure 1B)[44]. Collectively, these results indicate dual bi-directional contribution of Nfe2l1 to the positive and negative regulation of ARE-driven genes by Nfe2l2 or Nfe2l1α, respectively.

Figure 1. Distinct effects of Nfe2l1<sup>−/−</sup> and Nfe2l2<sup>−/−</sup> on basal expression of mouse α-Pal<sup>NRF1</sup>, TFAM, and relevant genes in MEFs.

(A) The mRNA levels of Nfe2l1 and Nfe2l2, as well as indicated antioxidant genes, were determined by real-time qPCR of Nfe2l1<sup>−/−</sup> and Nfe2l2<sup>−/−</sup> MEFs. The data are shown as mean ± SEM (n=3×3) with significant decreases (*p<0.01, **p<0.001) or increases ($p<0.01, $$p<0.001). (B) Distinct Nfe2l1 isoforms, along with a loading control β-actin, were also examined by Western blotting of Nfe2l1<sup>−/−</sup> and Nfe2l2<sup>−/−</sup> MEFs. (C) Changes in basal protein levels of Nfe2l2 and antioxidant enzymes HO-1, GCLM, SOD1 and Aldh1a1 between Nfe2l1<sup>−/−</sup> and Nfe2l2<sup>−/−</sup> MEFs were also observed. (D) Alterations in the basal mRNA expression levels of α-pal<sup>NRF1</sup>, COX5a, TFAM, Ndufv1, Ndufb6 and SOD1 were unraveled by real-time qPCR of Nfe2l1<sup>−/−</sup> and Nfe2l2<sup>−/−</sup> MEFs. The results are shown as mean ± SEM (n=3×3) with significant
Further RT-qPCR analysis of Nfe2l1−/− MEFs revealed that loss of Nfe2l1α also led to massive decreases in mRNA expression levels of α-PalNRF1 and its target genes TFAM, COX5α (cytochrome c oxidase subunit 5A), Ndufβ6 (NADH:ubiquinone oxidoreductase core subunit V1), Ndufβ6, and SOD1 were down-regulated by loss of Nfe2l1 to different lower extents, when compared to their equivalent levels measured in wild-type (Nfe2l1+/+) cells. The latter notion is corroborate by evidence showing significant decreases in the constitutive protein expression of HO-1, GCLM, SOD1 and Aldh1α (Figure 1H). Interestingly, Western blotting revealed that the full-length Nfe2l1α abundance was only marginally reduced in Nfe2l1−/− MEFs, but its processed isoforms of protein-B to -D were largely abolished by Nfe2l1−/−, also as accompanied by a remarkable increased abundance of Nfe2l1β (Figure 1I). These suggest that possibly proteolytic processing of Nfe2l1α to yield distinct isoforms may be influenced by Nfe2l1.

Comparative analysis of Nfe2l2−/− and wild-type MEFs unraveled almost no changes in mRNA expression levels of α-PalNRF1 and TFAM (Figure 1J). However, both protein levels of α-PalNRF1 and TFAM were markedly down-regulated by loss of Nfe2l2 (Figure 1K), implying that their stabilization may be monitored by Nfe2l2 (Figure 1L). Intriguingly, mRNA expression of COX5α, Ndufβ1 and Ndufβ6, besides SOD1, were down-regulated to varying degrees in Nfe2l2−/− MEFs (Figure 1J). This suggests that Nfe2l2 is likely required for controlling the basal expression of these three mitochondrial respiratory genes regulated by an α-PalNRF1-independent mechanism (Figure 1L).

2.3 Significant increases of Nfe2l1, Nfe2l2, α-PalNRF1, TFAM and other target genes in Keap1−/− MEFs

Knockout of the Nfe2l2-inhibitor Keap1 caused significant increases in protein abundances of Nfe2l2 and its downstream targets HO-1, GCLM, Aldh1α and SOD1 in Keap1−/− MEFs (Figure 2A), as consistent with the previous work (45). Of note, basal abundances of Nfe2l1-α, ΔN, γ and δ, but not -β, isoforms were incremented in Keap1−/− MEFs (Figure 2B), albeit its mRNA expression was unaltered by loss of Keap1 (Figure 2C). However, a substantial decrease of Nfe2l2 at its basal mRNA expression levels was determined in Keap1−/− MEFs (Figure 2C). These observations demonstrate that increased abundances of Nfe2l2, and also possibly Nfe2l1, proteins are negatively monitored by Keap1-mediated degradation. Such co-activation of Nfe2l2 and Nfe2l1 by Keap1−/− led to distinct extents of up-regulation of ARE-driven genes HO-1, GSTα1, Aldh1α, GCLM and SOD1, but not GSTp or MT-1 (Figure 2C). In fact, GSTp was unaffected, whilst MT-1 was marginally suppressed, by Keap1−/−-led co-active Nfe2l2 and Nfe2l1 (Figure 2C), even though GSTp and MT-1 were substantially down-regulated in either Nfe2l1−/− or Nfe2l2−/− MEFs (Figure 1, A & G), no matter whether Nfe2l1β was decreased in Nfe2l1−/− (Figure 1B), but conversely increased in Nfe2l2−/− MEFs (Figure 1H). Thereby, it is inferable
that both GSTp and MT-1 genes (and possibly Nfe2l2 per se) are also likely subjected to the putative dominant negative regulation by, at least, a not-yet-identified transcription factor competitively against the positive effects of Nfe2l2 and Nfe2l1 in Keap1−/− MEFs, as described by Hayes, et al (46).

Figure 2. Distinct roles of key redox control genes in basal expression of mouse α-Pal
NRF1, TFAM, and relevant genes.
(A) Distinct protein levels of keap1 and Nfe2l2, as well as indicated antioxidant enzymes, in between Keap1−/− and Keap1+/+ MEFs were visualized by Western blotting. (B) Altered abundances of distinct Nfe2l1 isoforms between Keap1−/− and Keap1+/+ MEFs were observed. (C) Basal mRNA levels of keap1, Nfe2l1 and Nfe2l2, as well as indicated antioxidant genes, were determined by real-time qPCR of Keap1−/− and Keap1+/+ MEFs. The data are shown as mean ± SEM (n = 3×3) with significant decreases (*p<0.01, **p<0.001) or significant increases ($, p<0.01, $$, p<0.001). (D) Basal mRNA levels of α-Pal51, COX5a, TFAM, Ndufv1, Ndufb6 and SOD1 were also determined as described above. (E) Altered protein levels of α-Pal51 and TFAM were revealed by Western blotting of Keap1−/− and Keap1+/+ MEFs. (F) A model is proposed to present effects of Keap1−/− on Nfe2l1, Nfe2l2, α-Pal51, TFAM, and related genes (and their proteins) in MEFs. (G) Within the promoter region of mouse α-Pal51 gene, the putative ARE sites (each with the core sequence 5′-TGAC/GnnnGC-3′) were marked (as purple dots, left panel). Six distinct ARE-driven reporters (i.e. ARE1 to ARE6-luc) and their respective mutants were constructed into the pGL3-Promoter vector (right panel). (H) Each pair of indicated ARE-luc and mutants was co-transfected with the internal control pRL-TK, together with each of expression constructs for mouse Nfe2l1, Nfe2l2 or empty pcDNA3.1 into RL34 cells for 8 h, before being allowed for 24-h recovery. Subsequently, distinct ARE-driven luciferase activity was measured. The resultant data are shown as mean ± SEM (n=3×3) with significant increases ($, p<0.01, $$, p<0.001) or decreases (*p<0.01). ND, no statistical difference.
By contrast, further examination of Keap1\(^{-}\) MEFS uncovered remarkable increases of α-Pal\(^{NRF1}\) and TFAM in both mRNA and protein expression levels (Figure 2,D & E). This demonstrates up-regulation of both α-Pal\(^{NRF1}\) and TFAM by Keap1\(^{-}\)-led co-activation of Nfe2l2 and Nfe2l1. However, Ndufv1 and Ndubf6 (both encoding two distinct subunits of the mitochondrial respiratory chain complex I) were only slightly promoted, whilst expression of COX5a was roughly unaltered, in Keap1\(^{-}\) MEFS (Figure 2D). This implies a putative negative transcription factor competitively against the positive effects of α-Pal\(^{NRF1}\) on transcriptional expression of its three mitochondrially-targeted genes Ndufv1, Ndubf6 and COX5a encoded in the nucleus of Keap1\(^{-}\) MEFS (Figure 2F).

2.4 Induction of ARE-driven α-Pal\(^{NRF1}\) luciferase reporter genes mediated by ectopic Nfe2l1 and/or Nfe2l2.

To further determine the transcriptional regulation of α-Pal\(^{NRF1}\) by Nfe2l1 and Nfe2l2, we herein created 6 pairs of the wild-type luciferase reporters driven by the indicated ARE consensus sites from mouse α-Pal\(^{NRF1}\) promoter and their corresponding mutants (in Figure 2G). Amongst them, basal activity of ARE2, ARE3, and ARE5 was obviously prevented by their respective mutants (Figure 2H). This implies the putative regulation of these three reporters by endogenous ARE-binding factors Nfe2l1 and/or Nfe2l2. Further co-transfection of RL34 cells with an Nfe2l1\(^{NRF1}\) expression construct revealed that transcriptional expression of the other 5 ARE-, except ARE4-, driven luciferase reporters was activated by Nfe2l1 (Figure 2H). Such Nfe2l1-mediated activity of only ARE5 and ARE6 situated within the first exon was suppressed by their mutants, but other three ARE1, ARE2 and ARE3 activity mediated by Nfe2l1 was largely unaffected by their mutants (Figure 2H). By contrast, transcriptional activity of ARE1-, ARE2- and ARE3-luc reporters was not only activated by Nfe2l2, but also reduced by their respective mutants to relative lower degrees. Together, these indicate that ARE1, ARE2 and ARE3 are Nfe2l2-specific regulatory sites within the mouse α-Pal\(^{NRF1}\) promoter region, whilst ARE5 and ARE6 are Nfe2l1-specific regulatory sites within the 5' non-coding exon one-encoded region of α-Pal\(^{NRF1}\). In addition, ARE1-, ARE2- and ARE3- mutant reporters were also activated by Nfe2l1, but not by Nfe2l2. This suggests a possibility that the three ARE mutants from the α-Pal\(^{NRF1}\) promoter region could also serve as artificial consensuses sites recruiting Nfe2l2 downstream transcription factors. Thus, it is inferable that up-regulation of ARE1, ARE2 and ARE3 activity to mediate α-Pal\(^{NRF1}\) expression may also be mediated by Nfe2l1 directly and/or indirectly its target downstream factors.

2.5 Down-regulation of mouse Nfe2l1, Nfe2l2 and ARE-driven genes by heterogeneous deletion of α-Pal\(^{NRF1}\) in MEFS.

In turn, to explore whether α-Pal\(^{NRF1}\) contributes to Nfe2l1, Nfe2l2 and ARE-driven gene expression, we employed the CRISPR-Cas9-mediated genome-editing of wild-type MEFS to create a cell line called α-Pal\(^{NRF1-/-}\). This cell line was further confirmed to be true by its DNA sequencing and RT-qPCR (Figures 3A & S1). Accordingly, basal expression levels of α-Pal\(^{NRF1}\)-target genes TFAM, Ndufv1, Ndubf6, COX5a and SOD1 were markedly decreased, as α-Pal\(^{NRF1}\) was deleted heterogeneously in α-Pal\(^{NRF1-/-}\) MEFS (Figures 3, A & B). Further RT-qPCR analysis revealed that expression of Nfe2l1, Nfe2l2 and ARE-driven genes GCLM, MT-1, Aldhqa1, GSTa1 and GStP1, besides SOD1, were reduced by α-Pal\(^{NRF1-/-}\) to different lower extents, when compared with those equivalents of α-Pal\(^{NRF1+/+}\) cells (Figure 3C). Western blotting of α-Pal\(^{NRF1-/-}\)-cells unraveled substantial decreases in distinct isoforms of mouse Nfe2l1 and Nfe2l2 proteins (Figure 3, D & E). Consistently, abundances of HO-1, GCLM, Aldhqa1 and SOD1 proteins were strikingly decreased in α-Pal\(^{NRF1-/-}\) MEFS (Figure 3E). Collectively, these findings demonstrate a putative contribution of α-Pal\(^{NRF1}\) (and its signalling) to expression of Nfe2l1, Nfe2l2 and ARE-driven target genes (Figure 3F). In addition to their transcriptional expression, their post-translational processes may also be influenced by α-Pal\(^{NRF1}\) signalling. This is based on the observations that significantly decreases in abundances of Nfe2l1 and HO-1 proteins were, rather, accompanied by less or no changes in their mRNA expression levels, by comparison of α-Pal\(^{NRF1-/-}\) with wild-type (α-Pal\(^{NRF1+/+}\)) MEFS (Figure 3, C-E).
Figure 3. Distinct effects of mouse α-pal on the expression of Nfe2l1, Nfe2l2, TFAM and related genes.

(A) Altered mRNA levels of α-pal, COX5α, TFAM, Ndufv1, Ndufb6 and SOD1 in α-pal MEFs were compared with wild-type (α-Pal). The data are shown as mean ± SEM (n=3×3) with significant decreases (*p<0.01, **p<0.001). (B) Significant changes in α-Pal TFAM and SOD1 proteins were detected by Western blotting of α-pal MEFs, as compared with α-Pal MEFs. The results are shown as mean ± SEM (n=3×3) with significant decreases (*p<0.01, **p<0.001). (C) Altered abundances of distinct Nfe2l1 isoforms in between α-pal and α-Pal MEFs were also visualized. (E) Altered protein levels of Nfe2l2 and indicated antioxidant enzymes (HO-1, GCLM, SOD1 and Aldh1a1) were further unraveled by Western blotting of α-pal and α-Pal MEFs. (F) A model is proposed for distinct effects of α-pal on the nuclear- to- mitochondrial respiratory and antioxidant genes in MEFs.

2.6 No alterations of α-PalNF1 in hNfe2l1α−− or hNfe2l2α−−ΔTA are accompanied by opposing changes of TFAM.

Next, we examined the inter-regulatory effects of between human Nfe2l1 and Nfe2l2 on α-PalNF1, TFAM and other target genes. Unexpectedly, almost no changes in protein and mRNA expression levels of α-PalNF1 were determined in either hNfe2l1α−− or hNfe2l2α−−ΔTA cells (both lines were established by Qiu, et al (38,47)), when compared with those equivalents obtained from wild-type cells (Figures 4, A6 & B). Accordingly, no or less alterations in basal expression of Ndufv1, Ndufb6 and COX5α by hNfe2l1α−− or hNfe2l2α−−ΔTA were also observed (Figure 4B). However, α-PalNF1-target TFAM at its protein and mRNA levels was strikingly down-regulated in hNfe2l1α−− cells, but rather significantly up-regulated in hNfe2l2α−−ΔTA cells, by comparison with their wild-type controls (Figures 4, A7 & B). These observations were further substantiated by transcriptomic sequencing (Figure 4C). Collectively, these results indicate that both Nfe2l1 and Nfe2l2 contributes respectively to the putative positive and negative regulation of human TFAM expression, possibly through a mechanism independent of α-PalNF1. This notion is supported by the evidence showing that a substantial increase in protein abundances of TFAM, rather than α-PalNF1, was resulted from over-expression of ectopic Nfe2l1 (i.e., Nrf1-V5, in Figure 4, cf. D3 with D4).

In addition, the inter-regulatory effects of between human Nfe2l1 and Nfe2l2 on the ARE-driven genes were also validated, as consistent with our previous reports (38,47). Of note, knockout of hNfe2l1α−− caused an marked increase in human Nfe2l2 protein abundances, but not its mRNA expression levels (Figure 4, A2, B and C). In turn, hNfe2l2α−−ΔTA cells gave rise to an obvious reduction of post-synthetically-processed Nfe2l1 isoforms and its mRNA levels (Figures 4, A1, B and C).
Figure 4. Distinct changes of human α-PalNRF1 and TFAM in HepG2-derived hNfe2l1α−/− and hNfe2l2−/− cell lines.

(A) Distinct protein levels of human Nfe2l1, Nfe2l2, α-PalNRF1, TFAM, as well as other relevant proteins were determined by Western blotting of hNfe2l1α−/−, hNfe2l2−/− and wild-type HepG2 cells. (B) Basal mRNA expression levels of Nfe2l1, Nfe2l2, α-PalNRF1, TFAM, and other indicated genes were examined by real-time qPCR of hNfe2l1α−/−, hNfe2l2−/− and wild-type HepG2 cells. The resultant data are shown as mean ± SEM (n=3×3) with significant decreases (*p<0.01, **p<0.001) or significant increases ($, p<0.01, $$, p<0.001). (C) The FPKM (Reads Per Kilobase per Million mapped reads) value of Nfe2l1, Nfe2l2, α-PalNRF1, TFAM, and other indicated genes were obtained by RNA-Sequencing of hNfe2l1α−/−, hNfe2l2−/−, hNfe2l1α−/+siNfe2l2 and hNfe2l1/2−/−. (D) Different protein levels of Nfe2l1, α-PalNRF1 and TFAM were examined in HepG2 cells that had been transfected with a hNfe2l1 expression construct or empty pcDNA3.1. (E) Distinct inducible alterations in abundances of Nfe2l1, Nfe2l2, α-PalNRF1, TFAM, HO-1, GCLM and SOD1 were determined by Western blotting of either hNfe2l1α−/− or hNfe2l1α−/− that had been or not been treated with 50 μmol/L tBHQ. (F, G) Distinct inducible mRNA levels of Nfe2l1, Nfe2l2, α-PalNRF1, HO-1, GCLM, TFAM, COX5a and SOD1 were revealed by real-time qPCR of both tBHQ-stimulated lines of hNfe2l1α−/− cells (F) and hNfe2l1α−/− cells (G). The resultant data are shown as mean ± SEM (n=3×3) with significant increases (*p<0.01, **p<0.001). (H) A model is assumed to present cross-talks between human Nfe2l1 and Nfe2l2, along with distinct effects on human α-PalNRF1, TFAM and other gene expression, particularly upon stimulation by tBHQ.

Western blotting of hNfe2l1α−/− revealed that massive increases of both GCLM and HO-1 proteins were coincided with hyper-active Nfe2l2 (Figure 4, A3 & A4). RT-qPCR analysis unraveled that mRNA expression of HO-1 was substantially up-regulated in hNfe2l1α−/− cells, but also significantly down-regulated in hNfe2l2−/−/TA cells (Figure 4B), whereas GCLM expression was roughly unaltered in these two cell lines, when compared to wild-type controls. Further
transcriptomic sequencing unveiled that basal GCLM expression was only repressed by hNfe2l1α−/−-siNrf2 (Figure 4C), implying that it is co-regulated by both Nfe2l1 and Nfe2l2. Furthermore, GSTp1 was up-expressed in hNfe2l1α−/− cells, and also further incremented in hNfe2l1α−/−+siNrf2 cells, but rather unaltered in hNfe2l2α−/−TA cells, when compared to wild-type controls (Figures 4, B & C). By contrast, mRNA expression of MT1E (encoding metallothionein 1E) was almost completely abolished in hNfe2l1α−/− or hNfe2l1α−/−+ siNfe2l2 cells, but also enormously augmented in hNfe2l2α−/−TA cells (Figures 4, B & C). Overall, these demonstrate that Nfe2l1 and Nfe2l2 contributes to the positive and negative regulation of MT1E, respectively, on which Nfe2l1 exerts its dominant effect, but GSTp1 and HO-1 expression is Nfe2l2-dependent. However, SOD1 expression is Nfe2l1α-dependent, because its protein and mRNA levels were reduced in hNfe2l1α−/− or hNfe2l1α−/−+siNfe2l2 cells, but largely unaffected in hNfe2l2α−/−TA cells (Figures 4, A5, B & C).

2.7 Induction of α-PalNRF1 and TFAM by tert-butylhydroquinone (tBHQ) is completely abolished in hNfe2l1α−/− cells.

Here, we determined effects of hNfe2l1α−/− on tBHQ-stimulated expression of α-PalNRF1 and TFAM. As anticipated, abundances of α-PalNRF1, TFAM and SOD1 proteins were evidently increased following 50 μmol/L tBHQ treatment of wild-type (hNfe2l1α+/+) cells, when compared with the vehicle DMSO-treated controls (Figure 4, E5 & E6). However, similar increases of α-PalNRF1, TFAM and SOD1 were not observed in hNfe2l1α−/− cells, even though hyper-active Nfe2l2 was further incremented by tBHQ (cf. E2 with E5-E7). Subsequently, RT-qPCR analysis revealed that mRNA expression levels of α-PalNRF1, TFAM, COX5a and SOD1 were induced, to greater or less extents (Figure 4F), by tBHQ stimulation of Nfe2l1, but not Nfe2l2, in hNfe2l1α−/− cells (Figures 4, E & F). This is based on the fact that tBHQ-inducible increases of α-PalNRF1, TFAM, COX5a, rather than SOD1, appeared to be completely abolished in hNfe2l1α−/− cells, albeit Nfe2l2 was hyper-expressed by tBHQ (Figure 4G). Altogether, these demonstrate transcriptional regulation of α-PalNRF1, TFAM and COX5a dominantly by tBHQ-inducible Nfe2l1, but not Nfe2l2, whilst SOD1 expression is co-regulated by both CNC-bZIP factors (Figure 4H). In addition, tBHQ treatment of hNfe2l1α−/− cells led to significant increases in protein and mRNA levels of HO-1 and GCLM (Figures 4, E3, E4 & F). Similar induction of HO-1 and GCLM by tBHQ was also obtained in hNfe2l1α−/− cells (Figures 4, E3, E4 & G). Thus, it is inferable that Nfe2l2 makes a major contribution to induction of HO-1 and GCLM expression by tBHQ (Figure 4H).

2.8 Another contribution of α-PalNRF1 to transrepression of human Nfe2l1, Nfe2l2 and ARE-driven genes

To clarify putative contributions of α-PalNRF1 to transcriptional expression of Nfe2l1, we herein made two luciferase reporters driven by mouse and human Nfe2l1 gene promoter regions, called mNfe2l1-luc and hNfe2l1-luc, respectively. As unexpected, ectopic α-PalNRF1-V5 over-expression only caused a slight reduction in activity in mNfe2l1-luc reporter (Figure 5A), albeit this reporter gene was significantly induced by tBHQ (Figure 5B, b1). Similarly, activity of hNfe2l1-luc reporter was substantially activated by tBHQ (Figure 5B, b2), but also significantly suppressed by ectopic expression of α-PalNRF1-V5 (Figure 5C, c1 & c3). Such over-expression of ectopic α-PalNRF1-V5 also led to transrepression of GSTa2-ARE-x6-luc reporter (Figure 5C, c2 & c3). These indicate a possible contribution of α-PalNRF1 to transrepression of Nfe2l1-luc and ARE-x6-luc reporter genes.

Western blotting of α-PalNRF1-expressing cells revealed that its targets TFAM and SOD1 were evidently enhanced, whilst abundances of Nfe2l1 and Nfe2l2 proteins were markedly diminished by ectopic α-PalNRF1-V5 (Figure 5D, d1-d5). Accordingly, HO-1 and GCLM abundances were also partially inhibited by α-PalNRF1-V5 (Figure 5D, d6 & d7). Conversely, knockdown of α-PalNRF1 by its specific siRNA (Figure 5, E & M1) only caused a marginal reduction of TFAM (Figure 5, F & M2), implying coordinated transcription regulation of human TFAM by α-PalNRF1 with another factor (e.g. GABPRNRF1). By contrast, both mRNA and protein levels of SOD1 were modestly promoted by silencing of α-PalNRF1 (Figure 5,G & M3), implying one of other putative transcription factors competitively against knockdown of α-PalNRF1. Similar results were also obtained from the case of COX5a (Figure 5H).
Figure 5. A negative effect of α-PalNRF1 on Nfe2l1, Nfe2l2 and other antioxidant genes in HepG2 cells.

(A) HepG2 cells were co-transfected for 8 h with mNfe2l1-luc reporter and the pRL-TK control, along with an expression construct for mouse α-PalNRF1 or an empty pcDNA3.1, and then allowed for a 24-h recovery before the luciferase activity was measured (A1). Total lysates were also subjected to identification by Western blotting with distinct antibodies against α-PalNRF1 (A2) or V5 tag (A3). (B) HepG2 cells were co-transfected for 8 h with mNfe2l1-luc (B1) or hNfe2l1-luc (B2), plus pRL-TK, and then treated with 50 μmol/L tBHQ or the DMSO vehicle for 24 h, before being allowed for additional 24-h recovery. Subsequently, these samples were subjected to dual luciferase assays. The results are shown as mean ± SEM (n=3×3) with significant increases ($, p<0.01). (C) HepG2 cells were co-transfected for 8 h with hNfe2l1-luc (C1) or AREx6-luc (C2) together with pRL-TK, plus a human α-PalNRF1 expression construct or an empty pcDNA3.1 and then allowed for 24-h recovery from co-transfection, before the reporter activity was measured. The data are shown as mean ± SEM (n=3×3) with significant decreases (*p<0.01). Total cell lysates were also subjected to characterization by Western blotting with distinct antibodies against α-PalNRF1 (C3) or V5 tag (C4). (D) Distinct protein levels of α-PalNRF1, TFAM, SOD1, Nfe2l1, Nfe2l2, HO-1 and GCLM were determined by Western blotting of HepG2 cells that had been transfected with α-PalNRF1 expression plasmid or an empty pcDNA3 vector. (E-L) Distinct changes in mRNA levels of α-PalNRF1 (E), TFAM (F), SOD1 (G), COX5a (H), Nfe2l1(J), Nfe2l2(J), HO-1(K) and GCLM(J) were analyzed by real-time qPCR of HepG2 cells that had been transfected with 0, 25, 50 and 100 nM of siRNA against α-PalNRF1. The resulting data are shown as mean ± SEM (n=3×3) with significant decreases (*p<0.01, **p<0.001) or increases ($, p<0.01). (M) Such siRNA-transfected cell lysates were subjected to Western blotting analysis of distinct protein abundances as indicated. (N) A model is proposed to present disparate effects of α-PalNRF1 over-expression or its knockdown on the nuclear-to-mitochondrial respiratory and antioxidant genes in HepG2 cells.

Further examinations revealed that modestly increased proteins of Nfe2l1, Nfe2l2 and HO-1 (Figure 5M, M4-6) were coincidently accompanied by marginal enhancements of their mRNA expression levels, particularly following transfection of HepG2 cells with 50 nM siRNA against α-PalNRF1 (Figure 5, S-I-K). In addition, GCLM protein and mRNA levels were almost unaffected by silencing of α-PalNRF1 (Figure 5, L & M7). Taken together, these results indicate that α-PalNRF1 contributes to the negative regulation of human Nfe2l1, Nfe2l2 and HO-1 (Figure 5N). However, no dose-responses of Nfe2l1, Nfe2l2 and HO-1 to different concentrations of α-PalNRF1-silenced siRNAs indicate a possible
involvement of other transcription factors (e.g., Pitx2, GABPNRF2). Moreover, α-PalNRF1 exerts disparate effects on GCLM, possibly depending on whether Nfe2l1, Nfe2l1 and other unidentified transcription factors were also stimulated by α-PalNRF1 over-expression or its RNA-silencing.

Figure 6. Identification of pitx2 as an upstream regulator of Nfe2l1, besides α-palNRF1.

(A) HepG2 cells were co-transfected for 8 h with mNfe2l1-luc (A1) or empty pGL3-Basic (A2), together with the pRL-TK control, plus a Pitx2 expression construct or empty pcDNA3.1, and then allowed for a 24-h recovery before the luciferase activity was measured. The data are shown as mean ± SEM (n=3×3) with significant increases ($, $p<0.01$) or NS (not significance). (B) Putative cis-regulatory binding sites for Pitx2, α-PalNRF1 and AREs within the human Nfe2l1 promoter region were indicated. Various lengths of hNfe2l1-luc were cloned into the pGL3-Basic vector as shown schematically. (C) HepG2 cells were co-transfected for 8 h (i) with hNfe2l1-luc and pRL-TK, and also treated for 24 h with 50 μmol/L tBHQ or the DMSO vehicle (C1); (ii) with hNfe2l1-luc (C2), hNfe2l1-luc1 (C3), or hNfe2l1-luc2 (C4), along with the pRL-TK control, plus a Pitx2 expression construct or an empty pcDNA3.1, before being allowed for additional 24-h recovery. The samples were then subjected to dual luciferase assays. The results are shown as mean ± SEM (n=3×3) with significant increases ($, $p<0.01$). (D) HepG2 cells were co-transfected for 8 h with each of PitxRE-luc reporters or their mutants, together with pRL-TK plus a Pitx2 expression construct or an empty pcDNA3.1, and then allowed for 24-h recovery. Thereafter, the reporter activity was detected and calculated as mean ± SEM (n=3×3) with significant increases ($, $p<0.01$). (E) Distinct mRNA levels of Pitx2, Nfe2l1 and HO-1 were detected by real-time qPCR of HepG2 cells that had been transfected with an expression construct for Pitx2 or an empty pcDNA3.1 vector. (F) Pitx2-expressing HepG2 cells were subjected to Western Blotting of Pitx2, Nfe2l1, Nfe2l2, HO-1, GCLM, α-PalNRF1, TFAM and SOD1. (G-N) Distinct mRNA levels of Pitx2 (G), α-PalNRF1 (H), TFAM (I), Nfe2l1 (J), HO-1 (J), GCLM (L), COX5a (M) and SOD1 (N) were determined by real-time qPCR analysis of HepG2 cells that had been transfected with three different siRNAs against Pitx2. The results are shown as mean ± SEM (n=3×3) with significant decreases (*$p<0.01$, **$p<0.001$). (O) A model is proposed for potential effects of Pitx2 on Nfe2l1, Nfe2l2, α-PalNRF1, TFAM and other genes in HepG2 cells.
2.9 Identification Pitx2 as a upstream regulator to mediate transactivation of human Nfe2l1 gene.

Clearly, \(\alpha\text{-Pal}^{\text{NRF1}}\) was identified as a direct target of Pitx2/3 (pituitary homeobox 2/3, also paired like homeodomain 2/3) (39). Here, we determine whether Pitx2 also acts as a direct upstream factor to mediate transactivation of human Nfe2l1. As shown in Figure 6A, activity of mNfe2l1-luc reporter was significantly transactivated by ectopic Pitx2, when compared with the basal activity measured from its co-transfection with an empty pGL3-Basic vector. Similar results were also obtained from those hNfe2l1-luc reporters (Figure 6, B & C). Of note, over-expression of ectopic Pitx2 caused gradual increments in the trans-activity of hNfe2l1-luc, hNfe2l1-luc1 and hNfe2l1-luc2 reporters (Figure 6C, C2-C4). The hNfe2l1-luc activity was also strikingly induced by tBHQ to the extent of hNfe2l1-luc1 transactivation mediated by Pitx2 (Figure 6C, cf. C1 with C3). In addition, four distinct consensus Pitx-response elements (PitxREs), which are situated at the upstream of the indicated promoter region to yield hNfe2l1-luc1 (Figure 6B), were also identified here. The results revealed that only PitxRE2-luc activity was modestly activated by Pitx2, but basal activity of PitxRE3-luc and PitxRE4-luc was partially suppressed by Pitx2 (Figure 6D). Together, these indicate that transcriptional expression of human Nfe2l1 gene is likely co-regulated by Pitx2 and its target factors.

RT-qPCR analysis revealed that endogenous mRNA expression of human Nfe2l1 and HO-1 was increased by Pitx2 over-expression (Figure 6E). Western blotting of Pitx2-expressing cells unraveled significant increases in abundances of all 7 examined proteins Nfe2l1, Nfe2l2, HO-1, GCLM, \(\alpha\text{-Pal}^{\text{NRF1}}\), TFAM and SOD1 (Figure 6F, F2-F8). These demonstrate that Pitx2 may also serve as a upstream regulator to mediate transcriptional expression of Nfe2l1 (and Nfe2l2), besides \(\alpha\text{-Pal}^{\text{NRF1}}\). This notion is further supported by the evidence obtained from silencing of Pitx2 by its three distinct siRNA sequences (as listed in Table S1). Consequently, silencing of Pitx2 led to varying decreases in basal mRNA expression levels of \(\alpha\text{-Pal}^{\text{NRF1}}\), TFAM, Nfe2l1, HO-1, GCLM, COX5a and SOD1 to less extents than their equivalent negative controls (Figure 6, G-N). Thereby, these results unveil that Pitx2 is required for mediating transcriptional expression of Nfe2l1, \(\alpha\text{-Pal}^{\text{NRF1}}\) and their target genes (Figure 6O).
note, mitochondria-targeting sequences (MTS), nuclear localization signal (NLS) and DNA-binding MHG-box were also indicated. Both MT51 (aa 1-18) and MT52 (aa 21-38) were wheeled into two similar α-helical structures. Basic arginine and lysine residues were placed on blue backgrounds, nucleophilic serine and threonine residues are on purple backgrounds, an unamiable proline residue was on a green background, and all hydrophobic amino acids were on yellow backgrounds, except for small alanine and glycine on grey backgrounds. (B) The putative consensus ARE sites and other cis-regulatory binding sites for Pitx2, α-Pal\textsuperscript{NRF2}, or GABP within the human TFAM gene promoter region were indicated. (C) Four distinct ARE-driven (i.e. ARE1-luc to ARE4-luc) and another Pitx2RE-luc reporters were constructed into the pGL3-Promoter vector. (D) HepG2 cells were co-transfected with PitxRE-luc and pRL-TK, plus a Pitx2 expression plasmid or an empty pcDNA3.1, and then allowed for 24-h recovery before the luciferase activity was measured. The data are shown as mean ±SEM (n=3×3) with significant increase ($, p<0.01). (E) HepG2 cells were co-transfected with each of ARE1-luc to ARE4-luc, together with pRL-TK plus an expression construct for Nrf1, Nrf2 or empty pcDNA3.1, and then allowed for 24-h recovery, before such ARE-driven activity was detected. The resultant data are shown as mean ± SEM (n=3×3) with significant increases ($, p<0.01) or decreases (*p<0.01). (F) A model is proposed to explain the transcriptional regulation of TFAM by Nfe2l1, Nfe2l2, Pitx2 and α-Pal\textsuperscript{NRF2} in HepG2 cells.

### 2.10 Identification of TFAM as another direct co-target of human Nfe2l1, Nfe2l2 and Pitx2.

Although TFAM is known as a direct target of α-Pal\textsuperscript{NRF2} (18,48,49), we further determined whether it also serves as another direct co-target of Nfe2l1, Nfe2l2 and Pitx2. The amino acid sequences of three nuclearly-encoded TFAM from the human and mouse were aligned (as illustrated in Figure 7A), revealing that two mitochondria- targeting sequences are located within the N-terminal region of this MHG-box-binding transcription factor. Further analysis of human TFAM promoter showed the putative consensus cis-regulatory elements, such as AREs, PitxRE and α-Pal-binding site (Figure 7B). Amongst them, ARE- and PitxRE-driven luciferare reporters were established (Figure 7C). As a result, the luciferase assays of both PitxRE-Luc and ARE3-Luc activity demonstrated that transcriptional expression of TFAM is co-regulated by human Pitx2, Nfe2l1 and Nfe2l2 (Figure 7, D-F).

### 3. Discussion

In this study, we have, for the first time, provided a better interpretation of two totally distinctive Nrf1 transcription factors (i.e. Nfe2l1\textsuperscript{NRF1} and α-Pal\textsuperscript{NRF1} renamed here). This is an attempt to rectify the previously-confusing explanations of both Nrf1 factors from their commonly-shared abbreviations in the literature as far as we have known(17,37,50), in which one of the most typical representative is the publication confused by L'Honore, et al (39). Similarly, another two Nrf2 transcription factors (51,52) are also referred to as Nfe2l2\textsuperscript{NRF2} and GABPα\textsuperscript{NRF2}, respectively. Of note, the antioxidant master Nfe2l2\textsuperscript{NRF2} is evolutionarily conserved with Nfe2l1\textsuperscript{NRF1}, but not with the nuclear respiratory factors α-Pal\textsuperscript{NRF2} and GABPα\textsuperscript{NRF2}, of which the latter two factors have also no any homology with each other. Collectively, our present study has elucidated synergistic and antagonistic roles of between Nfe2l1\textsuperscript{NRF1} (and/or Nfe2l2\textsuperscript{NRF2}) and α-Pal\textsuperscript{NRF2} in integrative regulation of the signalling to the nuclear-to-mitochondrial respiratory and antioxidant transcription networks, which differ between the mouse and human (Figure 8).

### 3.1 Synergism of mouse Nfe2l1\textsuperscript{NRF1}, Nfe2l2\textsuperscript{NRF2} and α-Pal\textsuperscript{NRF2} to coordinate the nuclear-to-mitochondrial respiratory and antioxidant gene responses in MEFs.

Clearly, Nfe2l1 and Nfe2l2 are two highly-conserved members of the CNC-bZIP transcription factors predominantly regulating distinct subsets of ARE-driven cytoprotective genes against oxidative stress (37,53). These target genes are critically involved in maintaining cellular homeostasis and organ integrity during normal development and growth, as well as healthy life process, in which Nfe2l1 and Nfe2l2 cannot only exert their combinational and/or overlapping roles, and also manifest their distinctive functions. Importantly, Nfe2l1 can elicit its unique dispensable physio-pathological functions, because its loss in the mouse leads to distinct pathological phenotypes, even in the presence of Nfe2l2 (37). This implies a fact that the loss of Nfe2l1 cannot be compensated by Nfe2l2, albeit the latter Nfe2l2 has been accepted as a master regulator of antioxidant, detoxification and cytoprotective responses (53,54). Such significant distinctions
in the functioning of between Nfe2l1 and Nfe2l2 are dictated by their respective intrinsic features.

Figure 8. Two distinct models for integrative regulation of cellular respiratory and antioxidant transcription networks.

(A) A model is proposed on the base of experimental evidence obtained from MEFs, to give a better understanding of regulatory cross-talks between Nfe2l1\textsuperscript{Ntrp}, Nfe2l2\textsuperscript{Ntrp} and \(\alpha\)-Pal\textsuperscript{Ntrp}, along with Pitx2, which are responsible for the nuclear-to-mitochondrial respiratory and antioxidant gene transcription networks. Of note, Nfe2l1\textsuperscript{Ntrp} can make opposing contributions to the bi-directional regulation of Nfe2l2\textsuperscript{Ntrp} and \(\alpha\)-Pal\textsuperscript{Ntrp} by itself and target proteasome (PSM) at two distinct layers. Nfe2l2\textsuperscript{Ntrp} can also determine putative post-transcriptional regulation of Nfe2l1\textsuperscript{Ntrp} and \(\alpha\)-Pal\textsuperscript{Ntrp}, but the detailed mechanisms remain unclear. In turn, \(\alpha\)-Pal\textsuperscript{Ntrp} also has a capability to positively regulate Nfe2l1\textsuperscript{Ntrp} and Nfe2l2\textsuperscript{Ntrp}, albeit no canonic GC-rich \(\alpha\)-Pal-binding sites within these mouse CNC-bZIP gene promoters (Table S2). Such nucleus-controlled mitochondrial respiratory and oxidative phosphorylation is also a primary source of byproduct reactive oxygen species (ROS) in cells, which can, in turn, trigger putative physiological activation of Nfe2l1\textsuperscript{Ntrp}, Nfe2l2\textsuperscript{Ntrp} and \(\alpha\)-Pal\textsuperscript{Ntrp}. Besides, GABP\textsuperscript{Ntrp} is also required for this process, but not yet identified herein. In addition to negative regulation of Nfe2l2\textsuperscript{Ntrp}, Keap1 can rather positively regulate transcription of this CNC-bZIP factor. (B) Another model is proposed, based on experimental evidence obtained from HepG2 cells, to give a better explanation of distinct cross-talks amongst Nfe2l1\textsuperscript{Ntrp}, Nfe2l2\textsuperscript{Ntrp} and \(\alpha\)-Pal\textsuperscript{Ntrp}, along with Pitx2. All these factors are converged on the nucleus-encoded mitochondria-targeting TFAM, but Nfe2l2\textsuperscript{Ntrp} may contribute to dual opposing effects on this mitochondrial transcription factor. Furthermore, \(\alpha\)-Pal\textsuperscript{Ntrp} can also make a negative contribution to transcription of human Nfe2l1\textsuperscript{Ntrp} and Nfe2l2\textsuperscript{Ntrp}, albeit all three factors are activated by redox inducer tBHQ. Of note, Nfe2l2\textsuperscript{Ntrp} is negatively regulated by Nfe2l1\textsuperscript{Ntrp}. In addition, human Nfe2l1\textsuperscript{Ntrp} is also essential for stabilization of Keap1, but whether the adaptor subunit of Cullin 3-based E3 ubiquitin ligase is involved in the proteolytic processing of Nfe2l1\textsuperscript{Ntrp} remains elusive.

Interestingly, Nfe2l1, but not Nrf2, with several domains being more highly conserved with its ancestral CNC, Skn-1 and Nach proteins (55), is located in the ER and its connected nuclear envelope membranes. Of note, there exist two extra functional domains (i.e. NTD and NST) within Nfe2l1, rather than Nfe2l2. The ER-targeting NTD of Nfe2l1 enables it to be topologically anchored within and around the membranes (56-58), whilst its NST glycodomain facilitates its proper protein folding and subsequent processing (59-61). The membrane-topology of Nfe2l1 determines its selective proteolytic processing by proteasomes and/or other cytosolic proteases in close proximity to the ER, in order to yield
distinct lengths of its isoforms, before its mature CNC-bZIP factor is translocated into the nucleus (44,61,62). Such the membrane-bound Nfe2l1 factor can also be activated in the unfolded protein response to the ER stress stimulated by tunicamycin (to inhibit its N-linked glycosylation) (38), in addition to its proteasomal ‘bounce-back’ response (63,64). By contrast, the water-soluble Nfe2l2 is segregated by Keap1 within the cytoplasmic compartments, where it is targeted for its ubiquitination-mediated proteasomal degradation (40,53). Upon stimulation of Nfe2l2 by oxidative stress, this CNC-bZIP factor is dissociated from the cytoplasmic Keap1, so that it is translocated into the nucleus and transactivates ARE-driven target genes. Collectively, these distinctions of Nfe2l1 from Nfe2l2 demonstrate disparate selection of their tempo-spatial activation or inactivation insomuch as to finely tune distinct subsets of target genes. As such, this also presages synergism and antagonism of between Nfe2l1 and Nfe2l2 in regulating distinct cognate gene expression.

In fact, mouse Nfe2l1/−/− embryonic lethality occurred at middle to late gestation starting at E13.5 (65), whereas the double knockout of Nfe2l11/−/−:Nfe2l21/−/− caused an earlier death of the mouse embryos at E10.5 due to extensively increased apoptosis and growth retardation induced by severe endogenous oxidative stress (66). The elevated ROS levels resulted from severely impaired expression of antioxidant defense genes (e.g. Mt-1, Gclm, Gclc, Ferritin H, Ho-1, Nqo1) in Nfe2l11/−/−:Nfe2l21/−/− MEFs, when compared with the individual knockout of Nfe2l1/−/− or Nfe2l2/−/−. Hence, it is inferred that Nrf2 is also allowed for a partial compensation for the loss of Nrf1 function in synergistically regulating critical genes for the intracellular redox homeostatic setting at the robust threshold state during embryogenesis. Such partially overlapping functions of both Nfe2l1 and Nfe2l2 are determined by co-expression patterns of the two CNC-bZIP factors (67-69) and their similarity of conserved sequences (37), which are also, though, driven by their respective ARE-containing gene promoters (Table S2).

It is, to our surprise, that the evidence presented herein reveals that knockout of Nfe2l1 in mice leads to significant decreases of both mRNA and protein levels of Nfe2l2 expressed in Nfe2l1/−/− MEFs. By contrast, almost no changes in mRNA expression levels of Nfe2l2 in Nfe2l2/−/− MEFs, but the loss of Nfe2l2 results in obvious decreases in abundances of the full-length Nfe2l1α and its processed proteins (i.e. isoform-B, C & D), as accompanied by an increased Nfe2l1β. Collectively, these results demonstrate that Nfe2l2 acts as a dominant positive regulator to monitor basal constitutive expression of Nfe2l2, at least in MEFs (Figure 8A). In turn, it does not hold true, but Nfe2l12 is required for stabilization of Nfe2l1α and its proteolytic processing to yield a mature CNC-bZIP factor. This notion is further substantiated by the evidence obtained from Keap1/−/− MEFs, showing that obvious accumulation of Nfe2l2 is accompanied by significant increases in abundances of Nfe2l1α and its derivates, but basal mRNA expression of Nfe2l1 remains to be unaffected.

Recently, emerging evidence showed that the regulatory cross-talks of between Nfe2l12 (but not Nfe2l1) with either α-PalNRF1 or GABPαNRF2 are involved in the nuclear control of mitochondrial biogenesis and relevant biological functions (51,52,70). In this study, we unravel that knockout of Nfe2l1 causes significant decreases in mRNA and/or protein levels of α-PalNRF1 and its target genes TFAM, Ndufv1, Ndub6, COX5a and SOD1 in Nfe2l1/−/− MEFs, whereas knockout of Nfe2l2/−/− leads to marked decreases in protein abundances of α-PalNRF1 and TFAM, but almost unaltered mRNA levels α-PalNRF1 and TFAM were observed in Nfe2l2/−/− MEFs. These results indicate that Nfe2l1 acts as a dominant regulator to monitor transcriptional expression of α-PalNRF1, TFAM and other target genes in MEFs, whilst stability of both α-PalNRF1, TFAM proteins may be monitored by Nfe2l1-mediated mechanisms. This is supported by another evidence showing that Keap1/−/− MEFs gave rise to evident increases in basal abundances of Nfe2l2, Nfe2l1α and its processed isoforms, as accompanied by obvious increased proteins of α-PalNRF1 and TFAM. However, only modest increases in their mRNA expression levels of α-PalNRF1 and TFAM were examined in Keap1/−/− MEFs, with an exception of significantly reduced mRNA levels of Nfe2l2, but not of Nfe2l1. This exception implies that transcriptional expression of Nfe2l2 requires for a putative positive feedback mechanism mediated by Keap1, albeit this Nfe2l2 inhibitor negatively regulates stability of this CNC-bZIP protein. Moreover, our further luciferase assays also revealed that both Nfe2l1 and Nfe2l2 contribute to

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transcriptional expression of distinct ARE-driven $\alpha$-Pal$^{\text{NRF1}}$ reporters. Conversely, marked decreases in both mRNA and protein levels of Nfe2l1 and Nfe2l2 resulted from heterogeneous deletion of mouse $\alpha$-Pal$^{\text{NRF1}}$−/−. Overall, these indicate bidirectional cross-talks of Nfe2l1 and Nfe2l2 with $\alpha$-Pal$^{\text{NRF1}}$ at distinct layers to coordinate the extra-nuclear signalling to the nuclear-to-mitochondrial respiratory and antioxidant transcription networks (as modeled in Figure 8A).

3.2 Cross-talks between human Nfe2l1$^{\text{NRF1}}$, Nfe2l2$^{\text{NRF2}}$ and $\alpha$-Pal$^{\text{NRF1}}$ to coordinate the nuclear-to-mitochondrial respiratory and antioxidant gene transcription networks.

Intriguingly, we found almost no effects of hNfe2l1$^{\text{−/−}}$ or hNfe2l2$^{\text{−/−}}$ on mRNA and protein levels of human $\alpha$-Pal$^{\text{NRF1}}$ in this experimental setting, albeit both CNC-ZIP genes contain at least one consensual $\alpha$-Pal binding site within their promoters (Table S3). This is also further confirmed by transcriptomics sequencing of hNfe2l1$^{\text{−/−}}$ +siNfe2l2, as compared with those obtained from hNfe2l1$^{\text{−/−}}$ or hNfe2l2$^{\text{−/−}}$ cells. Such results are really contrary to those obtained from mouse Nfe2l1$^{\text{−/−}}$ and Nfe2l2$^{\text{−/−}}$ as described above. Conversely, significantly decreases of human Nfe2l1 and Nfe2l2 protein levels were caused by forced expression of ectopic $\alpha$-Pal$^{\text{NRF1}}$. Similarly, transcriptional activity of hNfe2l1-luc, rather than mNfe2l1-luc, reporters was also markedly diminished by ectopic $\alpha$-Pal$^{\text{NRF1}}$. By contrast, a recovery of human Nfe2l1 and Nfe2l2 from inhibition of $\alpha$-Pal$^{\text{NRF1}}$ was acquired after this respiratory factor was silenced. Notably, silencing of $\alpha$-Pal$^{\text{NRF1}}$ can only cause a modest decrease in its target TFAM expression, implying that this mitochondrial transcription factor is also monitored by other factors (e.g. GABP$^{\text{NRF2}}$ and/or Pitx2) beyond $\alpha$-Pal$^{\text{NRF1}}$. In this study, we also found that TFAM was down-regulated in hNfe2l1$^{\text{−/−}}$ cells (with accumulation of Nfe2l2), and hence up-regulated in Nfe2l2$^{\text{−/−}}$ cells. Our further evidence reveals that TFAM along with $\alpha$-Pal$^{\text{NRF1}}$ are significantly induced by a redox inducer tBHQ, but such inducible expression levels of both factors are almost completely abolished by hNfe2l1$^{\text{−/−}}$. Collectively, these indicate that Nfe2l1 and Nfe2l2 contribute, respectively, to the putative positive and negative regulation of TFAM, though both CNC-ZIP factors are inhibited by $\alpha$-Pal$^{\text{NRF1}}$ through as-yet-unidentified mechanisms (Figure 8B). Accordingly, the positive regulation of TFAM by Nfe2l1 is further corroborated by its consensus ARE3-driven reporter assays. However, it should also be noted that the opposing effects of Nfe2l2 on the endogenous TFAM and its consensus ARE3-luc reporter could depend on distinct ARE3-adjoining promoter contexts.

Importantly, we have presented the evidence that activity of hNfe2l1-luc reporter is transactivated by Pitx2 (albeit it serves as a direct upstream regulator of $\alpha$-Pal$^{\text{NRF1}}$ (39)). Further evidence also reveals that endogenous expression of Nfe2l1 (and Nfe2l2) was significantly up-regulated by over-expression of Pitx2, but rather down-regulated by silencing of this homeobox factor. Such Pitx2-directed alternations of Nfe2l1 and Nfe2l2 are also accompanied by corresponding changes of HO-1, GCLM, as well as $\alpha$-Pal$^{\text{NRF1}}$, TFAM and COX5a. In addition to human Nfe2l1, TFAM is another potential target of Pitx2, because its consensus PitxRE-luc reporter was transactivated by this homeobox factor. Altogether with our previously-reported evidence (38,47), these demonstrate multiple regulatory cross-talks between Nfe2l1, Nfe2l2 and $\alpha$-Pal$^{\text{NRF1}}$, along with Pitx2 and its target TFAM (Figure 8B), are integrated from the extra-nuclear signalling to the nuclear-to-mitochondrial controls of distinct cellular respiratory and antioxidant gene transcription networks. Yet, they differ between the mouse and human.

4. Conclusion

Generally, biological functions and physiology responses at different levels are determined by a range of regulatory mechanisms from various signaling pathways to multiple transcription factor-mediated gene networks. Such being the case, these transcription factors and other regulatory molecules could be simplified as key modules which cross-talk among them, in order to form a hierarchical network. In this study, Nfe2l1 and Nfe2l2 are embedded in such a complex molecular interaction network, responsible for antioxidant, detoxification and cytoprotective adaptation to distinct physiological stresses during life process. Of note, Nfe2l1 is endowed with unique dispensable biological
functions. This fact confers Nfe2l1 to be distinguished from Nfe2l2 at regulating distinct subsets of ARE-driven cognate genes (e.g., Aldh1a1 and GSTa1). But, the inter-regulatory synergism of Nfe2l1 and Nfe2l2 confers both factors to exert their overlapping roles for co-target genes (e.g., MT-1, GSTp and SOD1) in MEFs. By contrast, apparent synergistic and antagonistic relationships of between human Nfe2l1 and Nfe2l2 are also demonstrated. Nfe2l1 is a dominant repressor whilst Nfe2l2 is positively regulated by Nfe2l1 in HapG2 cells. Such function of Nfe2l1 is considered as a brake to avoid Nfe2l2 overshoot. For this simplification to be valid, there should always be a correlation between Nfe2l1 and Nfe2l2, so that both CNC-bZIP factors along with cognate target genes are finely tuned in order to meet the changing needs of cells under all conditions. In fact, Nfe2l1 and Nfe2l2 cannot be reduced as a simple module alone. Now, the question becomes what is the minimal modular network to reproduce the observed data and why it is so evolved. At least three of them α-PalNRF1, TFAM and Pitx2 should be included, in addition to Nfe2l1 and Nfe2l2. This defines that the nuclear controls of mitochondrial respiration and biogenesis, as well as protein synthesis and degradation, are physiologically integrated with the extra-nuclear redox signalling to antioxidant cytoprotective responses mediated by Nfe2l1 and/or Nfe2l2. However, in view of mutual inter-regulation of between Nfe2l1 and Nfe2l2, it should be taken severe cautions to interpret the experimental results from loss of Nfe2l1, Nfe2l2 or both.

5. Materials and methods

5.1 Chemicals, antibodies and other reagents

All chemicals were of the highest quality commercially available. tert-Butylhydroquinone (tBHQ) was from Sangon Biotech (Shanghai, China). Specific antibodies against Nfe2l1 were made from our laboratory (57), antibodies against α-PalNRF1 or V5 ectope were from Abcam and Invitrogen, respectively, whilst β-actin and secondary antibodies were from ZSGB-BIO (Beijing, China). The detailed information about other antibodies, as well as all other key reagents and resources used in this study, was all shown in Table S1.

5.2 Expression constructs, Reporter plasmids, and other oligos used for sgRNA or siRNA.

Besides four expression constructs for human and mouse Nfe2l1 or Nfe2l2 saved by our group (44,47,62), another four expression constructs for human and mouse Pitx2, and α-palNRF1, were here made by cloning each of those full-length cDNA sequences into the pcDNA3.1 vector. Particularly, the CRISPR/Cas9 plasmid constructs containing guide RNAs specifically targeting mouse α-palNRF1 were created to generate a heterogeneous (α-palNRF1+/−) knockout cell line from MEFs. Such sgRNAs (listed in Table S1) were designed with highly specific targets for precision genomic positions (as shown in Figure S1), before being employed in the sgRNA-directed gene-editing of α-palNRF1.

Furthermore, several specific cis-regulatory luciferase reporter plasmids were prepared from cloning the indicated gene promoter regions. The mouse Nfe2l1 Promoter region (~2047 to +1210) was amplified by PCR from its genomic loci and then inserted into the pGL3-Basic vector. Another group of the cis-regulatory consensus, e.g., ARE and PitxRE (Pitx2 response elements)-adjointing sequences was cloned from the indicated gene promoter regions, such as Nfe2l1, TFAM, and α-palNRF1 and then inserted into the pGL3-Promoter vector. In addition to those intact reporter genes, such as PitxRE-Luc and ARE-Luc, relevant point-mutant reporters were engineered here. The fidelity of the above-described constructs was all confirmed to be true by sequencing. All these primers in the above gene manufacture, and other oligos for siRNAs-mediated knockdown of the indicated genes, were listed in Table S1, which all were synthesized by Tsingke (Chengdu, China).

5.3 Cell lines, culture and transfection.

Wild-type mouse embryonic fibroblasts (MEFs), were given as a gift by Akira Kobayashi. Their relevant knockout MEF lines, e.g., Nfe2l1−/−, Nfe2l2−/− and Keap1−/− were also obtained from the groups of Profs. Kobayashi and Hayes. Of note,
these cell lines were originally prepared from Prof. Yamamoto’s laboratory. But, another heterogeneous knockout line of α-pal$^{−/−}$ in mice was established by gene-editing in our own laboratory as described below. Besides, the human wild-type (i.e., hNfe2l1/2$^{+/+}$) hepatocellular carcinoma HepG2 cells were originally from the American Type Culture Collection (ATCC, Manassas, VA, USA). The fidelity was conformed to be true by its authentication profiling and STR (short tandem repeat) typing map (by Shanghai Biowing Applied Biotechnology Co., Ltd) (38). On this base, hNfe2l1α$^{−/−}$ and hNfe2l2$^{−/−}$ΔTA were established and characterized in our own laboratory (47). These experimental cell lines were maintained for growth in Dulbecco’s modified Eagle’s medium (DMEM) supplemented with 5 mM glutamine, 10% (v/v) fetal bovine serum (FBS), 100 units/mL penicillin-streptomycin, in the 37 °C incubator with 5% CO$_2$. Subsequently, the indicated cells were subjected to transfection for 8 h, which was performed by using Lipofectamine 3000 (Invitrogen, Carlsbad, CA, USA), containing different combinations of indicated plasmids, and then allowed for 24-h recovery from transfection in the fresh medium before relevant experimentation.

5.4 Real-time qPCR analysis.

Experimental cells were subjected to isolation of total RNAs by using the RNA simple Kit (Tiangen Biotech Co., Beijing, China). Then, 500 ng of total RNAs were added in a reverse-transcriptase reaction to generate the first strand of cDNA (with the Revert Aid First Strand Synthesis Kit from Thermo, Waltham, MA, USA). The synthesized cDNA was served as the template for qPCR, in the GoTaq$qPCR Master Mix (from Promega), before being deactivated at 95 °C for 10 min, and then amplified by 40 reaction cycles of the annealing at 95 °C for 15 s and then extending at 60 °C for 30 s. The final melting curve was validated to examine the amplification quality, whereas the mRNA expression level of β-actin served as an optimal internal standard control. All the primers used for qPCR (Table S1) were synthesized by Tsingke (Chengdu, China).

5.5 Western Blotting analysis.

Experimental cells were harvested in a lysis buffer (0.5% SDS, 0.04 mol/L DTT, pH 7.5), which was supplemented with the protease inhibitor cOmplete Tablets EASYpack. The lysates were denatured immediately at 100 °C for 10 min, sonicated sufficiently, and diluted in 3 × loading buffer (187.5 mmol/L Tris-HCl, pH 6.8, 6% SDS, 30% Glycerol, 150 mmol/L DTT, and 0.3% Bromphenol Blue) at 100 °C for 5 min. Then, equal amounts of protein extracts were subjected to separation by SDS-PAGE containing 5–12% polyacrylamide, and subsequent visualization by immunoblotting with distinct primary antibodies as indicated (in Table S1). On some occasions, the blotted membranes were stripped for 30 min and then were re-probed with additional primary antibodies. β-actin served as an internal control to verify equal loading of proteins in each of electrophoretic wells.

5.6 Distinct cis-regulatory reporter gene assays.

Equal numbers (1.4 × 10$^5$) of indicated experimental cells were plated into 12-well plates. When allowed for growth to the density reaching 70–80% cell confluence, they were then transfected with Lipofectamine 3000 reagent (Invitrogen). For distinct lengths of the gene promoter studies, the pGL3-basic vector containing 5-kb (−2248 to +2777), 2.7-kb (−2248 to +483) or 3kb (−259 to +2777) of human Nfe2l1 promoter, or 3.2kb (−2047 to +1210) of mouse Nfe2l1 promoter, or an empty pGL3-basic vector as a blank control, was co-transfected for 8 h with an indicated expression construct or an empty pcDNA3.1 as a control, plus another internal control pRL-TK reporter. Subsequently, the cells were allowed for a recovery from transfection in a fresh complete medium for 24 h, before they were lysed in a passive lysis buffer (E1910, Promega, Madison, WI, USA) for the dual-luciferase assay. About 20 µl of the supernatant of cells was assayed for the luciferase activity. Both firefly and renilla luciferase activities in each of the same samples were measured by the Dual-Luciferase reporter assay system (Promega). For the short consensus sequences of the
indicated transcription factor-binding sites, the specific driven luciferase plasmids or the paired point-mutants were co-transfected with the internal control pRL-TK, together with an expression construct for Nrf1, Nrf2, Pitx2 or an empty pcDNA3.1. All the resultant data were normalized and calculated as a fold change (mean ± S.D) relative to the activity of the control group (at a given value of 1.0).

5.7 Statistical analysis
The statistical significance of changes was determined using the Student’s t-test or Multiple Analysis of Variations (MANOVA). All the data presented in this study are shown as a fold change (mean ± S.D), each of which represents at least 3 independent experiments undertaken on separate occasions that were each performed in triplicate.

Data Availability: All data needed to evaluate the conclusions in the paper are present in this publication and/or the Supplementary Information that can be found at xx. Additional data related to this paper may also be requested from the authors.

Author contributions: S.Z. performed the most experiments with help of Y.X., S.H. and L.Q., except that Y.D. did the remaining experiments and repeated part of the work by S.Z. Both S.Z. and Y.D. collected relative data and also made draft of this manuscript with most figures and supplemental tables. Y.Z. designed and supervised this study, analyzed all the data, helped to prepare all figures with cartoons, wrote and revised the paper.

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