

Running title: HIF-1 predicted target genes

Title: An integrative genomics approach identifies Hypoxia Inducible Factor-1 (HIF-1) target genes that form the core response to hypoxia.

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Abstract

The transcription factor Hypoxia-inducible factor 1 (HIF-1) plays a central role in the transcriptional response to oxygen flux. To gain insight into the molecular pathways regulated by HIF-1, it is essential to identify the downstream target genes. We report here a strategy to identify HIF-1 target genes based on an integrative genomic approach combining computational strategies and experimental validation. To identify HIF-1 target genes microarrays data sets were used to rank genes based on their differential response to hypoxia. The proximal promoters of these genes were then analyzed for the presence of conserved HIF-1 binding sites. Genes were scored and ranked based on their response to hypoxia and their HIF binding site score. Using this strategy we recovered 41% of the previously confirmed HIF-1 target genes that responded to hypoxia in the microarrays and provide a list of predicted HIF-1 targets. We present experimental validation for *ANKRD37* as a novel HIF-1 target gene. Together these analyses demonstrate the potential to recover novel HIF-1 target genes and the discovery of mammalian regulatory elements operative in the context of microarray data sets.

Introduction

Maintenance of oxygen homeostasis in mammalian cells is fundamental to the survival of the organism. One of the pivotal mediators of the cellular response to hypoxia is hypoxia-inducible factor (HIF), a transcription factor that contains a basic helix-loop-helix motif as well as PAS domain. There are 3 known members of the HIF family (HIF-1, HIF-2, and HIF-3) and all are α/β heterodimeric proteins. HIF-1 was the first factor to be cloned and is the best understood isoform (1). HIF-3 is a distant relative of HIF-1 and little is currently known about its function and involvement in oxygen homeostasis. HIF-2, however, is closely related to HIF-1 and both activate hypoxia-dependent gene transcription. In all three isoforms the α -subunit senses oxygen levels (2-5). In normoxia the α -subunit is ubiquitously expressed but is rapidly degraded through interaction with the *VHL* ubiquitin ligase complex (6). In hypoxic conditions, it is stabilized through multiple mechanisms that are transcriptional, post-transcriptional, as well as post-translational (6-9). The β -subunit is widely expressed and generally not regulated by hypoxia. Once stabilized HIF-1 and HIF-2 interact with coactivators such as *CREBBP/EP300* and bind to a consensus sequence element (5'-RCGTG-3') in the proximal promoters of hypoxia-regulated genes. Together these genes control cellular process including a switch from oxidative to glycolytic metabolism, inhibition of cellular proliferation, and stimulation of oxygen delivery through erythropoiesis and angiogenesis (10). Metabolic dysregulation is the final outcome if the adaptive response is inadequate.

Hypoxia can arise in a variety of developmental, physiological, and pathological states. Solid tumors, such as breast cancer, quickly outgrow their blood supply and manipulate the hypoxia pathways to promote their own survival. The role of HIF-1 in tumor onset, progression, invasion and metastasis has been demonstrated in several solid tumors (11,12). In addition, cancer specific regulatory roles for HIF-2 have been demonstrated in an expanding list of cancers (13). For instance, in clear renal cell carcinoma the normal predominance of *HIF1A* expression is altered in favor of *EPAS1 (HIF2 α)* expression and promotes pro-survival rather than pro-apoptotic factors (14,15). As a result HIF target genes have emerged as potential targets for cancer specific therapy (16,17).

HIF-1 is an important metabolic regulator that allows rapid adaptation to oxygen availability. This effect is mediated through key regulators of bioenergetics and growth. For instance, *PDK1* is directly induced by HIF-1 resulting in attenuation of mitochondrial function and oxygen consumption (18) and *CDKN1A* is induced leading to growth arrest at the G1 phase (19). Identifying such HIF target genes is central to our understanding of the HIF network and the mechanism of cellular pathways modulation during hypoxia. In addition, identifying additional binding sites in HIF regulated genes might contribute to the paradigm of inferring function from sequence.

Currently, studies attempting to identify novel HIF target genes rely on microarray expression profiles to detect genes that respond to changes in HIF protein levels. Typically a gene of interest is selected and experimentally validated for HIF binding to its promoter. Kim et al. identified 25 transcripts that increase by at least 4 fold during hypoxia in a B cell line. *PDK1* was selected for further validation due to its role in regulating the TCA cycle. Consequently they were able to show that HIF-1 binds to the *PDK1* promoter (18). Shen et al. used a more rationale microarray design where tissues from *C. elegans* were profiled in normoxia and in hypoxia in a wild type, HIF-1 knockout and a VHL mutant strain (20). This study resulted in 63 HIF-1 dependent genes that respond to hypoxia but only 12 of those had a human homolog. Elvidge et al. compared expression profiles of human breast cancer cells in normoxia, hypoxia and in normoxia treated with a 2-OG-dependent dioxygenase inhibitor, dimethylxalylglycine (DMOG) which activates HIF-1. In addition, they compared expression profiles in hypoxia and in hypoxia treated with siRNAs to *HIF1A* and *EPAS1* (*HIF-2 α*) (21). Manalo et al. profiled arterial endothelial cells in normoxia and in hypoxia as well as in normoxia in the presence of a HIF-1 α constitutively active form (22). Only 45 genes were identified in both studies as HIF-1 dependent. Although these approaches are more likely to filter out genes that are not dependent on HIF-1, it remains challenging to determine whether the affected transcripts were directly or indirectly modulated by HIF.

Several methods for *in-silico* identification of transcription factor binding sites (TFBS) have been proposed (23-29). These methods fall into two categories. First, identification of TFBS based on predefined position weight matrices (PWM). Second, de novo prediction of sequence

motifs over-represented in proximal promoters compared to control sequences (for a review see (30,31)). Examples for the former include the STORM in CREAD (27), **CORE_TF (28) and GeneAct (29)** and for the latter DME (32) and the genomic identification of motifs described by Xie et al. (26). PWMs of HIF-1 have been previously used to identify genome-wide target genes. For instance, the Gene Set Enrichment Analysis program contains a set of HIF-1 target genes as part of its Molecular Signature Database (26,33). However, these approaches do not take into consideration promoter availability. In addition, the consensus HIF binding sequence is very short, has low information content and is ubiquitously present in the human genome making *in-silico* genome-wide prediction unreliable. To generate a reliable prediction we propose to reduce the search space to a subset of genes expressed in specific tissues under specific conditions. This can be achieved by microarray expression profiles under the assumption that promoters of genes that respond to a stimulus are available for TF binding. Several groups previously demonstrated that microarray expression profiles can be used to improve TFBS prediction (32,34-36) and that cis-regulatory modules in proximal promoters correlate with differential expression of downstream target genes (27).

In this study we present an integrative genomic approach combining both computational and experimental strategies to identify HIF target genes. Using this approach we recovered 41% of the known HIF-1 target genes that were differentially expressed in hypoxia, defined a ranked list of HIF target genes and experimentally validated *ANKRD37* as a novel HIF-1 target.

Material and Methods

Microarrays

Raw microarray data was obtained from GEO (37) and ArrayExpress (38). **Microarray studies were filtered to identify those that profiled the same tissue in normoxia and hypoxia on Affymetrix platform, used at least 2 replicates and provided raw data.** Affymetrix based data sets were normalized using the GCRMA module (39) of bioconductor (40) and present-absent calls were calculated for each probe using the MAS5 module. All probes with no present calls were

removed and from the remaining at least one sample was required to have an expression value larger than $\log_2(100)$, as recommended by Affymetrix. In all experiments, only pairwise comparisons were made with respect to normoxia. After the initial filtering was applied, the expression values were centered to the mean for each probe with replicates. Only probes for which the expression values of the replicates were all positive or all negative were further tested for differential expression. The limma module (41) of biocoductor was used to fit a linear model for each probe and p-values were corrected using the false discovery rate method (42).

Promoters

Promoter sequences of human genome build 18 were obtained from UCSC genome browser (43). For each protein-coding gene, the proximal promoter was defined as 700 bases upstream and 300 bases downstream of the transcription start site. In cases where multiple transcripts were annotated all alternative promoters were obtained and analyzed individually. Due to restriction of conservation analysis programs, for all genes the forward strand sequence of the genome was used. Background promoters for enrichment analysis were selected randomly from the promoter collection to match the CpG content and base composition of the foreground promoters. We obtained CpG sequence location from UCSC genome browser (43) and matched their location to the promoters defined. Each promoter was classified as CpG or non-CpG and for the background set the same proportion of CpG and non CpG promoters were selected randomly according to the ratio in the foreground set. Next we verified that the base composition matched within $\pm 2\%$ for each nucleotide with the foreground data set. For all enrichment purposes a set of 1,000 promoters was used as a background.

Enrichment of binding sites

The program MOTIFCLASS v1.40 (27) was employed to identify binding sites over-represented in promoters of a foreground set (genes differentially expressed in microarrays) compared to a background set of 1,000 randomly selected promoters. The relative error-rate was optimized for each motif and a p-value was calculated using 10,000 permutations. Finally, only motifs with an enrichment specificity of at least 0.5 were reported.

De-novo prediction of motifs

The program DME (v2.0) (27,32) was employed using the ZOOPS model to identify motifs of length 5-12 bases compared to a background set. Only the top 50 enriched motifs were reported and compared to known motifs using the program MATCOMPARE in CREAD (27).

Binding site prediction

The program STORM in CREAD (27,44) was used to match PWMs to genomic DNA and was employed using a p-value cutoff of $1e-4$. This cutoff was found to be optimal since a cutoff of $p < 1e-3$ was not stringent enough predicting nearly every promoter in the genome as having a HIF-1 site while $p < 1e-5$ was too stringent predicting only a handful of promoters in the genome with a HIF-1 site. Conservation information of 28 species genome alignments (43) was used in two approaches. First, the software multiSTORM (also in CREAD (27)) was employed to identify the number of genomes in which the PWM could still be matched with the same p-value cutoff as used in STORM. Second, the software site-cons was employed to calculate the level of conservation at each binding site compared to the flanking 100 bases (27). The site-cons p-value was obtained by extracting 100 bases upstream and downstream of the binding site and sampling randomly a number of columns equal to the length of the predicted binding site. A conservation score was then calculated for these columns and the process was iterated 10,000 times to obtain a distribution. Finally the p-value was calculated by comparing the original score for the binding site to the distribution. Conservation information was obtained from the 28-genome alignments available at UCSC genome browser (43). Namely, human (hg18), chimpanzee (panTro2), rhesus (rheMac2), bushbaby (otoGar1), tree shrew (tupBel1), mouse (mm8), rat (rn4), guinea pig (cavPor2), rabbit (oryCun1), shrew (sorAra1), hedgehog (eriEur1), dog (canFam2), cat (felCat3), horse (equCab1), cow (bosTau3), armadillo (dasNov1), elephant (loxAfr1), tenrec (echTel1), opossum (monDom4), platypus (ornAna1), lizard (anoCar1), chicken (galGal3), frog (xenTro2), fugu (fr2), tetraodon (tetNig1), stickleback (gasAcu1), medaka (oryLat1) and zebrafish (danRer4).

Transcription network

For each predicted HIF target gene, the single best scoring HIF site was selected and other binding sites were identified within ± 25 , ± 50 , ± 75 , ± 100 , ± 125 and ± 150 bases of that site as

well as in the entire promoter. To obtain a p-value the frequency of each site within that window was compared to a randomly selected background set of 1,000 promoters from genes that respond to hypoxia but had no detectable HIF binding site. Sequence composition for the foreground and background set were matched as described above. In each of the background promoters a single binding site was randomly selected and binding sites were identified within the window size as selected for the HIF site. A chi-square test was performed for each TF, comparing the occurrence of binding sites in the neighborhood of HIF to their occurrence in the neighborhood of the randomly selected binding site in the background set. This process was iterated 100 times and the average p-value for each TFBS was used as the final p-value. No correction for p-values was performed.

Functional pathway analysis

The KEGG database (release 47) (45) was obtained and used to place predicted HIF target genes into molecular pathways. Statistical analysis was performed using a hypergeometric distribution as described in the GOhyperGAll module of Bioconductor for gene ontology terms (40). The R program was employed (v2.6.2) with the following command: `phyper(x-1, m, n-m, k, lower.tail = FALSE)`, where x is the number of predicted target gene within a specific pathway; m, the number of genes in that pathway; n total number of unique genes in KEGG; and k, the number of predicted HIF target genes that have an entry in any of the KEGG pathways. **P-values were not corrected for multiple testing. This statistical analysis was repeated using the Reactome pathway database (46), the curated gene sets of Gene Set Enrichment Molecular Signature database (33) and the microRNA predicted targets database TargetScan (47). Enrichment for protein interactions was performed by first compiling a list of interactors for each human protein (Data obtained from NCBI Gene database). The HomoloGene database (48) was used to identify interaction in other species that can be mapped to human proteins. Finally, enrichment was calculated as described for KEGG by considering all interactors of each protein. Protein domains were obtained from Interpro (49) and enrichment was calculated for each domain.**

Selection of mitochondrial genes

Genes that localize to the mitochondria were selected by identifying (I) all human Swiss-Prot proteins annotated as localized in the mitochondria (50); (II) genes annotated with Gene Ontology terms that include the keywords: mitochondria, mitochondrion or mitochondrial (51); and (III) A predicted catalog of genes localized to the mitochondria (52).

Cell Culture

DLD-1, HCT116, SW480, Lovo, Panc-1, HeLa and MCF7 cells were maintained in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum (FBS). Hypoxic conditions were achieved by culturing cell lines in a sealed hypoxia chamber (Billups-Rothenberg) for 18 hours after flushing with a mixture of 1% O₂, 5% CO₂, and 94% N₂ (53). To minimize the effect of serum growth factors, the culture medium was switched to serum-free UltraCulture (Chambrex) before the cells were subjected to hypoxia.

Quantitative polymerase chain reaction analysis (qPCR)

Total RNA was isolated from cultured cells using the RNeasy kit (Qiagen) and reverse transcription with random hexanucleotide primers and SuperScript Reverse Transcriptase III (Invitrogen) was performed. The resulting cDNA was amplified by real-time polymerase chain reaction using the iQ5 Real-Time PCR Detection System (BioRad) and Power SYBR Green PCR Master Mix (Applied Biosystems). Primer sequences were 5'-GTCGCCTGTCCACTTAGCC-3' and 5'-GCTGTTTGCCCGTTCTTATTACA-3' for *ANKRD37*, 5'-AGGCCAGCACATAGGAGAGA-3' and 5'-TTTCTTGCGCTTTCGTTTTT-3' for *VEGFA* and 5'-CGGCTACCACATCCAAGGAA-3' and 5'-GCTGGAATTACCGCGGCT-3' for 18S rRNA. Transcript levels of *ANKRD37* were normalized to 18S rRNA.

Western blotting

Cells were lysed in chilled lysis buffer (20 mM Tris-HCl, pH 7.5, 150 mM NaCl, 1mM Na₂EDTA, 1mM EGTA, 1% Triton, 2.5mM sodium pyrophosphate, 1 mM β-glycerophosphate, 1 mM Na₃VO₄, 1 mM leupeptin) supplemented with the Complete protease inhibitor cocktail (Roche). 50 μg of protein extracts were resolved on a 3–8% NuPAGE Tris-Acetate SDS polyacrylamide gel (Invitrogen) and transferred onto a polyvinylidene difluoride membrane (Millipore). The blots were probed with anti-*HIF1A* (Transduction Laboratories; 1:500) and

anti- β actin (Sigma; 1:100,000) antibodies. Immunoreactive proteins were visualized using the Western Lighting Chemiluminescence Reagent Plus (PerkinElmer Life Sciences).

Plasmid Constructions

Fragments from -325 bp to +230bp -166 bp to +230 bp or -78 bp to +230 bp relative to the transcriptional start site of the human *ANKRD37* promoter were amplified by polymerase chain reaction (PCR) using 1 μ g of human genomic DNA extracted from DLD-1 cells. The PCR primers were as follows: -325bp sense primer; 5'-AACCAAACGCGTCCAGTTTCCTGGTTACGTG-3', -166bp sense primer; 5'-AACCAAACGCGTTCTCACGCCCACTGACTTA-3' , -78 bp sense primer; 5'-AACCAAACGCGTATCCACAGCTGGCCAATCG-3' and +230bp antisense primer; 5'-GTGGTTGAGATCTTAAGGCAGATGACAAGAGTCC-3'. The PCR-amplified products were digested with MluI and BglII and subcloned into the pGL3-basic vector (Promega). Site directed mutations were introduced at 3 potential HIF binding sites (1, 2 and 4). To prepare site 1 and site 4 mutants, the -325*ANKRD37*-luc pGL3 plasmid was digested with MluI / PstI or PmlI / Tth111I, respectively, and ligated with a double-stranded oligonucleotide in which the **consensus HIF binding site** was disrupted. The oligonucleotide sequences were as follows: 5'-CGCGTCCAGTTTCCTGGTTAAAAGCGCGCCGGCAGAGCCAAAACCTGCA-3' and 5'-GGTTTTGGCTCTGCCGGCGCGCTTTTAACCAGGAAACTGGA-3' for site 1 at -310bp and 5'-GTGCCAGTGTGTTGTGTA AAAAGCGGCCGTGGCGGGGCTGGACA-3' and 5'-CTGTCCAGCCCCGCCACGGCCGCTTTTACACAAACACTGGCAC-3' for site 4 at +14 bp. To prepare the site 2 mutant, PCR-based site-directed mutagenesis was performed using primers 5'-TACCGGGAGAAAAGTCAA ACTCA-3' and 5'-TGAGTTTGACTTTTCTCCCGGTA-3'. The nucleotide sequences of all constructs were confirmed by sequencing.

Transfections and Reporter Assays

Transient transfections were performed using Fugene 6 (Roche) in 24-well tissue culture plates according to the manufacturer's specifications. 150 ng of *ANKRD37*-luciferase pGL3 reporter constructs were co-transfected with 2 ng of pRL-CMV (Promega) as a control. Ten hours after transfection, the culture medium was switched to UltraCulture and cells were grown in normoxic

or hypoxic conditions for 18 hours. Luciferase activity was measured with a dual luciferase reporter assay system (Promega). The experiments were performed in triplicate wells a minimum of three times.

RNA interference

HCT116 cells were transfected with 20 nM siRNA duplex oligos directed to *HIF1A* or a non-specific control siRNA using Lipofectamine RNAiMAX (Invitrogen) according to the manufacturer's instructions. Nucleotide sequences of siRNAs were as follows: *HIF1A*, 5'-r(AUCCAGAGUCACUGGAACU)d(TT)-3', and control, 5'-r(GCGCGCUUUGUAGGAUUCG)d(TT)-3'. The silencing effect was confirmed by Western blotting 48 h after transfection. *ANKRD37* promoter reporter constructs were transfected 12 h after siRNA transfection.

Electrophoretic Mobility Shift Assay (EMSA)

Nuclear extracts were prepared from MCF7 cells cultured in either normoxic or hypoxic conditions for 12 hours utilizing NE-PER nuclear extraction reagent (Pierce). The *ANKRD37* promoter sequence utilized as an oligonucleotide probe was 5'-CTACCGGGAGACGTGTCAAACCTCAG-3'. The 5'-end of the oligonucleotide was labeled with biotin, and a complementary oligonucleotide was annealed to generate double-stranded fragments. EMSA was performed using LightShift chemiluminescent kit (Pierce) as previously described (54). Specificity of shifts was confirmed by utilizing 200-fold molar excess of unbiotinylated oligonucleotides as a specific competitor. Mutagenesis was performed to further define the elements responsible for the specific shifts obtained. The sequence of the mutant oligonucleotide probe that includes point mutations in the **HIF consensus binding site** was: 5'-CTACCGGGAGAAAAGTCAAACCTCAG-3'.

Chromatin immunoprecipitation (ChIP)

MCF7 cells were cultured in either normoxic or hypoxic conditions for 6 hours and then fixed with 1% formaldehyde at 37°C for 10 min. The ChIP assays were performed using a Chromatin Immunoprecipitation Assay Kit (Upstate) according to the manufacturer's protocol. Briefly, cells were lysed and sonicated to achieve DNA sizes ranging from 200 to 1,000 bp. Diluted supernatants were pre-cleared by incubating with salmon sperm DNA/protein-A agarose, 50%

slurry at 4C for 30 min. Supernatants were then incubated with anti-HIF-1 α antibody (Novus Biologicals number 100-105) or normal mouse IgG (Santa Cruz) at 4C overnight, or directly processed to the next step without antibody. Immunocomplexes were collected with salmon sperm DNA/protein A-agarose, 50% slurry, washed, eluted, and cross-linkage was reversed by heating at 65°C for 4 hours. The eluates were then digested with proteinase K at 45C for 1 hour. The precipitated DNAs were recovered using PCR Purification Kit (Qiagen) and amplified by PCR using PrimeSTAR HS DNA Polymerase (Takara Bio). The PCR primers used for amplification of site2 (primers A) and a non-HIF region upstream of site2 (primers B) were as follows: sense primer A; 5' - CCAGTTTCCTGGTTACGTGC -3', anti-sense primer A; 5' - TAAGTCAGTGGGCGTGAGAG -3', sense primer B; 5' - TGGAGGCACTTTCACCACAC -3' and anti-sense primer B; 5' - TGTGAGGTGAGCACACGTTG -3'.

Results

HIF-1 and HIF-2 and their downstream target genes are activated in response to hypoxia. To identify HIF target genes we first identified genes that responded to hypoxia using publicly available microarray data sets. **NCBI GEO and EBI ArrayExpress were searched for experiments where the same tissue was profiled comparing normoxia and hypoxia. Experiments that used replicates, were profiled on Affymetrix platform and provided raw data were accepted for further analysis (Table S1).** The same identical analysis protocol was applied to all experiments (see methods). Although all microarrays were profiled on Affymetrix arrays, the number of genes differentially expressed in each cell type varied significantly and ranged from 486 genes in monocytes to 2,119 genes in HeLa, with a surprisingly small overlap. The differentially expressed genes in each cell type are the potential HIF target genes and were subject to *in-silico* analysis of HIF binding sites.

***In-silico* optimization of HIF binding site prediction**

Two databases of PWMs were obtained and searched for HIF-1 PWM. The Jaspar collection (v3.0) contained no HIF-1 PWM while the TRANSFAC collection (v8.2) contained 2 HIF-1 PWMs (M00466, M00797). These PWMs are 12 and 14 bases long and were compiled based on only 12 and 23 validated binding sites, respectively. We compiled an additional HIF-1 PWM based on 104 validated binding sites in human, mouse and rat collected by Wenger et al. (10) (see Supplementary Figure S1; submitted to Jaspar). Despite the apparent variability in PWM length, it is clear from the alignment in Supplementary Figure S1 that most of the information content is within the **HIF consensus binding site: RCGTG**. The composition preference in the region flanking the core RCGTG observed in the Transfac matrices is a consequence of using a small number of validated HIF-1 binding sites.

Proximal promoters were defined from 700 bases upstream to 300 bases downstream of the transcription start site (TSS) of each transcript. **Initially, HIF-1 PWMs were used to identify binding sites, however, we observed a too small overlap between the 3 HIF-1 PWMs for any given p-value and conservation filtering criteria. Differences in PWM length (12-18bp) and in**

the sequences flanking the consensus binding site were found to introduce a bias in HIF-1 binding site prediction since calculation of p-values and conservation consider the entire length of the matrix and all bases defined within. To avoid this bias all HIF consensus binding sites sequences (RCGTG) were extracted from each promoter and tested for conservation in other species (see methods). A shift from A to G and vice versa in the first position was allowed for the purpose of conservation. Next, the software site-cons in CREAD was employed to calculate the level of conservation at each binding site compared to the flanking 100 bases. A site was predicted as a HIF binding site if it was conserved in at least 10 species (including human) or if conserved in 4 species with a site-cons p-value < 0.05. When the HIF consensus site is preceded by a C, it may form the E-box binding site CACGTG which is a known binding site for several bHLH transcription factors including HIF-1. In 43% of the E-box sites other TFs were predicted to bind at the same location as HIF-1, compared to only 2% of the non-Ebox sites. The transcription factors that are most commonly predicted at the same location as HIF are *ARNT* (HIF-1 β ; as homodimer), *AHR:ARNT*, *MYC*, *MAX*, *MYCN*, *CLOCK:ARNTL* and *USF1* (see Supplementary Figure S2). We only accepted genes with at least one non-Ebox HIF site as HIF target genes. Throughout this strategy our filtering criteria were very stringent in order to obtain a catalogue of high confidence at the expense of not recovering some known HIF targets. Each gene was scored as follows:

$$\text{HIF site score} = \text{number of species} \times (-\log(\text{conservation p - value}))$$

$$\text{Hypoxia score} = \text{abs}\left(\sum\left(\frac{\text{hypoxia}}{\text{normoxia}}\right)\right)$$

The hypoxia/normoxia ratio was inverted and assigned a negative value for genes that were down-regulated in hypoxia. Each gene was assigned two ranks, one based on the highest scoring HIF site and one on the hypoxia score. Finally, the sum of both ranks was calculated and all genes were ranked based on that value. For instance, the gene *BNIP3*, a bona fide HIF-1 target, was ranked 515 by HIF site score and 15 by hypoxia score. Using the sum of ranks *BNIP3* was ranked 56 among all genes. This scoring scheme is biased towards genes that respond to hypoxia in multiple cells. While some genes could be HIF targets in only one cell, we reason that a gene that responds to hypoxia in more than one cell is more likely to be a HIF target. This strategy is

summarized in Figure 1. Despite the stringent selection criteria of this approach we were able to identify a HIF binding site in 35/86 promoters of known target genes. A list of previously identified known HIF-1 target genes is shown in Table S2.

The majority of hypoxia responsive genes lack a HIF binding site

HIF target genes were predicted for each data set separately with the criteria outlined in materials and methods. Of the known and validated HIF target genes that responded to hypoxia in each data set, we recovered 37%-55% (Table 1). On average 70% of the hypoxia responsive genes did not contain a detectable HIF binding site in their proximal promoter (Table 1). To verify this observation and to test that no bias was introduced by our stringent conservation filtering above, genes that responded to hypoxia in each data set were divided to two groups. Those with a predicted HIF binding site (A) and those with no detectable HIF binding site (B). Each group was tested for over-representation of any PWM compared to a random set of promoters with similar base composition and CpG content. This analysis was performed using the program MOTIFCLASS in CREAD and is independent from the prediction analysis and selection criteria outlined above. In addition, MOTIFCLASS does not consider conservation and is based on sequence analysis alone. As expected HIF PWMs were identified in the top 20 over-represented binding sites in group A and none of the HIF PWMs were detected in the top 20 PWMs from group B. The results for the top 20 enriched motifs in each group in MCF7 breast cancer cells are shown in Figure 2A-B. The highest scoring PWM was a HIF-1 matrix that had a classification error of 0.407. In each of the six data sets we observed HIF-1 enrichment in group A while group B varied significantly between cell types (Table S3). We did not observe any significant HIF enrichment within the top 20 PWMs in group B throughout all data sets.

The general response to hypoxia is dependent on a small number of genes

Previous studies have suggested that the response to hypoxia varies by cell type (55-57). However, we expected a core set of genes to be shared, e.g. genes that control the shift from oxidative to glycolytic metabolism and inhibition of cellular proliferation. Yet, the cellular

response to hypoxia was surprisingly selective between cells. Only 17 genes responded to hypoxia in all studied cell types. These genes include HIF targets such as *ENO1*, *BHLHB2* and *BNIP3*. We observed a positive correlation between the number of cells in which a gene responded to hypoxia and the identification of HIF binding sites in its promoter (Figure 2C). Only 23% of the genes that responded to hypoxia in a single cell type had a predicted HIF binding site in their promoter compared to 59% of the genes that responded in 6 cell types. The top scoring gene was *TMEM45A* which responded to hypoxia in all studied cell types with an average of 21.6 fold induction and a HIF binding site conserved in 13 species with a conservation p-value < 0.0001 compared to the flanking 100bp. At least 5 of the top 10 genes have been previously identified as HIF-1 target genes, namely *DDIT4* (58,59), *STC2* (60), *P4HA1* (61), *JMJDIA* (62), and *ALDOC* (63). We did not find any correlation between the response to hypoxia and the HIF binding site score for the top 100 predicted HIF target genes. **To obtain a cutoff of high confidence, the top 500 ranked genes were plotted versus the cumulative number of previously validated HIF-1 targets (supplementary Figure S3). The resulting curve showed a logarithmic increase in validated targets for genes ranking below 200 and approaches saturation between 200 and 500. Therefore, the 200th gene rank was used as a cutoff of high confidence. Table S4 summarizes our prediction results for the top 500 HIF target genes.**

In the top 200 predicted HIF target genes, 81 responded to hypoxia in at least 3 cell types (Figure 3). We hypothesize that these genes are likely to be part of the shared response to hypoxia that is not cell specific. In addition, these genes have a higher probability of being HIF-1 targets since their response to hypoxia was detected in multiple experiments. Of the 81 genes, 22 genes were previously reported to be HIF target genes and 60 genes (74%) were up-regulated in hypoxia. In addition, 80 (99%) of the genes contained a CpG island in their proximal promoter, significantly higher than the 51% CpG containing promoters in our entire promoter database. CpG islands are thought to be non-tissue specific (64), further supporting the selection of the 81 genes as a shared response to hypoxia. The Kyoto Encyclopedia of Genes and Genomes (KEGG) database was used to identify over-represented pathways and processes within the 81 genes. In Figure 4A a metabolic map of HIF-1 target genes was constructed from the resulting analysis (Table S5). The metabolic map contained several known HIF-1 target genes, such as *LDHA*, *ALDOC* and

GAPDH and also several novel targets such as *GYS1* in starch and sucrose metabolism (65) and fumarate hydratase (*FH*) in the TCA cycle (66). One of the key cellular responses to HIF-1 in hypoxia is a metabolic shift from oxidative phosphorylation to glycolytic production of ATP. To highlight direct targets that may be involved in HIF-1 regulation of the mitochondria the predicted HIF targets that localize to the mitochondria (see methods) were used to create a mitochondrial map (Figure 4b). Eight of eleven genes were down-regulated in hypoxia and are involved in critical steps of mitochondrial function including two ribosomal subunits, cytochrome C, the iron transporter *SLC25A28* and the iron-sulfur assembly and repair protein *ISCU*.

Classification of novel HIF targets

All previously validated HIF-1 targets (Supplementary Tables S2 and S4) were tested for functional enrichment in KEGG pathway databases, Reactome database, Gene Set Enrichment Molecular Database (GSEA), protein interactions, InterPro protein domains and microRNA target prediction database TargetScan (see methods). This analysis allows identification of pathways or attributes that are highly represented by the HIF targets compared to an equivalent random list of genes. We next mapped novel HIF targets to these significantly enriched attributes as demonstrated by selected examples in Table 2 (full analysis shown in supplementary Table S6). Analysis of protein domains identified 2-oxoglutarate and Fe(II)-dependent oxygenase family as highly enriched in validated HIF targets (5 of 19 proteins, $p < 2e-7$). This family includes the prolyl hydroxylases known to regulate HIF-1 α as part of the oxygen sensing mechanism. PLOD1, is a novel predicted HIF target that is part of the same family. Analysis of microRNA targets identified five microRNAs that target validated HIF targets. miR-1/206, for instance, is predicted to target 583 human genes, of which 9 are known to be HIF-1 targets and 14 are predicted HIF targets. Analysis of gene sets from GSEA highlighted a group of 104 genes that predict a poor breast cancer prognosis and included 9 validated HIF targets ($p = 1e-7$) and 4 predicted ones. A graphical representation of protein interactions and Reactome pathways is shown in supplementary Figure S4 and highlights genes such as PCAF. PCAF interacts with 4 validated HIF targets and 6 predicted targets.

***ANKRD37* is a novel HIF target gene**

To demonstrate the utility of our method in identifying novel HIF-1 target genes, we selected 5 genes that were previously unknown to be HIF-1 targets, *ANKRD37* (ranked 8), *KLF10* (ranked 24) *WSB1* (ranked 32), *GYS1* (ranked 34) and *ELL2* (ranked 465). Using quantitative PCR, *ANKRD37* was induced up to 35 fold in hypoxia compared to normoxia, *KLF10* up to 2.5 fold, *WSB1* up to 4.9 fold, *GYS1* up to 7.8 fold, *ELL2* was not induced in hypoxia and *VEGFA* that was used as a positive control was induced up to 8.3 fold (Figure 5 & Supplementary Figure S5A). The gene *ANKRD37* was studied further due to its extreme induction in hypoxia and its high ranking within the predicted targets. *ANKRD37* is a short (158 amino acids, 17KDa) ankyrin repeat protein with unknown function that is conserved in mammals and zebrafish. *ANKRD37* responded to hypoxia in 4 of 6 cell types and 4 HIF-1 binding sites were predicted within the proximal promoter. The response to hypoxia was validated under hypoxic conditions across 7 cell lines. We observed a strong induction of *ANKRD37* in all cell lines but most significantly in the colon cancer cell lines DLD-1, HCT116, and SW480 (Figure 5A). *ANKRD37* hypoxic induction was measured after 4, 8, and 12 hours of incubation in hypoxic conditions in HCT116 cells and compared to *VEGFA*. HIF-1 protein levels were determined by western blot and showed a significant induction after 4 and 8 hours compared to normoxia and a slight decrease after 12 hours (Figure 5B). *ANKRD37* and *VEGFA* mRNA levels showed a similar profile that matched the HIF-1 induction, however, *ANKRD37* was induced 3 fold over the level of *VEGFA* induction (Figure 5C).

We next investigated the HIF binding sites in the *ANKRD37* promoter. We identified 4 HIF-1 binding sites that matched our filtering criteria and were located at -311 to -306 bp (site1), -228 to -223 bp (site2), -142 to -137 bp (site3) and +12 to +17 bp (site4). As shown in Figure 6A, 3 *ANKRD37* promoters encompassing these different HIF binding sites were cloned upstream of a luciferase reporter. Promoter1 was induced 4.1, 7.4 and 10.7 fold in hypoxia compared to normoxia in DLD-1, HCT116 and MCF7 cells, respectively. In contrast the induction observed with promoters 2 and 3 was in the range of 1.5-3 fold (Figure 6B). To determine whether the hypoxia induction was HIF-1 dependent, luciferase activity of *ANKRD37* promoter1 was measured in HCT116 cells in the presence of *HIF1A* siRNA. Endogenous *HIF1A* knockdown

was confirmed by western blot (Supplementary Figure S5A). The 5-fold induction of promoter1 in hypoxia was reduced to 1.3 fold in the presence of *HIF1A* siRNA (Supplementary Figure S5B). These results suggested that sites 1 and 2 are the physiologically relevant HIF-1 binding sites. Therefore, sites 1, 2 and 4 in promoter1 were selectively mutated at the **HIF consensus binding site** (ACGTG > AAAAG). As shown in Figure 6C, the hypoxic induction of promoter1 was maximally inhibited by a mutation in site2 while the other mutations had a minimal effect.

To establish whether endogenous HIF-1 protein binds to site2 in the *ANKRD37* promoter, EMSA assays were performed using nuclear extracts from MCF7 cells incubated in either normoxia or hypoxia. A unique band shift was obtained only when nuclear extracts from cells grown in hypoxic conditions were incubated with the probe corresponding to site2 (Figure 6D, lane 3). When non-biotinylated probe was co-incubated as a competitor, or a probe with specific mutations in the HIF consensus binding site (ACGTG > AAAAG) was utilized, the band obtained in hypoxic conditions was lost (Figure 6D, lane 4,5). Nuclear extracts from cells grown in hypoxia were then incubated with an antibody specific to HIF-1 α or control mouse IgG prior to performing EMSA assays. Incubation with an antibody against HIF-1 α resulted in a supershift of this specific band (Figure 6E). To further address whether HIF-1 α physiologically binds to site2, chromatin immunoprecipitation assays were performed using MCF7 cells incubated in either normoxia or hypoxia. Cross-linked cell lysates were immunoprecipitated with or without anti- HIF-1 α antibody or control mouse IgG and PCR was performed to amplify a 178bp or 220bp fragment of the *ANKRD37* promoter using primers corresponding to site2 (primers A) and a region upstream of site2 (primers B), respectively. DNA bound to HIF-1 α was detected when DNA-protein complexes from hypoxic cells were precipitated with an anti-HIF-1 α antibody and amplified with primers A, whereas no binding was observed at an upstream promoter region with primers B (Figure 6F). These data indicate that site2, the most conserved and highest scoring HIF site, is indeed a HIF-1 binding site in DLD-1, HCT116 and MCF7 cells.

The HIF transcriptional network

To identify transcription factors that are part of the HIF network we analyzed the presence of other binding sites in the 81 genes that ranked in top 200 and responded to hypoxia in at least 3 cell types. Matrices for validated transcription factors from the TRANSFAC and Jaspar collections were used to identify binding sites within 150 bases away from the highest scoring HIF binding site in each of the promoters as well as within the entire promoter. For this analysis we used STORM with p-value $< 1e-4$ and accepted only binding sites predicted in at least 4 species and significantly ($p < 0.05$) more conserved compared to the flanking 100 bases (see methods). To obtain a p-value for co-occurring binding sites, a chi-square analysis was performed compared to TFBS occurrence in a background set of 1000 promoters of genes that responded to hypoxia in at least one cell type but had no detectable HIF binding (see methods). The analysis was performed in increments of 25 bases from the highest scoring HIF site and the most significant p-value for each PWM was selected. Only binding sites that were not predicted at the **HIF consensus binding** site were considered. We identified 10 TFBS that were significantly enriched within a specific distance from the highest scoring HIF site including *ATF2*, *CREB1*, *SP1*, *WT1* and *JUN* which have been previously linked to hypoxia and HIF-1 (Table S6). When considering the entire promoter, we observed enrichment for P53:P73 binding sites and multiple members of the forkhead family, including FOXO4, FOXD1 and FOXF2. **To test for potential mechanism in up or down regulation of HIF target genes, a similar analysis was employed to up-regulated and down-regulated transcripts separately. Most of the sites co-occurring for all HIF targets above were also enriched for the up-regulated genes, albeit with more significant p-values. SP-1 and NF-Y were the only TFs significantly co-occurring within a specific distance from the HIF site in down-regulated genes. Surprisingly, 4 of 5 predicted NF-Y targets (*ABCF2*, *CYCS*, *FH*, *MRPL4*) were genes localized to mitochondria (Table S7).**

HIF-1 motifs are identified de-novo in predicted HIF-1 target genes

To identify de-novo motifs over-represented in the promoters of the 81 HIF target genes selected above, DME2 was employed. For each motif length in the range of 5-12 bases we identified the top 50 over-represented motifs compared to a suitable background set (see methods). These motifs were compared to the TRANSFAC and Jaspar collections of PWMs using the CREAD

program MATCOMPARE. Comparison was estimated using a divergence score in the range of 0 to 1, where a divergence of 0 indicates the motif predicted de-novo is identical to a PWM. HIF-1 PWMs were matched best to 6 bases long de-novo motifs. For motifs longer than 7 bases, no HIF-1 PWMs were ranked within the top 50 (Table S8). Comparing all available PWMs to *de-novo* predicted motifs with a divergence of 0.25 or lower identified ARNT (HIF-1 β), ATF2, NF-Y and ATF-6 as the most enriched in the data set (Table S9). Other motifs that were predicted de-novo include *CREB1*, AP-1 and *EVII* and *MIZF* (Table S9). Some of these are also identified above as part of the HIF transcriptional network.

Discussion

In this study we presented a computational strategy to identify HIF-1 target genes. This strategy integrates gene expression profiles and computational binding site analysis of proximal promoters. The utility of our strategy in detecting novel HIF target genes was demonstrated by recovering known HIF-1 target genes and experimentally validating *ANKRD37*. *ANKRD37* is a previously uncharacterized protein that contains 4 ankyrin repeats. Ankyrin repeats are thought to mediate protein-protein interactions (67) and are known to be involved in regulation of key transcription factors such as NF κ B and *TP53* (68-70). *ANKRD37* induction was 3 fold higher than *VEGFA* (Figure 5E), the validated HIF-1 binding site was conserved in 10 species and was significantly induced in hypoxia in multiple cell types analyzed here. Taken together, these data suggest this gene is likely to be an important regulator in hypoxia.

The cellular response to hypoxia was different between cell types, consistent with previous reports (55,56). The union of all differentially expressed genes in the data sets presented here contained over 6,000 unique genes. Even when comparing studies that attempted to detect a HIF dependent response to hypoxia (21,22,71), only 45 genes were differentially expressed in all 3. Importantly the analysis presented here indicates that 60% of the transcripts that responded to hypoxia did not have a detectable conserved HIF binding site in their proximal promoter. This observation was also supported by MOTIFCLASS enrichment, which is an independent analysis that does not consider conservation and did not detect any enrichment for HIF binding sites in those promoters. In addition, transcripts with no detectable HIF site were enriched for other

TFBS that were previously shown to participate in the cellular response to hypoxia including, *DEAF1*, *ELK1*, *POU2F1* and *IRF1* (72,73). Moreover, genes that responded to hypoxia and did not have a detectable HIF binding site were used as a background for the HIF-1 transcriptional network. One possible mechanism that may explain the different hypoxic response between cells is that genes directly regulated by HIF are involved in key processes and their regulation mediates a robust effect. As illustrated in the mitochondrial map, where several predicted down-regulated genes affect key steps in the mitochondria. The predicted HIF target genes *SLC25A28*, an iron transporter in the mitochondria and *ISCU*, an iron-sulfur scaffold protein are both down regulated in hypoxia. These two genes could affect several of the mitochondria iron-sulfur proteins including, NADH dehydrogenase, Coenzyme Q - cytochrome c reductase and Succinate - coenzyme Q reductase, which are critical to the function of the electron transport chain and the TCA cycle. In addition, the predicted HIF targets *MRPL4* and *MRPS12* are components of the mitochondrial ribosome that are required for mitochondrial protein translation. Additional examples include cell growth arrest by inhibition of *CAD*, a component of pyrimidine synthesis (74); *RRP9*, a component of snoRNP predicted to participate in processing and modification of pre-ribosomal RNA (75); *EIF2B3*, a translation initiation factor subunit; and *CCNB1*, a regulatory protein involved in mitosis (74). The HIF-1 pathway map also supports this observation where except for the glycolysis pathway, only one or two HIF targets were identified in each metabolic pathway. One novel predicted HIF target that is highlighted by the map is *GYS1*, a gene involved in glycogen biosynthesis (65,76) that was validated as responsive to hypoxia by qPCR in multiple cell types.

To highlight predicted HIF targets of interest and to suggest potential functional roles for these targets, a bioinformatics analysis of validated HIF targets was performed and predicted targets that were not previously validated were mapped to the significantly enriched functional categories. This analysis is summarized in Supplementary Table S6 and identifies several attractive predicted HIF targets. The family of 2-oxoglutarate and Fe(II)-dependent oxygenase has 19 members in the human genome of which 5 are bona fide HIF targets, including the HIF-1 α regulators *EGLN1* and *EGLN3*. The predicted HIF target *PLOD1*, is a member of that family and a lysyl hydroxylase involved in collagen synthesis and localized to the endoplasmic

reticulum (77). Mutations in *PLOD1* have been associated with type VI Ehlers-Danlos syndrome, a genetic disorder caused by defects in collagen synthesis (78). In another example, microRNA target predictions from TargetScan were analyzed and validated HIF targets were enriched for five microRNAs including miR-1/206 and miR-130/301. miR-1/206 were shown to be up regulated in a rat model of myocardial infarction (79) and miR-130 was shown to regulate angiogenesis (80). Both are relevant to the HIF pathway and would be attractive to study further with respect to the specific validated and predicted targets. Finally, protein interaction data presented in Figure S4 can be used to identify potential regulators, co-factors or adapter proteins that play a role in the HIF pathway. Finally, P300/CBP-associated factor (PCAF) interacts with 4 validated HIF targets and 6 predicted targets. PCAF was previously shown to be a HIF-1 α co-factor that regulates p53 transcriptional activity in hypoxia (81). The specific HIF targets that interact with PCAF are attractive candidates for further studies.

The method presented here is not without limitation. First, the microarray itself presents a limitation since only genes represented on the microarray are considered. However, this could be improved by using multiple platforms that offer complete coverage of annotated genes. **Of the 86 previously validated HIF-1 targets (supplementary Table S2), only 56 responded to hypoxia in at least one cell type.** One example of a bona fide HIF target gene that was not recovered by our analysis is *EPO* (erythropoietin). A close examination of the data for *EPO* revealed that the probe did not respond to hypoxia in any of the cells that were profiled. *EPO* was previously reported to be highly induced in the kidney (82). **Second, some HIF binding sites may be located outside the promoter region we defined or may not be conserved in other species.** The binding site for the well-characterized HIF-1 target *VEGFA* is located at -985bp (83) and therefore was not recovered in the present analysis. HIF-1 binding sites have been identified as far as 12Kb downstream (*PHD3*, (84) and 5Kb upstream (eNos; (85)) of the TSS. The defined promoter region was found optimal to capture most of the known sites (60% of known HIF-1 binding sites) while minimizing potential false positive prediction.

In this study we provide a ranked catalogue of genes predicted to be direct HIF target genes. Given the different hypoxia response between cell types, it is currently difficult to estimate how many HIF target genes exist. **Our analysis across 6 cell types was stringent in an effort to obtain**

the highest specificity and the top 200 ranked genes are of high confidence. The ranking system by itself offers a level of confidence for the prediction and was shown as reliable by high ranking for previously validated targets (Supplementary Figure S3). Currently, almost all known HIF target genes are up-regulated in hypoxia. While majority of predicted HIF targets were up-regulated in hypoxia, nearly all down-regulated genes are novel. The top ranking down-regulated gene is *EDEM3*, an α 1,2-mannosidase involved in quality control of misfolded proteins (86). In addition, a subset of down-regulated genes were highlighted in the mitochondrial map are consistent with the observed attenuation of oxidative phosphorylation by HIF-1 (87). We also identified NF-Y as significantly co-occurring adjacent to the highest scoring HIF-1 site in four of these down-regulated mitochondrial genes. It is currently unclear whether NF-Y is part of the hypoxic regulation of those genes. However, it was previously shown in yeast that the NF-Y homolog regulates the mitochondrial enzyme COX (88), which was also shown to be regulated by HIF-1 to optimize efficiency of mitochondrial respiration (89).

To describe the transcriptional network of HIF, we identified additional TFBS over-represented within ± 150 bp from the highest scoring HIF site as well as TFBS enriched in the entire promoter. We identified only a few TFs within a specific distance from the HIF site, however, almost all were previously associated with HIF-1, including *CREB1*, *ATF2* and *SP1* (90-92). The recovery of these TFs increases the confidence in the genes predicted as HIF targets and also identifies specific gene targets in Table S6 as predicted targets with higher confidence. *WSB1*, for instance, is a novel predicted HIF-1 target that contains binding sites for *CREB1*, *ATF6*, *ATF2* and *JUN:ATF2*, a profile very similar to *LDHA* that is a bona fide HIF-1 target. *WSB1* was previously shown to be involved in the ubiquitination and degradation of *HIPK2* (93), a kinase that was shown to repress HIF-1 α transcription (94). *WSB1* was also confirmed to be hypoxia responsive by qPCR (Supplementary Figure S5). Taken together these data suggest *WSB1* is highly likely to be a direct HIF-1 target and to be part of a feedback loop that includes HIF-1 α , *WSB1* and *HIPK2*. All TFs that were previously associated with HIF-1 appear to be enriched only in genes up-regulated during hypoxia. YY-1 and NF-Y were detected as enriched in down-regulated genes. Further studies will be necessary to validate these observations and to

determine their functional relevance to HIF-1.

De-novo motif prediction suggested that no significant information flanking the **HIF consensus binding site** could be found in the predicted HIF target genes. This is consistent with the observation that enhancing the number of validated HIF binding sites reduces the information content of the flanking nucleotides (Supplementary Figure S1). Conservation was not considered in the *De-novo* prediction process. Yet, several TFs identified as part of the HIF transcriptional network have also been identified de-novo, including, *CREB1*, *JUN:ATF2*, *ATF2*, *ATF6* and AP-1. The ability to recover these TFs de-novo confirms their significant over-representation and demonstrates the utility of this approach in recovering previously validated TFs and co-factor that are part of the HIF network. **Furthermore, novel TFs that may be part of the HIF transcriptional network are currently supported by sequence analysis data alone and additional studies are required to validate these findings.**

HIF-1 and HIF-2 are both key transcription factors with that modulate metabolic pathways, bioenergetics and processes relevant to cancer onset and progression. This study not only gives insights into the genes potentially regulated by HIF but also serves as a guide to study direct targets of other transcription factors.

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Figure Legends

Figure 1: Prediction strategy for identifying HIF-1 target genes. Candidate genes that respond to hypoxia were first identified by microarrays. Each data set was subjected to a computational analysis in which HIF binding sites were detected in proximal promoters. Each gene was scored for its response to hypoxia and for the best HIF binding site. No cutoff was set for determining HIF target genes. Finally, all genes were ranked.

Figure 2: (A, B) Binding site enrichment analysis. The program MOTIFCLASS was employed to identify binding sites significantly over-represented in the promoters of genes that respond to hypoxia in B cells. (A) 770 promoters of genes that responded to hypoxia in which a detectable HIF-1 binding site was identified. HIF-1 PWMs were identified as the most enriched. (B) 1,456 promoters of genes that responded to hypoxia but do not contain a detectable HIF-1 binding site. No HIF-1 PWM was identified in the top 20 matrices. Sn: sensitivity, Sp: specificity, Error: classification error rate, Pval: p value. (C) Correlation between the number of HIF target genes and the number of cells in which they responded to hypoxia. Only 31% of the genes that responded to hypoxia in 1 of 6 cells was predicted as a HIF target gene, compared to 71% of the genes that responded to hypoxia in 6 of 6 cell lines.

Figure 3: HIF dependent response to hypoxia across 6 cell types for 81 selected genes that respond to hypoxia in at least 3 cell types and were ranked within the top 200 HIF target genes. The heatmap shows a fold induction compared to normoxia within each cell type. White blocks indicate the gene did not respond to hypoxia in that cell type.

Figure 4: (A) Metabolic map of HIF target genes. The KEGG pathway database was employed to map 81 HIF target genes defined as the core response to hypoxia to pathways. Metabolism related process are shown here (black objects) and those over-represented with a p-value < 0.05 are shown with a dotted white frame. Up regulated genes are shown as red nodes while

down-regulated genes as green nodes. Previously identified HIF-1 target genes are indicated by a diamond shape. (B) Mitochondrial map. Genes within the top 200 predicted HIF targets that localize to the mitochondria were mapped according to their functional annotation. Up regulated genes are shown as red nodes and down regulated as green nodes. Genes indicated in bold responded to hypoxia in at least 3 cell types. Dotted lines from iron-sulfur protein assembly and repair illustrate a few of the iron-sulfur proteins that are key to mitochondrial function, such as NADH dehydrogenase.

Figure 5: *ANKRD37* response to hypoxia. (A) *ANKRD37* mRNA levels were monitored by qPCR across 7 cell lines and normalized to 18S rRNA. (B, C) *ANKRD37* hypoxic induction over time during hypoxia. (B) Endogenous *HIF1A* protein levels determined after 0, 4, 8 and 12 hours of hypoxic incubation by western blot. (C) mRNA levels of *ANKRD37* and *VEGFA* measured by qPCR after 0, 4, 8 and 12 hours of hypoxic incubation.

Figure 6: Mapping of HIF-1 site in *ANKRD37* promoter. (A) Genome browser view of the 4 HIF binding sites identified in the *ANKRD37* promoters and the 3 promoter sequences that were cloned to identify the dominant HIF-1 site. The site score is shown in parenthesis for each site, higher is better. The larger box of the *ANKRD37* transcript (green) indicates the coding sequence. Note that the conservation shown on the plot is computed by PhastCons which scores conservation based on the evolutionary distance and does not necessarily reflect the number of species (95). (B) DLD1, HCT116 and MCF7 cells were transiently transfected and incubated under normoxic or hypoxic conditions. Luciferase activity of the 3 promoters was measured and normalized to promoter1 in normoxic conditions. All studies were performed in triplicate and data represent the mean \pm standard deviation for 3 different wells. (C) Luciferase activity of promoter1 in normoxia vs hypoxia with mutations in sites 1, 2 and 4 in DLD1, HCT116 and MCF7 cells. Experimental procedure and data analysis was performed as described for panel B. (D) in vitro binding of HIF-1 protein to site2 in the *ANKRD37* promoter. EMSAs were performed using biotinylated probe corresponding to HIF binding site2. Nuclear extracts (NE)

from MCF7 cells cultured in either normoxia (N) or hypoxia (H) were utilized. The asterisk indicates the specific shift obtained in hypoxia. 200xM excess of non-labeled probe as a specific competitor or probe with a specific mutation in the HIF binding site2 (ACGTG > AAAAG) was utilized to confirm specificity. WT = wild type probe. MT = mutant probe. (E) Nuclear extracts from MCF7 cells grown in hypoxia were incubated with antibody specific to HIF-1 α or normal mouse IgG. The double asterisk indicates the super-shift obtained only with a HIF-1 α antibody. N.S.; nonspecific band. (F) *In-vivo* binding of HIF-1 α protein to site2 in the *ANKRD37* promoter. ChIP assays were performed using primer sets corresponding to HIF binding site2 (primer A) or a region upstream of site2 (primer B). DNA-protein complexes from MCF7 cells cultured in either normoxia (N) or hypoxia (H) were immunoprecipitated with or without antibody specific to HIF-1 α or normal mouse IgG. Precipitated DNA or input samples were amplified by PCR.

Table Legends

Table 1. Transcriptional response to hypoxia across six different cell types as determined by microarrays.