Zinc Finger Nuclease Mediated Knockout of ADP-Dependent Glucokinase in Cancer Cell Lines: Effects on Cell Survival and Mitochondrial Oxidative Metabolism

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Abstract

Zinc finger nucleases (ZFN) are powerful tools for editing genes in cells. Here we use ZFNs to interrogate the biological function of ADPGK, which encodes an ADP-dependent glucokinase (ADPGK), in human tumour cell lines. The hypothesis we tested is that ADPGK utilises ADP to phosphorylate glucose under conditions where ATP becomes limiting, such as hypoxia. We characterised two ZFN knockout clones in each of two lines (H460 and HCT116). All four clones had frameshift mutations in all alleles at the target site in exon 1 of ADPGK, and were ADPGK-null by immunoblotting. ADPGK knockout had little or no effect on cell proliferation, but compromised the ability of H460 cells to survive siRNA silencing of hexokinase-2 under oxic conditions, with clonogenic survival falling from 21 ± 3% for the parental line to 6.4 ± 0.8% (p = 0.002) and 4.3 ± 0.8% (p = 0.001) for the two knockouts. A similar increased sensitivity to clonogenic cell killing was observed under anoxia. No such changes were found when ADPGK was knocked out in HCT116 cells, for which the parental line was less sensitive than H460 to anoxia and to hexokinase-2 silencing. While knockout of ADPGK in HCT116 cells caused few changes in global gene expression, knockout of ADPGK in H460 cells caused notable up-regulation of mRNAs encoding cell adhesion proteins. Surprisingly, we could discern no consistent effect on glycolysis as measured by glucose consumption or lactate formation under anaerobic, or extracellular acidification rate (Seahorse XF analyser) under oxic conditions in a variety of media. However, oxygen consumption rates were generally lower in the ADPGK knockouts, in some cases markedly so. Collectively, the results demonstrate that ADPGK can contribute to tumour cell survival under conditions of high glycolytic dependence, but the phenotype resulting from knockout of ADPGK is cell line dependent and appears to be unrelated to priming of glycolysis in these lines.

Introduction

The identification of large numbers of candidate genes through genomic analysis has created a pressing need for new approaches for ascribing biological function. Highly sequence-specific zinc-finger nucleases (ZFN) have utility for targeted gene editing in live cells [1–6] and are one of the emerging functional genomics tools for exploring genotype/phenotype relationships. Specifically, dimeric ZFNs capable of recognising 18–42 base pair sequences can be used to introduce double strand DNA breaks at unique locations in the genome. These DNA breaks initiate error-prone non-homologous end joining repair to generate site-specific, heterogeneous mutations (predominantly small indels that disrupt gene function) or, in the presence of a donor DNA sequence, to introduce defined mutations via homology-directed repair. Recent studies confirm the high sequence specificity of custom-designed ZFNs in cells [7–10].

Here we utilise ZFN technology to interrogate the biological function of a human gene, ADPGK, which encodes an ADP-dependent glucokinase (ADPGK). Surprisingly, given extensive investigation of glucose phosphorylation as the central reaction of intermediary metabolism for many decades [11], mammalian ADPGK was discovered only recently through its sequence similarity to archaeal ADP-dependent glucokinases [12]. Phylogenetic analysis suggests the ancestral gene was laterally transferred from Archaea early in metazoan evolution [12]. The purified recombinant murine [12] and human [13] enzymes have been confirmed to phosphorylate glucose, with the unusual feature (as for the archaeal enzymes [14]) that the phosphoryl donor is ADP in contrast to the well-studied ATP-dependent vertebrate hexokinase isoforms (HK1–4). Murine ADPGK is quite specific for glucose, with lesser ability to phosphorylate mannose and fructose (20% and 10% respectively of the rate with glucose); it has a low apparent $K_m$ for both glucose (96 μM) and ADP (260 μM), and is
inhibited by high concentrations of glucose and by its product AMP but, unlike HK1-4, not by glucose-6-phosphate. The biological role of eukaryotic ADPGKαs is not well understood; RNAi screens in C. elegans and HeLa cells have not identified a phenotype [15–17], although a recent report has demonstrated a role of ADPGK in T-cell receptor signalling through diversion of glycolytic flux to the glycerol-3-phosphate dehydrogenase shuttle, resulting in stimulation of mitochondrial production of reactive oxygen species (ROS) [18]. However, the biochemical properties of ADPGK, particularly its ability to utilise ADP, led us to hypothesise that it may play a role in priming glycolysis under stress conditions where ATP becomes limiting [12], such as under hypoxia when cells become highly dependent on glycolytic ATP generation [19].

Given the importance of glucose phosphorylation in tumour metabolism, we focus here on the role of ADPGK in human tumour cell lines. Tumour cells are highly dependent on glycolysis, as first observed by Otto Warburg during the 1920s [20,21], and the associated metabolic reprogramming has recently been suggested as a possible hallmark of cancer [22]. In particular, elevated glycolytic flux in tumour cells is considered to provide intermediates for anabolic pathways and to increase antioxidant defenses through NADPH generation via the pentose phosphate pathway [23,24]. Expression of hexokinases is often up-regulated in cancer cells as part of this metabolic switch [25]. ADPGK is highly expressed in human tumours and tumour cell lines, at both the mRNA and protein levels, although there is little indication of up-regulation relative to normal tissues and (unlike many glycolytic enzymes) it is not up-regulated by anoxia, hypoxia or HIF-1 in tumour cell cultures and shows little dependence on extracellular glucose concentration [13]. However, given that an emergency response to ATP depletion would be mounted most rapidly by a constitutively expressed enzyme, the lack of regulation of ADPGK, particularly its ability to utilise ADP, led us to hypothesise that it may play a role in priming glycolysis under these conditions.

Our initial attempt to test this hypothesis examined the effect of suppressing ADPGK expression, with and without suppression of HK2, in HCT116 and H460 human tumour cell lines using RNA interference [13]. This study showed higher mRNA and protein expression of both ADPGK and HK2 in H460 than in HCT116 cells, but did not demonstrate any significant effect on anaerobic glycolysis (glucose consumption and lactate formation), or on clonogenic cell survival under short term anoxia, hypoxia or HIF-1 in tumour cell cultures and shows little dependence on extracellular glucose concentration [13]. However, given that an emergency response to ATP depletion would be mounted most rapidly by a constitutively expressed enzyme, the lack of regulation of ADPGK expression by hypoxia does not preclude a role in priming glycolysis under these conditions.

In the present study we circumvent the incomplete silencing of ADPGK by using specific ZFNs to effect multi-allelic mutational inactivation of the gene, generating ADPGK-null H460 and HCT116 cell lines. The pair of ZFNs used here target a genomically unique 37 base pair recognition sequence within the first exon of the ADPGK gene. Two independent ADPGK-null clones with confirmed frameshift mutations were generated in each genetic background. These clones were characterised with respect to proliferation, clonogenic survival and glycolytic flux under aerobic and anaerobic conditions. Extracellular acidification (as a measure of glycolysis) and mitochondrial oxygen consumption were also measured using a Seahorse XF analyser. Finally, the ability of these cell lines to grow as tumour xenografts, and the steady state proportion of hypoxic cells in the resulting tumours, were compared with parental lines.

## Results

### Generation of ADPGK-null Cell Lines using ZFNs

ADPGK was knocked out in two genetic backgrounds (HCT116 and H460) using CompoZr™ ZFNs custom-designed to introduce double-strand breaks at a genomically unique target site in the first exon of the ADPGK gene (Figure 1A). The ability of the ZFNs to introduce mutations at this site was tested in HCT116 cells using the Surveyor™ mutation detection assay (Figure 1B), following lipid-based co-transfection with a GFP plasmid and FACS sorting 24 h later to enrich for transfected cells. A 473 bp region surrounding the ZFN cut site was amplified by PCR and the products were denatured and re-annealed to generate mismatch bubbles at ZFN cut sites. CEL-II nuclease [26] cleavage of the mismatch bubbles resulted in the predicted products (256 and 217 bp) for cleavage at the target site. Band densitometry of the image in Figure 1B showed that the ratio of the summed cleavage products to parental band was 66% (0.399/0.601) for the ZFN-treated DNA supplied by the manufacturer (lane 2) and 68% (0.403/0.597) for ZFN-transfected HCT116 cells (lane 4) in this experiment, indicating a high frequency of site-specific mutations. In later experiments, electroporation was used instead of lipid-based transfection to further increase transfection efficiencies.

Clones isolated from ADPGK ZFN-treated populations were screened by immunoblotting for the absence of the characteristic 54-kDa ADPGK band. Two candidate knockouts (HCT116 C3 and IC10) with no detectable ADPGK protein (Figure 1C) were identified from two different rounds of transfection (C3 from screening of 12 clones after FACS enrichment, and IC10 from 131 clones after electroporation without flow sorting using conditions which gave transfection efficiencies of ~70% using a GFP plasmid), indicating a low overall frequency of bi-allelic knockout leading to complete loss of immunodetectable protein. A higher proportion of clones appeared to show reduced ADPGK protein expression (data not shown), possibly due to mutational inactivation of a single allele. To test whether the low frequency of null lines (2/143 clones) reflects compromised survival or proliferation in bi-allelic knockouts, we followed the frequency of mutations in a ZFN-transfected HCT116 pool using the Surveyor (PCR/CEL-II nuclease) assay. The 256 and 217 bp bands diminished over two weeks in culture (Figure S1A), although a similar decrease over time was seen with a separate ZFN pair targeting the 6th exon of POR (Figure S1B), which encodes NADPH-cytochrome P450 oxidoreductase. POR-null HCT116 clones were isolated at higher frequency (3/14) using the POR ZFN pair. Thus the progressive loss of ADPGK and POR mutations is more likely to reflect compromised proliferation/survival of cells with the highest plasmid copy number after transfection.

Copy number within the ADPGK gene was assessed for the two ADPGK null clones (C3 and IC10) by qPCR using primer pairs flanking the ZFN target sequence (CNV2 and 3) and another recognising exon 7 (CNV1) >31 kb away (Figure 1D). This showed the presence of two copies of ADPGK in the knockouts, as for the parent line (consistent with the Sanger Cancer Genome Project; www.sanger.ac.uk/cgi-bin/genetics/CGP/cghviewer/CghViewer.cgi), except for a single copy region near the ZEN target site in HCT116 clone C3. Sequencing across the ZFN target site of genomic DNA from these null clones demonstrated frameshift mutations in both (Figure 1E). These frameshifts generate premature stop codons resulting in predicted truncated proteins of 75 and 84 amino acids, lacking the ADP kinase domain located between amino acids 52 and 497 of the full length isoform (www.uniprot.org), and are thus expected to be catalytically inactive. The finding of only one mutated (and no WT) sequence
for clone 1C10, coupled with a copy number of two at CNV2 and 3, suggests homologous recombination using the initial ZFN-induced mutation as template resulted in reduction to homozygosity. HCT116 C3 also provided only a single sequence at the ZFN target site, but the copy number of one at CNV2 and 3 suggested a large deletion. This was confirmed by amplifying and sequencing an extended region, identifying a 2963 deletion spanning the CNV2 and CNV3 sites (Figure S2).

Transfection of H460 cells with the same ADPGK ZFN plasmids yielded no ADPGK-null clones from screening of 127 clones after nucleofection alone and screening of 24 clones after nucleofection and FACS enrichment. This low efficiency may reflect the presence of three ADPGK alleles in H460 (Sanger Cancer Genome Project), which we confirmed with the qPCR-based copy number assay (Figure S3). Two clones showed reduced ADPGK protein levels (ID5 and VD6; Figure 2A), suggesting they may carry mutant alleles, were therefore subjected to a second round of ZFN transfection (electroporation and FACS), providing 5/121 clones with no detectable ADPGK protein from which two were chosen for further analysis (IID10 from ID5 and IIE5 from VD6) (Figure 2A). Copy number determination (Figure 2B) in conjunction with sequencing of the ZFN target site (Figure 2C) showed a homozygous frameshifting compound deletion/base substitution mutation for clone H460 IIE5 giving a predicted truncated protein of 89 amino acids. Clone IID10 had a 62-bp deletion in at least one allele, potentially generating a protein of 62 amino acids, while

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**Figure 1. ADPGK knockout in HCT116 cells using zinc-finger nucleases.** (A) Features of the ADPGK gene, with location of primer pairs and the dimeric ZFN targeting site. (B) PCR/CEL-II nuclease (Surveyor) assay for mutation detection at the ZFN target site. HCT116 cells were transfected with a pair of ADPGK ZFNs and a GFP plasmid. One day later genomic DNA was prepared from pooled FACS sorted GFP positive cells for the assay (Lane 4). Lane 1: DNA ladder. Lane 2: positive control DNA from ADPGK ZFN-treated K562 cells. Lane 3: Untreated HCT116 cells. (C) ADPGK ZFN-treated HCT116 cells cloned and screened for ADPGK by western blot. (D) Genomic DNA copy number by qPCR for primer pairs CNV1-3. Results are plotted relative to WT DNA which has two ADPGK alleles. (E) Sequencing across ZFN recognition site (predicted cut site in lower case) resulted in deletions (−) and insertions (underlined) for ADPGK-null HCT116 clones C3 and IC10. The inferred copy number for each allele is shown.

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the other allele(s) carry a number of duplications of a segment of DNA downstream from the ZFN cutting site, which were not fully identified.

Proliferation and Clonogenicity of ADPGK Knockout Cell Lines

The ADPGK-null cell lines from both genetic backgrounds showed similar doubling times to the WT lines when cultured under standard aerobic cell culture conditions (Figure 3A and B), with a possible slight reduction in cell proliferation for the HCT116 IC10 line. Colony morphology by phase contrast microscopy was also similar to the parental cell lines (Figure 3C and D) although the H460 IID10 cells were somewhat more prone to rounding up and detaching from the dish.

To further investigate proliferation, HCT116 and H460 cell lines were cultured under normoxia for 54 and 72 h, respectively, and cell number, cell volume, cell cycle distribution and clonogenicity was measured (Table 1). No significant differences were observed for HCT116 C3 compared to WT; however a two-fold increase in G1 phase cells was seen for HCT116 IC10, consistent with the reduction in proliferation noted above. Plating efficiency was similar for all three HCT116 cell lines, but the slower proliferation of HCT116 IC10 was reflected in a significantly decreased colony radius. Both H460 ADPGK-null clones showed a small but significant decrease in cell number, and a small increase in G2/M phase cells. Additionally, H460 IID10 had an increased mean cell volume and showed a trend towards decreased plating efficiency as well as decreased colony radius, possibly due to the detachment of cells from the colonies. Overall, the results suggest a minor effect on proliferation but this was not a consistent finding across cell lines and clones.

Global Gene Expression in ADPGK-null Lines

To investigate whether knockout of ADPGK affects gene expression, two ADPGK –null clones (HCT116 C3 and H460 IIDE5) with similar proliferation and colony morphology to their parental lines were chosen for microarray analysis using Affymetrix Human Gene 1.0 ST microarrays. Single cultures of the HCT116 C3 ADPGK-null line and HCT116 parental cells were compared in a first experiment, and duplicate cultures of both the HCT116 and H460 pairs in a second experiment. The transcriptome of the ADPGK–null HCT116 C3 line appeared to be broadly similar to that of the WT HCT116 line (Figure 4A) and no differentially expressed transcripts were identified when the false discovery rate was controlled to 5% by the Benjamini-Hochberg method. While this analysis suggested that the number of apparently differentially expressed transcripts was no greater than expected due to chance, it remains possible that small numbers of mRNA transcripts may be authentically regulated following ADPGK gene inactivation in HCT116 cells. There was no evidence for changes in expression of glycolytic genes other than an apparent 2-fold decrease of glucose transporter SLC2A3. Intriguingly though, within the top-ranked 22 probe sets (Table S1), transcripts from eight Y-chromosome genes were down-regulated in the knockout line. On comparing

Figure 2. ADPGK knockout in H460 cells using zinc-finger nucleases. (A) Western blots of H460 cells after transfection with ADPGK ZFNs (clones ID5 and VD6), and ADPGK-null clones derived from these in a second round of ZFN transfection (IID10 and IIE5). (B) Genomic DNA copy number by qPCR for primer pairs CNV1-3. Results are plotted relative to WT DNA which has three ADPGK alleles. (C) Sequencing across the ZFN cut site shows deletions (−) and insertions (underlined) for the ADPGK alleles in H460 clones IID10 and IIE5.

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the karyotype of HCT116 C3 with the WT line, we noted that the latter contains a subpopulation of cells retaining a Y chromosome while the HCT116 C3 line (and the HCT116 1C10 line) comprises only a single karyotype lacking the Y chromosome (Table S2). Thus the down-regulation of Y-chromosome transcripts may be an artifact resulting from clonal selection of a Y-minus variant.

Knockout of ADPGK in H460 (clone IIE5) caused a visibly greater alteration in gene expression (Figure 4B). Most notably the probe set for cadherin 11 (CDH11) was significantly decreased, by 150-fold, in H460 IIE5 (p = 0.03). No other differentially expressed transcripts were identified when the false discovery rate was controlled to 5% by the Benjamini-Hochberg method, a conservative statistical threshold that is appropriate when so few replicates are available. Nevertheless, plotting the expression differences of the top-ranked 50 probe sets in a heatmap shows a visible but not statistically significant distinction between WT H460 line and the IIE5 H460 knockout clone duplicate cultures (Figure 4C). While there was no evidence for changes in the abundance of glycolytic mRNAs, two mRNAs encoding regulators of cellular metabolism did appear to be differentially expressed just below the level of statistical significance (PPARGC1A, 3-fold downregulated; and AKT3, 2.7-fold upregulated). Cadherins 2, 6 and 10 were also differentially expressed >2.5-fold but below the level of significance. The top-ranked 150 probe sets from H460 (Table S3) were chosen for further analysis with the gene ontology tool DAVID ([27]; http://david.abcc.ncifcrf.gov/tools.jsp). Close to 50% of the input genes were associated with the plasma membrane and predicted to be glycosylated, 20% were localised to the extracellular space and ~16% were associated with cell adhesion (Table S4). Analysis using the GeneSetDB pathway analysis tool [28] also revealed that the top-ranked 150 probe sets

Figure 3. ADPGK knockout clones of HCT116 (A, C) and H460 (B, D) show growth and morphology similar to the respective WT lines in vitro. (A/B). Cell density after seeding 24-well plates at 10⁵/ml. Values are mean and SEM for triplicate cultures. (C/D). Phase contrast microscopy (10× objective magnification) of WT and knockout clones in T flasks. doi:10.1371/journal.pone.0065267.g003
from H460 cells were significantly enriched (p < 0.05) for Gene Ontology (GO, http://www.geneontology.org/) categories of ‘Adherens junction organisation’ and ‘Cell junction assembly’, and for the Reactome (http://www.reactome.org/) molecular

Table 1. Proliferation and clonogenicity of HCT116 and H460 cell lines under normoxia.

| Sample          | Fold increase in cell number | Mean cell volume (fl) | Cell cycle   | Clonogenic assay   |
|-----------------|-------------------------------|-----------------------|--------------|--------------------|
|                 |                               |                       | G1/G0 | S    | G2/M | Plating efficiency (%) | Colony radius (mm) |
| HCT116 (54 h incubation) |                               |                       |       |      |      |                       |                      |
| HCT116 WT       | 3.32±0.17                     | 1722±17.8             | 30.1±0.7 | 46.7±0.4 | 22.0±0.4 | 113.0±5.7 | 0.91±0.004 |
| C3              | 3.18±0.26                     | 1722±0.3              | 26.1±0.8 | 48.3±0.5 | 24.6±0.5 | 115.7±4.5 | 0.92±0.002 |
| IC10            | 3.00±0.38                     | 1676±9.3              | 58.7±1.0 * | 25.6±0.6 * | 14.5±0.3 * | 966.6±6.3 | 0.64±0.016 * |
| H460 (72 h incubation) |                               |                       |       |      |      |                       |                      |
| H460 WT         | 12.87±0.10                    | 1814±43.0             | 60.3±0.8 | 29.5±1.0 | 8.8±0.3 | 92.0±2.3 | 0.54±0.007 |
| IIE5            | 9.38±0.29 *                   | 1824±36.0             | 59.4±0.1 | 28.6±0.1 | 10.3±0.3 * | 92.1±5.9 | 0.54±0.004 |
| IID10           | 9.44±0.83 *                   | 2338±38.8 *           | 61.0±0.9 | 28.0±0.8 | 10.0±0.2 * | 75.9±14.7 | 0.43±0.007 * |

Asterisks indicate significant (p < 0.05) difference from WT by one-way ANOVA/Holm-Sidak. Proliferation parameters of respective cell lines are displayed as mean ± SEM for three biological replicates.

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Figure 4. Global gene expression in ADPGK-null HCT116 (clone C3) and H460 (clone IIE5) cell lines. RNA was analyzed using Affymetrix Human Gene 1.0 ST microarrays (A) Scatterplot showing mean expression values for HCT116 C3 versus WT (3 cultures each). (B) Scatterplot showing mean expression values for H460 IIE5 versus WT (2 cultures each). (C) Heat map of the 50 top-ranked differentially expressed probe sets in duplicate cultures of H460 WT and H460 IIE3. (D) qPCR of RNA from 3 replicate cell cultures each for H460 WT and ADPGK knockout clones IIE5 and IID10, normalised against 18S rRNA.

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pathway categories of ‘Adherens junctions interactions’ and ‘Cell junction organisation’.

In order to confirm suppression of mRNA for cadherin 11 and other cell adhesion molecules that appeared to be differentially expressed following ADPGK knockout (NCAM2, L1CAM and CDH2), their expression was quantified by qPCR in H460 WT and both the ADPGK-null clones IIE5 and IID10 (Figure 4D). ADPGK mRNA was also quantified by qPCR, and demonstrated low transcript abundance in the mutant clones consistent with nonsense-mediated decay. Expression of CDH11 was strongly suppressed in the ADPGK knockouts (>10,000-fold in H460 IIE5 and ~200-fold in H460 IID10), NCAM2 and L1CAM RNA were decreased in the range of 30 to 40-fold and 3 to 4-fold, respectively, in both the ADPGK-null clones. CDH2 was only decreased in H460 IIE5 (~1000-fold). In contrast, this suppression of CDH11, NCAM2 and L1CAM was not detected when ADPGK was knocked down to 80% of WT levels by siRNA (Figure S4) suggesting that complete loss of gene function may be required for this phenotype.

Effect of ADPGK Knockout on Cell Survival and Glycolysis in HK2-depleted Cells and Under Anoxia and Hypoxia

The above studies indicated little if any effect of ADPGK knockout on cell proliferation or plating efficiency (clonogenicity) under normal growth conditions. We therefore tested whether ADPGK might contribute to cell survival when glucose phosphorylation is restricted by treatment with HK2 siRNA, or when glycolytic demand is increased under strictly anaerobic conditions (6-h anaerobia). One day after transfection of H460 WT, IIE5 and IID10 with HK2 siRNA or GC-matched control siRNA, HK2 knockdown as measured by qPCR was in the range 70-80% (Figure 5A). Two days after transfection with control siRNA, cell numbers of knockout clones were not significantly different from WT, although a small trend towards reduced proliferation was noted for H460 IID10 as above (Figure 5B). HK2 siRNA significantly reduced cell numbers in WT cultures relative to control siRNA, and both knockout clones showed a small but significant further decrease in cell number compared to HK2 siRNA treated WT (Figure 5B). Plating efficiency of the cells treated with control siRNA, scored 10 days after re-plating cells, was also reduced for the IID10 line (~50% of that for H460 WT), but not for IIE5 (Figure 5C).

The ability of glycolytic restriction (HK2 siRNA) or increased glycolytic demand (anaoxia) to further suppress clonogenicity was evaluated by calculating the surviving fraction (plating efficiency as a fraction of that for the normoxic control siRNA-treated cells). HK2 siRNA killed 79% of H460 WT (surviving fraction 0.21) in Figure 5D) and the resulting colonies were smaller (40% reduction in mean colony radius; data not shown). Notably, both HK2 siRNA transfected ADPGK-null cell lines showed an additional highly significant ~4-fold loss of clonogenicity (Figure 5D), with no further change in colony size, compared to WT also treated with HK2 siRNA. When cells were re-plated in an anaerobic chamber and exposed to 6 h anaoxia before being transferred to an aerobic CO2 incubator, clonogenic survival of WT cells decreased by 71% (Figure 5E) and colony radius by 30% (not shown). Both H460 ADPGK-null cell lines were significantly more sensitive to killing under anaoxia (Figure 5E), with no further change in colony radius. HK2 knockout in combination with anaoxia had a similar effect on viability to that seen under aerobic conditions, again with a significantly greater effect in the ADPGK-null than WT lines (Figure 5F).

Increased sensitivity of both ADPGK knockout H460 clones to anaoxia was confirmed in a second set of experiments, both with and without the glycolytic inhibitor 2-deoxy-D-glucose (Figure S5). These experiments clearly show that ADPGK has a protective effect against cell death under anaoxia and when HK2 is knocked down under aerobic or anaoxic conditions in the H460 cell line.

A similar study to that for H460 cell lines was conducted for HCT116 WT and its ADPGK-null derivatives C3 and IC10 (Figure S6). In this case, the only statistically significant effect of ADPGK knockout was a modest decrease in plating efficiency (of the control siRNA-treated cells) which appeared to be more pronounced than in the experiment without control RNA transfection reported in Table 1. Knockdown of HK2, and exposure to anaoxia for 6 h, caused less cell killing of HCT116 WT than H460 WT cells by a factor of ~2, and knockout of ADPGK did not further increase killing by HK2 siRNA or anaoxia in the HCT116 background.

We further investigated whether prolonged exposure of hypoxia (0.2% oxygen in gas phase) has a similar effect on H460 ADPGK-null clones as shown for anaoxia. All three cell lines proliferated at similar rates under hypoxia for 3 or 6 d, with no significant difference in the fold increase in clonogens per culture (Figure S7A). Similarly, ADPGK knockout had no consistent effect on growth of HCT116 clonogens under 0.2% oxygen for 3, 6, or 9 days (Figure S7B).

The apparent difference in effects of ADPGK knockout on survival of H460 cells under anaoxia versus 0.2% oxygen led us to test activation of the unfolded protein response (UPR), which is more pronounced under severe than moderate hypoxia [29,30]. XBP1 splicing by the IRE-1 endonuclease, a marker of UPR [31], showed similar increases in H460 A DP G K-null clones and WT cells after 6-h anaoxia (Figure S8).

Effects of ADPGK Knockout on Glycolysis and Mitochondrial Metabolism

We next tested whether the effects of ADPGK knockout on H460 survival under anaoxia reflect a role of ADPGK in glycolysis. Glucose consumption and lactate formation during 6-h anaoxia were suppressed when HK2 was knocked down in H460 (Figure 6A, B) and HCT116 (Figure 6C, D) cell lines, establishing that glucose phosphorylation is rate-limiting for glycolysis under these conditions. Surprisingly, there was no evidence for a lower glycolytic rate in the ADPGK knockouts, and glycolysis in the knockouts was no more sensitive to HK2 suppression. Similarly, knockdown of HK2 suppressed steady-state ATP levels (under either aerobic or anaerobic conditions) in H460 cell lines, but this effect was no greater for any of the ADPGK-null clones (Figure 7A). Anoxia and HK2 siRNA had only minor effects on ATP levels in HCT116 WT cells, consistent with the lesser effect of these treatments on clonogenic survival than in H460 cells, with no obvious differences in the ADPGK knockout clones (Figure 7B).

To further investigate the potential role of ADPGK in glycolysis, we also evaluated rates of aerobic glycolysis using a Seahorse XF24 Extracellular Flux Analyser. WT and ADPGK-null cells of both genetic backgrounds were assayed in unbuffered DMEM media, and extracellular acidification rates (ECAR) and oxygen consumption rates (OCR) were measured simultaneously. Knockout of ADPGK had no effect on ECAR, a proxy measure of glycolytic flux [32], in H460 when assayed in media containing 5 mM glucose, 1 mM pyruvate and 1 mM glutamate (Figure 8A) or media containing 5 mM glucose exclusively (Figure 8B). However, when glucose was decreased to 1 mM both ADPGK-null cell lines showed a small but statistically significant (p = 0.002) reduction in ECAR compared to H460 WT (Figure 8C). In HCT116 cells, knockout of ADPGK had no effect on ECAR (Figure 8D-F), with the exception of clone HCT116 C3, which
surprisingly showed an increase in ECAR in media containing pyruvate and glutamate additionally to glucose (Figure 8D). However, removal of pyruvate and glutamate from the media reduced ECAR in clone HCT116 C3 below that of HCT116WT cells (Figure 8E) and could suggest more complex interactions between multiple metabolic pathways in this particular clone.

Interestingly, knockout of ADPGK in both HCT116 and H460 cells resulted in clone- and glucose-dependent reductions in OCR. In H460 cells, the IID10 clone showed the most pronounced reductions in OCR, at all glucose concentrations, as did the IC10 clone in HCT116 cells. Residual oxygen consumption in the presence of the ATP synthase inhibitor oligomycin and complex III inhibitor antimycin A (i.e. non-mitochondrial oxygen consumption) was in most cases unchanged for the knockout lines relative to the parental cells (Figure S9).

To investigate whether these reductions in basal OCR were dependent on glycolytic flux, we examined OCR in media containing 5 mM glucose, 1 mM pyruvate and 1 mM glutamate, following the addition of 2-deoxy-D-glucose to block glycolytic flux. After the addition of 2-deoxy-D-glucose, ECAR decreased by 50%, while OCR was not altered, in all cell lines (Figure S10).

These data suggest that impaired glucose oxidation does not account for the oxidative phenotype observed. The 3-fold reduction in expression of peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PPARGC1A) in H460 clone IIE5 by microarray (Table S2) suggested a possible mechanism for the reduced OCR. In H460 cells, protein expression of components of the electron transport chain complexes I and II appeared to be reduced in the IID10 clone and was associated with a loss in mitochondrial membrane potential (Figure S11C). These data suggest that ADPGK can induce clonal dependent alterations in mitochondrial metabolism.

**ADPGK Knockout Tumours: Growth and Hypoxic Fraction of Xenografts**

To investigate whether ADPGK influences xenograft growth and/or hypoxic fraction in tumours, xenografts were grown from two ADPGK knockouts, HCT116 C3 and H460 IIE5, and their WT counterparts. No difference in growth as subcutaneous tumours was found for the ADPGK knockout clones (Figure 10A/B). Western blots from fresh frozen samples of each tumour that reached the endpoint size showed a reduction of the 54-kDa ADPGK band in most of the ADPGK knockout tumours, but a residual band of varying intensity was evident (Figure 10C). This presumably reflects a variable murine stromal component, given that the antibody also recognised murine ADPGK in mouse liver samples; this is consistent with the presence of a cross-reactive 25 kDa band in mouse liver and in the ADPGK knockout tumour samples with the most intense 54 kDa bands (Figure 10C).
H&E staining and immunohistochemistry for the hypoxic probe pimonidazole did not reveal any differences in necrotic or hypoxic tumour area for any of the groups or cell lines (Figure 10D and E). The analysis was not biased by the tumour size, since there was no significant difference in tumour weights between groups (data not shown). In a second small study with HCT116 WT and C3 xenografts, no obvious difference was seen in staining for pimonidazole, the proliferation marker bromodeoxyuridine or the TUNEL apoptosis assay (Figure S12).

Discussion

In this study we use a pair of ZFNs, custom-designed to target a genomically unique sequence in the ADPGK gene (Figure 1A), to generate human tumour cell lines with frameshift mutations at the target site and which completely lack ADPGK protein by immunoblotting. The truncated proteins predicted from sequencing the region near the ZFN target site represent 62–89 amino acid N-terminal fragments which would not be detected by the antibody we used, which recognises a C-terminal epitope [13]. However, these truncated proteins would almost entirely lack the ADP kinase catalytic domain (amino acids 52–497) and particularly the likely active site aspartate at position 481 and metal ion binding residues at 297 and 328 (www.uniprot.org), and are thus expected to be catalytically inactive. In addition the low abundance of the mutant ADPGK transcripts (Figure 4D), consistent with nonsense-mediated decay, indicates that any such N-terminal fragments are likely to be poorly expressed.

It is of note that two of the four ADPGK-null clones we isolated harboured homozygous mutations, including identical mutations in all three alleles in H460 IIE5. It is presumed that reduction to homozygosity occurred in these cases through ongoing ZFN-induced cutting of the wild type allele, resulting in homology-directed repair with the mutant allele as template, as has been suggested previously [33,34]. The frequency with which multi-allelic knockout was achieved was ~1.5%, with 2/143 screened HCT116 clones lacking ADPGK expression. This contrasts to the much higher proportion of mutations at the ZFN target site as demonstrated by the Surveyor mutation detection assay (Figure 1B), which detects monoallelic mutations as heteroduplexes (predominantly with the WT sequence). This suggests that reduction to homozygosity is a relatively infrequent event in the...
The efficiency of generation of ADPGK-null clones seemed to be even lower in H460, which required two rounds of ZFN transfection with 0/151 null lines in the first round and 5/121 on re-transfection of candidate partial knockouts; this lower efficiency may in part reflect the presence of three ADPGK alleles in this line. As yet there is little information to provide comparison with the efficiency of multi-allelic gene disruption by ZNF in other mammalian cell lines. Much higher rates have been reported for genes that are X-linked [30] or otherwise functionally haploid [39], or when the knockout provides a selectable phenotype [40,41], but rates vary widely at other loci [33,39,40,42]. The difficulties in distinguishing between low efficiency of multi-allelic knockout and rescue by compensating genetic/epigenetic changes with ZFN technology is likely to be particularly problematic with tumour cells given the dual problems of genomic instability and high gene copy number at many loci.

Clonal heterogeneity in tumour cell lines also represents a challenge for use of ZFN in that knockout clones and parental lines are unlikely to be strictly isogenic, and phenotypic differences may thus not have a causal relationship to the targeted mutations. Heterogeneity in the HCT116 line was evident in the karyotypic analysis; the parental line comprised subpopulations with and without a Y-chromosome as well as a polyploid variant, which is consistent with the karyotype reported by ATCC, while the ADPGK knockout clones were derived from the Y-minus pseudodiploid variant (Table S2) and lacked Y-chromosome transcripts (Table S1). Indeed a larger number of clones would have been evaluated in the present study, but this was precluded by the very low efficiency with which multi-allelic knockouts were recovered. Clonal heterogeneity is likely to be an important confounding factor in ZFN gene editing studies with tumour cell lines, and suggests that it would be advantageous to use cell lines that are relatively competent for homology-directed repair which would be expected to minimise genotypic diversity in the parental line as well as maximising gene conversion at the target locus (potentially leading to higher efficiency recovery of homozygous mutations).

Despite the low efficiency in production of null clones using ZFN, knockout of ADPGK in H460 resulted in a marked phenotype in relation to clonogenic survival under anoxia or when glycolysis is restricted with siRNA against HK2 (Figure 5D-F). This phenotype was consistent in both H460 clones, but appears to be cell line dependent given that no such effects were observed in the two HCT116 knockout clones. This difference might reflect the higher ADPGK protein levels in H460 than HCT116 [13], or differences in ADPGK activity as a result of post-translational modification. The mechanism of transient activation of ADPGK during T-cell receptor signalling is unknown, but it occurs in the absence of a change in protein levels and is dependent on PKC-θ [18] suggesting a possible role in the serine/threonine residues of full-length human ADPGK are potential phosphorylation sites, but this has yet to be investigated experimentally. In relation to the cell line dependence of ADPGK knockout, it is perhaps also relevant that HCT116 cells were more resistant to these glycolytic stresses as indicated by a lesser effect of HK2 suppression and anoxia on cell survival (Figure S6) than for H460. In our previous siRNA study [13], knocking down ADPGK by 70–90% in H460 cells did not increase sensitivity to clonogenic cell killing under anoxia. Thus ZFN-mediated knockout may provide a clearer phenotype than RNAi, as also suggested in the present study by the strong reduction in PPARGC1A expression on
knockout of ADPGK but not when it was knocked down with siRNA (Figure 9).

Given the clear effect of knocking out ADPGK on clonogenic survival of H460 under these stress conditions (Figure 5), we were surprised to find no observable effect on glycolysis in either H460 clone (or in the HCT116 knockouts). These studies used two independent measures of glycolysis (glucose consumption/lactate production in bulk cultures, and extracellular acidification rate in unbuffered media with a Seahorse analyser), and failed to reveal any defect in glycolysis even under conditions of HK2 knockdown and anoxia (Figure 6). In addition, knockout of ADPGK also did not further compromise steady-state ATP levels in cells in which glycolysis was inhibited with HK2 siRNA (Figure 7). Thus the effect of ADPGK on survival of H460 cells under these stress conditions appears not to be mediated by a direct effect on glycolytic flux. The studies with the Seahorse analyser also evaluated mitochondrial oxygen consumption in aerobic cultures, and interestingly, demonstrated a reduction in most ADPGK knockout clones in most media (Figure 8). This decrease in respiration on knockout of ADPGK is the reverse of the reported suppression of respiration in T-cells when ADPGK activity is stimulated through T-cell receptor/diacylglycerol signaling [18]. In addition, there was no consistent evidence for changes in oxygen consumption in the presence of oligomycin and antimycin A in the knockouts (Figure S9), as might be expected if ADPGK increases generation of ROS as in activated T-cells [18].

Figure 8. Reduced oxygen consumption rate (OCR) but not extracellular acidification rate (ECAR) in ADPGK knockout cells under aerobic conditions. Basal OCR and ECAR were measured in H460 (A–C) and HCT116 (D–E) ADPGK knockout cell lines and their respective wild types (WT) using a Seahorse XF analyser with monolayers in different media as indicated. Values are mean and SEM from two independent experiments with five biological replicates each.
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Figure 9. Effect of knockout of ADPGK, and its knockdown by siRNA, on expression of PPARC1A in H460 cells. PPARC1A expression was measured by qPCR in WT and the two ADPGK-null clones, and in H460 WT cells two days after treatment with control or ADPGK siRNA. Standard errors are shown for 3 replicate cultures with 3 technical replicates each.
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ADPGK does not appear to participate in an analogous signalling pathway in HCT116 or H460 tumour cells under the conditions we have tested. The marked decrease in expression of PPARGC1A in the H460 knockouts (Figure 9) suggested that compromised mitochondrial biogenesis might be responsible for the decrease in oxygen consumption. In support of this hypothesis, we did observe a decrease in electron transport chain complex I and II expression, which could limit the reduction of the electron transport chain and ultimately reduce oxygen consumption. Consistent with this finding, we also observed a decrease in mitochondrial membrane potential in the IID10 H460 clone. It is unclear whether this is due to a direct effect of ADPGK on mitochondrial biogenesis processes, or due to feedback to these same processes from altered metabolic flux. However, in an effort to explain the difference between our findings and those observed with oxygen consumption in activated T-cells, it is possible that these effects could also be context-dependent and determined by specific signaling to ADPGK, as we have suggested for the wider functions of ADPGK. Furthermore, variability between clones leaves open the question as to whether changes in oxygen consumption represent a real effect of ADPGK or a manifestation of clonal heterogeneity.

Given the important role of hypoxia as a driver of tumour angiogenesis [44], we sought to determine whether the reduced survival of H460 ADPGK knockouts under anoxia in vitro translates
into compromised growth as tumour xenografts. 

ADPGK knockout had no discernible effect on growth of the H460 or HCT116 clones, and steady state hypoxic fractions were unaffected in the resulting tumours (Figure 10). This apparent difference between in vitro and in vivo phenotypes let us to evaluate effects of moderate hypoxia (0.2% O2 gas phase) as distinct from anoxia in vitro; even for the H460 line showing greater sensitivity to anoxia, proliferation of clonogens under hypoxia was not compromised by knockout of ADPGK (Figure S7). Thus moderate levels of hypoxia in tumours, sufficient to induce HIF-1 stabilisation and angiogenesis, do not appear to result in ADPGK dependence. Our results suggest that ADPGK may not be a useful target for cancer therapy, although it needs to be born in mind that the current investigation explores just two clones from each of two human tumour cell lines. The intriguing observation of a clear effect of ADPGK on survival of H460 cells under certain stress conditions in vitro indicates that a deeper understanding of its role in tumour cell biology is needed. In particular, the effect on survival but not apparently glycolysis (despite the demonstrated ability of purified ADPGK to catalyse ADP-dependent glucose-6-phosphate formation [12,13]) raises the question whether this ancient gene might have been co-opted for other functions during metazoan evolution, perhaps analogous to the roles of mitochondrially-bound HK2 in suppressing apoptosis and ROS generation [45,46] and of PK-M2 as a co-activator of HIF-1 [47]. The recent demonstration of the diversion of glycolytic flux by ADPGK to hyper-reduce ubiquinone and drive mitochondrial generation of ROS, in response to T-cell receptor signaling, also raises the possibility that ADPGK might contribute to elevated ROS production in some tumour cells. However, we observed no consistent difference in oxygen consumption in the cells lines examined in the present study following antimiycin exposure, which in part reflects mitochondrial ROS generation, nor consistent alterations in mitochondrial membrane potential. This suggests that modulation of ADPGK levels in H460 and HCT116 cells did not affect the reduced state of the respiratory chain or ROS production. The gene expression changes observed in H460 cells suggest that ADPGK might also regulate expression of cell adhesion molecules in some contexts, indicating a possible avenue for further investigation. In addition, Adpgk knockout mouse embryonic stem cells are now available, providing another important opportunity for evaluation the role of this enigmatic gene in mammalian biology.

Materials and Methods

Ethics Statement

Animal experiments were conducted under protocols approved by the University of Auckland Animal Ethics Committee (approval number CR830).

Cell Culture and Generation of ADPGK-null Lines using Zinc-finger Nucleases

H460 and HCT116 cell lines were obtained from the American Type Culture Collection (ATCC), VA and used within 90 days passage from frozen stocks confirmed to be mycoplasma negative using a PCR-Elisa kit (Roche, Switzerland). All cell lines were grown in alphaMEM (Invitrogen, CA), supplemented with 5% foetal bovine serum (FBS). Cells were subjected to anoxia (0% oxygen in a 5% CO2/5% H2O290% N2 gas phase) in a Bactron Pd catalyst anaerobic chamber (Sheldon Manufacturing, OR), using plasticware and solutions equilibrated to anoxia for at least three days before the experiment.

Plasmids for expression of a pair of custom-designed COB-ZfTM Fok1 ZFNs against two 18 base pair target sites in the first exon of the human ADPGK gene (chromosome 15:73,043,636-73,076,126) were purchased from Sigma Aldrich, MO. The targeted region is: 5'-CGGGGACCGGTCTCCCGCGGGGCCCTCGG-3' and 5'-CAAGCTCCGACACTTCTCAGGG-3'. The Surveyor mutation detection assay, using the CEL-II nuclease, was performed as per the manufacturer's instructions (Transgenomic Inc., NE). Products were resolved on a 2% agarose gel and band densitometry was undertaken using Image J software.

Sequencing of the ZFN Cutting Site

Genomic DNA from WT cells and knockout clones was amplified by PCR using primers surrounding the ZFN cut site (ADPGK_P1): 5'-GGAGGACAATGGTGTGAAAGAACGTCAATCCGAGCTAGC-3' and 5'-GGAGGACAATGGTGTGAAAGAACGTCAATCCGAGCTAGC-3'. The Surveyor mutation detection assay, using the CEL-II nuclease, was performed as per the manufacturer's instructions (Transgenomic Inc., NE). Products were resolved on a 2% agarose gel and band densitometry was undertaken using Image J software.

Western Immunoblotting

SDS-PAGE and western blotting was performed as previously [13]. Primary antibodies were mouse monoclonals against ADPGK and HK2 (Abnova, Taiwan), rabbit polyclonal anti-GAPDH (Abcam, UK) and mouse monoclonal anti-
Karyotyping and qPCR Copy Number Variation (CNV) Assay

Log-phase cultures were treated with colcemid (50 ng/ml, 1 h) and metaphases were prepared for Trypsin-Giemsa staining using standard methods [38,49]; 20 metaphases were analysed for each cell line. qPCR was performed using the Platinum SYBR Green qPCR SuperMix-UDG with ROX module (Invitrogen, CA) and 10 ng of genomic DNA as template. Reactions were performed in quadruplicate in a total volume of 10 μl using the ABI 7900HT Fast Real-Time PCR System (Applied Biosystems, CA) with the following program: 50°C 2 min, 95°C 10 min, 40 cycles of 95°C 15 s, 60°C 30 s, 72°C 30 s. Primer sets were designed to assess copy number at three different sites, within exon 7 of ADPGK gene, immediately down and upstream of the ZFN cut site (see Figure 1A); CNV1 (5'-CTCACCACATCTGATTTGT-3', 5'-TTGTGCTTACGCGCTCTGT-3'); CNV2 (5'-TTGCTAATCCGGCCTGTTGCT-3', 5'-ACGGGTCCTCAAGAAGTTTCA-3'); CNV3 (5'-AGGGCTTGGAGAGGAGAAGG-3', 5'-ATCCGCCGAAFTAGGGAGTGG-3'). All values were normalized relative to the house keeping gene RPP21 (5'-AGGTTCTGGGTTGGTGTGAG-3', 5'-TGTTGTTTGGCAAGGTTGTA-3'). For analysis, the software package SDS 2.3 and RQ manager from Applied Biosciences, CA was used. Copy numbers were calculated by using the formula 2^-ΔΔCt (ΔCt = cycle threshold). HCT116 with two ADPGK copies (www.sanger.ac.uk/cgi-bin/genetics/CGP/cghviewer/CghViewer.cgi) was employed as calibrator.

Proliferation, Cell Volume, Cell Cycle Distribution and Clonogenicity

Cell number and cell volumes were determined from trypsinized monolayer cultures (combined with the original medium to include any floating cells) using a Beckman Coulter counter (Z2 Coulter Particle Count and Size Analyzer). Cell cycle distributions were determined after fixation in 70% ethanol and staining with propidium iodide (10 μg/ml in 0.1% Triton X-100, 100 μg/ml DNase-free RNase A in PBS) for 30 min using an LSR II flow cytometer (BD) and analyzed with FACSDIVA software (BD). 100 or 1000 cells were seeded in triplicate for clonogenic assay as previously [13].

mRNA Microarrays

Cell lines were seeded at 2.5×10^4 cells in T25 flasks. After four days, culture medium was removed and 750 μl TRIZOL® RNA extraction reagent (Invitrogen, CA) was added. RNA was extracted using Qiagen RNeasy Mini columns following the manufacturer’s instructions. The quality of the total RNA (1 μL) was checked using the Eukaryotic Total RNA 6000 Nano Assay on an Agilent 2100 Bioanalyzer according to the manufacturer’s protocol (Agilent, CA). Subsequently, total RNA was processed using the Affymetrix Whole Transcript (WT) Sense Target Labeling Assay Rev. 5, and fragmented, labelled single-stranded DNA was hybridised to Affymetrix GeneChip® Human Gene 1.0 ST arrays at 45°C in a hybridisation oven for 17 h. The arrays were washed and stained using the Affymetrix protocol FS450_0001 in an Affymetrix GeneChip Fluidics Station 450, and scanned in an Affymetrix GeneChip Scanner 7G. Data analysis was undertaken using R version 2.11.0 with the following Bioconductor packages and libraries: affy, limma, gdata, gplots and hguene1stprobeset.db. Specifically, raw microarray data at the probe level was normalised using the Robust Multiarray Analysis method with background correction [30], provided by the R ‘affy’ package. For quality control, Expression Console software (Affymetrix, CA) and R were used. The raw and normalized array data, and the relevant MIAME compliant metadata, can be accessed from GEO with accession number GSE39497 (www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE39497).

Quantitative Real-time PCR (qPCR)

qPCR was performed as detailed in [13] with additional primer pairs for CDH11 [51], CDH2 [52], NCLM2 [53], LIG3 [54] and PPARGC1A [55].

Measurement of Glycolysis, ATP and Oxygen Consumption

HK2 siRNA treatment, glucose and lactate measurements and ATP assays were performed as previously [13]. Extracellular acidification rate (ECAR) and oxygen consumption rate (OCR) were measured with a Seahorse XF analyser (Seahorse Bioscience, MA) in unbuffered DMEM (no serum, Sigma-Aldrich, MO) containing either 5 mM glucose, 1 mM glucose or 5 mM glucose/1 mM pyruvate/1 mM Glutamax™ (Invitrogen, CA) as substrates. Plates were incubated for 60 min in a non-CO2 incubator at 37°C before three basal measurements were undertaken determining oxygen and proton concentration in the medium. Then the glycolytic inhibitor 2-deoxy-D-glucose (100 mM) was injected, or (in separate studies) the ATP synthase inhibitor oligomycin (1 mM) and the complex III inhibitor antimycin A (1 μM) were injected serially, with three further measurements after each addition. Seahorse plates had all media removed, without disrupting the cell monolayer, and were frozen at −80°C, immediately after the conclusion of the assay. Cell number in each well was determined using the CyQUANT kit (Invitrogen, CA), according to manufacturer’s instructions. All OCR and ECAR values were normalized to 5×10^4 cells.

Tumour Xenografts

Immunodeficient female NIH-III nude mice (NIH-Lyst<sup>bg-Bfox</sup>-<sup>nu</sup>-<sup>Foxn1</sup>), approximately 21 g body weight, were housed in groups of 4–6 under specific pathogen-free, controlled ambient conditions (22±2°C, 12 h day/night lighting cycle) with standard rodent diet (Harlan Teklad diet 2018H) and sterile water supplied ad libitum. Tumour cells (7×10<sup>6</sup>/site) were inoculated subcutaneously on the right flank. Tumours were measured every 2–3 days using digital calipers and volumes were calculated as width<sup>2</sup>×length×π/6. Tumours were harvested at approximately 1 cm<sup>3</sup>, 90 min after dosing the mice intraperitoneally with 1000 mg/kg bromodeoxyuridine (Sigma-Aldrich, MO) and/or 60 mg/kg pinomitazol (HPI Inc.). Mice were culled by cervical dislocation and tumours were excised immediately. Half of each tumour was frozen in liquid nitrogen, stored at −80°C and subsequently pulverized using a liquid N<sub>2</sub>-cooled Biomixer (BioSpec Products, OK) and lyzed using Laemmli buffer. The other half was fixed with 10% neutral buffered formalin for 36–48 h, then 70% histology alcohol (18:1:1 ethanol/methanol/isopropyl alcohol) before paraffin embedding and cutting 5 μm sections.

Immunohistochemistry

FFPE sections were deparaffinised and antigen retrieval was carried out using 10 mM sodium citrate buffer pH 6.0 in a pressure cooker for 25 min, followed by cooling on ice for 10 min.
Non-specific binding was blocked by incubation with 10% goat serum in TBS (0.2 M Tris, 1.37 M NaCl pH 7.6) for 1 h in a humidified chamber. FITC-pimonidazole monoclonal antibody (Hypoxyprobe™, HPI Inc.) was diluted 1:25 in 5% goat serum in TBS and incubated overnight at 4°C in a dark humidified chamber. The next day, coverslips were mounted with ProLong® gold antifade reagent (Invitrogen, CA). Slides were stored at 4°C in the dark until imaging with a Nikon TE2000E Inverted microscope (montage function). The same tumour section were then stained with hematoxylin & eosin (H&E, Sigma-Aldrich, MO) and re-imaged. The percentage of necrotic and hypoxic regions in tumour sections was calculated using ImageJ.

Statistics
Descriptive statistics report the mean and SEM for biological replicates (separate cultures) unless otherwise indicated. Significance of difference between two groups was tested using Student’s t-test, and significance between more than two groups was evaluated by one-way ANOVA/Holm Sidak.

Supporting Information

Figure S1 Changes in mutation frequency in HCT116 pools during growth after transfection with ZFNs. HCT116 cells were co-transfected with a GFP plasmid and with plasmid pairs for ADPGK ZFNs (A) and POR ZFNs (B) by nucleofection, and 24 h later 25% of the cells with the brightest GFP fluorescence were sorted. Genomic DNA was prepared on the indicated day after transfection (day 1 sample obtained immediately after sorting), and the mutation frequency was assessed using the Surveyor mutation detection assay. For ADPGK the positive control is a reference DNA sample from ADPGK ZFN-treated K562 cells, provided by Sigma Aldrich, showing the predicted Surveyor products (256 and 217 bp, arrows). For POR the positive control is from a POR null clone (Hko3) with two mutant alleles (a M263L missense mutation and a one-bp insertion) at the ZFN target site that gives predicted Surveyor products of 417 bp and 248 bp (arrows).

Figure S2 Characterisation of the large ADPGK deletion in HCT116 clone C3. Yellow marks the binding site for primer pair ADPGK_P2. Grey marks the WT sequence deleted in HCT116 C3. The ADPGK start codon ATG is underlined and the ZFN recognition site is marked in red (with cutting site in lower case).

Figure S3 ADPGK copy number of HCT116, H460 and SiHa. Copy number was determined via qPCR with HCT116 as calibrator with known copy number of 2 (according to Sanger Institute, cancer genome project). Primers amplify a 175 bp sequence located within exon 7 of the ADPGK gene. Error bars show the SEM for four technical replicates. Boxed numbers indicate copy number identified by the Sanger Institute (www.sanger.ac.uk/cgi-bin/genetics/CGP/cghviewer/CghViewer.cgi). All cell lines were obtained from the American Type Culture Collection (ATCC), VA.

Figure S4 No decreased expression of cell adhesion molecules when ADPGK is knocked down in H460. RNA from three separate experiments was isolated one day after transfection (RNAiMAXTM, Invitrogen, CA) with both control siRNA and ADPGK siRNA (Invitrogen, CA). RNA was transcribed into cDNA and analysed by qPCR. All values are normalised against 18S rRNA, and error bars represent the standard error of three biological replicates each.

Figure S5 ADPGK KO reduces anoxic cell survival but does not lactate formation in H460, and 2-deoxy-D-glucose (2DG) has no effect on these parameters. H460 cells (WT, KO clone I1E5 and HI10) were plated in an anoxic chamber for 2 h before being treated with 2 concentrations of 2DG (1 mM, 10 mM, Sigma-Aldrich, MO) or saline only for 4 h. Graphs show results from 3 independent experiments with 3 experimental replicates each. A. Anoxic surviving fraction measured by clonogenic assay after exposure to 6 h anoxia. B. Lactate formation measured in culture medium after 4 h exposure to saline or 2DG.

Figure S6 Knockout of ADPGK in HCT116 does not affect clonogenic survival under anoxia and when HK2 is knocked down. HK2 was knocked down by siRNA in two independent experiments, combined here, each of which included three biological replicates for WT and two for each KO clone. (A) HK2 mRNA by qPCR one day after siRNA transfection. (B) Cell number two days after siRNA transfection, at which time cells were replated for clonogenic assay. (C) Plating efficiencies of two days after transfection with control siRNA. (D) Effect of HK2 siRNA on clonogenic surviving fraction two days after transfection, relative to cells transfected with control siRNA. E. Effect of 6 h anoxia on clonogenic surviving fraction, relative to oxic controls, determined by plating cells in an anoxic chamber two days after siRNA transfection and transferring to an aerobic incubator 6 h later. F. Effect of HK2 siRNA on clonogenic surviving fraction after exposure to 6 h anoxia, relative to an equivalent anoxic exposure after control siRNA.

Figure S7 Knockout of ADPGK in H460 (A) and HCT116 (B) does not affect cell growth or clonogenic survival under chronic hypoxia. Cells were seeded at 20,000, 1000 or 200 cells/well into 24-well plates and exposed to 3, 6 or 9 days of hypoxia (0.2% oxygen in gas phase), respectively. Cell number was measured using a Beckman Coulter counter and cells were re-plated for 10 days to measure clonogenic survival. Asterisks indicate significance (p<0.05) compared to WT. For HCT116 cell lines, two separate experiments were performed. Hypoxia (0.2% oxygen 5% CO2/ N2) was achieved with an anaerobic glove box system and an oxygen controller (Coy Laboratory Products, Inc.). For long-term exposure, plates were partially enclosed in plastic bags containing trays of water to maximise humidity.

Figure S8 XBP1 splicing under anoxia in H460 cell lines. RNA from H460 WT and two ADPGK-null clones was extracted after exposure to either 6-h normoxia (1 culture each) or anoxia (3 cultures each). RNA was transcribed into cDNA and analysed by qPCR. Two primer pairs, one reporting on total XBP1 (GGCATCCTGGCTTGCCTCCA; GCCCCCTCAGCAGTGTTC), and one reporting on spliced XBP1 (CGCTTTGGGGATGTGATGCCCTGG; CCTGGACCTGCTGCCGACT) were used. All values were normalised against 18S rRNA, and the ratio between spliced and total XBP1 was calculated. Error bars represent standard error.

Figure S9 Inhibition of oxygen consumption by oligomycin and antimycin. Oxygen consumption rate (OCR) in ADPGK-null clones and parental (WT) cell lines in the indicated culture media, determined using a Seahorse XF Analyser, and normalised to 50,000 cells. Values are mean and errors are SEM for five biological replicates, and are derived from two timepoints for basal
conditions and three measurements after addition of oligomycin (1 μM) and antimycin A (1 μM). Asterisks indicate significance (p<0.05) of differences from the respective WT.

**Figure S10** Inhibition of glycolysis by 2-deoxy-D-glucose (2DG). Five replicate cultures of each cell line were seeded in complete medium (5 mM glucose, 1 mM pyruvate, 1 mM glutamate), and EACR and OCR were measured with a Seahorse XF Analyser. After addition of 100 mM 2DG (Sigma-Aldrich) measurements were repeated. Asterisks indicate significance (p<0.05) of differences from the respective WT.

**Figure S11** Knockout of ADPGK in H460 and HCT116 has no effect on mitochondrial mass (A), but has clone-dependent effects on electron transport chain subunit expression (B) and mitochondrial membrane potential (C). For (A), cells were seeded at 25,000 cells per well in black, clear bottom 96 well plates. 24 hours later, cells were stained with 50 nM MitoTracker Green FM (Life Technologies) for 30 min. Media was replaced and the plate was scanned with a fluorescence plate reader at excitation 490 nm and emission 515 nm. For (B), protein lysates were separated using SDS-PAGE before immunoblotting with the Mitoprofile Total ADPKD antibody (Serotec, UK) and incubated for 1 h at RT in a humidified chamber. Substrate-chronogen DAB (EnVision™ Detection Systems Peroxidase/DAB, DAKO, Denmark) was applied for 8–10 min before being rinsed off. TUNEL assay was performed using the ApopTag® Red In Situ Apoptosis Detection kit (Chemicon International Inc.).

**Table S1** HCT116 microarray: top 50 probe sets in order of p values.

**Table S2** Karyotypes of HCT116 WT cells and ADPGK knockout clones.

**Table S3** H460 microarray: top 150 probe sets in order of p values.

**Table S4** Gene ontology (GO) analysis of potential differentially expressed genes in ADPGK knockout clone H460 IIE5 using DAVID.

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**Author Contributions**

Conceived and designed the experiments: SR RSR SLM WRW. Performed the experiments: JR JS SM TC. Analyzed the data: SR SLM WRW CGP. Wrote the paper: SR SLM WRW. Revised the manuscript critically for important intellectual content: SLM CGP RSR.

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