Figure S1. Tumor cell lines express low to undetectable levels of *EPOR* mRNA

*EPOR* mRNA levels were quantified in hematopoietic and non-hematopoietic cell lines using TaqMan primers and a probe located in EpoR exon 8 which encodes the cytoplasmic domain of *EPOR*. Positive controls included UT-7/Epo, OCIM-1, and erythroid progenitors differentiated from CD34+ cells. Low expression control was 769-P cells. *EPOR* mRNA levels from cell lines derived from human (A) breast, ovary, central nervous system (CNS), non-small cell lung carcinoma (NSCLC), small cell lung carcinoma (SCLC), and kidney tumors; and (B) colorectal, leukemia, lymphoma, skin, bladder, liver, and other (pancreatic, prostate, bone, soft tissue, embryonic, head, and neck) tumors are shown relative to housekeeping gene *ACTB* levels.

Figure S2. A82 western blots show the range of levels of EpoR protein detected from representative cell lines and erythroid progenitor cells

A82 western blot method used to estimate EpoR dimers/cell: A comparison of the band intensities for a two-fold step titration of known numbers of cells compared to a two-fold step titration of a known quantity of purified EpoR extracellular domain protein (EpoR ECD) where 150 fg EpoR ECD = 2 × 10^6 EpoR dimers. (A1) EpoR in erythroid progenitor cells differentiated in vitro from peripheral blood CD34+ cell estimated at 8,000–16,000 dimers/cell. (A2) EpoR in DMS-79 and NCI-H1299 cells estimated at 1600–3200 dimers/cell. (B) EpoR western blot showing the range of levels found in solid tumor cell lines (1.6 × 10^5 cells/lane). 769-P is the negative control; OCIM-1 is the positive control. CycloB is the loading control.

Figure S3. *EPOR* mRNA shows no significant fold increase with hypoxia treatment in 66 cell lines examined

Expression of *EPOR*, *CYCLOB*, *VEGF*, and *BNIP3* mRNA in human tumor cell lines following growth in normoxia (N) or hypoxia (H) was determined by bDNA assay the transcript level for each cell line from 3 independent cultures was averaged and normalized to the level of 18S rRNA (assay was repeated with the same lysates and results were averaged). Each point represents the ratio of the normalized RNA level in hypoxia divided by that of normoxia (fold-change) for an individual cell line and vertical bars represent the median for the population. The median value and fold-change for the population is indicated.

Figure S4. EpoR knockdown achieved for 8 different siRNAs and the relative affect on viability of each

EpoR knockdown was plotted as mean +/- standard deviation from replicate experiments. (A) UT-7/GM-CSF cells vs. normalized viability (mean +/- standard deviation) for the same siRNAs in UT-7/Epo cells. (B) EpoR knockdown vs normalized viability plotted for A2780 cells and (C) plotted for NCI-H1299 cells.
Figure S2

A

Erythroid Progenitor Cells

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<tr>
<th>Femtograms</th>
<th>2400</th>
<th>1200</th>
<th>600</th>
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B

EpoR dimers/cell

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<tr>
<th>SK-OV-3</th>
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<th>400-1600</th>
<th>1600-3200</th>
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</thead>
<tbody>
<tr>
<td>EpoR</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CycloB</td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>
Figure S3

- EpoR
- CycloB
- VEGF
- RNIP3

[Fold Change]_log

Hypoxia/Normoxia
Figure S4

A

Normalized Viability (UT-7/Epo)

% EPOR Knockdown (UT-7/GM-CSF)

R² = 0.6973

B

Normalized Viability

% EpoR Knockdown (A2780)

R² = 0.1201

C

Normalized Viability

% EpoR Knockdown (NCI-H1299)

R² = 0.0024