

# PNAS

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Supplementary Information for

**Intracellular Redox Potential is correlated with miRNA expression in MCF7 cells under Hypoxic Conditions**

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### Estimating the error on the Lagrange multipliers $\lambda_\alpha(p)$

The Lagrange multipliers  $\lambda_\alpha(p)$  is the weight of constraint  $\alpha$ ,  $\alpha = 0, 1, 2, \dots$ , at the oxygen pressure  $p$ . See equation [1] of the main text., reproduced here

$$\begin{aligned} \ln X_i(p) &= \ln X_i^0(p) + \sum_{\alpha=1,2,\dots} G_{i\alpha} \lambda_\alpha(p) \\ &= \sum_{\alpha=0,1,2,\dots} G_{i\alpha} \lambda_\alpha(p) \end{aligned} \quad \text{S.1}$$

$X_i(p)$  is the level of miRNA  $i$  at oxygen pressure  $p$ .  $\alpha = 0$  is the stable state. We compute the weight  $G_{i\alpha}$  of miRNA  $i$  in constraint  $\alpha$  by the method of SVD. This means that the different vectors  $G_\alpha$  are orthogonal,

$$\sum_i G_{i\alpha} G_{i\beta} = \delta_{\alpha,\beta} \cdot \quad \text{S.2}$$

It follows from equation [1] that an explicit result for the weight  $\lambda_\alpha(p)$  is

$$\lambda_\alpha(p) = \sum_i G_{i\alpha} \ln X_i(p) \quad \text{S.3}$$

and an uncertainty in the weight due a measurement error of each miRNA is

$$\delta \lambda_\alpha(p) = \sum_i G_{i\alpha} \delta(\ln X_i(p)) \quad \text{S.4}$$

The schwarz inequality of vector algebra yields an upper bound

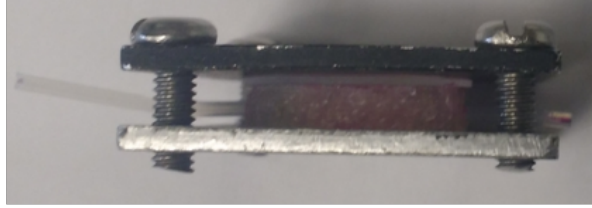
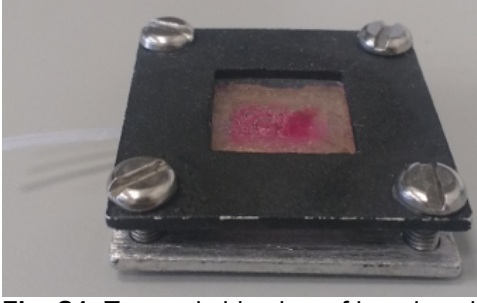
$$\delta \lambda_\alpha(p) \leq \left( \sum_{i=1}^N G_{i\alpha}^2 \right)^{1/2} \left( \sum_{i=1}^N \left( \frac{\delta X_i^p}{X_i^p} \right)^2 \right)^{1/2}$$

From equation S.2 the first sum is unity and the second sum can be approximated as

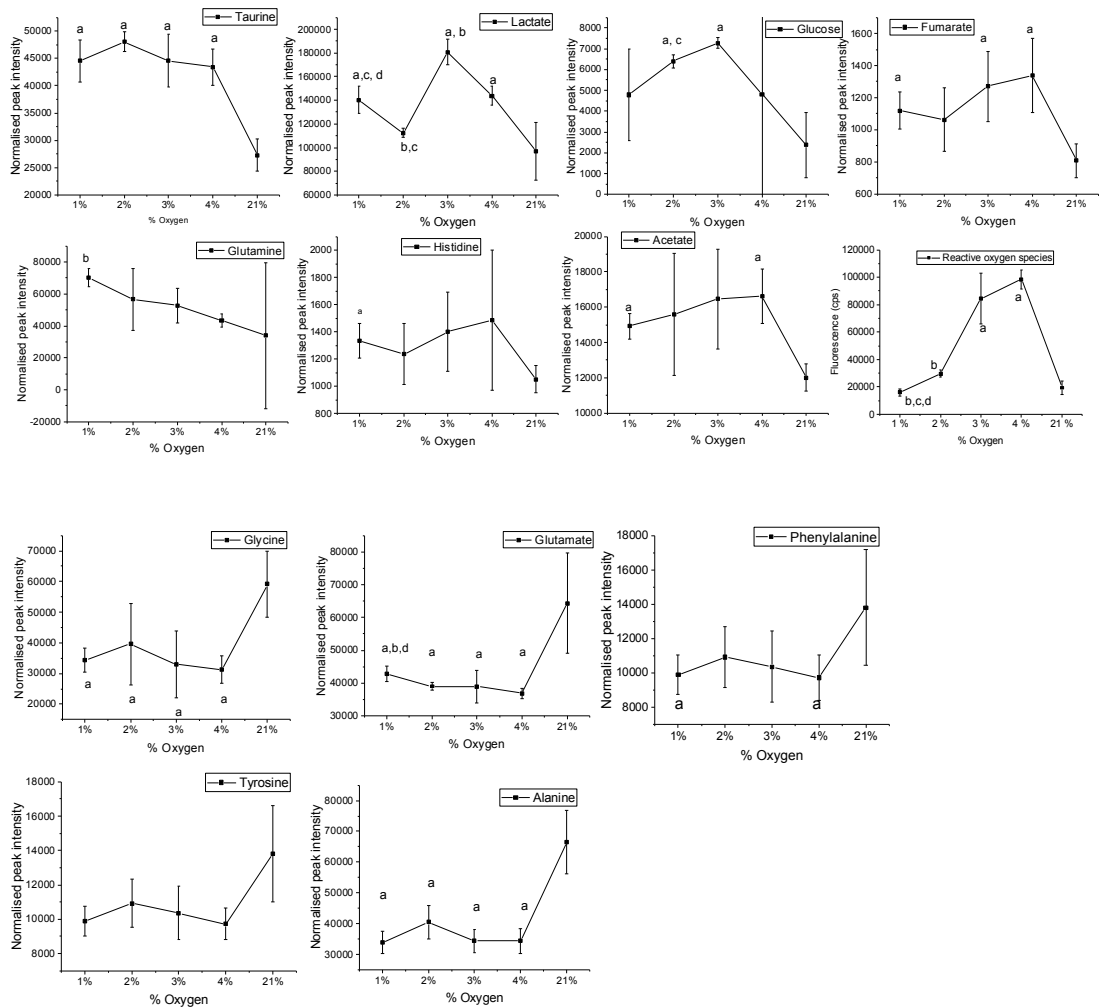
$(\delta X/X)(N)^{1/2}$  where  $(\delta X/X)$  is he mean error per reading and  $N$  is the number of readings.

We have  $N=69$ , so  $(N)^{1/2} = 8.31$  and for the six replicates we get

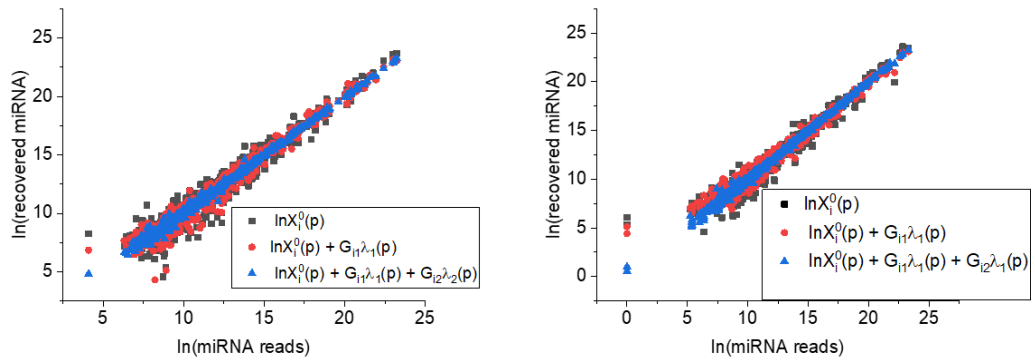
PO <sub>2</sub>	1%	2%	3%	4%	21%
$av(\delta X/X)$	0.12	0.12	0.16	0.16	0.6
$\delta \lambda_\alpha(p)$	1	1	1.32	1.32	1.32



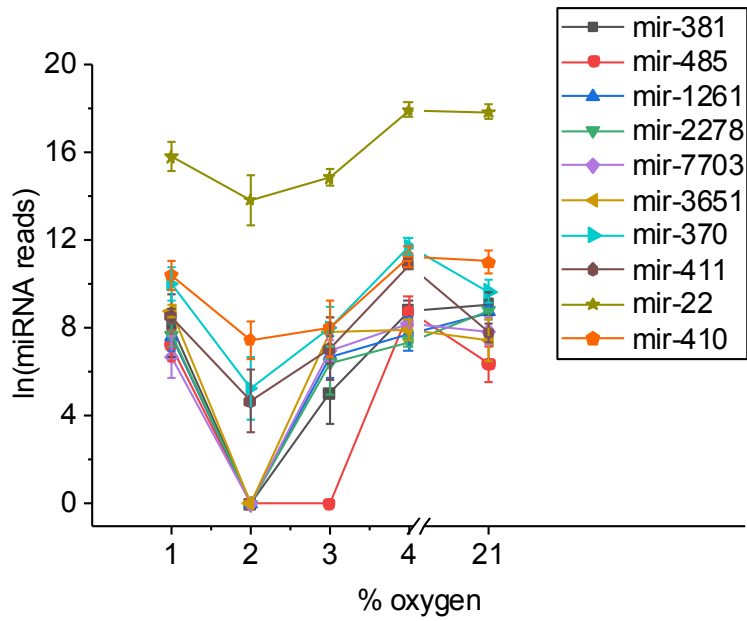
**Fig. S1.** Top and side view of imaging chamber.



**Fig. S2.** Concentration profile of a panel of measured metabolites. Error bars represent the standard deviation of 5 independent measurements. Letters as labels signify a p-value < 0.05 for a paired t-test versus 21% (a); 4% (b); 3% (c); 2% (d).



**Fig. S3.** Addition of  $\lambda_1$  and  $\lambda_2$  to the stable state improves the fit of the data at A - 4% O<sub>2</sub> and B - 21% O<sub>2</sub>.



**Fig. S4.** The top 10 miRNAs for which  $G_{i,\alpha=1} < 0$ . Error bars show the standard deviation of 3 independent measurements.

**Table S1.** Cellular pH at the oxygen concentrations used.

<b>O<sub>2</sub> of cell, %</b>	<b>Average pH of all replicates</b>	<b>STDEV of pH of all replicates</b>
<b>1</b>	<b>6.3</b>	<b>±0.12</b>
<b>2</b>	<b>6.1</b>	<b>±0.03</b>
<b>3</b>	<b>6.7</b>	<b>±0.24</b>
<b>4</b>	<b>6.6</b>	<b>±0.24</b>
<b>21</b>	<b>6.5</b>	<b>±0.05</b>

**Table S2.** Pearson correlation coefficient measuring the correlation between miRNA reads and ROS.

<b>miRNA</b>	<b>Correlation Coefficient</b>
mir-548p	0.9520
mir-769	0.9342
mir-6747	0.9130
mir-1306	0.8978
let-7c	0.8893
let-7g	0.8776
mir-767	0.8753
mir-340	0.8678
mir-1303	0.8588
mir-24	0.8552
mir-6807	0.8546
mir-6764	0.8428



**Table S3.** Pearson correlation coefficient measuring the correlation between ln(miRNA) and E.

<b>miRNA</b>	<b>Correlation coefficient</b>
mir-381	0.8188
mir-485	0.2237
mir-1261	0.8882
mir-2278	0.8869
mir-7703	0.8781
mir-3651	0.7577
mir-370	0.6649
mir-411	0.5421
mir-22	0.7799
mir-410	0.6519

**Table S4.** miRNA roles and known transcription factors for the top 10 miRNAs for which  $G_{i,\alpha=1} < 0$ .

miRNA	Role	Transcription factors (Genecards.org)
mir-381	Neural SC differentiation and proliferation. Upregulates Nestin. HES 1 target. <sup>1</sup> Tumor repressor Inhibitor of metastasis. <sup>2</sup>	Several Zn fingers identified
mir-485	Low levels poor prognostic for glioblastoma <sup>3</sup>  Suppresses breast cancer metastasis by inhibiting PGC1a <sup>4</sup>  Suppresses proliferation and invasion in hepatocellular carcinoma – targets stanniocalcin <sup>5</sup>	GATA (zn finger) ZNF680 (zn finger) ZFP3 (zn finger) MNT
mir-1261	Regulated by YAP member of mir29 family Inhibits PTEN expression. <sup>6</sup> Repressor. “Sponging” is associated with proliferation and invasion. <sup>7,8</sup>	YAP
mir-2278	Tumor suppressor targets STAT5A and induces apoptosis. <sup>9</sup>	ZNF169
mir-7703	Very little information	GLIS1(zn finger)
mir-3651	Down regulated in squamous cell carcinoma. <sup>10,11</sup> Repressor	C/EBP Beta (redox regulated) <sup>12</sup> ZNF348 (zn finger)
mir-370	TF (Ets) had disulfide in dna binding domain. Regulates cyp2d6 (drug metabolism) Inhibits fibrogenesis Supresses proliferation. <sup>13</sup> Downregulates FOXO1 and regulates redox. <sup>14</sup>	ELF3 SOX TFAP4 (two Cysteines) BCOR(zn finger)
mir-411	Inhibits proliferation and metastasis in breast cancer. Targets GRB2 <sup>15</sup> Targets SPRY4(a kinase inhibitor) inhibits proliferation in vitro and in vivo. <sup>16</sup>	No information
mir-22	Inhibits tumor growth in AML. <sup>17</sup>	C/EBP Beta (redox regulated) <sup>12</sup>
mir-410	Tumor suppressor in breast cancer. <sup>18</sup> Tumor enhancer in liver cancer. <sup>19</sup>	NFE2U, AP1 (redox regulated) <sup>20</sup>

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