Supplementary figure 2.10

```
$ ffq -l 2 CRX102291 -o metadata.json
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{
    "PRJNA102291": {
        "accession": "PRJNA102291",
        "title": "Genome-wide transcriptional responses of Saccharomyces cerevisiae to high car
bon dioxide concentrations",
        "description": "Physiological effects of carbon dioxide and impact on genome-wide trans
cript profiles were analysed in chemostat cultures of Saccharomyces cerevisiae. In anaerobic, g
lucose-limited chemostat cultures grown at atmospheric pressure, cultivation under CO2-saturate
d conditions had only a marginal (<10%) impact on the biomass yield. Conversely, a 25% decrease
 of the biomass yield was found in aerobic, glucose-limited chemostat cultures aerated with a m
ixture of 79% CO2 and 21% O2. This observation indicated that respiratory metabolism is more se
nsitive to CO2 than fermentative metabolism. Consistent with the more pronounced physiological
effects of CO2 in respiratory cultures, the number of CO2-responsive transcripts was higher in
aerobic cultures than in anaerobic cultures. Many genes involved in mitochondrial functions sho
wed a transcriptional response to elevated CO2 concentrations. This is consistent with an uncou
pling effect of CO2 and/or intracellular bicarbonate on the mitochondrial inner membrane. Other
 transcripts that showed a significant transcriptional response to elevated CO2 included NCE103
 (probably encoding carbonic anhydrase), PCK1 (encoding PEP carboxykinase) and members of the I
MD gene family (encoding isozymes of inosine monophosphate dehydrogenase Keywords: Dose reponse
 Overall design: Knowledge on the genome-wide transcriptional response of S. cerevisiae to high
 CO2 concentrations may provide a deeper insight into the molecular mechanisms of CO2 stress. S
uch insight is essential to develop metabolic-engineering strategies for improving CO2 toleranc
e. Furthermore, identification of ‘signature transcripts’ that uniquely respond to CO
2 stress may be applicable for diagnosing the CO2 status of industrial fermentations. It has re
cently been demonstrated that the combination of chemostat cultivation with DNA-microarray-base
d transcriptome analysis offers a powerful and reproducible approach to identify the transcript
ional responses of yeasts to environmental parameters For this reason, in the present study we
used chemostat cultures of S. cerevisiae to quantify the effect of CO2 on respiring and ferment
ing cells, and to determine the genome-wide transcriptional responses of this yeast to high CO2
 concentrations.",
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