Multiomics data for Yoneda *et al* (2016)

# Summary

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| --- | --- | --- | --- | --- |
| **Strain** | **Growth data**  [7 Phe and 1 Glc different conc]  {13 time samples, 8 rep}  (191210\_Ropacus\_Yoneda2016\_Fig2.xlsx) | **Growth in Phe/Glc/N with Phe consumption data**  {3-5 time samples}  (191210\_Ropacus\_Yoneda2016\_FigS3.xlsx) | **Growth data**  [Glc, lowP, highP]  {4-15 time samples, 2 replicates}  (191210\_Ropacus\_Yoneda2016\_transcriptomics\_growth.xlsx) | **Transcriptomics data**  [Glc, lowP, highP]  {single time sample, 3 replicates}  (<https://htcf.wustl.edu/files/5dGx8leZ/yoneda_2016/>) |
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| WT | **✓** | **✓** | **✓** | **✓** |
| evol33 | **✓** | **✓** | **✓** | **✓** |
| evol40 | **✓** | **✓** | **✓** | **✓** |

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# Details

Fig. 2 growth data. (191210\_Ropacus\_Yoneda2016\_Fig2) Note that this data is in a 96 well plate, and 1 g/L nitrogen source (ammonium sulfate), so the aeration will be different for this data set compared to growth in 50 mL tubes or 250 ml flasks.

Fig S3 growth and consumption data (191210\_Yoneda2016\_FigS3) WT, evol33, and evol40 at 1.5 g/L phenol as sole carbon source, 1 g/L nitrogen source (Fig S3). Note that phenol concentrations were calculated from absorbance at 280nm, and growth was 100 mL in 250 ml flask, so again, different aeration here.

The collection times for RNASeq for Yoneda et al were 14 h for glucose, 24 h for 0.75 g/L phenol, and 32 hours for 1.5 g/L phenol

Other growth data: preliminary growth curve to determine the optimal time to harvest transcriptomics samples at mid-exponential phase. (191210\_Yoneda2016\_transcriptomics\_growth). This growth curve was done at 100 mL volume in a 250 mL flask and low nitrogen (0.05 g/L nitrogen source).

**Winston’s yoneda\_2016 folder**: All the raw data as well as bowtie and featureCounts output for transcriptomics.