

README for 2020_01_15 high abundance transcript in mouse gut experiment

Based on RNA seq data paired with metagenomic sequencing done by Hao Zhou in Brito lab.

Sequence data in ../../probe_design/data

Probe design in ../../probe_design/runs/DSGN_001

Probes ordered in ../../orders/2020_01_07_high_abundance_transcripts.xlsx

Targeted Transcripts

- ndhM:
 - aerobic-type carbon monoxide dehydrogenase, large subunit CoxL
 - d__Bacteria;p__Firmicutes_A;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__UBA9475;s__
 - rpkM_average = 42,648
- argC:
 - Belongs to the NAGSA dehydrogenase family. Type 1 subfamily
 - d__Bacteria;p__Firmicutes_A;c__Clostridia;o__Oscillospirales;f__DTU089;g__Acutalibacter;s__Acutalibacter muris
 - rpkM_average = 3284

Probes

Transcript probes:

p.ndhM_322.27.27

p.ndhM_302.27.27

p.argC_553.25.25

p.argC_529.25.25

rRNA 16s probe:

EUB_R1

Branch Probes:

b.27.*27.*27.*28

b.25.*25.*25.*30

Adapter probes:

a.28.*28.*R2

a.30.*30.*R7

Readout probes:

R2* (Alexa 546)

R7* (Alexa 647)

R1* (Alexa 488)