

README

The folder contains R scripts for analysis and data from adipose tissue (Prokkola et al. 2022 pre-print).

File names shown like `this` . Explanations below.

Basic info: files

`Data_prep_final.R`

R code for compiling the complete dataset from several files:

`Sample_info_AT.txt` , `Oroboros_rawdat_AT.txt` , `MtDNA_qty_AT.txt` ,
`Cellsize_AT.txt` , and `sample_times_oroboros.txt` and calculating
respiration traits and coefficients.

`Resp_data_analysis_v1_Jul2022.R`

R code for statistical tests and plots. Using the output from data prep R code, i.e.,

`AdiposeTissue_data_all.txt` .

Variable names

In the final data, `AdiposeTissue_data_all.txt` , variables are:

`pit` = PIT ID of the individual

`id_sample` = Unique number given to each individual during sampling

`geno_vgll3` = `vgll3` genotype (EE = homozygous early maturation alleles, LL = homozygous late maturation alleles)

`orob.mes` = was the respiration measurement successful (yes/not good)

`date` = date of sampling and oroboros measurement

`sex` = female (F) or male (M), verified during sampling

`mass_gonads` = wet mass of gonads in g

maturation = index for maturation status based on size of gonads (different scale for females and males, always higher value = more mature)

tank = ID of fish rearing tank

feed = HF (high fat, i.e. control feed), LF = low fat feed

weight.7 = fish body mass one day prior to sampling

length.7 = fish for length one day prior to sampling

ID_ma = unique ID of mother

ID_pa = unique ID of father

relDNA2 = relative amount of mtDNA (mtDNA/gDNA/2)

mtDNA = average expression of mitochondrial genes

gDNA2 = average expression of nuclear genes / 2

MPG = respiration in the presence of malate, pyruvate, and glutamate

ADP = respiration in the presence of MPG and ADP

Cyt_c = respiration in the presence of MPG, ADP and Cytochrome c

Suc = respiration in the presence of MPG, ADP, Cytochrome c and succinate

Omy = respiration in the presence of MPG, ADP, Cytochrome , succinate and oligomycin

FCCP = respiration in the presence of MPG, ADP, Cytochrome , succinate, oligomycin and FCCP

Rot = respiration in the presence of MPG, ADP, Cytochrome , succinate, oligomycin, FCCP

Ama.baseline = respiration in the presence of MPG, ADP, Cytochrome , succinate, oligomycin, FCCP and antimycin

Asc.TMPD.CIV1. = respiration in the presence of MPG, ADP, Cytochrome , succinate, oligomycin, FCCP, antimycin and TMPD

Azide.CIV2. = respiration in the presence of MPG, ADP, Cytochrome , succinate, oligomycin, FCCP, antimycin, TMPD and azide

median_area = median adipocyte size in tissue cryosection for each individual

mean_area = mean adipocyte size in tissue cryosection for each individual

N_cells = number of adipocytes which area was measured for each individual

tissue_mg = wet weight of adipose tissue sample just before respiration measurements in mg

time_oro = time of oroboros measurement

time_sampling time = time when fish was sampled

time_biops = difference between sampling and oroboros measurement in hours (sample stored in BIOPS buffer)

For details on the rest of the variables, see manuscript and R code

`Data_prep_final.R` .