**Supplementary material S1**

**Article Title: Mitochondrial abundance and function in skeletal muscle and liver from beef cattle divergent for residual feed intake**

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**Journal Title: ANIMAL**

SAS code for predicting dry matter intake

(This example pertains to Bulls used in study, but the same code would have been used to calculate predicted dry matter intake (DMI) of heifers. Metabolic body weight (MWT)\_1 = metabolic body weight, average daily gain (ADG) SAS = ADG as predicted by SAS, backfat (BF).

Options linesize =**72** Pagesize=**54**;

**Proc** **Import** Out=Work.AllBulls

     Datafile="\\geax341\homeshares$\Clare.McKenna\RFI\Bull RFI\Predict DMI 2016.CSV"

     DBMS=CSV Replace;

     Getnames=Yes;

**Run**;

**Proc** **Print** data=AllBulls;

**Run**;**Quit**;

**Proc** **Means** data=AllBulls n nmiss mean min max stderr cv;

**Run**;**Quit**;

**Proc** **GLM** data=Allbulls;

Model DMI = MWT\_1 ADGSAS BF/solution;

**Run**;**Quit**;

SAS code for normalising data

(This example uses citrate synthase activity in liver as an example, but this analysis was done for all variables measured)

**proc** **reg** data=bulls;

model Cit\_Syn\_act\_liver= RFI day;

output out=residuals r=rCit\_Syn\_act\_liver ;

**run**;**quit**;

**proc** **print** data=residuals;

**run**;**quit**;

symbol1 v=circle i=rl;

**proc** **gplot** data=residuals;

plot rCit\_Syn\_act\_liver\*Cit\_Syn\_act\_liver/ vref=**0**;

**run**;

**proc** **univariate** data=residuals plot normal;

      var rCit\_Syn\_act\_liver;

      histogram rCit\_Syn\_act\_liver/ cfill=ltgray

                       normal kernel(color=black);

      inset n='Observations' MEAN='Averday' std='Standard Deviation'  / position=ne;

      label rCit\_Syn\_act\_liver = 'Residual Cit\_Syn\_act\_liver';

       qqplot rCit\_Syn\_act\_liver / normal (color=red);

**run**;**Quit**;

/\*If variable is not normally distributed then use the

code below to transform the variable\*/

/\* Cit\_Syn\_act\_liver looks not normally distributed - transformation necessary\*/

**PROC** **TRANSREG** DATA=bulls OUTTEST=TRANSFORM SS2 CLI;

MODEL BOXCOX(Cit\_Syn\_act\_liver)= IDENTITY (bull);

**RUN**;**quit**;

/\*A new variable is created in SAS using the code below - the transformed variable\*/

**data** bulls;

set bulls;

t Cit\_Syn\_act\_liver =(Cit\_Syn\_act\_liver)\*\*-**0.50**;

**Run**;**quit**;

/\*The new variable is tested for normal distribution below\*/

**proc** **reg** data=bulls;

model Cit\_Syn\_act\_liver= RFI day;

output out=residuals r=rCit\_Syn\_act\_liver ;

**run**;**quit**;

**proc** **print** data=residuals;

**run**;**quit**;

symbol1 v=circle i=rl;

**proc** **gplot** data=residuals;

plot rCit\_Syn\_act\_liver\*Cit\_Syn\_act\_liver/ vref=**0**;

**run**;

**proc** **univariate** data=residuals plot normal;

      var rCit\_Syn\_act\_liver;

      histogram rCit\_Syn\_act\_liver/ cfill=ltgray

                       normal kernel(color=black);

      inset n='Observations' MEAN='Averday' std='Standard Deviation'  / position=ne;

      label rCit\_Syn\_act\_liver = 'Residual Cit\_Syn\_act\_liver';

       qqplot rCit\_Syn\_act\_liver / normal (color=red);

**run**;**Quit**;

/\*The transformation was successful \*/

SAS code for analysis effect of residual feed intake (RFI) on traits

(This example uses RFI as an example, but this analysis was done for all variables measured such as DMI, ADG, BF, Initial trial weight, end trial weight, citrate synthase activity and activity of all complexes in the electron transport chain)

options Linesize=**72** Pagesize=**54**;

**Proc** **Import** Out=Work.allanimals

Datafile="\\geax341\homeshares$\Clare.Mckenna\Gender production traits\Mfile all.CSV"

DBMS=CSV Replace;

Getnames=yes;

**Run**;

**PROC** **PRINT** data=allanimals;

**Run**;**quit**;

**PROC** **MEANS** data=allanimals N NMISS MEAN STD MIN MAX CV Stderr;

**Run**;**quit**;

ods graphics on;

**Proc** **mixed** data=all animals;

Class RFI Gender RFI \* Gender;

Model RFI =RFI Gender Day/ residual influence;

Random sireno;

LSmeans RFI Gender Day/ pdiff adj=tukey;