Placement in manuscript and file location of figures.

Figure 1: glucocorticoid-induced insulin resistance

1. Human data BMI status---waist circumference?

* Github>CushingAcromegaly study>data>figures>cushing clinical bmi

1. Human data HOMA
   * Github>CushingAcromegaly study>data>figures>cushing clinical bmi
2. Mouse study design schematic—you can edit this file if you want, I don’t love the way it looks but I wanted to keep the vehicle/dex colors the same

* Harvey>mousework>dex>ncd/hfd combined>study design schematic

1. ITT
   * Harvey>mousework>dex>ncd/hfd combined>ITT>ITT analysis combined
2. Fasting glucose
   * Harvey>mouse work>dex>Qi data>ITT>ITT analysis combined
3. Glucose infusion
   * Harvey>mousework>dex>Qi data>glucose clamp data>figures
4. Endogenous glucose production
   * Harvey >mousework>dex>Qi data>glucose clamp data>figures
5. Glucose turnover
   * Harvey>mousework>dex>Qi data>glucose clamp data>figures
6. Glucose uptake in tissues
   * This figure has not been made—may go in to supplemental data
   * Excel file in qi data>glucose clamp

Figure 2: Liver steatosis

1. Human ALT serum levels
   * Github>CushingAcromegaly study>data>figures>cushing clinical bmi
2. Liver triglycerides
   * Harvey> mousework>dex>ncd/hfd combined>combined liver analysis
3. Liver H&E stain
   * Harvey>mousework>dex>ncd/hfd combined>histology> 2017-01-19>representative images
4. Liver mRNA
   * Bridges>mouse work>dex>hfd and dex> livers>mRNA>qPCR analysis/or/figures

Figure 3: Body Composition

1. Body mass
   * Harvey>mousework>dex>ncd/hfd combined>combined weight analysis
2. Lean mass
   * Harvey>mousework>dex>ncd/hfd combined>combined weight analysis
3. Fat mass
   * Harvey>mousework>dex>ncd/hfd combined>combined weight analysis
4. Fat pad mass
   * Harvey>mousework>dex>ncd/hfd combined>tissue weight analysis
5. Food consumption

* Figure not made
* Excel file (may need re-formatting): Harvey>mousework>dex>ncd/hfd combined>HFD and older chow dex food

Figure 4: Lipolysis

1. 3T3-L1 reduced tg
   * need to repeat experiment one more time to get N=3
   * no figures made
   * Excel file cell tg: Harvey>assays>tg assays>combined data for cont dex
2. 3T3-L1 increased media glycerol
   * no figures made
   * Excel file media glycerol: Harvey>assays>tg assays>2017-05-16 3t3-l1 lipolysis dex foll. Diff.
3. 3T3-L1 mRNA
   * No figures made in R (excel file probably needs to be reformatted)
   * Excel file Harvey>cell culture>3T3-L1 adipocytes>3T3L1 studies>diff followed by dex treatment> 2015-07-17 lipolysis genes
   * Excel file Harvey>cell culture>3T3-L1 adipocytes>3T3-L1 studies> diff followed by dex treatment>2017-06-22 3t3 lipolysis
4. 3T3-L1 protein
   * images of western
     1. Harvey>westerns>cell culture>3t3>dex studies>2015-12-15 dex foll diff folder>images
   * No R script for quantification
     1. Harvey>westerns>cell culture>3t3>dex studies>2015-12-15 dex foll diff folder> 2015-12-15 ATGL /gapdh blots from dex foll diff in 3T3-L1s spreadsheet