

# Collaborative **exercise**

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# GWAS workflow/pipeline - collaborative exercise

- Build your own workflow!
  - a. Download the data
  - b. Prepare the data (look at the phenotypes and genotypes!)
  - c. Filter the data
  - d. Impute missing genotypes
  - e. Run the GWAS
- Data on stump tail sperm defect of Swiss Large White boars

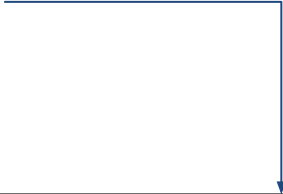
(<https://zenodo.org/record/4081475#.YKPfmnUzZhE>)



from: <https://petpigworld.com/large-white-pigs-the-essential-guide/>

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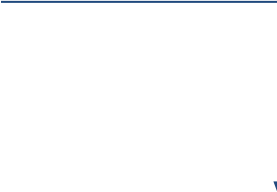


!! beware !! no missing SNP  
genotypes (data already filtered  
and imputed)

get data with missing SNP  
genotypes from here:  
[http://www.jackdellequerce.com/data/GWAS\\_cohort.tar.gz](http://www.jackdellequerce.com/data/GWAS_cohort.tar.gz)

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take a **subset of the SNPs** (to make calculations -and trial/errors- quicker), **e.g. chromosomes 10-14** (the mutation is on chromosome 12)



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- 1. Try on your own (individually, groups)
- 2. Let's do it all together!

