# Heritability estimates using LDSC

Installation:

We performed the analysis using version v1.0.1. We installed it using the conda installation provided on the

https://github.com/bulik/ldsc

**LD score calculation:**

**This step requires splitting the Genotype data by chromosome. This was achieved using**

**PLINK. The detailed steps are included in split_by_chr.sh**

Based on the average LD decay in the HS rats outbred population, we decided to use a 5Mb

window for the LD score calculation.

Detailed command is included in script **ld_score.sh**

**Munging summary statistics**

**This step involved some data wrangling in preparation for the heritability calculation.**

**The scripts we used are (in order) prepare_snplist.R, prep_for_munge.R and ldsc_munge.sh**

**Heritability estimation**

**The script we used is LDSC_h2.sh**

This step uses the munged summary statistics as well as the LD scores.