(ldsc) Irenes-MacBook-Pro:ldsc irenecho$ python /Users/irenecho/Desktop/final/ldsc/ldsc.py \

> --h2 /Users/irenecho/Desktop/final/ldscstep/step1/smoke/step1.sumstats.gz \

> --ref-ld-chr /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_enrichment/GenoSkylinePlus/GSplus\_Tier3\_1KGphase3. \

> --w-ld-chr /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_enrichment/weights/weights.hm3\_noMHC. \

> --overlap-annot \

> --frqfile-chr /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_enrichment/genotype/1000G.EUR.QC. \

> --out /Users/irenecho/Desktop/final/ldscstep/step3 \

>

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

\* LD Score Regression (LDSC)

\* Version 1.0.1

\* (C) 2014-2019 Brendan Bulik-Sullivan and Hilary Finucane

\* Broad Institute of MIT and Harvard / MIT Department of Mathematics

\* GNU General Public License v3

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

Call:

./ldsc.py \

--h2 /Users/irenecho/Desktop/final/ldscstep/step1/smoke/step1.sumstats.gz \

--ref-ld-chr /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_enrichment/GenoSkylinePlus/GSplus\_Tier3\_1KGphase3. \

--out /Users/irenecho/Desktop/final/ldscstep/step3 \

--overlap-annot \

--frqfile-chr /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_enrichment/genotype/1000G.EUR.QC. \

--w-ld-chr /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_enrichment/weights/weights.hm3\_noMHC.

Beginning analysis at Wed May 4 01:30:29 2022

Reading summary statistics from /Users/irenecho/Desktop/final/ldscstep/step1/smoke/step1.sumstats.gz ...

Read summary statistics for 1185267 SNPs.

Reading reference panel LD Score from /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_enrichment/GenoSkylinePlus/GSplus\_Tier3\_1KGphase3.[1-22] ... (ldscore\_fromlist)

Read reference panel LD Scores for 1190321 SNPs.

Removing partitioned LD Scores with zero variance.

Reading regression weight LD Score from /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_enrichment/weights/weights.hm3\_noMHC.[1-22] ... (ldscore\_fromlist)

Read regression weight LD Scores for 1187349 SNPs.

After merging with reference panel LD, 1172459 SNPs remain.

After merging with regression SNP LD, 1169499 SNPs remain.

Removed 0 SNPs with chi^2 > 632.802 (1169499 SNPs remain)

Total Observed scale h2: 0.0241 (0.0019)

Categories: GenoCanyon10KL2\_0 Mononuclear\_cells\_from\_peripheral\_bloodL2\_0 T\_cells\_CD3+L2\_0 T\_cells\_effector/memory\_CD4+\_CD25int\_CD127+L2\_0 T\_regulatory\_cells\_CD4+\_CD25+\_CD127-L2\_0 T\_helper\_cells\_CD4+\_CD25-L2\_0 T\_helper\_naive\_cells\_CD4+\_CD25-\_CD45RA+L2\_0 T\_helper\_cells\_PMA-I\_stimulated\_CD4+\_CD25-\_IL17-L2\_0 T\_helper\_17\_cells\_PMA-I\_stimulated\_CD4+\_CD25-\_IL17+L2\_0 T\_helper\_memory\_cells\_CD4+\_CD25-\_CD45RO+L2\_0 T\_helper\_memory\_cells\_from\_peripheral\_blood\_CD4+L2\_0 T\_memory\_cells\_CD8+L2\_0 T\_helper\_naive\_cells\_CD4+L2\_0 T\_naive\_cells\_CD8+L2\_0 Monocytes\_CD14+L2\_0 Hematopoietic\_stem\_cells\_G-CSF-mobilized\_CD34+L2\_0 B\_cells\_CD19+L2\_0 Natural\_killer\_cells\_CD56+L2\_0 GM12878\_lymphoblastoid\_cellsL2\_0 ThymusL2\_0 SpleenL2\_0 Brain\_hippocampus\_middleL2\_0 Brain\_substantia\_nigraL2\_0 Brain\_anterior\_caudateL2\_0 Brain\_cingulate\_gyrusL2\_0 Brain\_inferior\_temporal\_lobeL2\_0 Brain\_angular\_gyrusL2\_0 Brain\_dorsolateral\_prefrontal\_cortexL2\_0 NH-A\_astrocytesL2\_0 LungL2\_0 NHLF\_lung\_fibroblast\_primary\_cellsL2\_0 AortaL2\_0 Right\_atriumL2\_0 Left\_ventricleL2\_0 Right\_ventricleL2\_0 Muscle\_satellite\_cultured\_cellsL2\_0 Psoas\_muscleL2\_0 Skeletal\_muscleL2\_0 HSMM\_skeletal\_muscle\_myoblasts\_cellsL2\_0 HSMM\_cell\_derived\_skeletal\_muscle\_myotubes\_cellsL2\_0 Stomach\_smooth\_muscleL2\_0 Duodenum\_smooth\_muscleL2\_0 Colon\_smooth\_muscleL2\_0 Rectal\_smooth\_muscleL2\_0 EsophagusL2\_0 GastricL2\_0 Stomach\_mucosaL2\_0 Duodenum\_mucosaL2\_0 Small\_intestineL2\_0 Sigmoid\_colonL2\_0 Colonic\_mucosaL2\_0 Rectal\_mucosaL2\_0 PancreasL2\_0 Pancreatic\_isletsL2\_0 LiverL2\_0 Adipose\_nucleiL2\_0 Adipose\_derived\_mesenchymal\_stem\_cell\_cultured\_cellsL2\_0 Mesenchymal\_stem\_cell\_derived\_adipocyte\_cultured\_cellsL2\_0 Mesenchymal\_stem\_cell\_derived\_chondrocyte\_cultured\_cellsL2\_0 Bone\_marrow\_derived\_cultured\_mesenchymal\_stem\_cellsL2\_0 Osteoblast\_primary\_cellsL2\_0 NHDF-Ad\_adult\_dermal\_fibroblast\_primary\_cellsL2\_0 NHEK-epidermal\_keratinocyteprimary\_cellsL2\_0 Breast\_myoepithelial\_primary\_cellsL2\_0 Breast\_variant\_human\_mammary\_epithelial\_cells\_(vHMEC)L2\_0 HMEC\_mammary\_epithelial\_primary\_cellsL2\_0 OvaryL2\_0

Lambda GC: 1.4853

Mean Chi^2: 1.7319

Intercept: 1.1776 (0.0174)

Ratio: 0.2427 (0.0237)

Reading annot matrix from /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_enrichment/GenoSkylinePlus/GSplus\_Tier3\_1KGphase3.[1-22] ... (annot)