**Remaining analyses for the paper:**

**Previously urgent**

1. Do adjustment for covariates per each envir group separately
2. Do GWAS in the pooled sample of groups (to avoid range restriction)

**Urgent for first draft**

1. Finish indirect effect simulations/derivations
2. Finish assortative mating simulations/derivations
3. Use LMM approaches for EA by SES GWAS

**After first draft**

1. (?) Fig. 4: four panels for indirect-direct and assortative mating
2. (i) Figure out if the issue with simulated traits for Fig 3, (ii) simulate under low heritability
3. Compare sib and unrel sets properties: phenotype distributions, allele frequencies, etc.
4. (?) Consider removing age adjustments for BMI-age analysis
5. Correct hair color (remove “Other”) and blood pressure (adjust for medication)
6. (?) Check h2 explanations for fig1 (Arbel)
7. Look into differences between (1) standard GWAS with covariates and (2) standard GWAS on residualized covariates
   * effect size diff, and polygenic score difference
   * Prs along PCs
8. Redo LDSC across groups (adjusting for covariates as done in point 1 above)
9. Add additional phenotypes to Fig3

**Remaining writings for the paper:**

**Urgent for first draft**

1. Finalize main figures
   * Fig 1: update DBP with medication adjusted results, refine error bars, add significance, maybe incremental R2? (Arbel)
   * Fig 2 (Arbel)
   * Fig 3: finalize the list of traits in panel B, then update numbers in panel A
   * Update supp figure on p-value dependency of fig1 (Arbel)
   * Fig 3 (notes: add traits, reverse x axis, no legend)
   * Additional fig for simulations (?)
2. Collect supplemental figures in one file.
3. Supplement for indirect effect/assortative mating results (more concise than current versions) (notes: Hakha – unify notation; Arbel – edit assortative mating)

**After first draft**

1. Control for C effect in figure 3B: do trends persist?
2. Rethink correlation between effect sizes: should we focus on ascertained SNPs?
3. Nicer supplementary figure 1 for SES binary traits (Arbel)
4. Fig1 extra panels / new fig with h2 explanation (Arbel)
5. Edit/comment on Methods (Arbel)
6. Edit/comment on the Intro
7. Add references to intro (Molly)
8. Discussion section (when all above completed; Molly & JKP first draft)

**Shelved analyses:**

* Fish for an example where tail of PS distribution behave different than R2
* Consider other traits for sib vs pop GWAS: alcohol, tobacco, etc.
* Test for range restriction, change in Ve, Vg, etc. across envir groups
* Simulate range restriction, GxE, change in Ve, Vg, etc. across envir groups
* Use approaches like those in the height replication paper to test for stratification
* Effect size correlation across envir groups
* Variability in N\* + sib set
* Simulate a low heritability trait
* Ascertain SNPs in sib and matched unrel set (particularly for a high heritability trait, e.g. height) for qualitative comparison with current approach of ascertaining in a large unrel set
* Build PS using LDpred
* Use public large GWAS in the pipelines, e.g. GIANT, EA2, etc.
* LD reference from UKB not 1000G EUR for LDSC
* Some measure for AF and LD differences across groups
* Plots for PS decile vs phenotype
* Simulating assortative mating realistically
* For blood pressure analysis: consider medication taken for hypertension + number of children
* LD across chromosomes as a measure of assortative mating
* Simulate pop structure confounding
* “age at full time education” phenotype for Figs 1 and 3