**Lee et al., 2018 Gene discovery and polygenic prediction from a 1.1-million person GWAS of educational attainment:**

We conduct a large-scale genetic association analysis of educational attainment in a sample of ~1.1 million individuals and identify 1,271 independent genome-wide-significant SNPs. For the SNPs taken together, we found evidence of heterogeneous effects across environments. The SNPs implicate genes involved in brain-development processes and neuron-to-neuron communication. In a separate analysis of the X chromosome, we identify 10 independent genome-wide-significant SNPs and estimate a SNP heritability of ~0.3% in both men and women, consistent with partial dosage compensation. A joint (multi-phenotype) analysis of educational attainment and three related cognitive phenotypes generates polygenic scores that explain 11–13% of the variance in educational attainment and 7–10% of the variance in cognitive performance. This prediction accuracy substantially increases the utility of polygenic scores as tools in research.

**Group 1:**

**Use all the resources at your disposal to explain to the class what educational attainment is, in the context of this study.**

**Group 2:**

**Use all the resources at your disposal to understand Figure 1, and present it to the class.**