Anderson (2010). Data quality control in genetic case-control association studies. Nat Protoc. 5(9): 1564-1573.

- 1. What is a false positive (negative) association and how can a genome-wide study minimize these types of errors?
- 2. What is informative missingness?
- 3. What is the relationship between genomic coverage and the power of genetic association study?
- 4. How can mean heterozygosity be defined and what kind of information does it provide?
- 5. What is the difference between IBS and IBD?
- 6. What is meant by cryptic relatedness? Is it a concern when performing a population-based genome-wide association study? If not, explain. If so, how can it be dealt with in your GWA?
- 7. Is there a difference between QC-ing in candidate gene studies and genome-wide association studies? Explain.

- 8. What is the HapMap population? Can you describe it in a bit more detail? Why is it useful in the context of genetic association studies?
- 9. Which QC measures would you take differently (or in addition) when performing a genomewide association study using multiple families?
- 10. What does genomic ancestry mean and can this information be integrated in a genomewide association study?