

Questions and discussion items Freedman et al. (2011) 43: 513-518

1. What is a major reason to perform a genetic study and identify strong risk genes?
2. What is the greatest challenge after a genome wide association study?
3. Why is it important to identify the causal variant and/or the molecular basis of risk etiology
4. What is the underlying hypothesis with respect to how SNPs exert their effect i.e. confer risk to complex diseases?
5. What are 2 ways to assess the functionality / effect of a SNP?
6. What is different between these two methods.
7. What is a Tag SNP?
8. How could the SNP affect the epigenetically regulated gene expression?
9. What would be criteria for a strong candidate gene?
10. If a strong candidate gene is selected, likely to be affected by the genome wide association signal what would be next steps to proof causality to the disease.