



**Figure S1** Schematic of different strategies for genome-wide studies. QTL mapping and genome-wide association studies provide direct evidence for genetic regulation of distinct phenotypes. However, it is frequently difficult to infer functionality. Expression QTL (eQTL) studies use variation in transcript abundance, measured with expression arrays to provide evidence for functional transcripts co-segregating with traits of interest. A limitation is that RNA expression does not fully reflect effects on the phenotype. Using the proteome as a surrogate, which is more directly related to the phenotype level, might aid functional studies.