population context. The figure illustrates the differences in regulatory scope and pathways between these two classes, highlighting the transition from local regulatory effects to broader network-level influences.

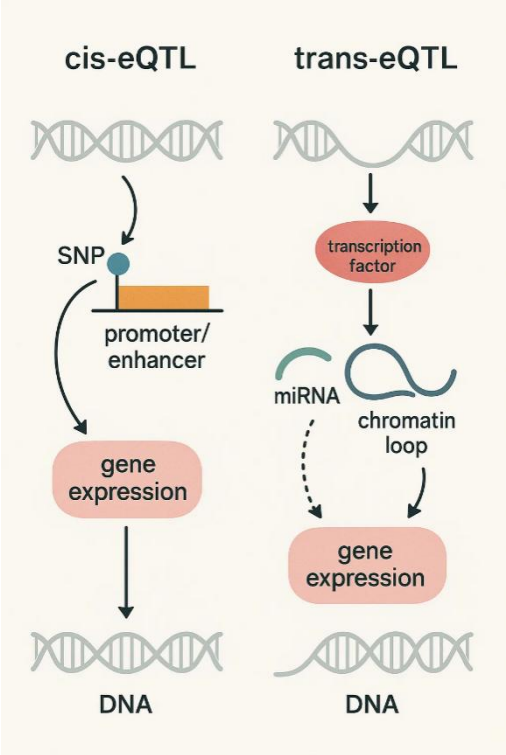

Figure 1 Regulatory patterns of cis- and trans-eQTL and their roles in integrative analyses

2.2 Tissue and cell-type specificity

eQTL effects often vary substantially across tissues and developmental stages (Fagny et al., 2017). Some loci exhibit consistent effects across multiple tissues, whereas others are highly tissue-specific, reflecting differences in chromatin states, regulatory programs, and cellular composition. For integrative analyses, prioritizing tissues that are relevant to the trait of interest generally improves interpretability. At the same time, reporting both shared and tissue-specific effects can help distinguish robust signals from context-dependent ones.

Cellular heterogeneity represents an important source of confounding in bulk tissue data. To address this, approaches such as deconvolution, interaction models, and environment-specific analyses can be used to better characterize context-dependent effects (Zhang and Zhao, 2023).

Single-cell eQTL (sc-eQTL) analyses further increase resolution by identifying regulatory effects at the level of individual cell types or states. Studies in immune and brain tissues have revealed a large number of cell-type-specific signals, as well as dynamic changes across conditions (Bryois et al., 2022). From a statistical perspective, pseudo-bulk aggregation and hierarchical modeling are often used to balance resolution and power. These data can provide more precise information about where regulatory effects are likely to act, which is valuable for downstream interpretation.

2.3 Extended QTL types: sQTL, pQTL, and meQTL

Beyond expression QTL, additional layers of molecular QTL provide further insight into regulatory mechanisms. Splicing QTL (sQTL) capture variation in transcript structure and may operate independently of total expression levels, allowing regulatory effects to be examined from both quantitative and structural perspectives (Zheng et al., 2020). Analyses at the transcript level or using multi-exposure models can help disentangle these contributions.

Protein QTL (pQTL) measure the effects of genetic variants on protein abundance and are often closer to the functional endpoints of many traits. While some cis-pQTL can serve as strong instruments, their relationship with eQTL is not always straightforward, reflecting additional layers of post-transcriptional regulation.