

The diagram illustrates the concept of eQTLs by showing how a specific SNP genotype can influence gene expression levels in different tissues. A human figure is shown with dashed lines connecting specific tissues (brain and arm) to corresponding scatter plots of gene expression levels across different SNP genotypes (A/A, A/C, C/C).

Brain Tissue: The scatter plot shows gene expression levels for three genotypes: A/A (high expression), A/C (medium expression), and C/C (low expression). This indicates a negative correlation between the C allele and gene expression in the brain.

Arm Tissue: The scatter plot shows gene expression levels for three genotypes: A/A (low expression), A/C (medium expression), and C/C (high expression). This indicates a positive correlation between the C allele and gene expression in the arm.

Figure 1 illustrates genotype-specific gene expression across three cell types: Neuron, Macrophage, and Oligodendrocyte. The y-axis represents Gene expression, and the x-axis represents SNP genotypes (A/A, A/C, C/C). The plots show that for each cell type, the A/A genotype generally has the highest expression, followed by A/C, and then C/C.