Immune infiltration-associated differentially expressed genes

Immune infiltration-associated differentially expressed genes refer to genes whose expression levels are altered in response to the presence of immune cells infiltrating a particular tissue or tumor. In other words, these genes are influenced by the immune response and can play critical roles in shaping the immune microenvironment of a tissue or tumor.

When immune cells, such as T cells, B cells, natural killer cells, macrophages, etc., infiltrate a tissue or tumor, they interact with the local cells and produce various signaling molecules, which can trigger changes in gene expression. These changes are essential for modulating the immune response, controlling inflammation, and influencing disease progression.

Identifying immune infiltration-associated differentially expressed genes can be crucial in understanding the immune response in various contexts, such as cancer, autoimmune diseases, infections, and inflammatory conditions. Analyzing such genes can shed light on the molecular mechanisms underlying immune regulation and may help identify potential therapeutic targets or diagnostic markers.

Researchers typically use various techniques such as transcriptomic profiling (e.g., RNA sequencing or microarray) and bioinformatics analyses to identify these differentially expressed genes associated with immune infiltration.

It's important to note that the list of immune infiltration-associated differentially expressed genes can vary depending on the specific disease or tissue being studied and the experimental conditions. Therefore, to obtain the most current and relevant information, it's best to refer to the latest scientific literature and research databases in the field of immunology and genomics.

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