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Genetic analysis of the role of the reprogramming gene LIN-28 in human embryonic stem cells

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Gene expression analysis enhances proper cancer subtyping, a better understanding of the molecular characteristics of cancer, and strategies for precision medicine. However, salivary gland cancer (SGC) subtyping remains largely unexplored because of its rarity and diverse histopathological and immunological characteristics. This study aimed to determine whether the histological origin and immunological characteristics of SGC subtypes are intrinsic tumor immunity factors. We performed immune profiling of 94 RNA-seq of SGC tissues and found that the SGCs that originated from the excretory duct (ED), such as the salivary duct and mucoepidermoid carcinomas, exhibit higher immunity than those from the intercalated duct (ID), such as the adenoid cystic and myoepithelial carcinomas, based on the computationally predicted immune score ($p < 0.001$), immune cell enrichment in the tumor immune microenvironment (TIME) ($p < 0.001$), T-cell receptor diversity ($p < 0.001$), and expression of signal I (major histocompatibility complex, MHC, $p < 0.001$) and signal II (co-stimulatory, $p < 0.001$ and co-inhibitory, $p < 0.001$) genes. Further analysis revealed that tolerogenic dendritic cell-induced dysfunctional T-cell populations and T-cell exclusion in the TIME are the major immune evasive mechanisms of the ED-and ID-derived SGCs, respectively.