Exploring the genetic landscape of immune evasion in colorectal cancer using single cell transcriptome

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Colorectal cancer remains a significant challenge due to its ability to evade the immune system, vital for tumor survival and proliferation. Immune checkpoint inhibitors are becoming critical therapeutic options to counter this phenomenon, though significant limitations still exist. In this study, using single-cell approaches, we uncovered the cellular heterogeneity within the tumor microenvironment and gained deeper insights into how different cell types contribute to immune evasion. Notably, we identified that Tumor Gene A, driven by TP53 mutations, plays a crucial role in promoting immune evasion by increasing CTLA-4 expression on T cells, thus enhancing the tumor's capacity to escape immune surveillance. This finding allowed us to gain a more refined understanding of the complex interactions within the tumor microenvironment at a single-cell level, suggesting the potential for developing novel targeted therapies to improve immunotherapy outcomes for a broader range of patients.