Search for molecular markers - predictors of a positive response to immunotherapeutic treatment according to single-cell RNA sequencing

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The aim of the study was to compare data on gene expression in people who respond to checkpoint immunotherapy and those who do not. Immunotherapy is a new approach in the treatment of malignant tumors, which consists in activating the patient's own immune response. The human immune system has self-regulation methods, one of which is checkpoints, membrane molecules on the surface of immune cells that inhibit the activity of the immune system. Tumor cells use this innate self-control system against the body, activating it under inappropriate conditions. Thus, by inhibiting checkpoint activity, it is possible to allow the immune system to develop an anti-tumor response. However, for the successful use of checkpoint inhibitors, it is necessary that tumor cells use this pathway to avoid the immune response, otherwise the therapy will not give results. To decide on the need for such therapy, tests are currently being carried out for the presence of various markers in patients that positively affect the outcome of therapy. Currently, there is an active search for such markers to increase the success of immune therapies. People who respond to immunotherapy will have changes in the expression of genes involved in regulating the immune system. The iTalk package allows you to find ligand-receptor pairs (using the built-in database of such interactions). Thus, we can find genes for proteins localized on the membrane and involved in signaling. Thus, a change in the expression of the HAVCR2 and CTLA4 genes, which are genes for checkpoint proteins, was found in the respondents. Differences were also found for checkpoint ligands and tumor necrosis factors: LGALS9, CD274, CD80 / CD86, TNFSF9.

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