ABSTRACT

Pathways of acquisition, efflux, storage, and regulation of iron are perturbed in several types of cancer, suggesting that the reprogramming of iron metabolism is a central aspect of tumor cell survival. We apply dimension reduction tools to a previously published single cell RNA sequencing expression dataset from melanoma patients to explore expression patterns that potentially affect iron metabolism in tumor cells and different immune cells. We hope to gain a new understanding regarding the links between oncogenic processes and iron regulation in melanoma.

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