



Single Cell Transcriptome Conservation in Cryopreserved Cells and Tissues

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Abstract

A variety of single cell RNA preparation procedures have been described. So far these protocols require fresh starting material, hindering complex study designs. We describe a sample preservation method that maintains transcripts in viable single cells and so allows to disconnect time and place of sampling from subsequent processing steps. To demonstrate the potential, we sequenced single cell transcriptomes from >1,000 fresh and conserved cells. Our results confirmed that the conservation process did not alter transcriptional profiles. This substantially broadens the scope of applications in single cell transcriptomics and could lead to a paradigm shift in future study designs.

<http://biorxiv.org/content/early/2016/08/04/067884>