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Linked References. Y. Hasin, M. Seldin, and A. Lusk, "Multi-omics approaches to disease," *Genome Biology*, vol. 18, no. 1, View at.

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Computational and analytical challenges in single-cell transcriptomics. Similarly another study by Bhasin et al. As a validation strategy they compared predicted protein abundance with experimental data. Both breast and hepatocellular cancer exhibited increased gene-metabolites associations in comparison to adjacent noncancerous tissues. Cancer Genome Atlas Research Network. Acquisition of cancer hallmarks allows the transition of a normal cell to a malignant cell.
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