



H3ABioNet

Pan African Bioinformatics Network for H3Africa

WELLCOME GENOME CAMPUS

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Next Generation Sequencing Bioinformatics Course 2021

Module 7: RNA-Seq Human Introduction to the Practical



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NGS Bioinformatics Course Africa 2021

Jon Ambler

Nyasha Chambwe

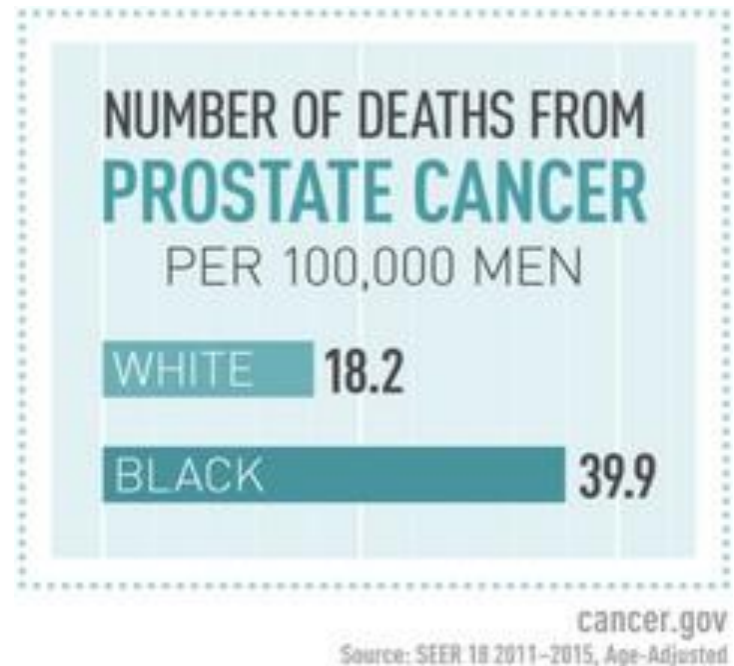
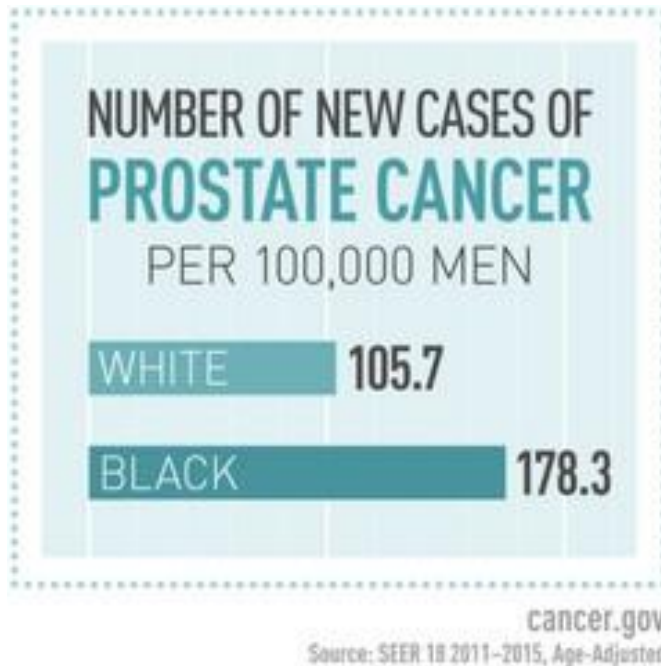
Phelelani Mpangase

Learning Outcomes

By the end of this practical you should be able to:

- Align RNA-Seq reads to a reference genome and transcriptome
- Visualise transcriptional data using standard tools
- Perform QC of NGS transcriptomic data
- Quantify transcript expression in a given set of samples and perform differential expression analysis between groups of samples

Practical: Analysis of Matched Tumour and Normal Prostate Cancer RNA-Seq Data



Research Question:

Is the prostate cancer associated transcriptome different between ethnicity groups where we see differences in cancer incidence and mortality?

Practical: Analysis of Matched Tumour and Normal Prostate Cancer RNA-Seq Data

Study Overview

Matched high-grade ($GS \geq 7(4+3)$) prostate tumor and adjacent normal specimens from **African American** and **European American** men were subjected to two replicate runs of RNA-sequencing.

Teslow, E. A., et. al. (2018). Molecular Oncology (PMID:[29741809](https://pubmed.ncbi.nlm.nih.gov/29741809/))

Mapping and microdissection of tumor and normal tissue

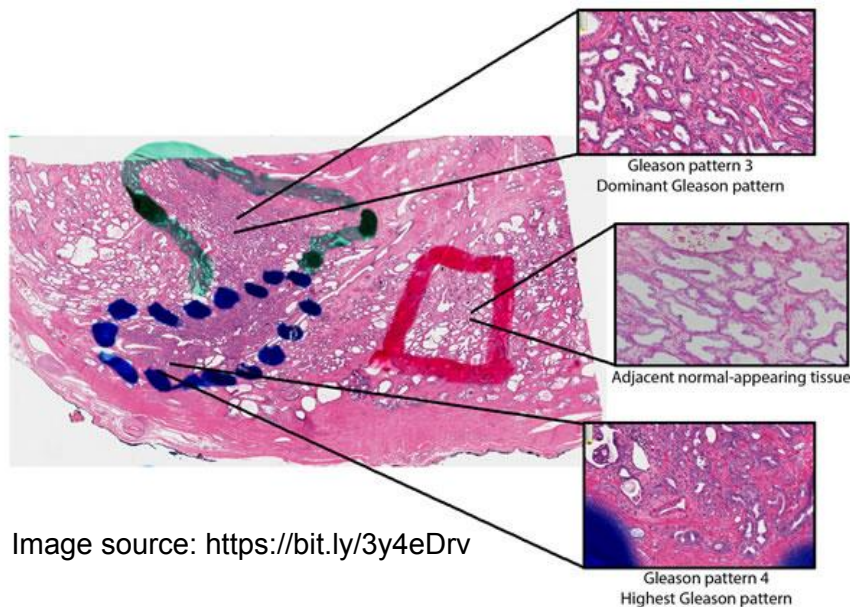


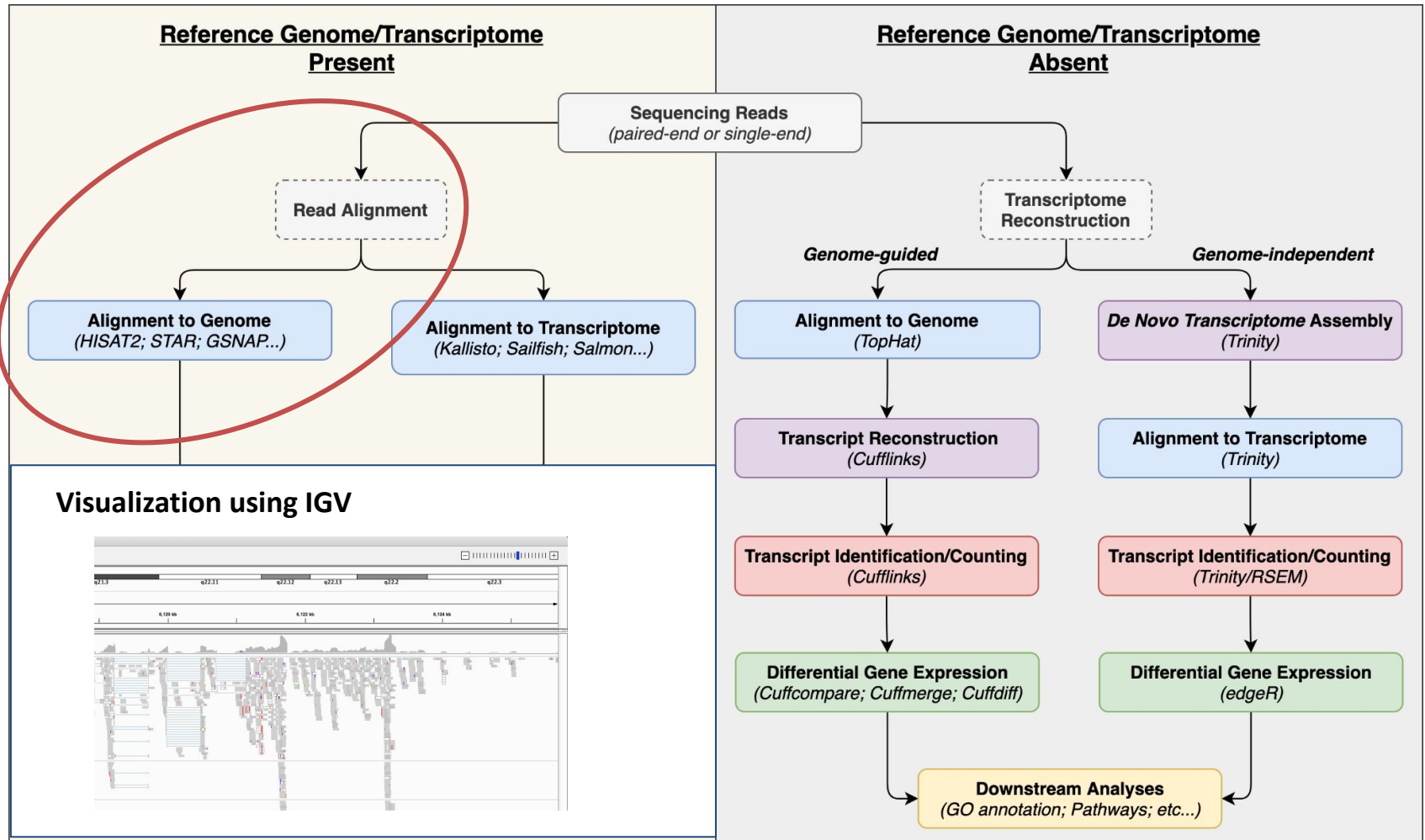
Image source: <https://bit.ly/3y4eDrv>

patientID	normalID	tumorID	ethnicity
487	NP4	PT4	AA
881	NP6	PT6	AA
2249	NP10	PT10	AA
376	NP2	PT2	EA
647	NP5	PT5	EA
3365	NP13	PT13	EA

NP Normal Prostate
PT Prostate Tumour

AA African-American
EA European-American

Practical: Analysis of Matched Tumour and Normal Prostate Cancer RNA-Seq Data



Practical: Analysis of Matched Tumour and Normal Prostate Cancer RNA-Seq Data

