Data Visualization

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Data Visualization

- Important communication skills to present data and provide clear "story"
- Help to find important patterns from vast amount of data
- Deliver key messages from "big data"

Data Visualization went Wrong

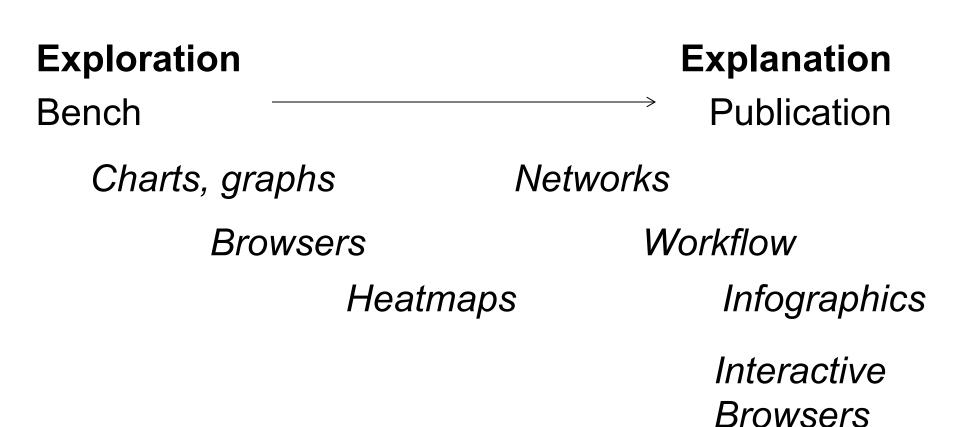
http://viz.wtf/

The Beauty of Data Visualization

http://www.ted.com/talks/david_m ccandless_the_beauty_of_data_vi sualization?language=en

Visual Representation

Integral to Research Trajectory



(Adapted from Bang Wong's slides)

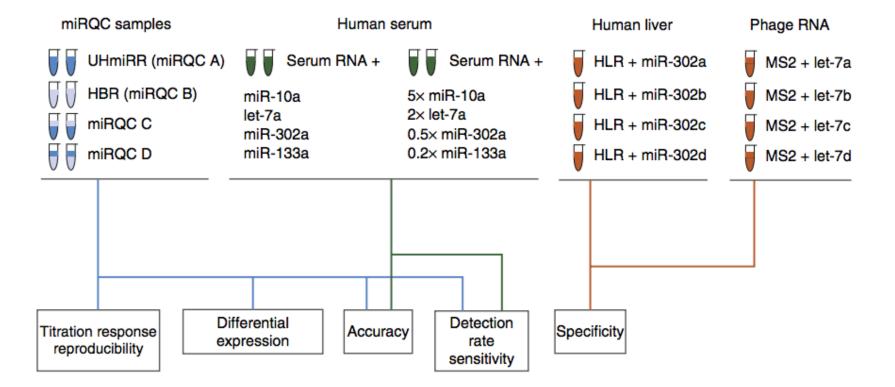
ANALYSIS

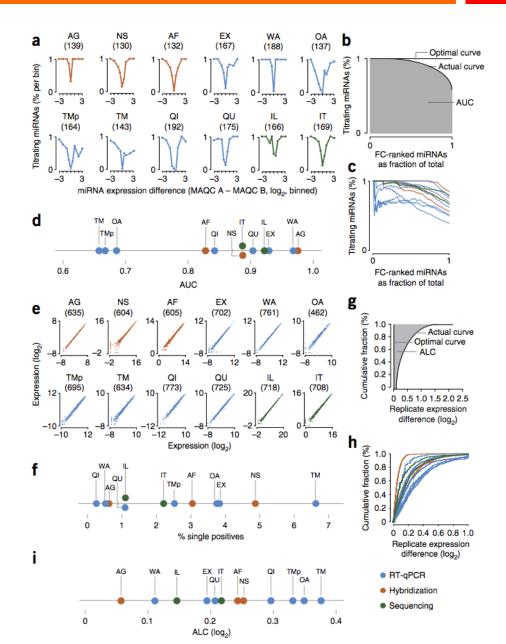
Evaluation of quantitative miRNA expression platforms in the microRNA quality control (miRQC) study

Pieter Mestdagh¹, Nicole Hartmann², Lukas Baeriswyl², Ditte Andreasen³, Nathalie Bernard⁴, Caifu Chen⁴, David Cheo⁵, Petula D'Andrade⁶, Mike DeMayo⁷, Lucas Dennis⁸, Stefaan Derveaux⁹, Yun Feng⁵, Stephanie Fulmer-Smentek⁶, Bernhard Gerstmayer¹⁰, Julia Gouffon⁷, Chris Grimley⁸, Eric Lader¹¹, Kathy Y Lee⁴, Shujun Luo¹², Peter Mouritzen³, Aishwarya Narayanan¹³, Sunali Patel⁴, Sabine Peiffer¹⁰, Silvia Rüberg¹⁰, Gary Schroth¹², Dave Schuster⁵, Jonathan M Shaffer¹¹, Elliot J Shelton⁴, Scott Silveria⁹, Umberto Ulmanella⁴, Vamsi Veeramachaneni¹³, Frank Staedtler², Thomas Peters², Toumy Guettouche¹⁴ & Jo Vandesompele¹

Nature Methods 2014

Quantitative PCR (PCR)	Hybridization (HYB)	RNA input (ng)
 EX miRCury (Exiqon) OA OpenArray (Life Technologies) TM TaqMan Cards (Life Technologies) * TMp TaqMan Cards preAmp (Life Technologies) QI miScript (Qiagen) QU qScript (Quanta BioSciences) WA SmartChip (WaferGen) 	AF microarray (Affymetrix) * AG microarray (Agilent) NS nCounter (Nanostring) *	EX 40 AF 400 OA 100 AG 100 TM 350 NS 100 TMp 50 50 50
	Sequencing (SEQ) IL TruSeq (Illumina) IT Ion Torrent (Life Technologies)	QI 500 IL 1,000 QU 800 IT 1,000 WA 1,000





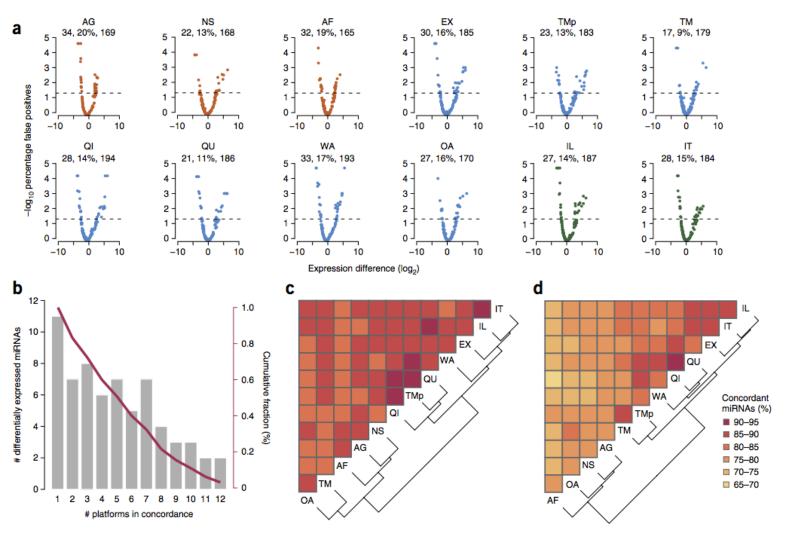


Figure 5 | Differential miRNA expression. (a) Volcano plot showing $-\log_{10}$ of the rank products percentage of false positives value as a function of the mean expression difference for miRQC A and C (n = 4) versus miRQC B and D (n = 4) samples. For each platform (abbreviated as in **Fig. 1**), total number of differentially expressed miRNAs, is indicated above the plot as an absolute number and as a percentage relative to the total number of miRNAs included in the analysis, also indicated above the plot. (b) Number of differentially expressed miRNAs identified by at least one or multiple platforms. (c) Hierarchically clustered heatmap indicating miRNA concordance between all platform combinations. (d) Hierarchically clustered heatmap indicating miRNA concordance between all platform rate.

Charts & Graphs (& Color & Design Principles)

• <u>https://vimeo.com/114252896</u>

Bang Wong's Blog (Broad Institute)
 – Nature Methods – Points of View
 – http://clearscience.info/wp/?p=546

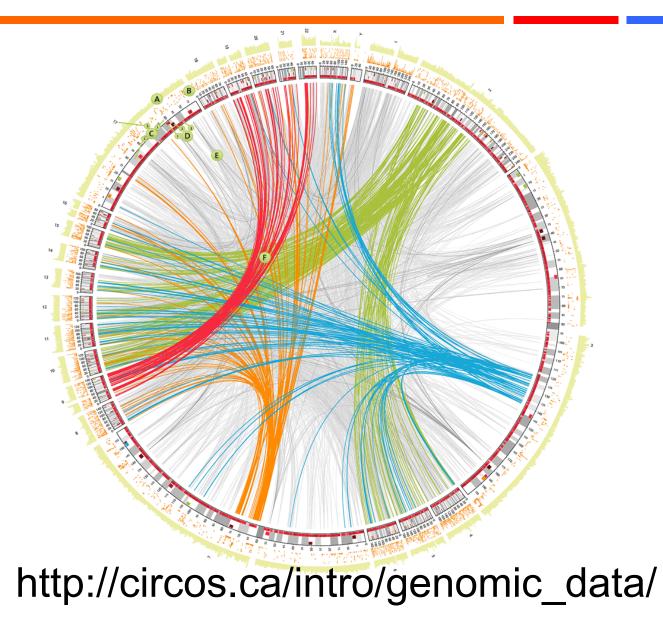
How to visualize Human Genome?

- ACTGACTG (3 billion characters)
- Chromosome Map (NCBI Map Viewer)
- https://www.ncbi.nlm.nih.gov/projects/map view/map_search.cgi?taxid=9606&build=1 07.0

Circos Plot

- CIRCULAR VISUALIZATION
- Circos is a software package for visualizing data and information. It visualizes data in a circular layout — this makes Circos ideal for exploring relationships between objects or positions. There are other reasons why a circular layout is advantageous, not the least being the fact that it is attractive.
- http://circos.ca/

Circos Plot for Human Genome



Browser

- Integrative Genomics Viewer (IGV)
- The Integrative Genomics Viewer (IGV) is a high-performance visualization tool for interactive exploration of large, integrated genomic datasets. It supports a wide variety of data types, including arraybased and next-generation sequence data, and genomic annotations.
- http://software.broadinstitute.org/software/i gv/

cBioPortal

- The cBioPortal for Cancer Genomics provides visualization, analysis and download of large-scale cancer genomics data sets.
- http://www.cbioportal.org/

ICGC Data Portal

- The ICGC Data Portal provides tools for visualizing, querying and downloading the data released quarterly by the consortium's member projects.
- https://dcc.icgc.org/

NCI Genomic Data Commons

- The NCI's Genomic Data Commons (GDC) provides the cancer research community with a unified data repository that enables data sharing across cancer genomic studies in support of precision medicine.
- https://gdc-portal.nci.nih.gov/

COSMIC – Sanger Institute

- COSMIC, the Catalogue Of Somatic Mutations In Cancer, is the world's largest and most comprehensive resource for exploring the impact of somatic mutations in human cancer.
- http://cancer.sanger.ac.uk/cosmic

GDSC – Sanger Institute

- GDSC Identifying molecular features of cancers that predict response to anticancer drugs.
- http://www.cancerrxgene.org/

LINCS Cloud

- Interactive Browser and Apps for Managing the functional genomics data generated in the LINCS Project (Broad Institute)
- https://clue.io/

D3 – Data-Driven Documents

- D3.js is a JavaScript library for manipulating documents based on data. D3 helps you bring data to life using HTML, SVG, and CSS. D3's emphasis on web standards gives you the full capabilities of modern browsers without tying yourself to a proprietary framework, combining powerful visualization components and a data-driven approach to DOM manipulation.
- https://d3js.org/

Interactive Visualization Tool

https://www.bloomberg.com/billionaires/

A workflow diagram depicts a series of actions that define a job or how work should be done. A workflow diagram visualizes how tasks will flow between resources, whether they're machines or people and what conditions allow the sequence to move forward. https://www.smartdraw.com/workflow-diagram/

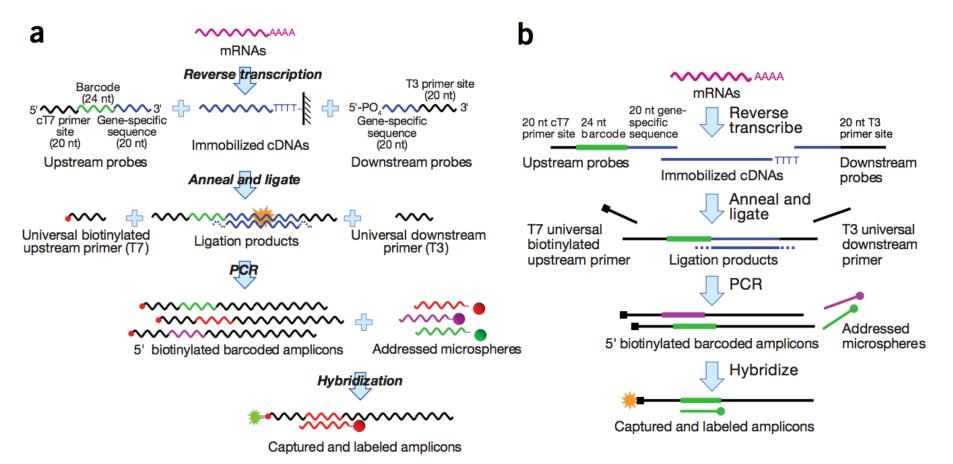
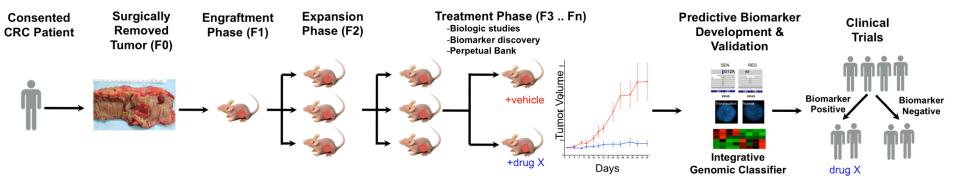
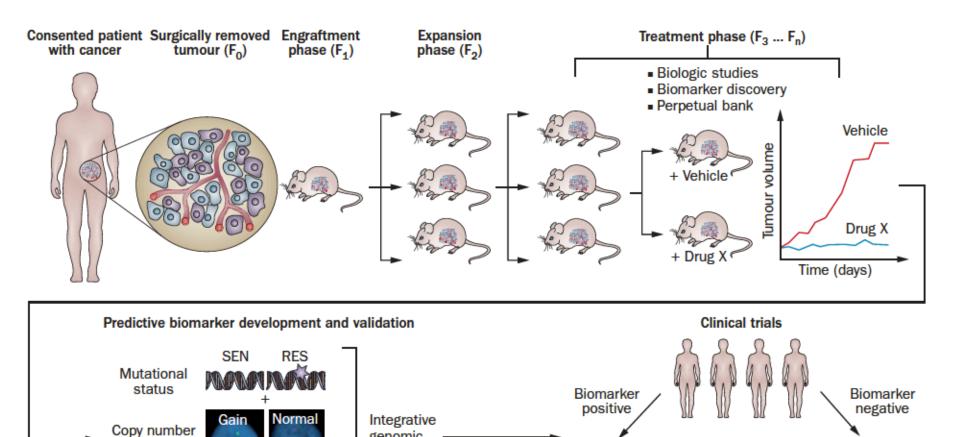


Figure 2 | Visual structure that matches the message. (a) Illustration showing a gene expression analysis technique. Reprinted from *Genome Biology*⁴. (b) The same elements organized according to the purpose of the illustration, which is to show a sequence of steps.

Wong B (2011) Nature Methods. http://www.nature.com/nmeth/journal/v8/n2/pdf/nmeth0211-101.pdf

Original Design





genomic

classifier

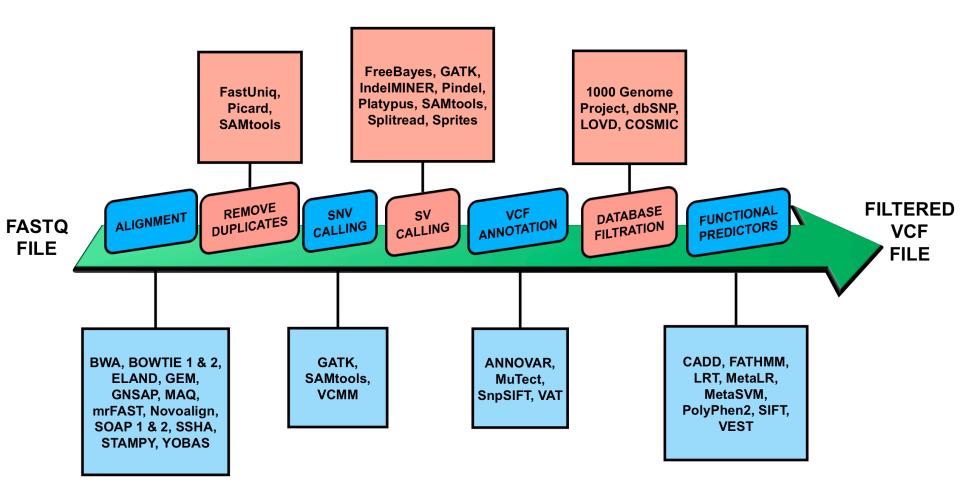
variation

Gene expression

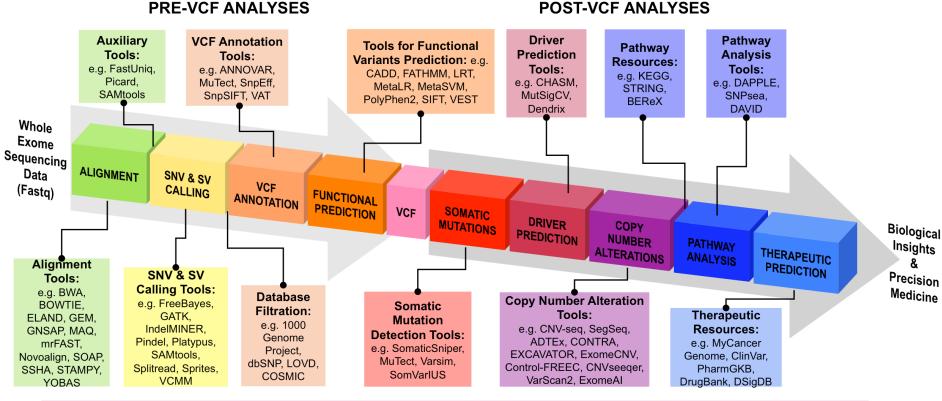
Final Design

(Tentler et al (2012). Nat Rev Clin Onc)

Drug X



Original Design



POST-VCF ANALYSES

WES Data Analysis Pipeline: e.g. SeqMule, Fastq2vcf, IMPACT, Genomes on the Cloud

Final Design

More Resource

 VizBi – visualization of Biological Data Conference

https://vizbi.org/