

Introduction to RNA-Seq

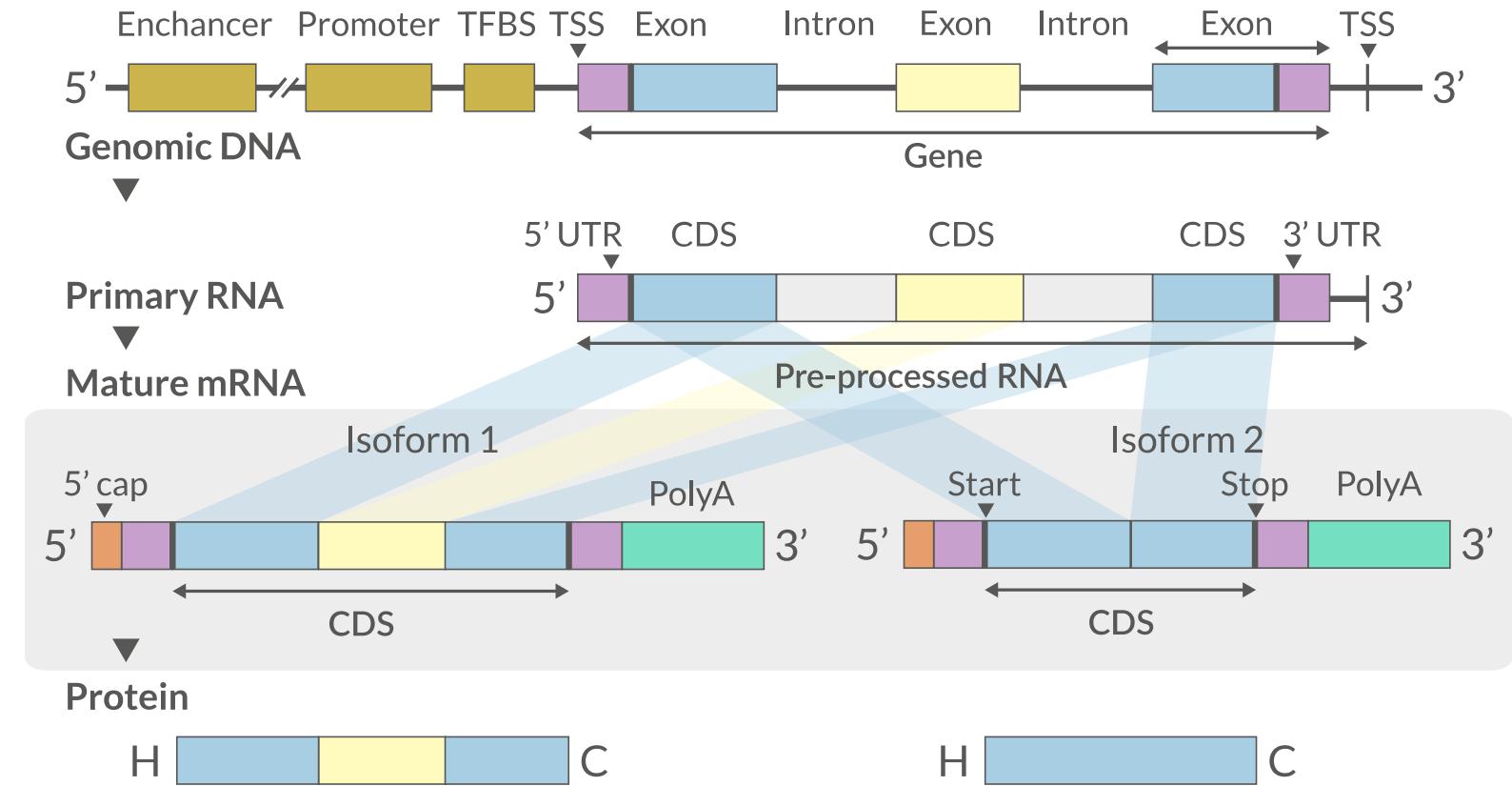
Introduction To Bioinformatics Using NGS Data

Roy Francis • 14-Apr-2019

Contents

- RNA Sequencing
- Workflow
- DGE Workflow
- ReadQC
- Mapping
- Alignment QC
- Quantification
- Normalisation
- Exploratory
- DGE
- Functional analyses
- Summary
- Help

RNA Sequencing

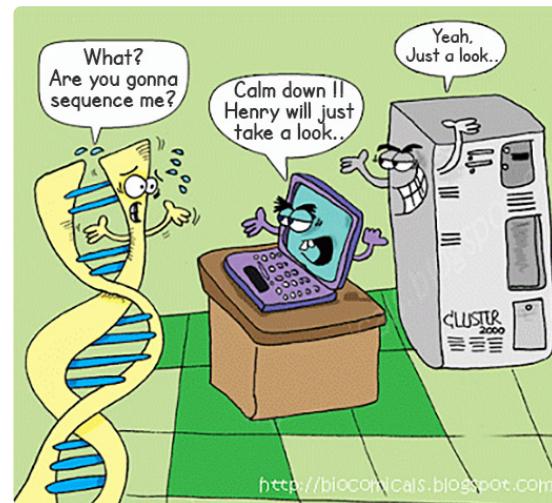
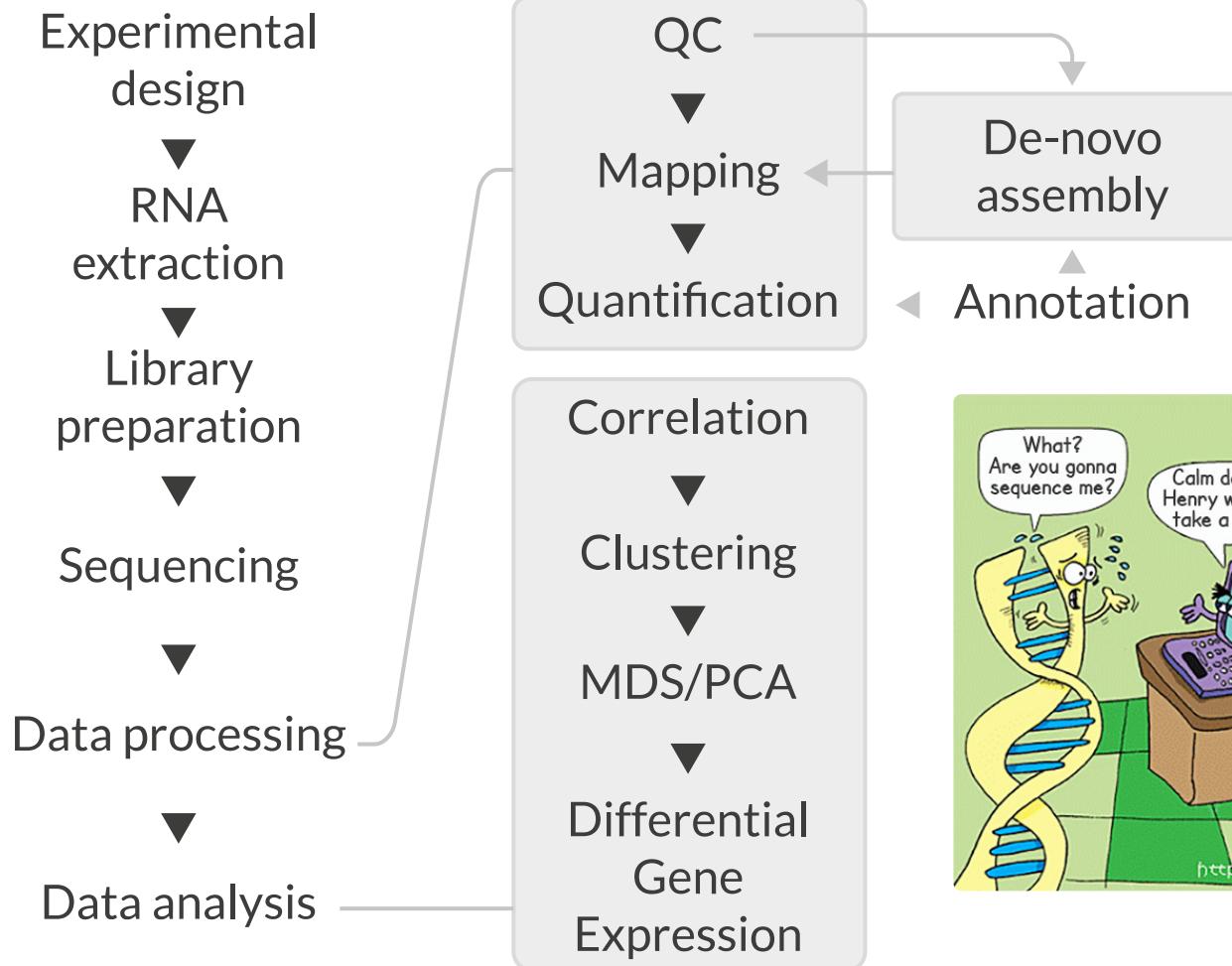


- The transcriptome is spatially and temporally dynamic
- Data comes from functional units (coding regions)
- Only a tiny fraction of the genome

Applications

- Identify gene sequences in genomes
- Learn about gene function
- Differential gene expression
- Explore isoform and allelic expression
- Understand co-expression, pathways and networks
- Gene fusion
- RNA editing

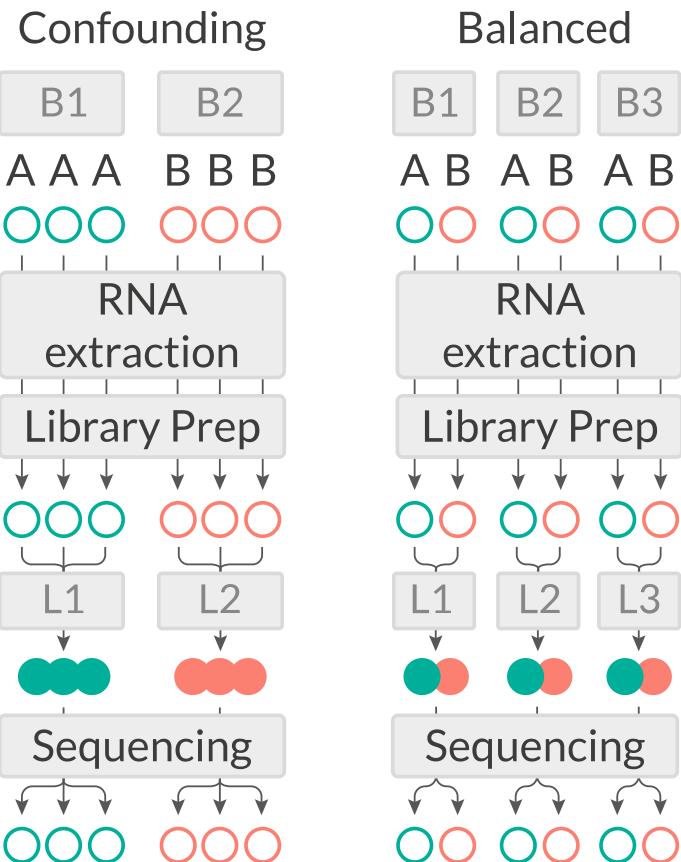
Workflow



Experimental design

- Balanced design
- Technical replicates not necessary ([Marioni et al., 2008](#))
- Biological replicates: 6 - 12 ([Schurch et al., 2016](#))
- ENCODE consortium
- Previous publications
- Power analysis

畏惧 [RnaSeqSampleSize](#) (Power analysis), [Scotty](#) (Power analysis with cost)



Busby, Michele A., et al. "Scotty: a web tool for designing RNA-Seq experiments to measure differential gene expression." *Bioinformatics* 29.5 (2013): 656-657

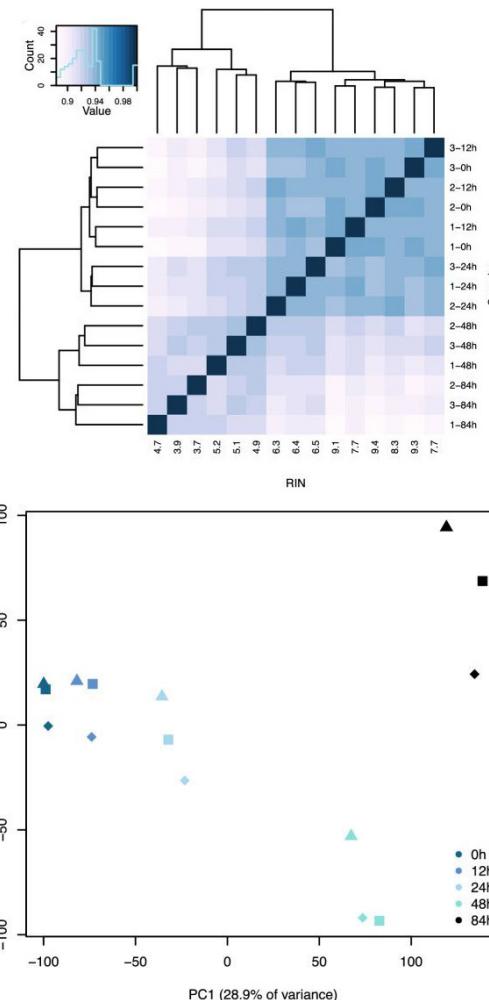
Marioni, John C., et al. "RNA-seq: an assessment of technical reproducibility and comparison with gene expression arrays." *Genome research* (2008)

Schurch, Nicholas J., et al. "How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use?." *Rna* (2016)

Zhao, Shilin, et al. "RnaSeqSampleSize: real data based sample size estimation for RNA sequencing." *BMC bioinformatics* 19.1 (2018): 191

RNA extraction

- Sample processing and storage
- Total RNA/mRNA/small RNA
- DNase treatment
- Quantity & quality
- RIN values (Strong effect)
- Batch effect
- Extraction method bias (GC bias)

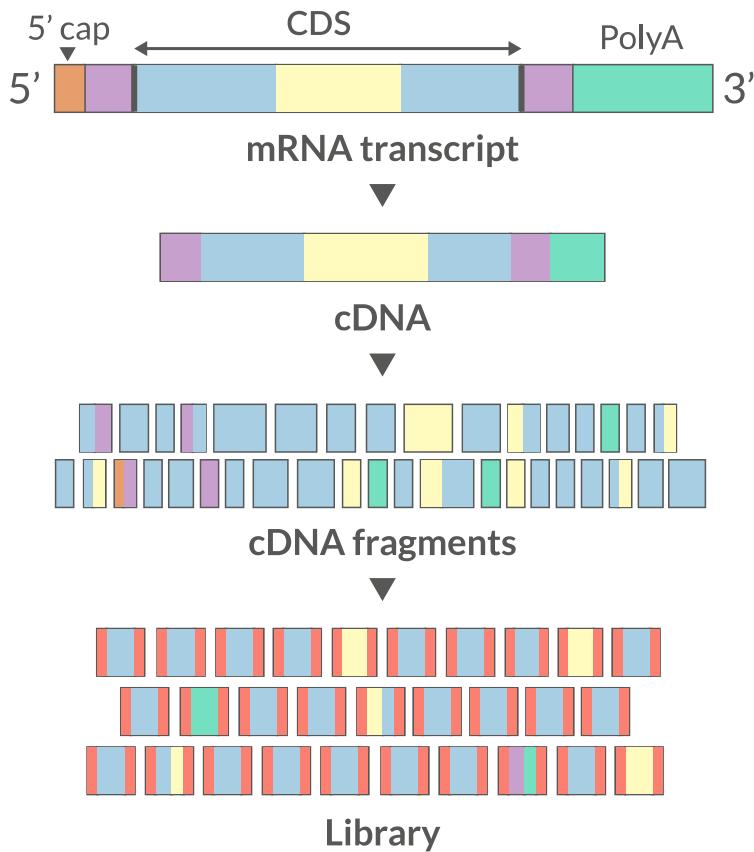


Romero, Irene Gallego, et al. "RNA-seq: impact of RNA degradation on transcript quantification." *BMC biology* 12.1 (2014): 42

Kim, Young-Kook, et al. "Short structured RNAs with low GC content are selectively lost during extraction from a small number of cells." *Molecular cell* 46.6 (2012): 893-895.00481-9.

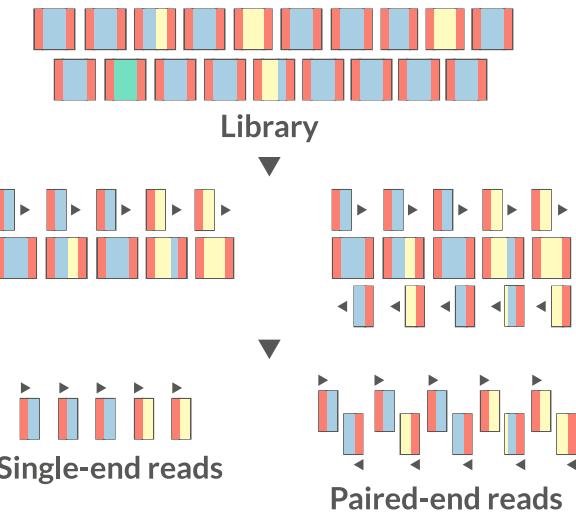
Library prep

- PolyA selection
- rRNA depletion
- Size selection
- PCR amplification (See section PCR duplicates)
- Stranded (directional) libraries
 - Accurately identify sense/antisense transcript
 - Resolve overlapping genes
- Exome capture
- Library normalisation
- Batch effect



Sequencing

- Sequencer (Illumina/PacBio)
- Read length
 - Greater than 50bp does not improve DGE
 - Longer reads better for isoforms
- Pooling samples
- Sequencing depth (Coverage/Reads per sample)
- Single-end reads (Cheaper)
- Paired-end reads
 - Increased mappable reads
 - Increased power in assemblies
 - Better for structural variation and isoforms
 - Decreased false-positives for DGE

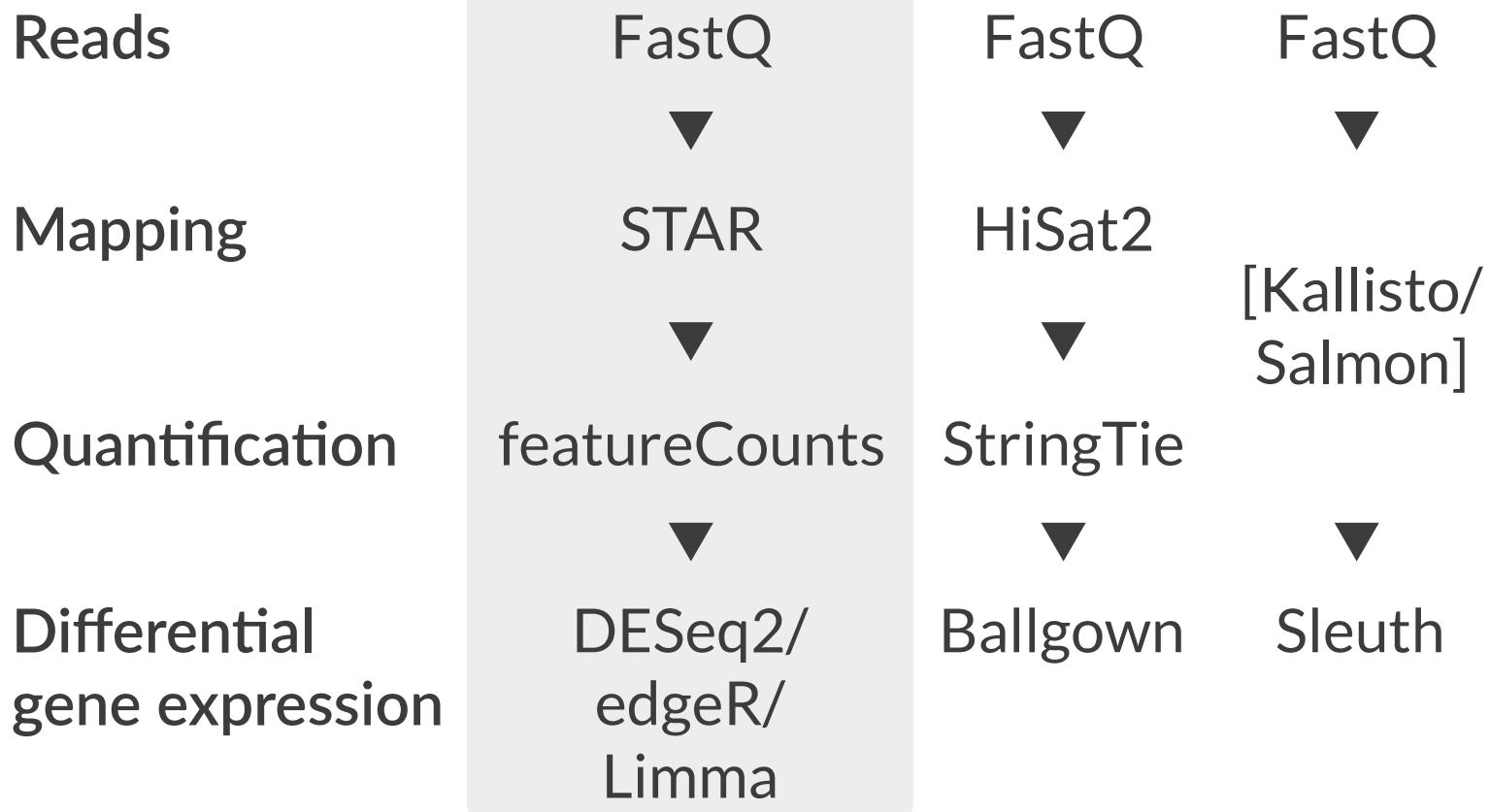


⌚ Chhangawala, Sagar, et al. "The impact of read length on quantification of differentially expressed genes and splice junction detection." *Genome biology* 16.1 (2015): 131

⌚ Corley, Susan M., et al. "Differentially expressed genes from RNA-Seq and functional enrichment results are affected by the choice of single-end versus paired-end reads and stranded versus non-stranded protocols." *BMC genomics* 18.1 (2017): 399

⌚ Liu, Yuwen, Jie Zhou, and Kevin P. White. "RNA-seq differential expression studies: more sequence or more replication?." *Bioinformatics* 30.3 (2013): 301-304 ⌚
Comparison of PE and SE for RNA-Seq, SciLifeLab

Workflow • DGE



De-Novo assembly

- When no reference genome available
- To identify novel genes/transcripts/isoforms
- Identify fusion genes
- Assemble transcriptome from short reads
- Assess quality of assembly and refine
- Map reads back to assembled transcriptome

_APPS Trinity, SOAPdenovo-Trans, Oases, rnaSPAdes

⌚ Hsieh, Ping-Han *et al.*, "Effect of de novo transcriptome assembly on transcript quantification" [2018 bioRxiv 380998](#)

⌚ Wang, Sufang, and Michael Gribkov. "Comprehensive evaluation of de novo transcriptome assembly programs and their effects on differential gene expression analysis." [Bioinformatics 33.3 \(2017\): 327-333](#)

Read QC

- Number of reads
- Per base sequence quality
- Per sequence quality score
- Per base sequence content
- Per sequence GC content
- Per base N content
- Sequence length distribution
- Sequence duplication levels
- Overrepresented sequences
- Adapter content
- Kmer content

FastQC, MultiQC

<https://sequencing.qcfail.com/>



 QCFAIL.com

Articles about common next-generation sequencing problems

FastQC Report

Thu 21 Dec 2017
good_sequence_short.txt

Summary

- ✓ Basic Statistics
- ✓ Per base sequence quality
- ✓ Per tile sequence quality
- ✓ Per sequence quality scores
- ✓ Per base sequence content
- ✓ Per sequence GC content
- ✓ Per base N content
- ✓ Sequence Length Distribution
- ✓ Sequence Duplication Levels
- ✓ Overrepresented sequences
- ✓ Adapter Content

Basic Statistics

Measure	Value
Filename	good_sequence_short.txt
File type	Conventional base calls
Encoding	Illumina 1.5
Total Sequences	250000
Sequences flagged as poor quality	0
Sequence length	40
%GC	45

Per base sequence quality

Quality scores across all bases (Illumina 1.5 encoding)

FastQC Report

Thu 21 Dec 2017
bad_sequence.txt

Summary

- ✓ Basic Statistics
- ✗ Per base sequence quality
- ✗ Per tile sequence quality
- ✓ Per sequence quality scores
- ! Per base sequence content
- ! Per sequence GC content
- ✓ Per base N content
- ✓ Sequence Length Distribution
- ! Sequence Duplication Levels
- ! Overrepresented sequences
- ✓ Adapter Content

Basic Statistics

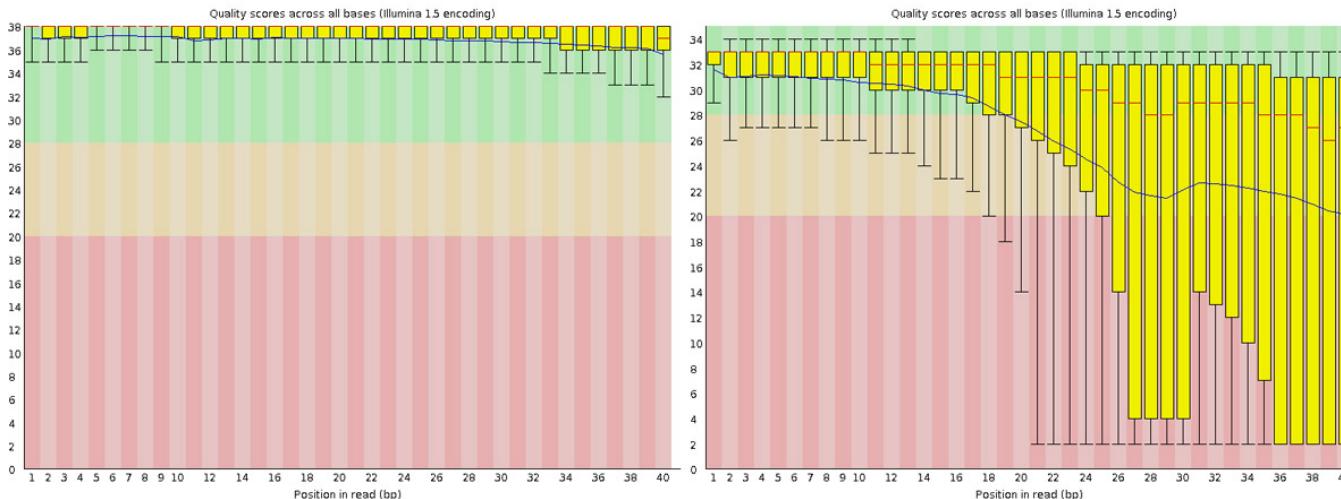
Measure	Value
Filename	bad_sequence.txt
File type	Conventional base calls
Encoding	Illumina 1.5
Total Sequences	395288
Sequences flagged as poor quality	0
Sequence length	40
%GC	47

✗ Per base sequence quality

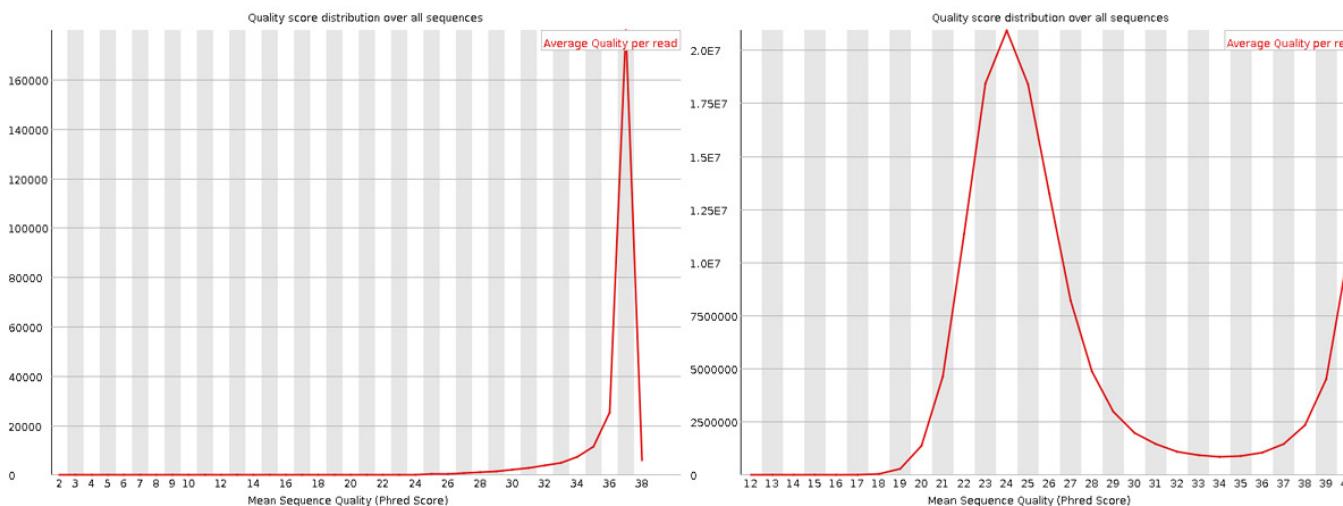
Quality scores across all bases (Illumina 1.5 encoding)

Read QC • PBSQ, PSQS

Per base sequence quality

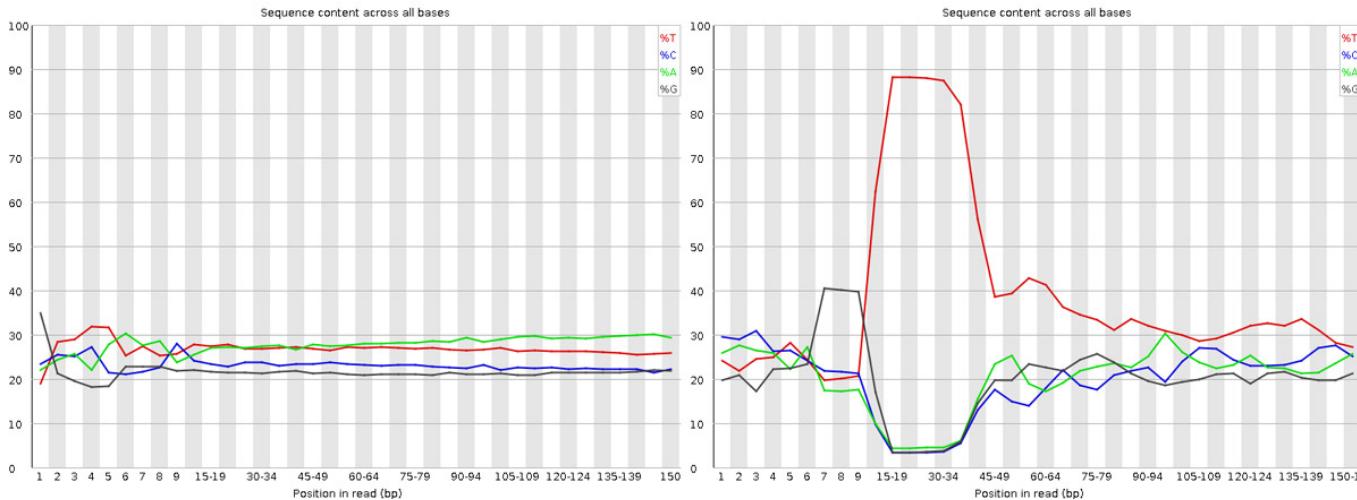


Per sequence quality scores

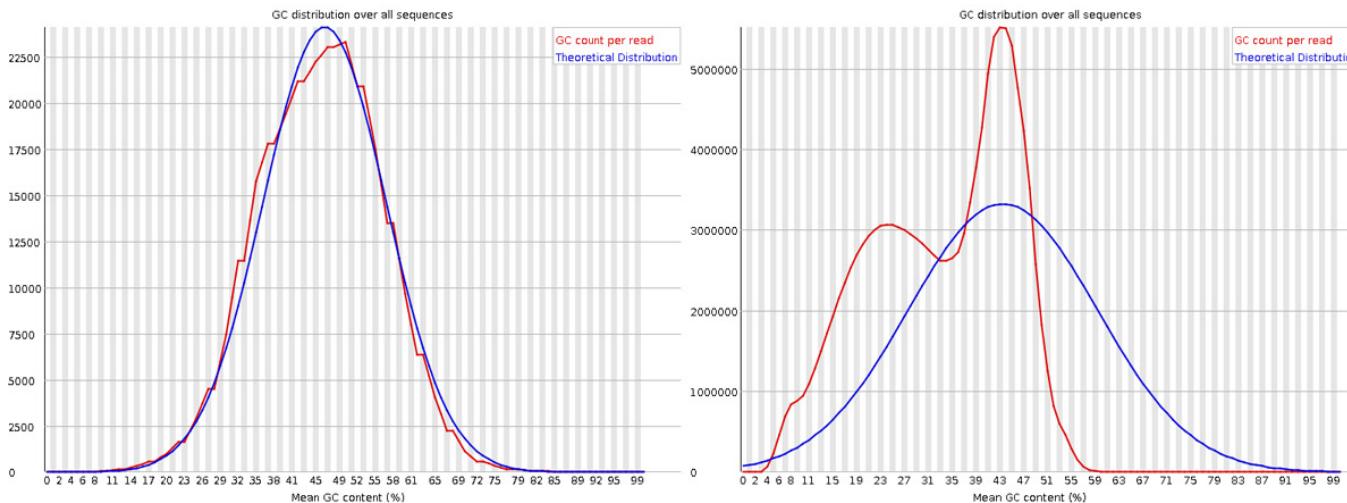


Read QC • PBSC, PSGC

Per base sequence content

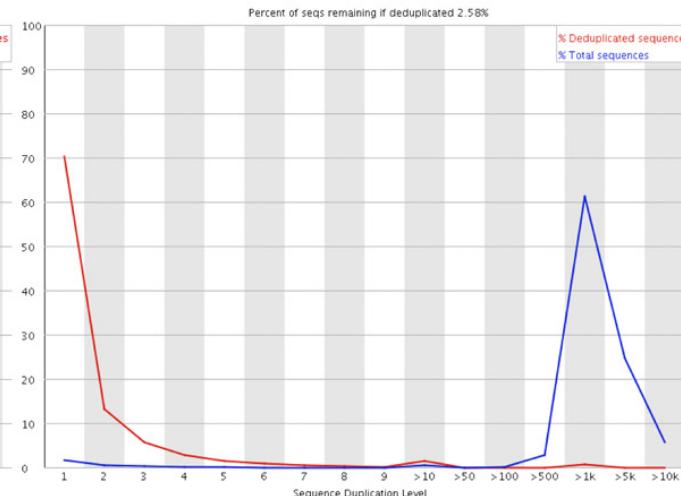
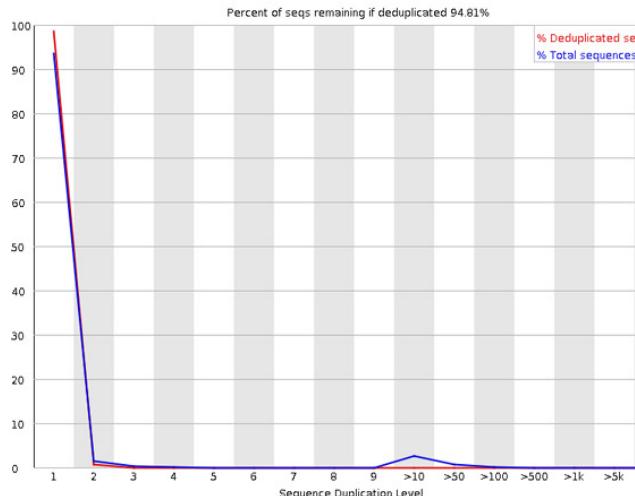


Per sequence GC content



Read QC • SDL, AC

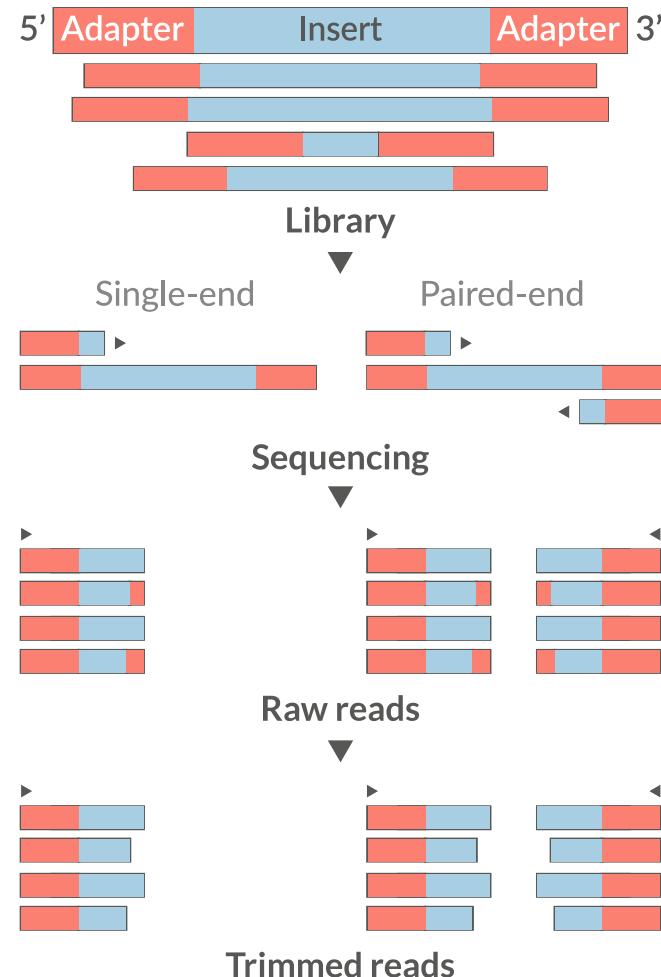
Sequence duplication level



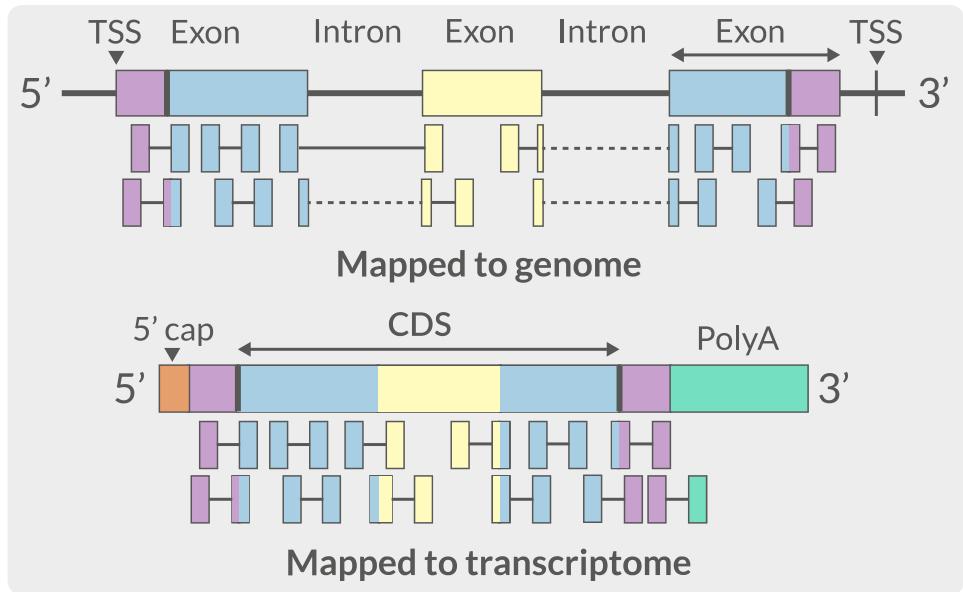
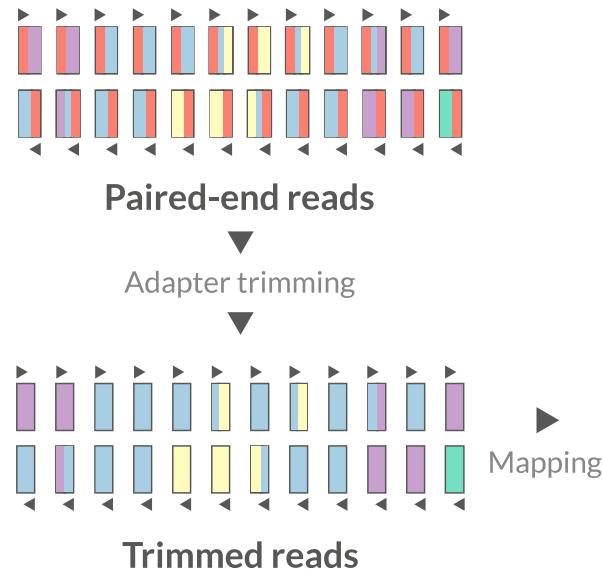
Trimming

- Trim IF necessary
 - Synthetic bases can be an issue for SNP calling
 - Insert size distribution may be more important for assemblers
- Trim/Clip/Filter reads
- Remove adapter sequences
- Trim reads by quality
- Sliding window trimming
- Filter by min/max read length
 - Remove reads less than ~18nt
- Demultiplexing/Splitting

_cutadapt, fastp, Skewer, Prinseq



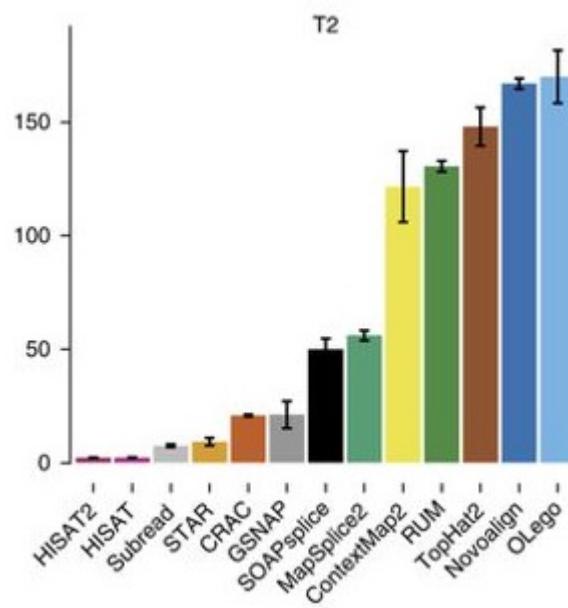
Mapping



- Aligning reads back to a reference sequence
- Mapping to genome vs transcriptome
- Splice-aware alignment (genome)

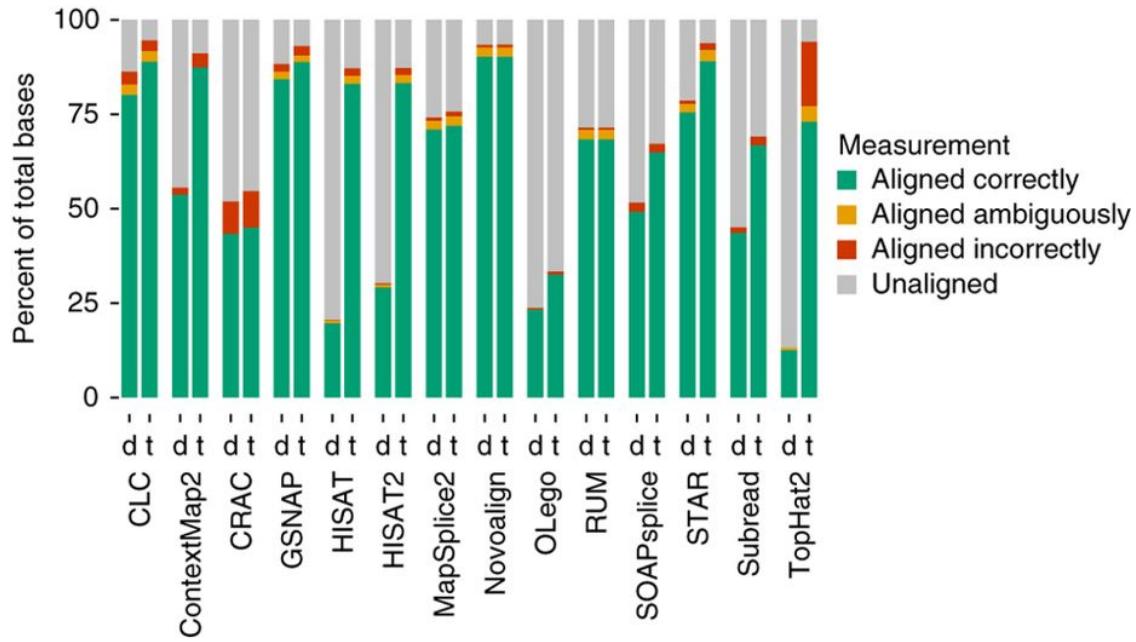
⌚ [STAR](#), [HiSat2](#), [GSNAP](#), [Novoalign](#) (Commercial)

Aligners • Speed



Program	Time_Min	Memory_GB
HISATx1	22.7	4.3
HISATx2	47.7	4.3
HISAT	26.7	4.3
STAR	25	28
STARx2	50.5	28
GSNAP	291.9	20.2
TopHat2	1170	4.3

Aligners • Accuracy



Increasing Accuracy ↑

- Novel variants / RNA editing
- Allele-specific expression
- Genome annotation
- Gene and transcript discovery
- Differential expression

🖨️ STAR, HiSat2, GSNAp, Novoalign (Commercial)

Mapping

- Reads (FASTQ)

```
@ST-E00274:179:HHYMLALXX:8:1101:1641:1309 1:N:0:NGATGT  
NCATCGTGGTATTGCACATCTTCTTCAAATAAAAGTTAACCTACTCAGTTATGCGCATACGTTTTGATGGCATTCCATAAACGATTTTTTT/  
+  
#AAAFAFA<-AFFJJJAFA-FFJJJJFFF AJJJJ-<FFJJJ-A-F-7--FA7F7-----FFFJFA<FFFFJ<AJ--FF-A<A-<JJ-7-7-<FF-FFFJAFFAA-
```

```
@instrument:runid:flowcellid:lane:tile:xpos:ypos read:isfiltered:controlnumber:sampleid
```

- Reference Genome/Transcriptome (FASTA)

```
>1 dna:chromosome chromosome:GRCz10:1:1:58871917:1 REF  
GATCTAAACATTATTCCCCCTGCAAACATTCAATCATTACATTGTCAATTCCCCTC  
CAAATTAAATTAGCCAGAGGCCACAACATACGACCTCTAAAAAGGTGCTGTAACATG
```

- Annotation (GTF/GFF)

```
#!genome-build GRCz10  
#!genebuild-last-updated 2016-11  
4 ensembl_havana gene 6732 52059 . - . gene_id "ENSDARG00000104632"; gene
```

```
seq source feature start end score strand frame attribute
```

Alignment

- SAM/BAM (Sequence Alignment Map format)

ST-E00274:188:H3JWNCCXY:4:1102:32431:49900 163 1 1 60 8S139M4S = 385

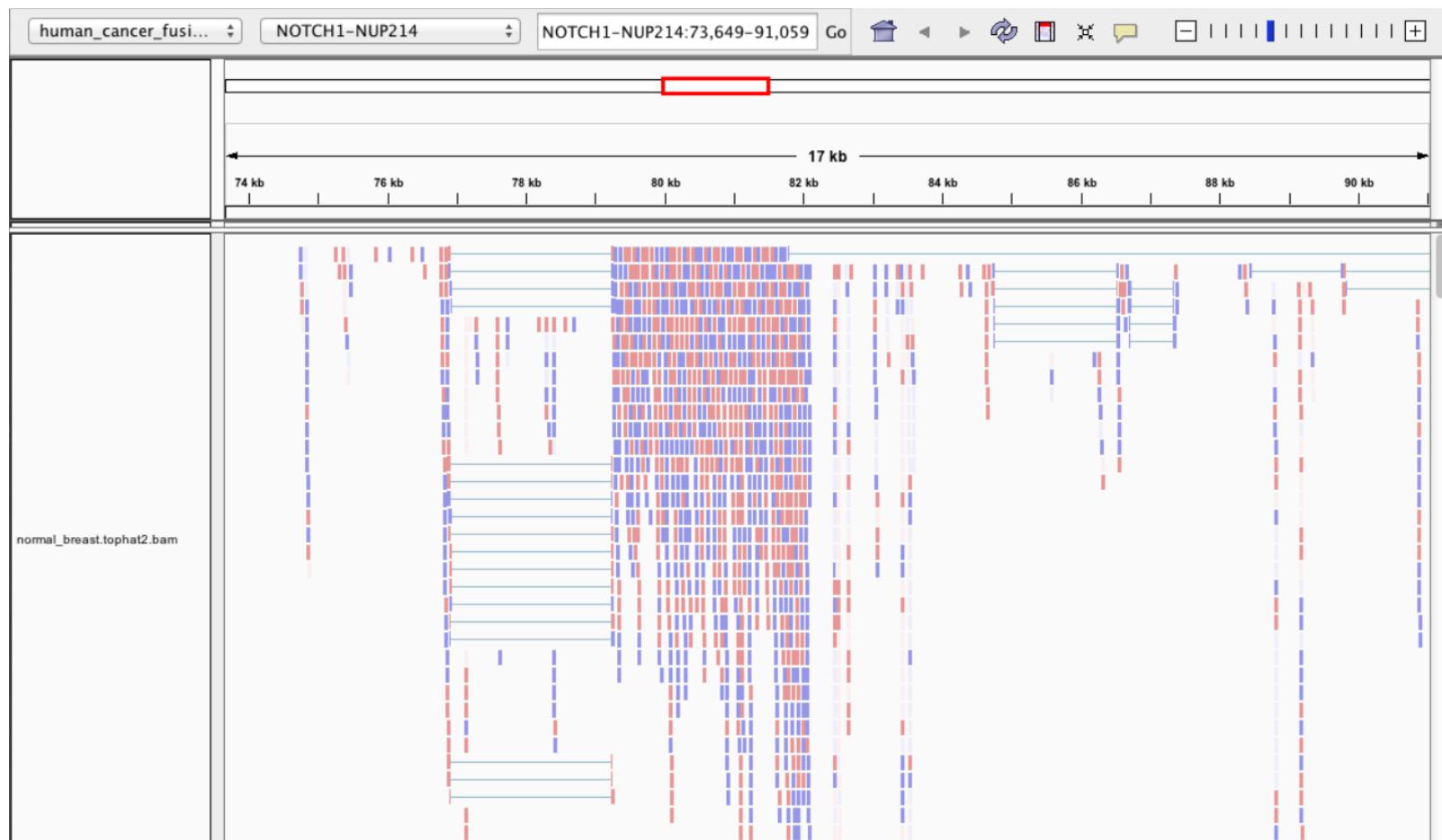
query flag ref pos mapq cigar mrnm mpos tlen seq qual opt

Format	Size_GB
SAM	7.4
BAM	1.9
CRAM lossless Q	1.4
CRAM 8 bins Q	0.8
CRAM no Q	0.26

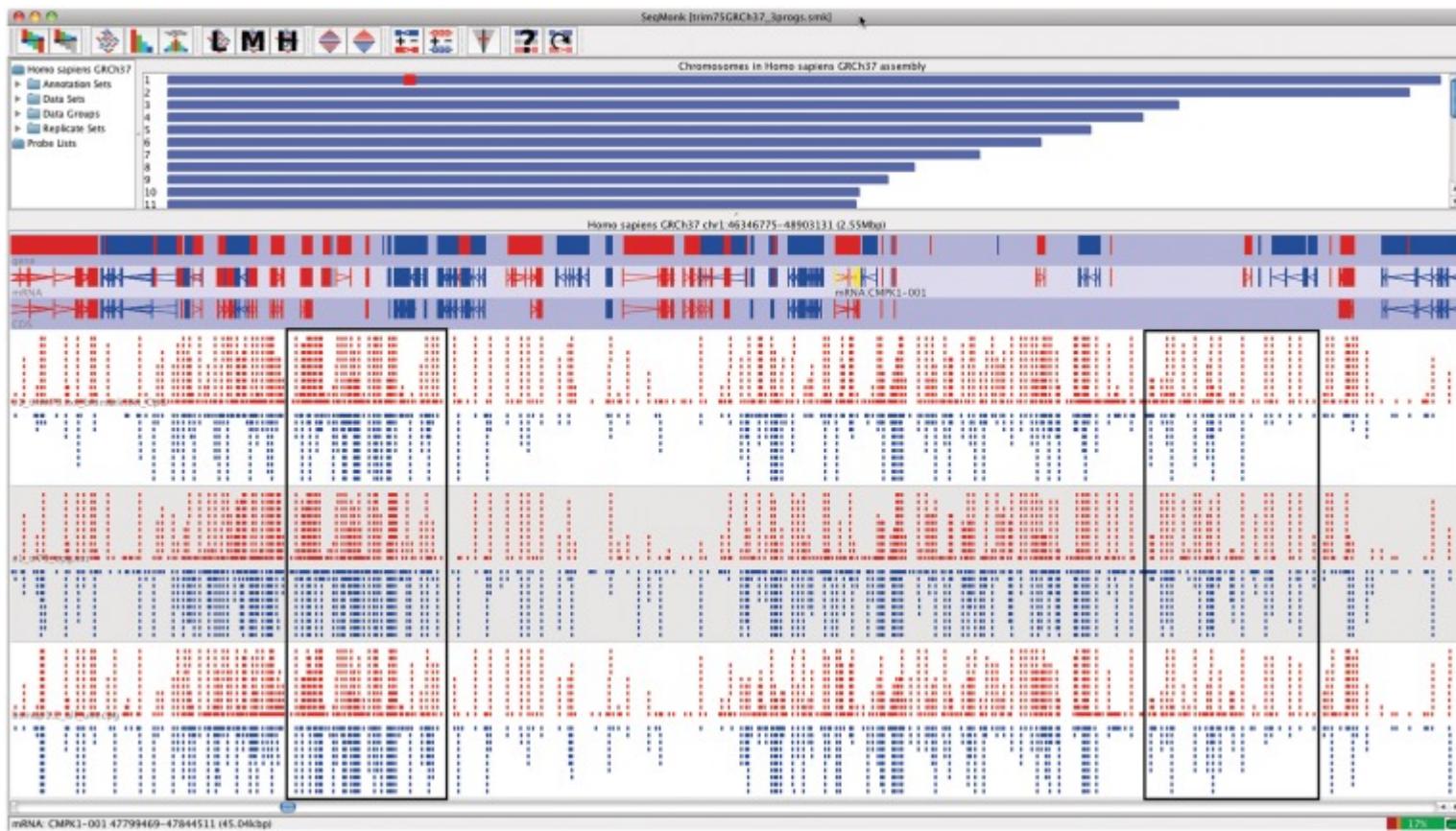
Visualisation • **tview**

```
 samtools tview alignment.bam genome.fasta
```

Visualisation • IGV



Visualisation • SeqMonk



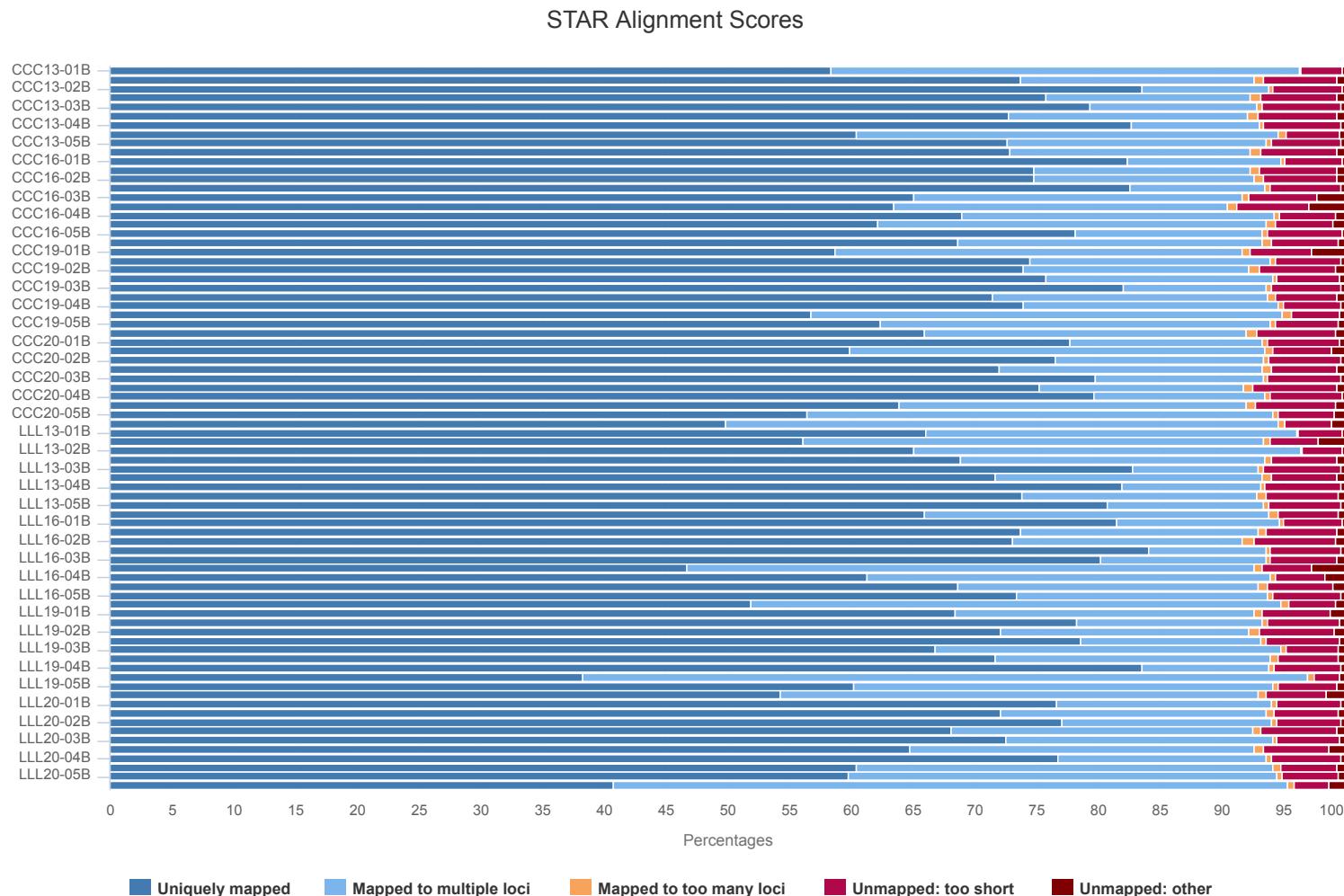
Alignment QC

- Number of reads mapped/unmapped/paired etc
- Uniquely mapped
- Insert size distribution
- Coverage
- Gene body coverage
- Biotype counts / Chromosome counts
- Counts by region: gene/intron/non-genic
- Sequencing saturation
- Strand specificity

📄 STAR (final log file), samtools > stats, bamtools > stats, [QoRTs](#), [RSeQC](#), [Qualimap](#)

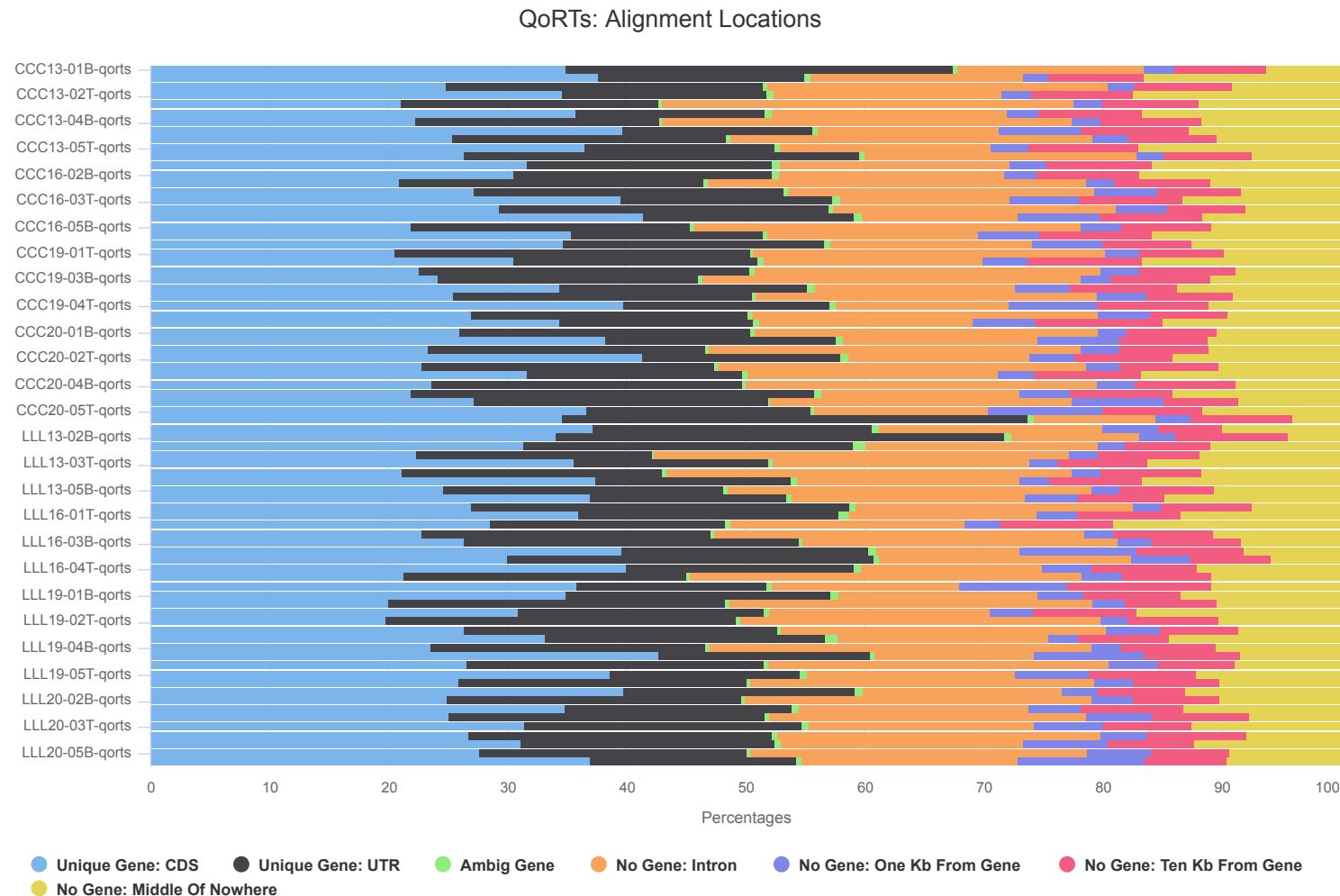
Alignment QC • STAR Log

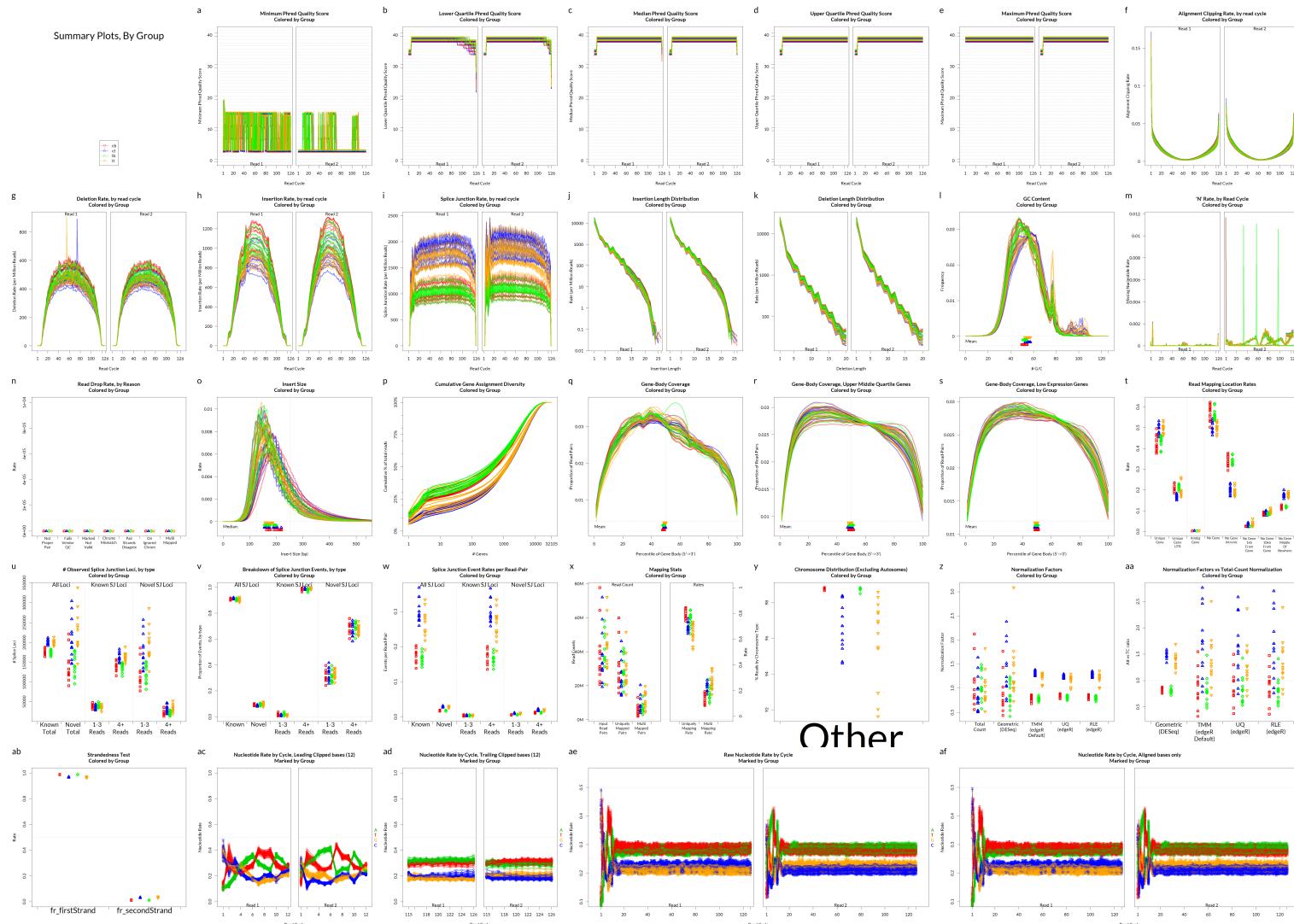
MultiQC can be used to summarise and plot STAR log files.



Alignment QC • Features

QoRTs was run on all samples and summarised using MultiQC.

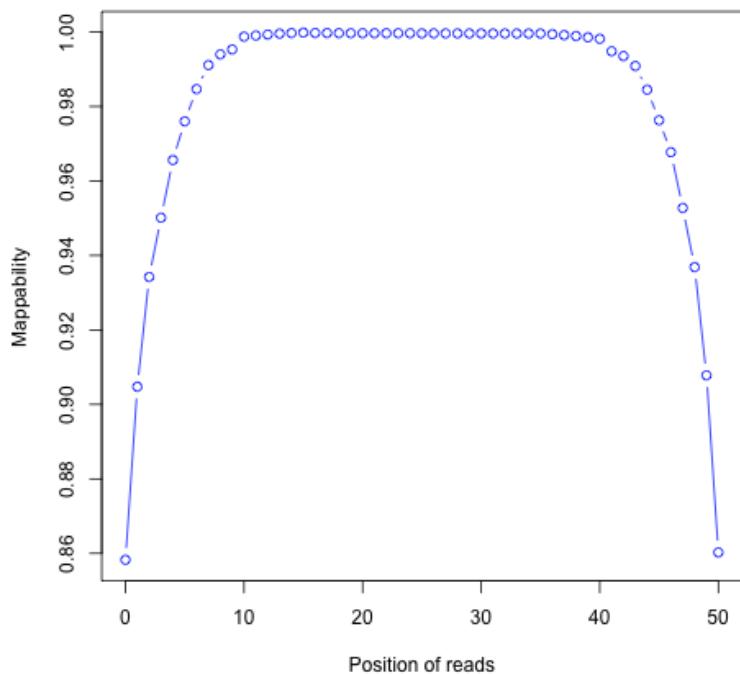




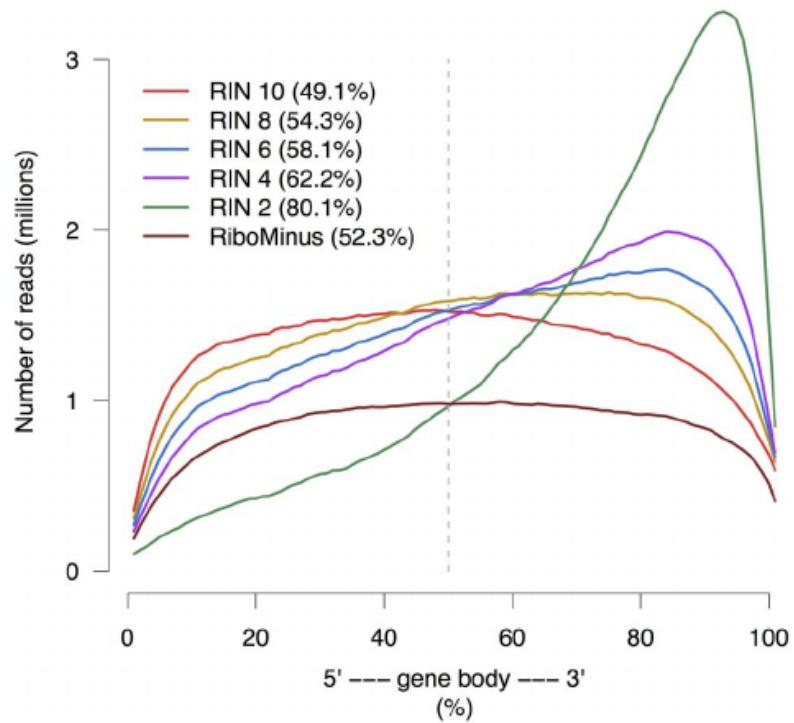
Other

Alignment QC

Soft clipping

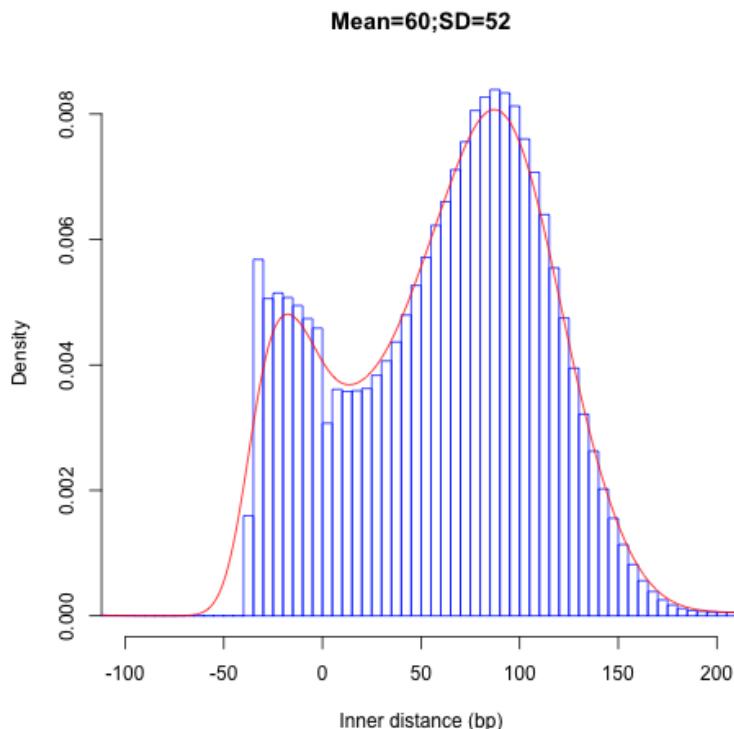


Gene body coverage

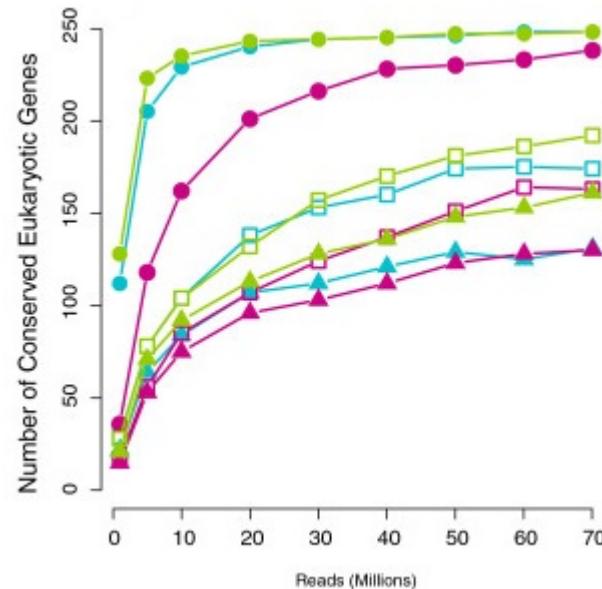


Alignment QC

Insert size

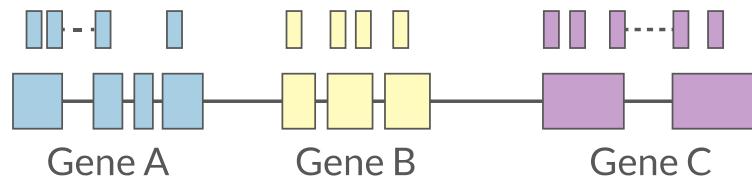


Saturation curve

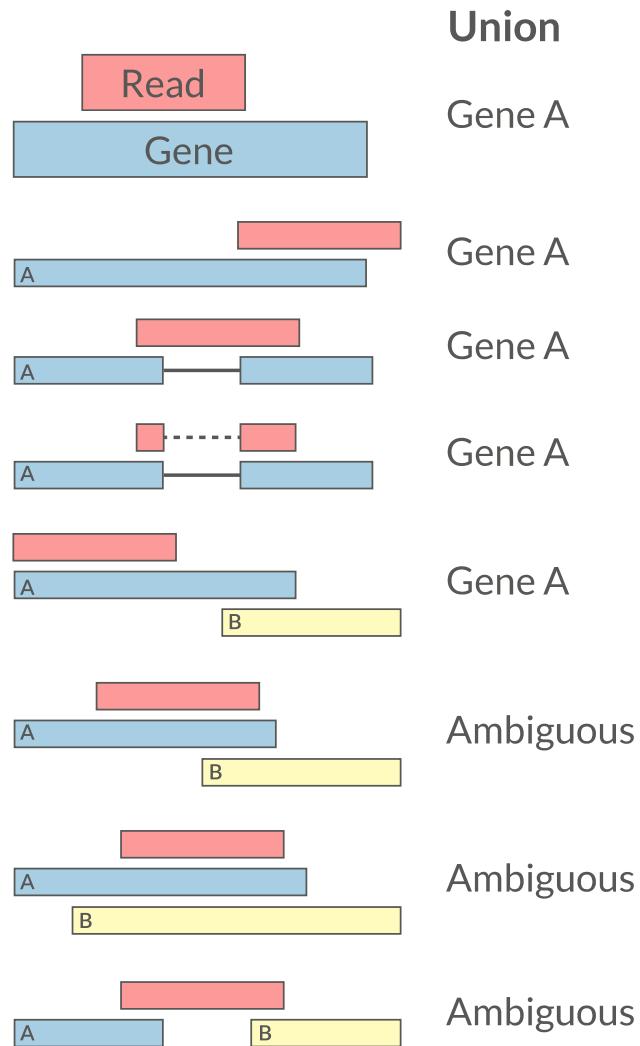


Quantification • Counts

- Read counts = gene expression
- Reads can be quantified on any feature (gene, transcript, exon etc)
- Intersection on gene models
- Gene/Transcript level



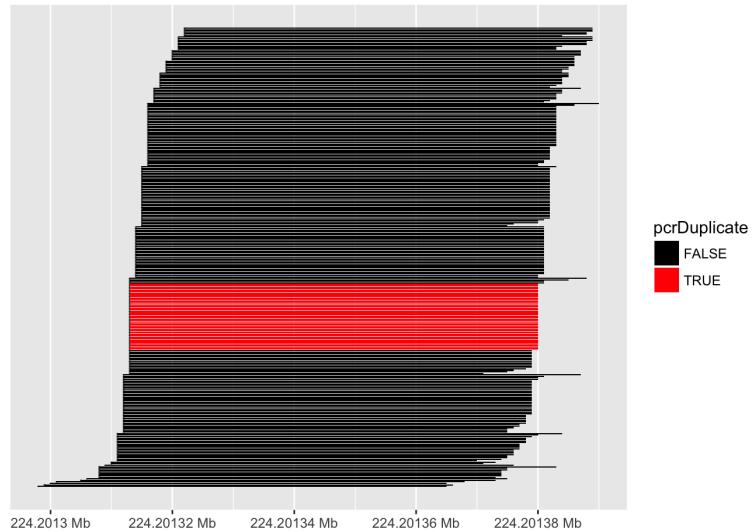
[featureCounts](#), [HTSeq](#)



Quantification

PCR duplicates

- Ignore for RNA-Seq data
- Computational deduplication (Don't!)
- Use PCR-free library-prep kits
- Use UMIs during library-prep



Multi-mapping

- Added (BEDTools multicov)
- Discard (featureCounts, HTSeq)
- Distribute counts (Cufflinks)
- Rescue
 - Probabilistic assignment (Rcount, Cufflinks)
 - Prioritise features (Rcount)
 - Probabilistic assignment with EM (RSEM)

✉ Fu, Yu, et al. "Elimination of PCR duplicates in RNA-seq and small RNA-seq using unique molecular identifiers." *BMC genomics* 19.1 (2018): 531

✉ Parekh, Swati, et al. "The impact of amplification on differential expression analyses by RNA-seq." *Scientific reports* 6 (2016): 25533

✉ Klepikova, Anna V., et al. "Effect of method of deduplication on estimation of differential gene expression using RNA-seq." *PeerJ* 5 (2017): e3091

Quantification • Abundance

- Count methods
 - Provide no inference on isoforms
 - Cannot accurately measure fold change
- Probabilistic assignment
 - Deconvolute ambiguous mappings
 - Transcript-level
 - cDNA reference

Kallisto, Salmon

- Ultra-fast & alignment-free
- Subsampling & quantification confidence
- Transcript-level estimates improves gene-level estimates
- Kallisto/Salmon > transcript-counts > `tximport()` > gene-counts

 [RSEM](#), [Kallisto](#), [Salmon](#), [Cufflinks2](#)

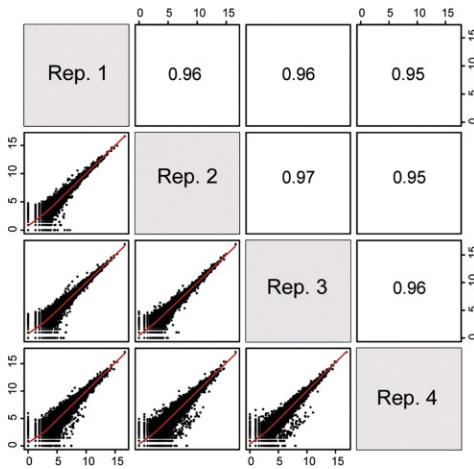
⌚ Soneson, Charlotte, et al. "Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences." [F1000Research 4 \(2015\)](#)

⌚ Zhang, Chi, et al. "Evaluation and comparison of computational tools for RNA-seq isoform quantification." [BMC genomics 18.1 \(2017\): 583](#)

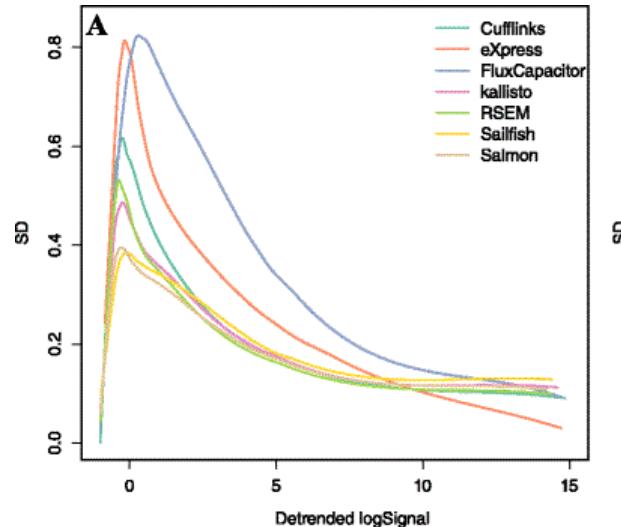
Quantification QC

ENSG000000000003	140	242	188	143	287	344	438	280	253
ENSG000000000005	0	0	0	0	0	0	0	0	0
ENSG000000000419	69	98	77	55	52	94	116	79	69
ENSG000000000457	56	75	104	79	157	205	183	178	153
ENSG000000000460	33	27	23	19	27	42	69	44	40
ENSG000000000938	7	38	13	17	35	76	53	37	24
ENSG000000000971	545	878	694	636	647	216	492	798	323
ENSG00000001036	79	154	74	80	128	167	220	147	72

- Pairwise correlation between samples must be high (>0.9)



- Count QC using RNASeqComp



RNASeqComp

MultiQC
v1.6

- General Stats
- featureCounts
- STAR
- Cutadapt
- FastQC
- Sequence Counts
- Sequence Quality Histograms
- Per Sequence Quality Scores
- Per Base Sequence Content
- Per Sequence GC Content
- Per Base N Content
- Sequence Length Distribution
- Sequence Duplication Levels
- Overrepresented sequences
- Adapter Content

MultiQC

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

Report generated on 2018-08-04, 01:51 based on data in: /Users/ewels/GitHub/MultiQC_website/public_html/examples/rna-seq

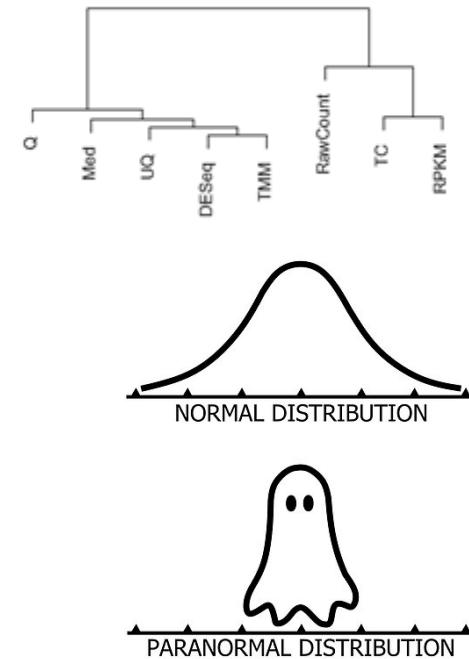
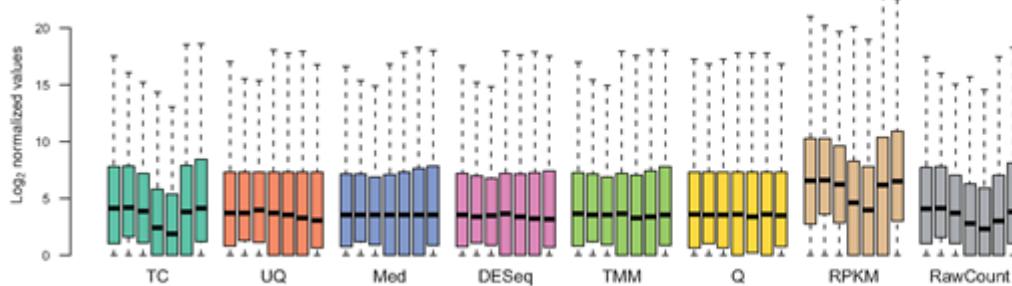
General Statistics

Copy table
 Configure Columns
 Plot
Showing 8/8 rows and 8/10 columns.

Sample Name	% Assigned	M Assigned	% Aligned	M Aligned	% Trimmed	% Dups	% GC	M Seqs
SRR3192396	67.5%	71.9	93.7%	97.8	4.0%	78.9%	51%	104.4
SRR3192397	66.6%	63.0	94.7%	87.1	3.5%	77.2%	49%	92.0
SRR3192398	50.9%	36.5	88.2%	58.7	5.0%	55.3%	47%	66.6
SRR3192399	52.3%	42.3	88.2%	65.6	5.0%	57.4%	47%	74.3
SRR3192400	70.3%	63.4	77.3%	73.4	7.2%	74.1%	45%	94.9
SRR3192401	71.2%	63.8	76.4%	72.8	6.3%	76.3%	45%	95.2
SRR3192657	73.1%	67.1	91.2%	85.0	3.1%	82.2%	51%	93.1
SRR3192658	71.2%	66.9	89.7%	87.1	3.4%	82.3%	52%	97.1

Normalisation

- Control for Sequencing depth & compositional bias
- Median of Ratios (DESeq2) and TMM (edgeR) perform the best



- For DGE using DGE packages, use raw counts
- For clustering, heatmaps etc use VST, VOOM or RLOG
- For own analysis, plots etc, use TPM
- Other solutions: spike-ins/house-keeping genes

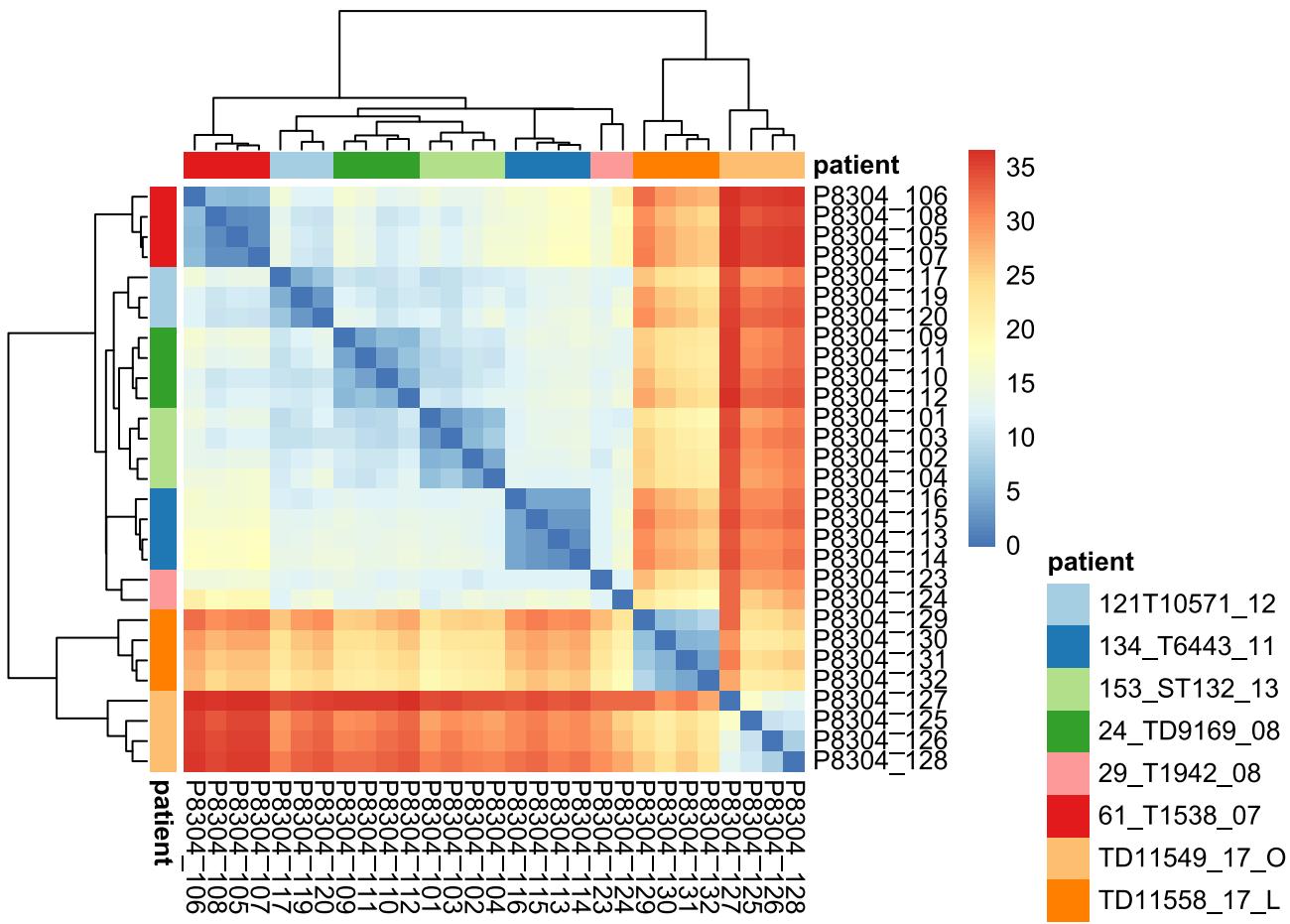
Dillies, Marie-Agnes, et al. "A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis." *Briefings in bioinformatics* 14.6 (2013): 671-683

Evans, Ciaran, Johanna Hardin, and Daniel M. Stoebel. "Selecting between-sample RNA-Seq normalization methods from the perspective of their assumptions." *Briefings in bioinformatics* (2017)

Wagner, Gunter P., Koryu Kin, and Vincent J. Lynch. "Measurement of mRNA abundance using RNA-seq data: RPKM measure is inconsistent among samples." *Theory in biosciences* 131.4 (2012): 281-285

Exploratory • Heatmap

- Remove lowly expressed genes
 - Transform raw counts to VST, VOOM, RLOG, TPM etc
 - Sample-sample clustering heatmap



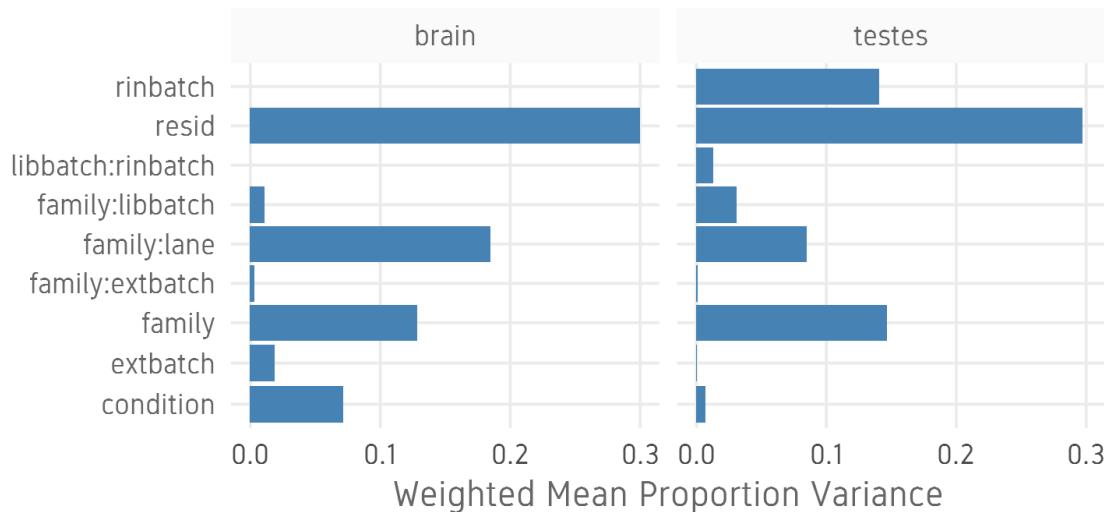
Exploratory • MDS



- 121T10571_12
- 134_T6443_11
- 153_ST132_13
- 24_TD9169_08
- 29_T1942_08
- 61_T1538_07
- TD11549_17_O
- TD11558_17_L

Batch correction

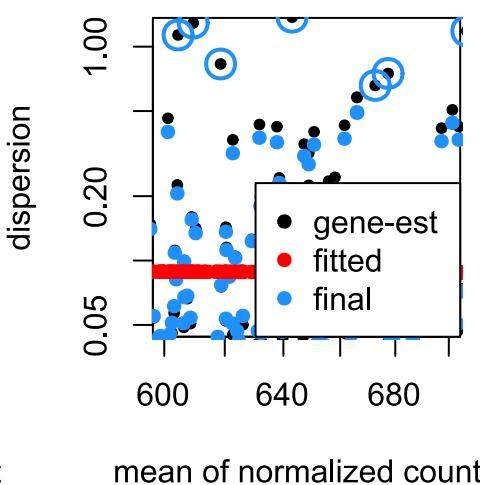
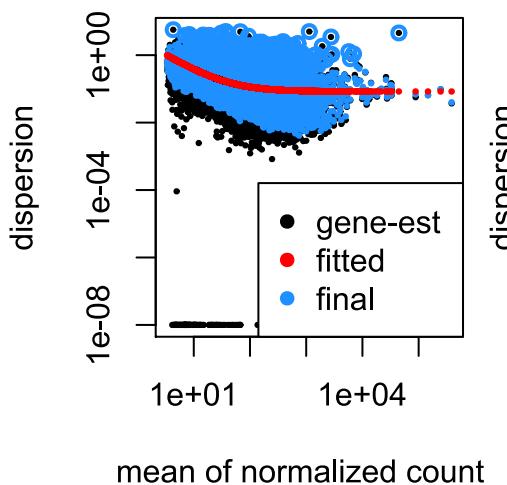
- Estimate variation explained by variables (PVCA)



- Find confounding effects as surrogate variables (SVA)
- Model known batches in the LM/GLM model
- Correct known batches (ComBat)(Harsh!)
- Interactively evaluate batch effects and correction (BatchQC)

camera icon SVA, PVCA, BatchQC

- DESeq2, edgeR (Neg-binom > GLM > Test), Limma-Voom (Neg-binom > Voom-transform > LM > Test)
- DESeq2 `~age+condition`
 - Estimate size factors `estimateSizeFactors()`
 - Estimate gene-wise dispersion `estimateDispersions()`
 - Fit curve to gene-wise dispersion estimates
 - Shrink gene-wise dispersion estimates
 - GLM fit for each gene
 - Wald test `nbinomWaldTest()`



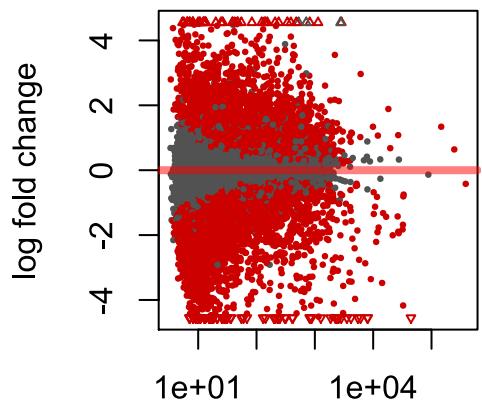
- Results `results()`

```
## log2 fold change (MLE): type type2 vs control
## Wald test p-value: type type2 vs control
## DataFrame with 1 row and 6 columns
##           baseMean    log2FoldChange        lfcSE
##          <numeric>      <numeric>      <numeric>
## ENSG000000000003 242.307796723287 -0.932926089608558 0.114285150312515
##             stat       pvalue        padj
##            <numeric>      <numeric>      <numeric>
## ENSG000000000003 -8.16314356727411 3.2641615028674e-16 1.36240610016877e-14
```

- Summary `summary()`

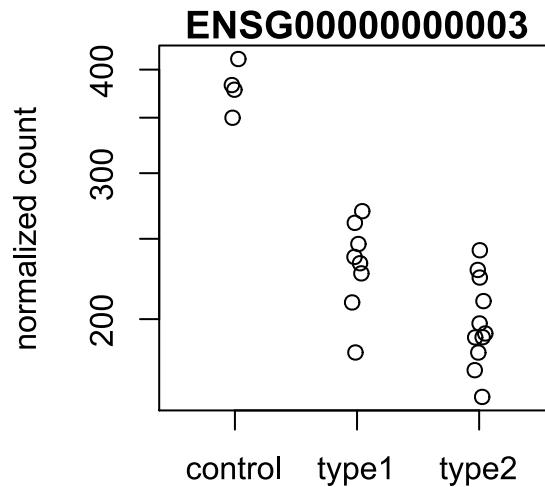
```
## 
## out of 17889 with nonzero total read count
## adjusted p-value < 0.1
## LFC > 0 (up)      : 4526, 25%
## LFC < 0 (down)    : 5062, 28%
## outliers [1]       : 25, 0.14%
## low counts [2]     : 0, 0%
## (mean count < 3)
## [1] see 'cooksCutoff' argument of ?results
## [2] see 'independentFiltering' argument of ?results
```

- MA plot `plotMA()`



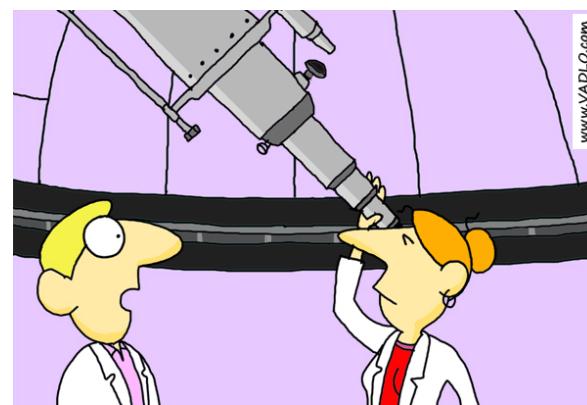
mean of normalized count

- Normalised counts `plotCounts()`



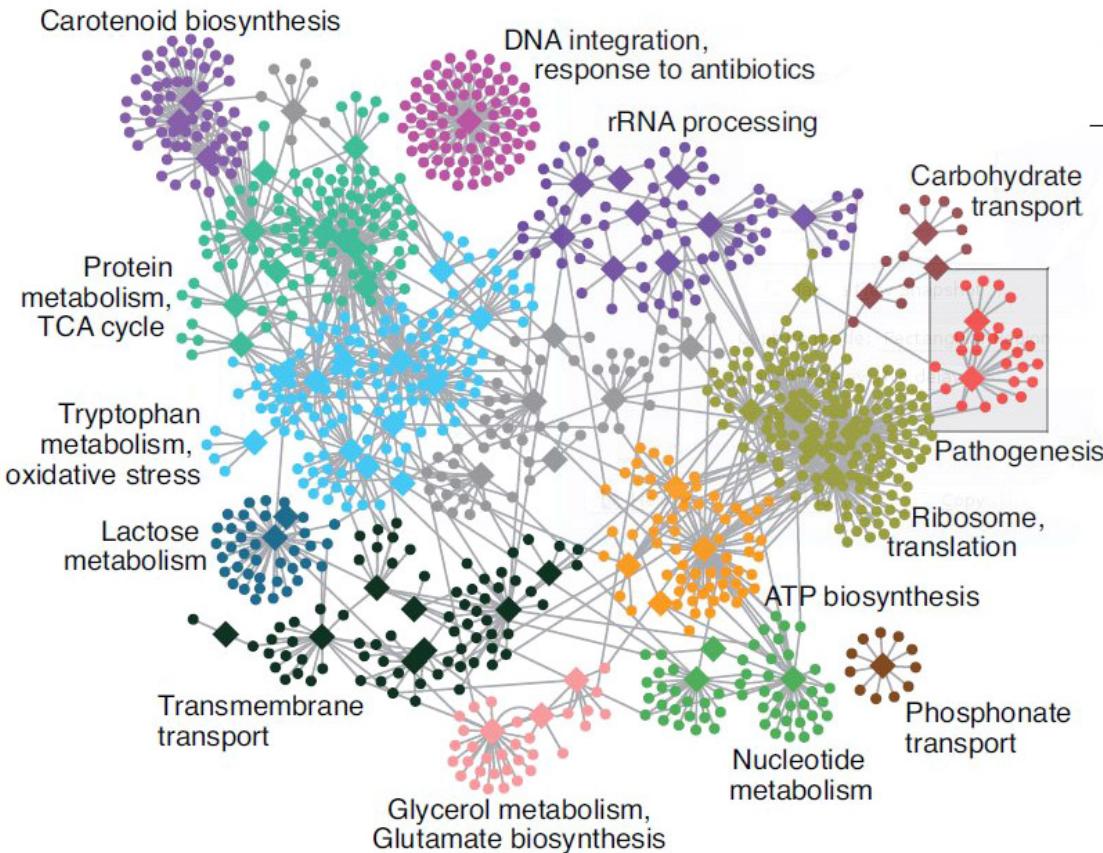
control type1 type2

- Volcano plot

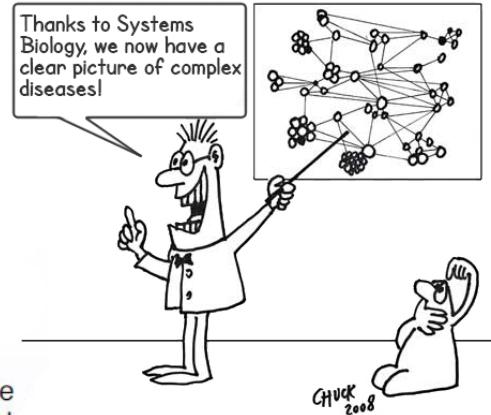


Functional analysis • GO

- Gene enrichment analysis
- Gene set enrichment analysis (GSEA)
- Gene ontology / Reactome databases

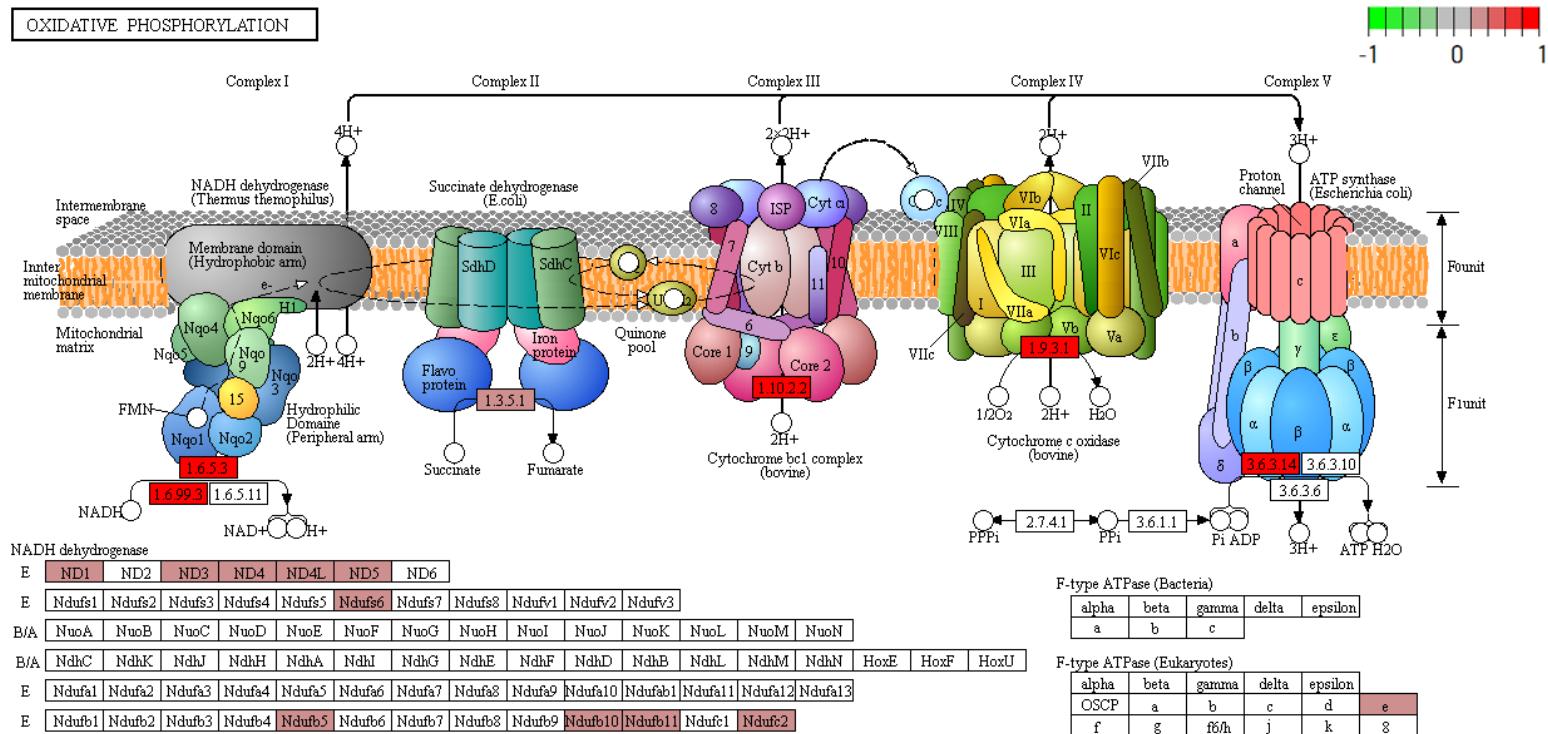


Thanks to Systems Biology, we now have a clear picture of complex diseases!



Functional analysis • Kegg

- Pathway analysis (Kegg)



DAVID, clusterProfiler, ClueGO, ErmineJ, pathview

Summary

- Sound experimental design to avoid confounding
- Plan carefully about lib prep, sequencing etc based on experimental objective
- Biological replicates may be more important than paired-end reads or long reads
- Discard low quality bases, reads, genes and samples
- Verify that tools and methods align with data assumptions
- Experiment with multiple pipelines and tools
- QC! QC everything at every step

🔗 Conesa, Ana, et al. "A survey of best practices for RNA-seq data analysis." *Genome biology* 17.1 (2016): 13

Thank you. Questions?

R version 3.5.2 (2018-12-20)

Platform: x86_64-pc-linux-gnu (64-bit)

OS: Ubuntu 18.04.2 LTS

Built on : 📅 14-Apr-2019 at ⏱ 21:18:55

2019 • SciLifeLab • NBIS

Hands-On tutorial

Main exercise

- 01 Check the quality of the raw reads with **FastQC**
- 02 Map the reads to the reference genome using **Star**
- 03 Assess the post-alignment quality using **QualiMap**
- 04 Count the reads overlapping with genes using **featureCounts**
- 05 Find DE genes using **edgeR** in R

Bonus exercises

- 01 Functional annotation of DE genes using **GO/Reactome/Kegg** databases
- 02 Visualisation of RNA-seq BAM files using **IGV** genome browser
- 03 RNA-Seq figures and plots using **R**
- 04 De-novo transcriptome assembly using **Trinity**

Data: </sw/courses/ngsintro/rnaseq/>

Work: </proj/g2019007/nobackup/<user>/rnaseq/>

Hands-On tutorial

- Course data directory

```
/sw/courses/ngsintro/rnaseq/
```

```
rnaseq/
+-- bonus/
|   +-- assembly/
|   +-- exon/
|   +-- funannot/
|   +-- visual/
+-- documents/
+-- main/
|   +-- 1_raw/
|   +-- 2_fastqc/
|   +-- 3_mapping/
|   +-- 4_qualimap/
|   +-- 5_dge/
|   +-- 6_multiqc/
+-- reference/
|   +-- mouse/
|   +-- mouse_chr11/
+-- scripts/
```

- Your work directory

```
/proj/g2019007/nobackup/[user]/
```

```
[user]/
rnaseq/
+-- 1_raw/
+-- 2_fastqc/
+-- 3_mapping/
+-- 4_qualimap/
+-- 5_dge/
+-- 6_multiqc/
+-- reference/
|   +-- mouse/
|   +-- mouse_chr11/
+-- scripts/
+-- funannot/
+-- assembly/
```