**Algorithms**

* Bowtie

Langmead B, Trapnell C, Pop M, Salzberg SL. “Ultrafast and memory-efficient alignment of short DNA sequences to the human genome”, Genome Biology <<http://genomebiology.com/2009/10/3/R25>>.

* Tophat

Trapnell C, Pachter L, Salzberg SL, TopHat: discovering splice junctions with RNA-Seq, Bioinformatics, 25(9):1105-1111 <http://bioinformatics.oxfordjournals.org/cgi/content/abstract/btp120>.

* Cufflinks

Trapnell C, Williams BA, Pertea G, Mortazavi AM, Kwan G, van Baren MJ, Salzberg SL, Wold B, Pachter L.Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation <<http://dx.doi.org/10.1038/nbt.1621>> Nature Biotechnology

* BWA

Li et al " Fast and accurate short read alignment with Burrows­Wheeler transform" <http://bioinformatics.oxfordjournals.org/content/25/14/1754.abstract>

**File Manipulation tools**

* Samtools - <http://samtools.sourceforge.net/>
* Picard - <http://picard.sourceforge.net/index.shtml>
* FastQC - <http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>
* HTSeq - http://www-huber.embl.de/users/anders/HTSeq/doc/overview.html

**Data Standards**

* <http://encodeproject.org/ENCODE/dataStandards.html>
* Sam format - http://samtools.sourceforge.net/SAM1.pdf
* <http://www.ebi.ac.uk/arrayexpress/>
* http://www.ebi.ac.uk/ena/

**Normalization**

Oshlack A. et al "From RNA-seq reads to differential expression results." Genome Biology

Robinson and Oshlack "A scaling normalization method for differential expression analysis of RNA-seq data." Genome Biology

<http://www.biomedcentral.com/1471-2105/12/480/abstract> - GC content normalization

<http://www.bepress.com/ucbbiostat/paper291/> - GC bias

**Differential Expression**

Tarazona et al. Differential expression in RNA-seq: A matter of depth, 2011,

*Genome research* 21 (12) p. 2213-23

< http://genome.cshlp.org/cgi/content/abstract/gr.124321.111v1>

Anders and Huber, "Differential expression analysis for sequence count data", 2010, Genome Biology, 11 (10) p. R106

<<http://genomebiology.com/2010/11/10/R106>>

Robinson et al, "edgeR: a Bioconductor package for differential expression analysis of digital gene expression data", 2010, *Bioinformatics (Oxford, England)* 26 (1) p. 139-40

< http://bioinformatics.oxfordjournals.org/content/26/1/139.long>