Introduction to bioinformatics (NGS data analysis)

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Got your sequencing data - now, what to do with it?

- File size: several Gb
- Number of lines: >1,000,000

```
@M02443:17:000000000-ABPBW:1:1101:12675:1533 1:N:0:1
TCGATAATTCTTACTTTCTCTCTGGTCTGAGCGTTTCACATCAACGACAAGCTCGA
TTCTTCCTTTTCTCTTTTTTTCTTCTCTTCCTCTTTTTTCCTTTTCTCCCTCTTCT
TTTTTTTTCTTCTT
+
8B6-@-,CFFED9CFAE@@C6;@,CFEEF9<@6FGGF9F<CC,,CB,@::8CF,6+
,,3733>>@@,,,388@,,8*,773333,3,333738,*,,,,,,76,,2,,2,,2
0*).1.))(0*)***
@M02443:17:000000000-ABPBW:1:1101:18658:1535 1:N:0:1
TCCCTAATTCTCTGTCTTCAAATTTTCCTTCTCTAAATCGTCCCTCGTTTCTACCT
TTTCTTGTTTTTTTATTTCCTCCTCTTCCTTTTTTACTTCCACCTTCTTTTCTGCC
TTTTCTTCTTTTTCT
+
-<<9-@CCEF9CE-<,,,,,;,,<C,=,6,C9,C<=C,,,;,86C,6:C,,,;<;,,
,,,,5,5:,,9++4,,,:,,,,,,,,,,38,853,5,,3,,7,,,6,,,,,7,,,,
+0,()+++)11.*)*
```

Before library preparation

What you need to know to steer your way through the analysis

- Research question
  - Identify adaptive genes
  - *De novo* genome assembly
  - Population genetic structure
  - Phylogenetic relation
- Experimental design
  - Number of individuals
  - Treatment of samples (e.g. heat stress)
- Sample collection
  - Samples degraded (e.g. stored in Formalin)
  - Tissue (reproductive, vegetative)
- What genetic sources are further available?
  - Lucky, if you have a reference genome

Library preparation

- DNA-seq, RNA-seq, Bis-Seq, Chip-Seq...
  - RNA reads (which lack introns) requires splice-aware mappers.
  - Bis-seq changes GC ratio (bisulphite converts cytosine to uracil, but leaves 5-methylcytosine unaffected)
  - Chip-Seq enriches binding-sites of DNA-associated proteins
- Pooled samples?
  - Demultiplexing
  - Remove barcodes
- Adapter sequences for trimming
- Targeted coverage

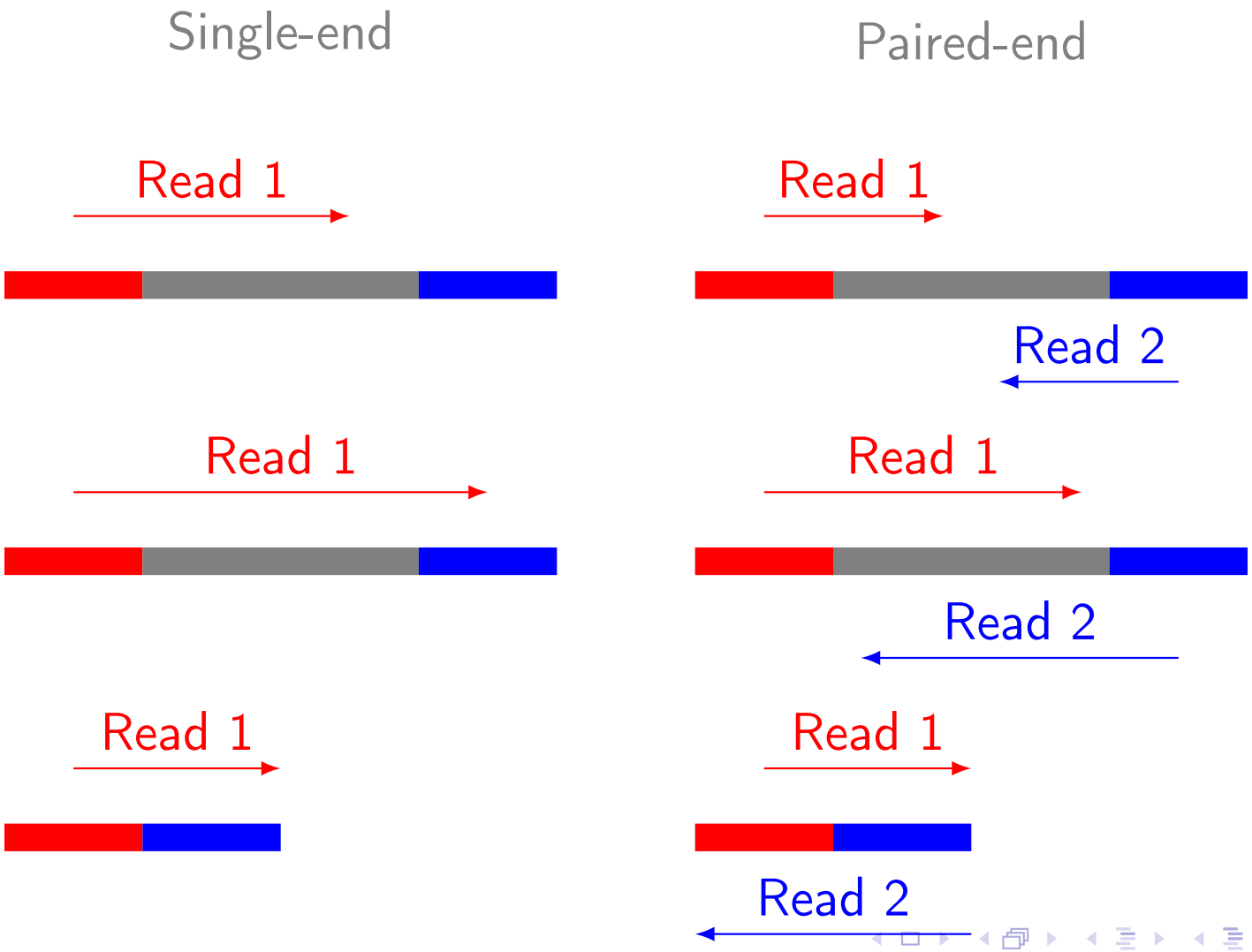
Single- or Paired end sequencing, read length

Library fragment

Adapter
Flowcell/bead binding sequences
Amplification primers
Sequencing primers
Barcodes

Adapter
Flowcell/bead binding sequences
Amplification primers
Sequencing primers
Barcodes

Single- or paired-end sequencing, read length - why does it matter



Expected read lengths and sequencing qualities for the most common sequencing platforms

Platform	Max read length	Reads/run or lane	Consideration
Illumina HiSeq 3/4000	2x300	312,500,000	
Illumina MiSeq v3	2x600	25,000,000	
Roche 454 GS FLX+/FLX	700	700,000	High error rate
Ion PGM 318	400	4,000,000	
PacBio RSII	14,000	47,000	High error rate
SoliD 5500xl W	2x100	266,666,667	Low error rate Color-space

Primary analysis

- Demultiplexing
- Adapter trimming
- Quality control

Fastq file

4 lines that contain

- sequence id
  - @, instrument name, flowcell lane, tile number, and flowcell x,y coordinates
  - barcode sequence and pair number for paired-end sequencing
- sequence
- quality scores

```
@HWI-ST141_0365:2:1101:2983:2114#TTAGGC/1
GATTTGGGGTTCAAATTAGTATCGATCAAATAGTAAATCCATTTGTTCAACTC
+
!''*((((***+))%%%++)(%%%%).1***-+*''))**55CCF>>>>>>CC
```

Trimmig: Adapter removal

Adapters disturb assembly and alignment

GATTTGGGGTTCAANNNNNNNNATTAGTATCGAT

GATTTGGGGTTCAANNNNNNNNATTAGTATCGAT

TTGGGGTTCAANNNNNNNNATTAGTATCGAT

GATTTGGGGTTCAANNNNNNNNATTAGTATCGAT

ATTTGGGGTTCAANNNNNNNNATTAGTATCGAT

GATTTGGGGTTCAANNNNNNNNATTAGTATCGAT

Demultiplexing of pooled samples (if barcoded)

AATTANNNNNNNNNNNNNNNN	File 1
AGTCGNNNNNNNNNNNNNNNN	File 2
AGTCGNNNNNNNNNNNNNNNN	File 2
GCCATNNNNNNNNNNNNNNNN	File 3
AATTANNNNNNNNNNNNNNNN	File 1
GCCATNNNNNNNNNNNNNNNN	File 3
AGTCGNNNNNNNNNNNNNNNN	File 2

Trimmig of low-quality bases

- Trim bases with a Phred quality score <20
- $Quality = -10 * log_{10} P$

Phred Score	Probability of incorrect base	Base call accuracy
10	1 in 10	90%
20	1 in 100	99%
30	1 in 1000	99.9%

Fastq file contains both sequence reads and base quality scores

Fastq file

```
@SEQ_ID
GATTTGGGGTTCAAATTAGTATCGATCAAATAGTAAATCCATTTGTTCAACTC
+
!''*((((***+))%%%++)(%%%%).1***-+*''))**55CCF>>>>>>CC
```

Fasta file

```
>SEQ_ID
GATTTGGGGTTCAAATTAGTATCGATCAAATAGTAAATCCATTTGTTCAACTC
```

Base qualities are encoded in ascii format

ASCII stands for American Standard Code for Information Interchange. An ASCII code is the numerical representation for a character.

Dec	Hx	Oct	Char	Dec	Hx	Oct	Html	Chr	Dec	Hx	Oct	Html	Chr	Dec	Hx	Oct	Html	Chr
0	0	000	NUL (null)	32	20	040		Space	64	40	100	@	@	96	60	140	`	`
1	1	001	SOH (start of heading)	33	21	041	!	!	65	41	101	A	A	97	61	141	a	a
2	2	002	STX (start of text)	34	22	042	"	"	66	42	102	B	B	98	62	142	b	b
3	3	003	ETX (end of text)	35	23	043	#	#	67	43	103	C	C	99	63	143	c	c
4	4	004	EOT (end of transmission)	36	24	044	$	$	68	44	104	D	D	100	64	144	d	d
5	5	005	ENQ (enquiry)	37	25	045	%	%	69	45	105	E	E	101	65	145	e	e
6	6	006	ACK (acknowledge)	38	26	046	&	&	70	46	106	F	F	102	66	146	f	f
7	7	007	BEL (bell)	39	27	047	'	'	71	47	107	G	G	103	67	147	g	g
8	8	010	BS (backspace)	40	28	050	(	(	72	48	110	H	H	104	68	150	h	h
9	9	011	TAB (horizontal tab)	41	29	051	)	)	73	49	111	I	I	105	69	151	i	i
10	A	012	LF (NL line feed, new line)	42	2A	052	*	*	74	4A	112	J	J	106	6A	152	j	j
11	B	013	VT (vertical tab)	43	2B	053	+	+	75	4B	113	K	K	107	6B	153	k	k
12	C	014	FF (NP form feed, new page)	44	2C	054	,	,	76	4C	114	L	L	108	6C	154	l	l
13	D	015	CR (carriage return)	45	2D	055	-	-	77	4D	115	M	M	109	6D	155	m	m
14	E	016	SO (shift out)	46	2E	056	.	.	78	4E	116	N	N	110	6E	156	n	n
15	F	017	SI (shift in)	47	2F	057	/	/	79	4F	117	O	O	111	6F	157	o	o
16	10	020	DLE (data link escape)	48	30	060	0	0	80	50	120	P	P	112	70	160	p	p
17	11	021	DC1 (device control 1)	49	31	061	1	1	81	51	121	Q	Q	113	71	161	q	q
18	12	022	DC2 (device control 2)	50	32	062	2	2	82	52	122	R	R	114	72	162	r	r
19	13	023	DC3 (device control 3)	51	33	063	3	3	83	53	123	S	S	115	73	163	s	s
20	14	024	DC4 (device control 4)	52	34	064	4	4	84	54	124	T	T	116	74	164	t	t
21	15	025	NAK (negative acknowledge)	53	35	065	5	5	85	55	125	U	U	117	75	165	u	u
22	16	026	SYN (synchronous idle)	54	36	066	6	6	86	56	126	V	V	118	76	166	v	v
23	17	027	ETB (end of trans. block)	55	37	067	7	7	87	57	127	W	W	119	77	167	w	w
24	18	030	CAN (cancel)	56	38	070	8	8	88	58	130	X	X	120	78	170	x	x
25	19	031	EM (end of medium)	57	39	071	9	9	89	59	131	Y	Y	121	79	171	y	y
26	1A	032	SUB (substitute)	58	3A	072	:	:	90	5A	132	Z	Z	122	7A	172	z	z
27	1B	033	ESC (escape)	59	3B	073	;	;	91	5B	133	[	[	123	7B	173	{	{
28	1C	034	FS (file separator)	60	3C	074	<	<	92	5C	134	\	\	124	7C	174			|
29	1D	035	GS (group separator)	61	3D	075	=	=	93	5D	135	]	]	125	7D	175	}	}
30	1E	036	RS (record separator)	62	3E	076	>	>	94	5E	136	^	^	126	7E	176	~	~
31	1F	037	US (unit separator)	63	3F	077	?	?	95	5F	137	_	_	127	7F	177	&#127;	DEL

Source: www.LookupTables.com

ASCII encodings of sequencing platforms

```
 SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS.....................................................
 .........................XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX.....................
 ............................IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII.....................
 ..............................JJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJ.....................
 LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL.....................................................
 !"#$%&'()*+,-./0123456789:;<=>?@ABCDEFGHIJKLMNOPQRSTUVWXYZ[\]^_`abcdefghijklmnopqrstuvwxyz{|}~
 |                         |    |       |                              |                     |
33                        59   64      73                             104                   126
 0........................26...31.......40
                          -5....0........9.............................40
                               0........9.............................40
                                  3.....9.............................40
 0.2......................26...31.........41

S - Sanger        Phred+33,  raw reads typically (0, 40)
X - Solexa        Solexa+64, raw reads typically (-5, 40)
I - Illumina 1.3+ Phred+64,  raw reads typically (0, 40)
J - Illumina 1.5+ Phred+64,  raw reads typically (3, 40)
    with 0=unused, 1=unused, 2=Read Segment Quality Control Indicator (bold)
    (Note: See discussion above).
L - Illumina 1.8+ Phred+33,  raw reads typically (0, 41)
```

Figure : Quality score encodings

Quality control tool: FastQC

Informs on:

- Base quality
- Duplication
- Overrepresentation of sequences
  - contamination?
  - adapters?
- GC content (should be around 50%, in Bis-Seq lower)

Quality before trimming

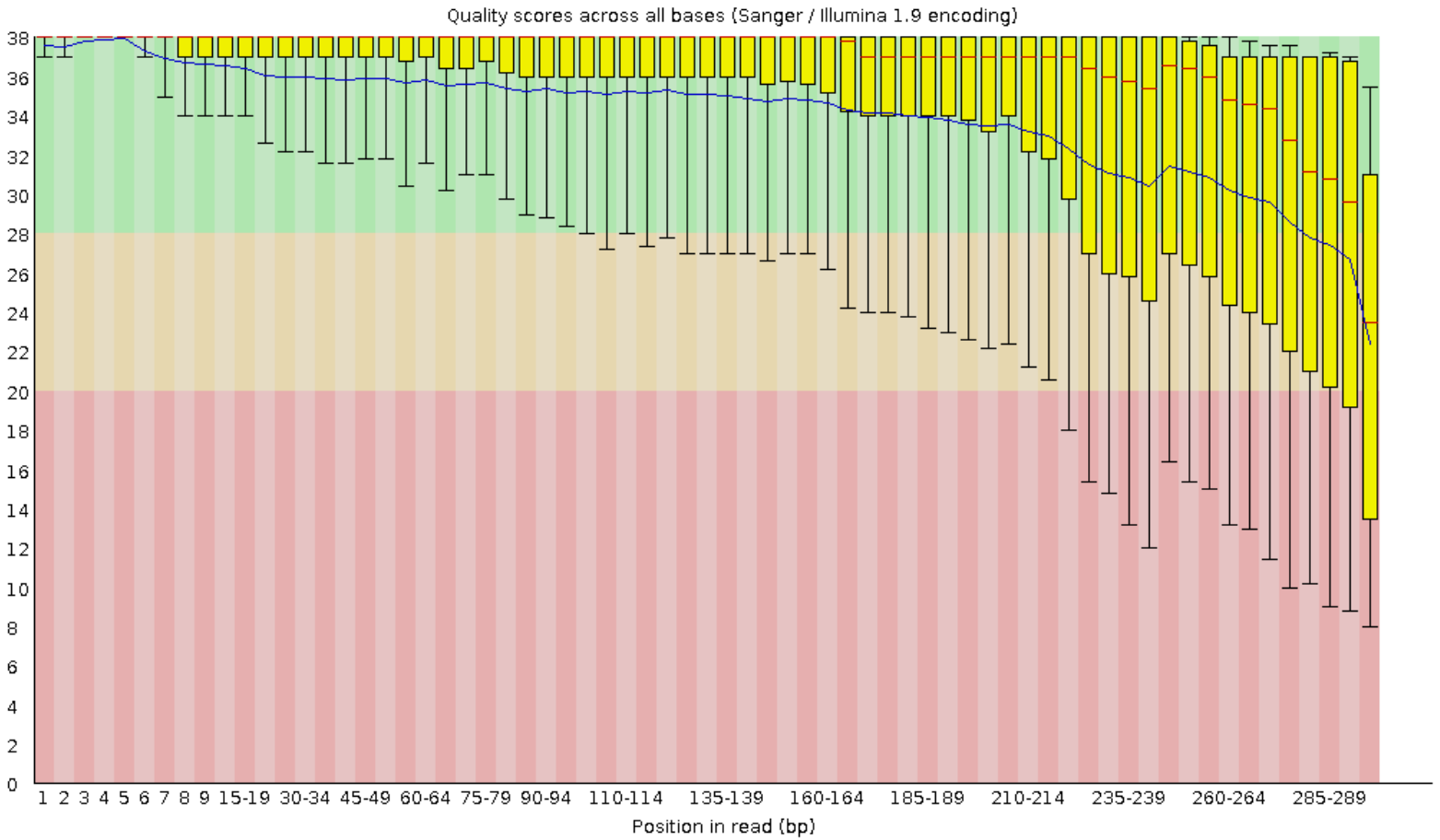


Figure : Base-quality generally decreases with increasing sequencing length

Quality after trimming

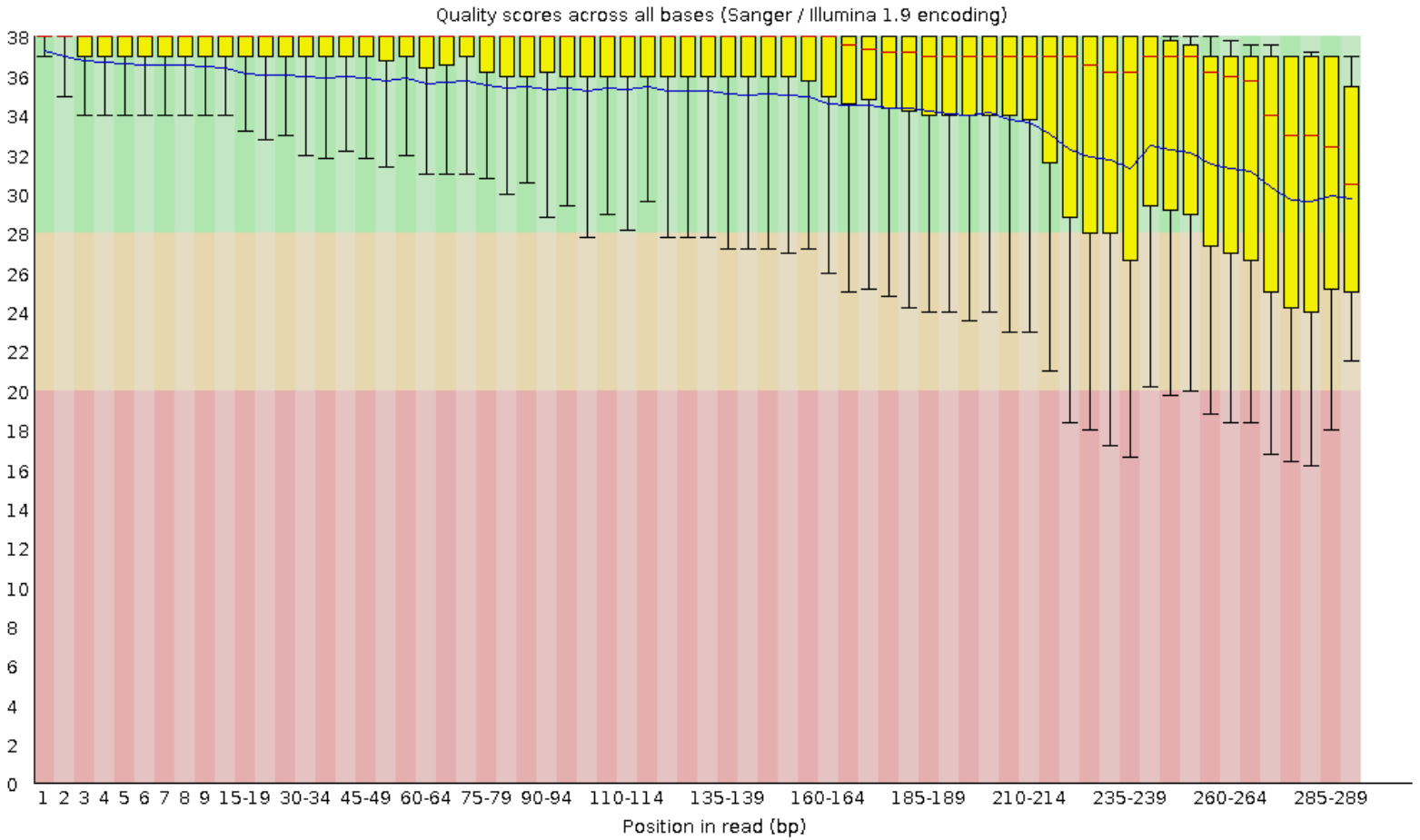


Figure : Quality after trimming

Sequence bias in first few bases of illumina RNAseq

Due to 'random' hexamer primers for reverse transcription

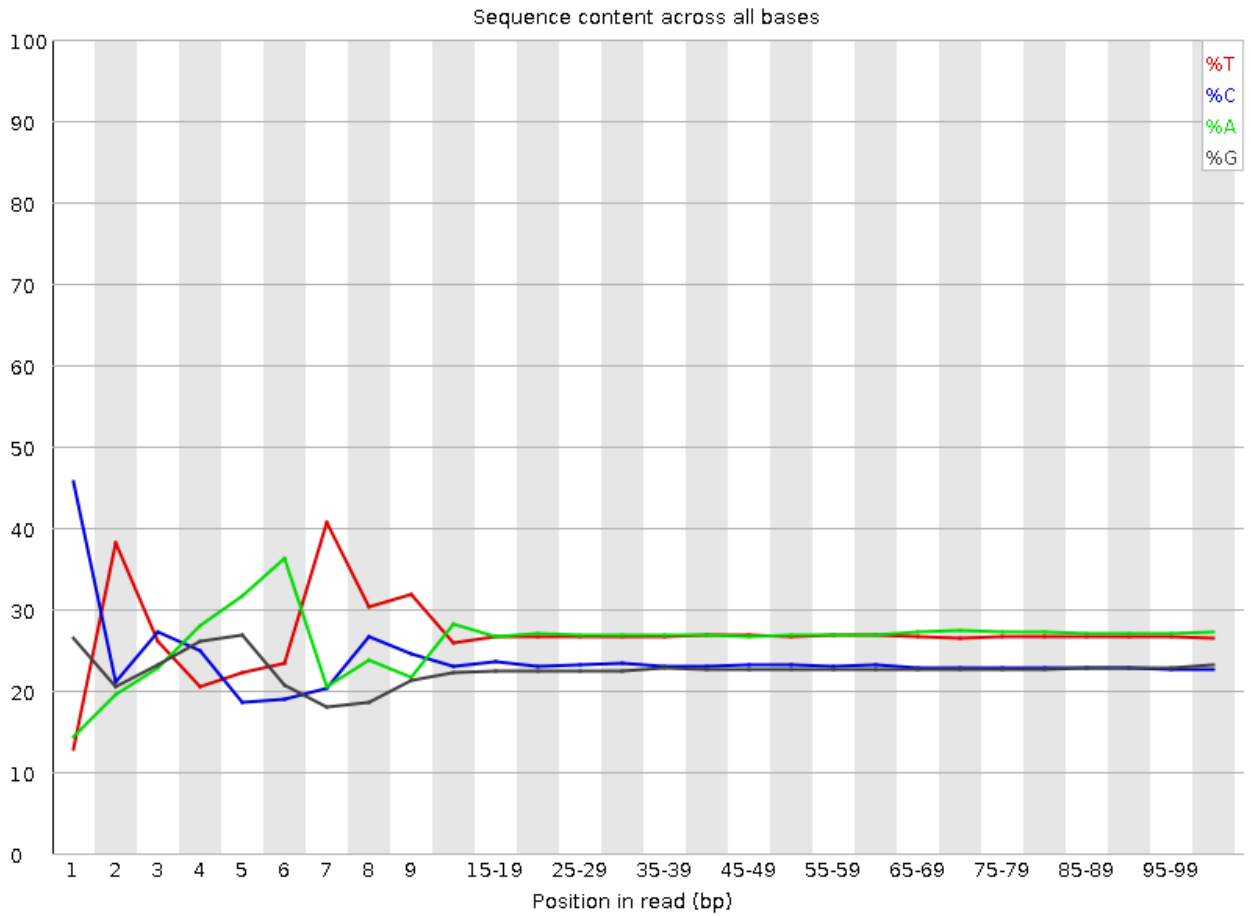
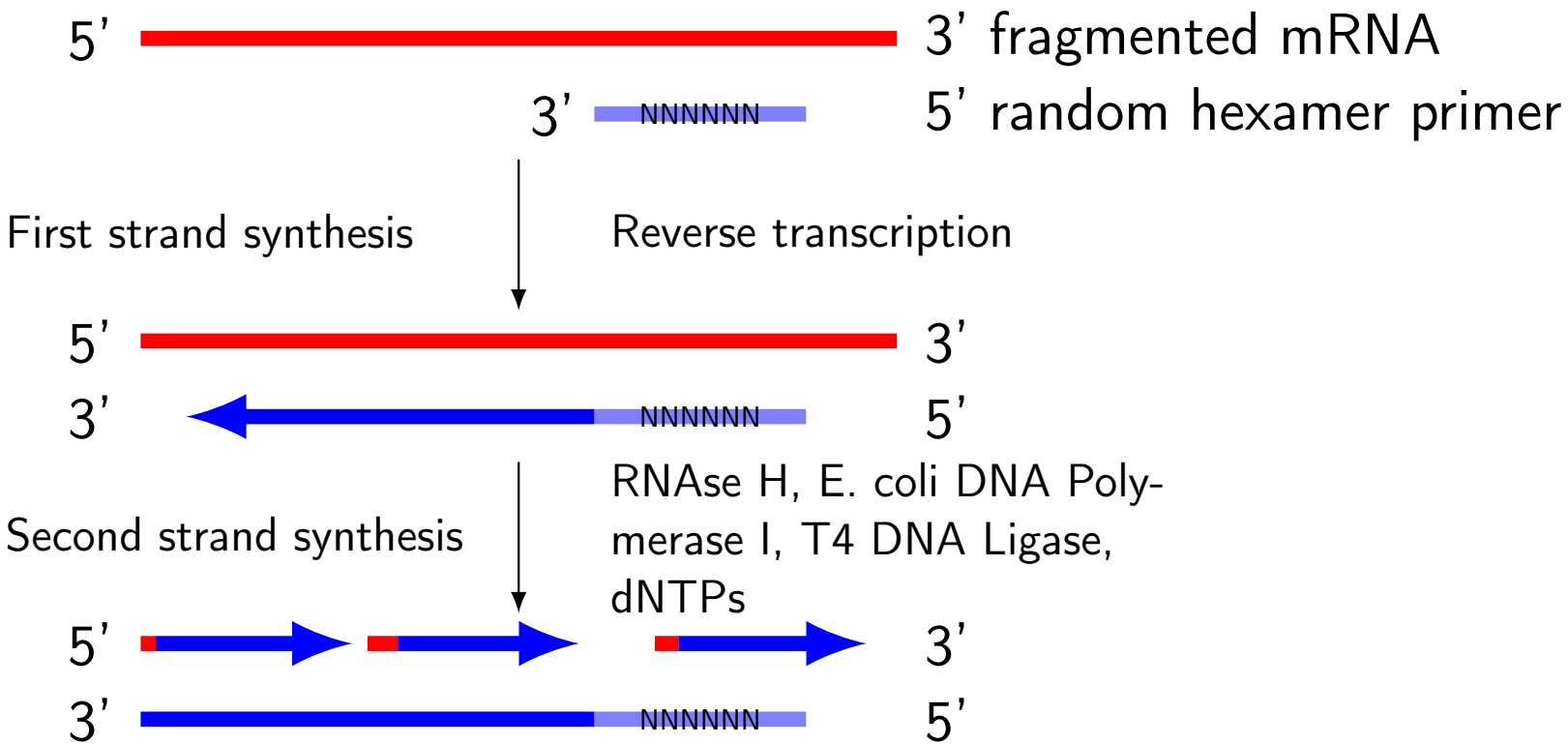


Figure : Per base sequence content (FastQC output)

(Hansen et al., 2010)

Hexamer primers for cDNA synthesis cause sequence bias



PCR Duplicates

Duplicates are generally removed in quantitative analyses (e.g. RNA-seq)

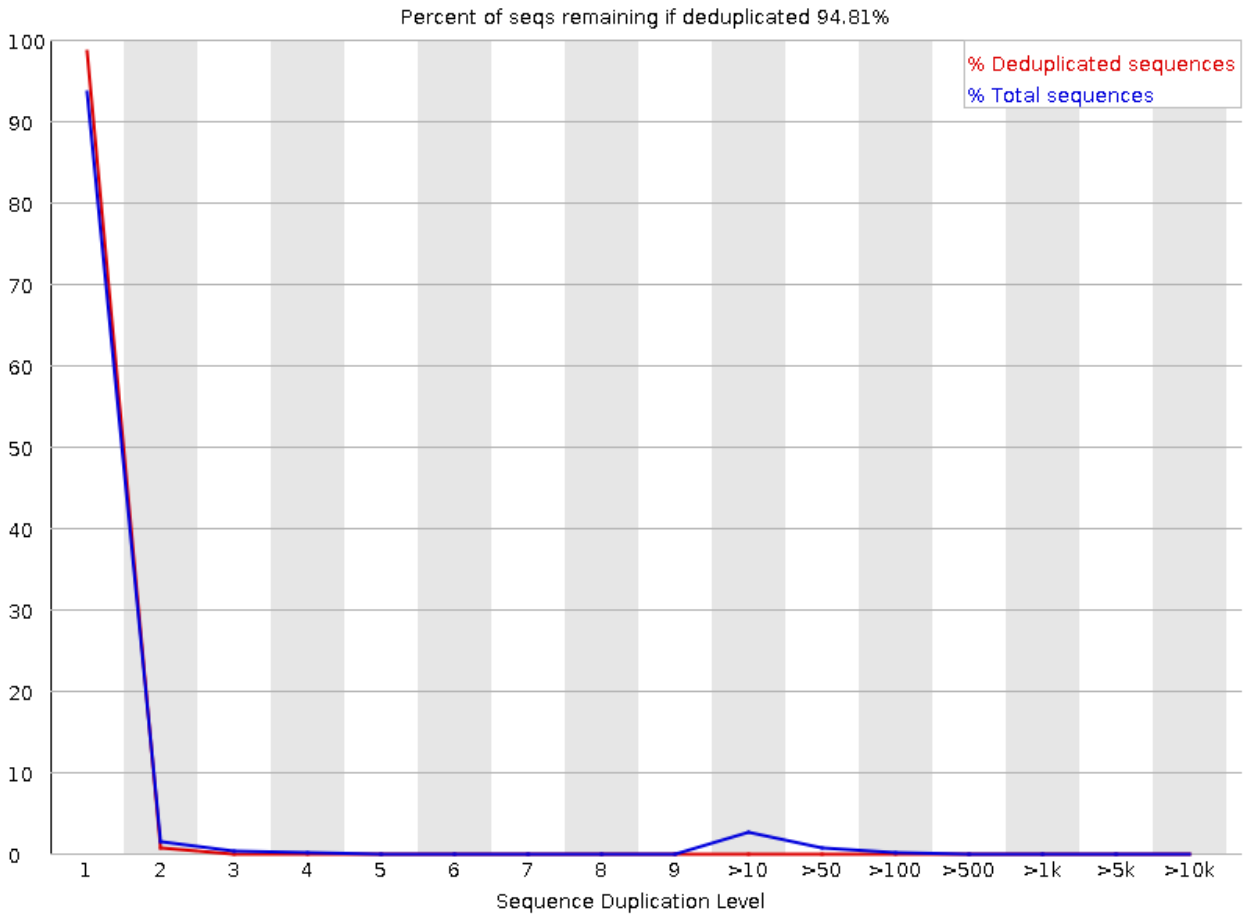


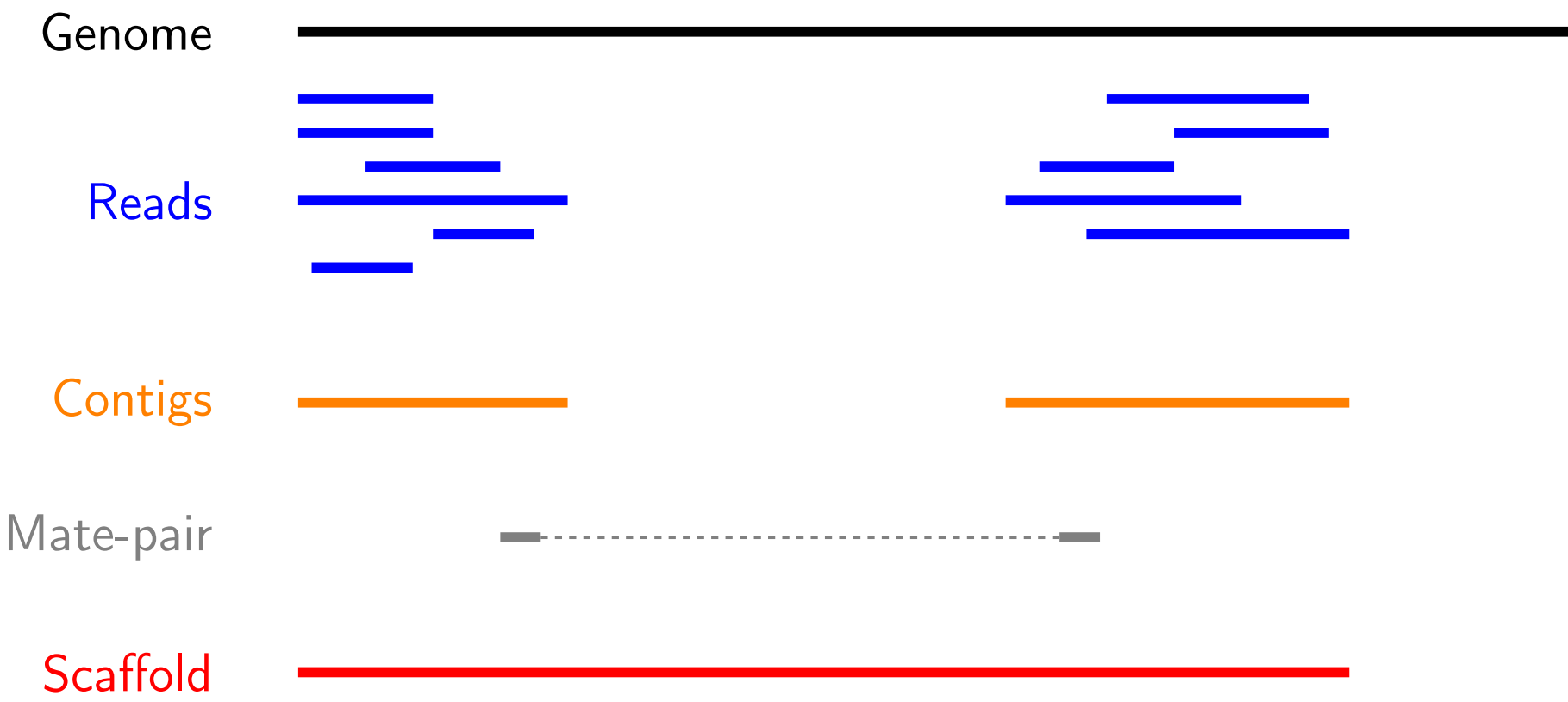
Figure : Duplication levels (FastQC output)

De Novo assembly

Task: Look for overlapping regions and create contigs (contiguous sequences)

- Genome assembly
  - SOAP de NOVO
  - Velvet
- MIRA
- Transcriptome assembly
  - Review: Martin and Wang (2011)
  - Trinity
  - MIRA

De Novo assembly: Step by step



De NOVO assembly: The N50 metric

N50 is a single measure of the contig length size distribution in an assembly

- Sort contigs in descending length order
- Size of contig above which the assembly contains at least 50% of the total length of all contigs

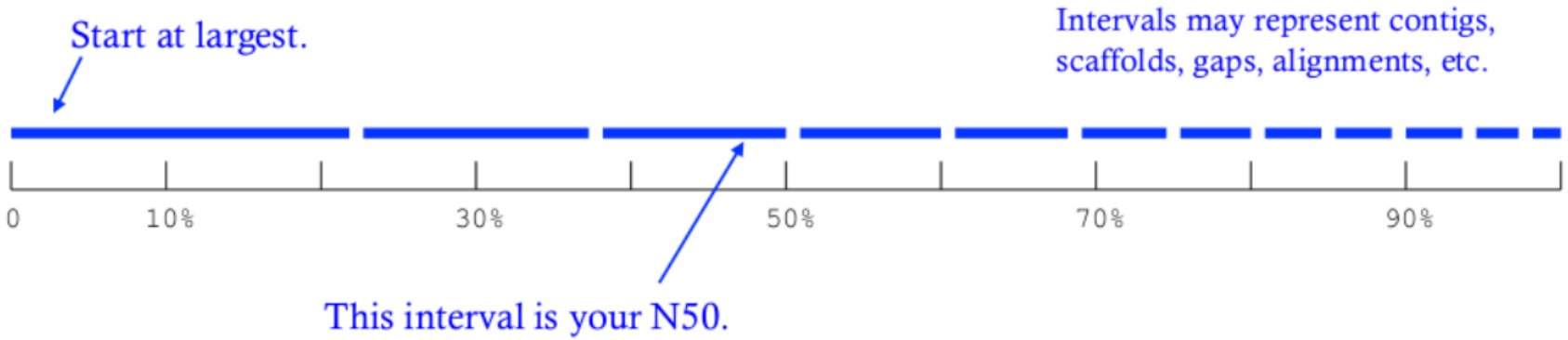


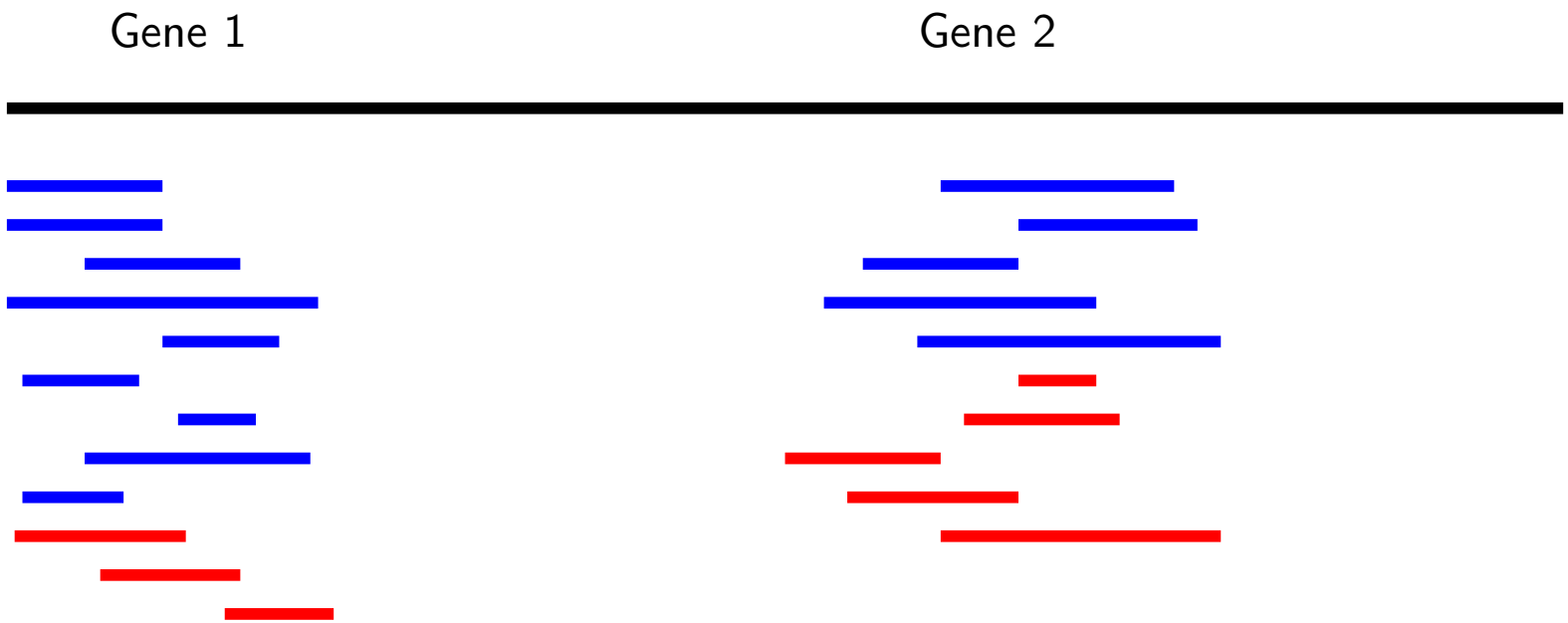
Figure : From Kane, N.C.

Mapping against reference genome/transcriptome

- Main purposes:
  - Identify variants (SNPs, InDels)

Mapping against reference genome/transcriptome

- Main purposes:
  - Quantify gene expression



Mapping: Global versus local alignment

- Global alignment (e.g. BWA, Bowtie2)
  - Needleman-Wunsch algorithm
  - aligns sequences in their full length
  - typically used for multiple sequence alignment when sequences are similar

Figure : Global vs local alignment from rosalind.info

- Local alignemt
  - Smith-Waterman algorithm
  - clipping of terminal unmatched bases
  - Only aligned bases contribute to the alignment's score
  - used to target smaller portions of genes with high similarity

Splice-aware alignment of RNAseq reads

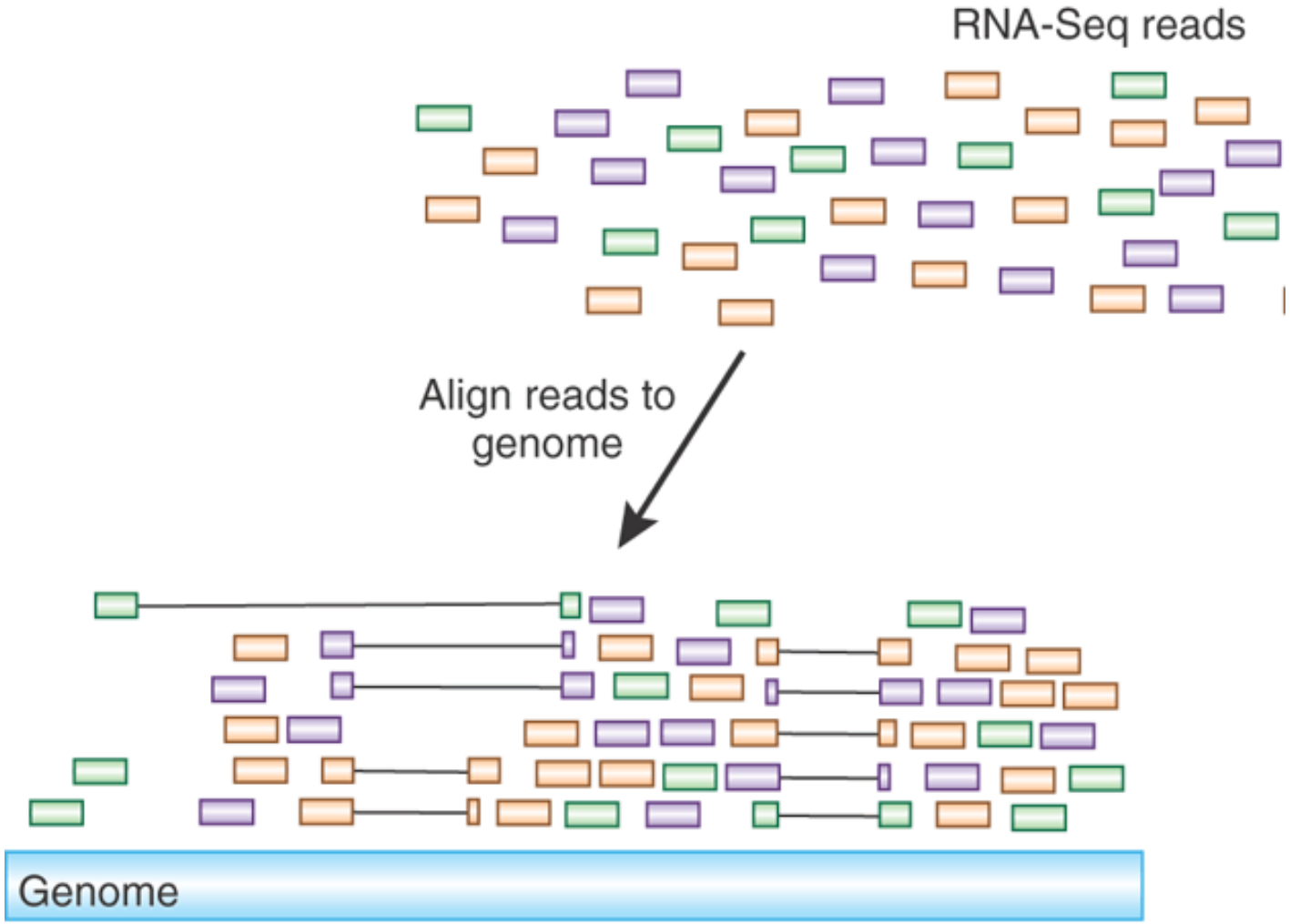


Figure : Adapted from Haas and Zody (2010)

Mapping: SAM/BAM files example

Output format of most alignment programs

- Header lines preceded by `@`
- One tab-delimited line per read

```
@HD    VN:1.0
@SQ    SN:chr20 LN:62435964
@RG    ID:L1 PU:SC_1_10 LB:SC_1 SM:NA12891
@RG    ID:L2 PU:SC_2_12 LB:SC_2 SM:NA12891
read_28833_29006_6945 99  chr20 28833 20 10M1D25M = 28993 195 \
       AGCTTAGCTAGCTACCTATATCTTGGTCTTGGCCG <<<<<<<<<<<<<<<<<<<<:<9/,&,22;;<<< \
       NM:i:1 RG:Z:L1
read_28701_28881_323b 147 chr20 28834 30 35M      = 28701 -168 \
       ACCTATATCTTGGCCTTGGCCGATGCGGCCTTGCA <<<<<;<<<<7;:<<<6;<<<<<<<<<<<7<<<< \
       MF:i:18 RG:Z:L2
```

Figure : Example from `http://samtools.sourceforge.net/SAM1.pdf`

- SAM files are large
- BAM: Compressed binary versions, not human-readable

Mapping: Mandatory fields in SAM files

Col	Field	Type	Regexp/Range	Brief description
1	QNAME	String	`[!-?A-~]{1,255}`	Query template NAME
2	FLAG	Int	`[0,2^16-1]`	bitwise FLAG
3	RNAME	String	`\*|[!-()+-<>-~][!-~]*`	Reference sequence NAME
4	POS	Int	`[0,2^31-1]`	1-based leftmost mapping POSition
5	MAPQ	Int	`[0,2^8-1]`	MAPping Quality
6	CIGAR	String	`\*|([0-9]+[MIDNSHPX=])+`	CIGAR string
7	RNEXT	String	`\*|=|[!-()+-<>-~][!-~]*`	Ref. name of the mate/next read
8	PNEXT	Int	`[0,2^31-1]`	Position of the mate/next read
9	TLEN	Int	`[-2^31+1,2^31-1]`	observed Template LENgth
10	SEQ	String	`\*|[A-Za-z=.]+`	segment SEQuence
11	QUAL	String	`[!-~]+`	ASCII of Phred-scaled base QUALity+33

Explanation of the flag field (click here: Link1, Link2)

Mapping: CIGAR string in SAM files

Op	BAM	Description
M	0	alignment match (can be a sequence match or mismatch)
I	1	insertion to the reference
D	2	deletion from the reference
N	3	skipped region from the reference
S	4	soft clipping (clipped sequences present in SEQ)
H	5	hard clipping (clipped sequences NOT present in SEQ)
P	6	padding (silent deletion from padded reference)
=	7	sequence match
X	8	sequence mismatch

Variant calling

Consistent mismatches in the alignment indicate:

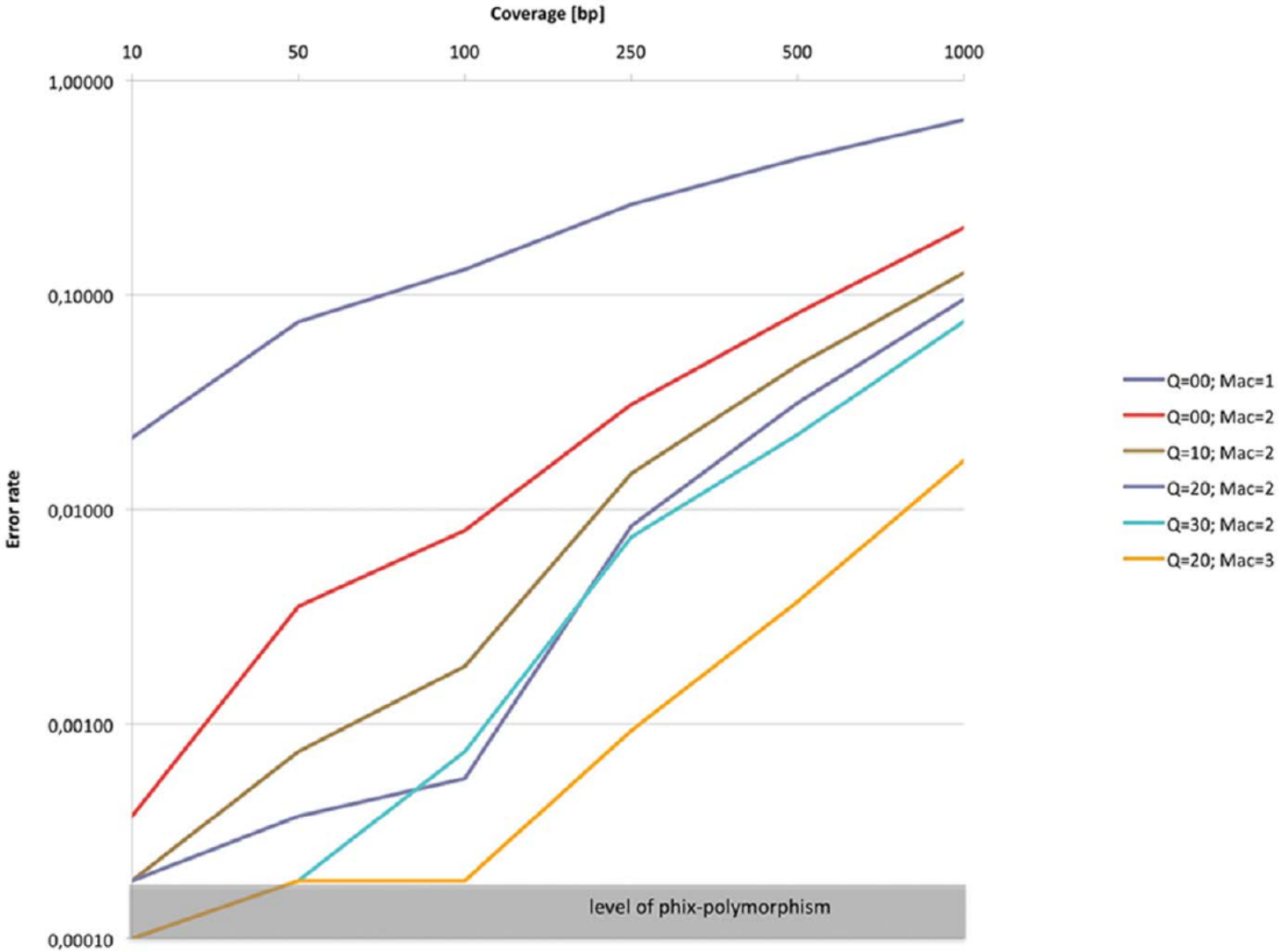
- Single Nucleotide Polymorphisms (SNPs)
- Insertions/Deletions (InDels)

Difficulty in discriminating sequencing errors from real SNPS

- Minimum coverage of 50 recommended (Schlötterer et al., 2014)

Variant Calling

Minimum count threshold decreases error rate

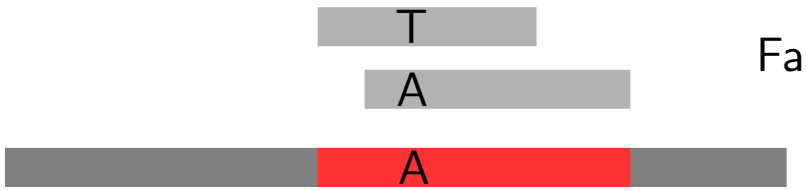


(Kofler et al., 2011)

Variant calling: Copy number variations

Sequenced specimen (2 copies)

Reference sequence (1 copy)



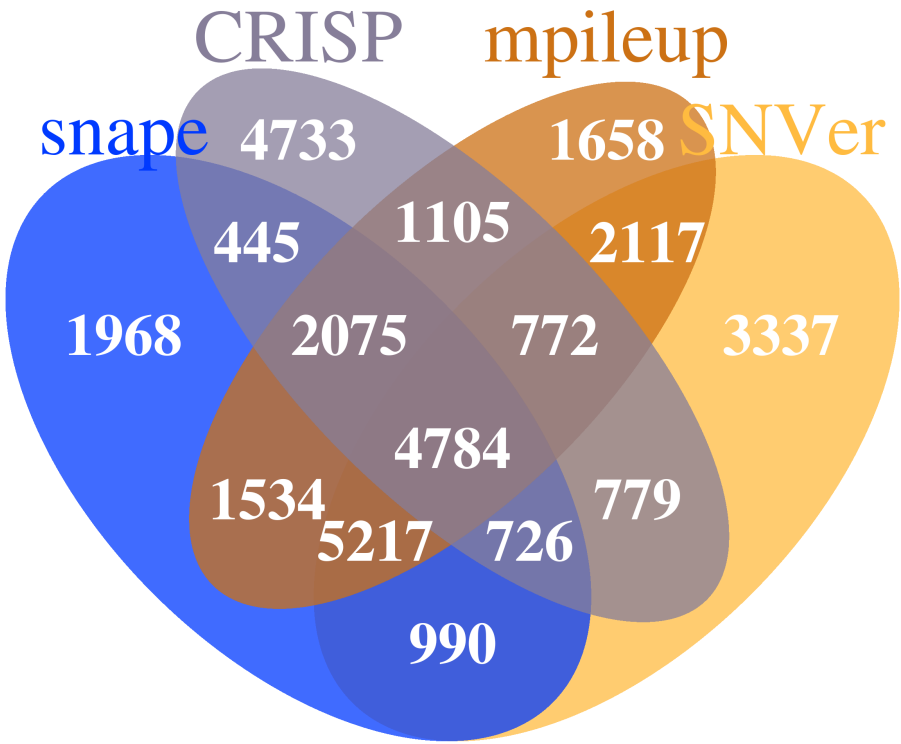
False positive SNP

Based on Kofler, R. (link)

Remove reads of excessive coverage

Identified SNPs vary between programs/algorithms

Venn diagram of the number of SNPs (coverage >400) called with four programs from the same alignment file (ddRAD tags mapped against the genome of Guppy).



VCF file format

Variant call format

- described in `http://www.1000genomes.org/node/101`
- informs on location and quality of each SNP

VCF file information

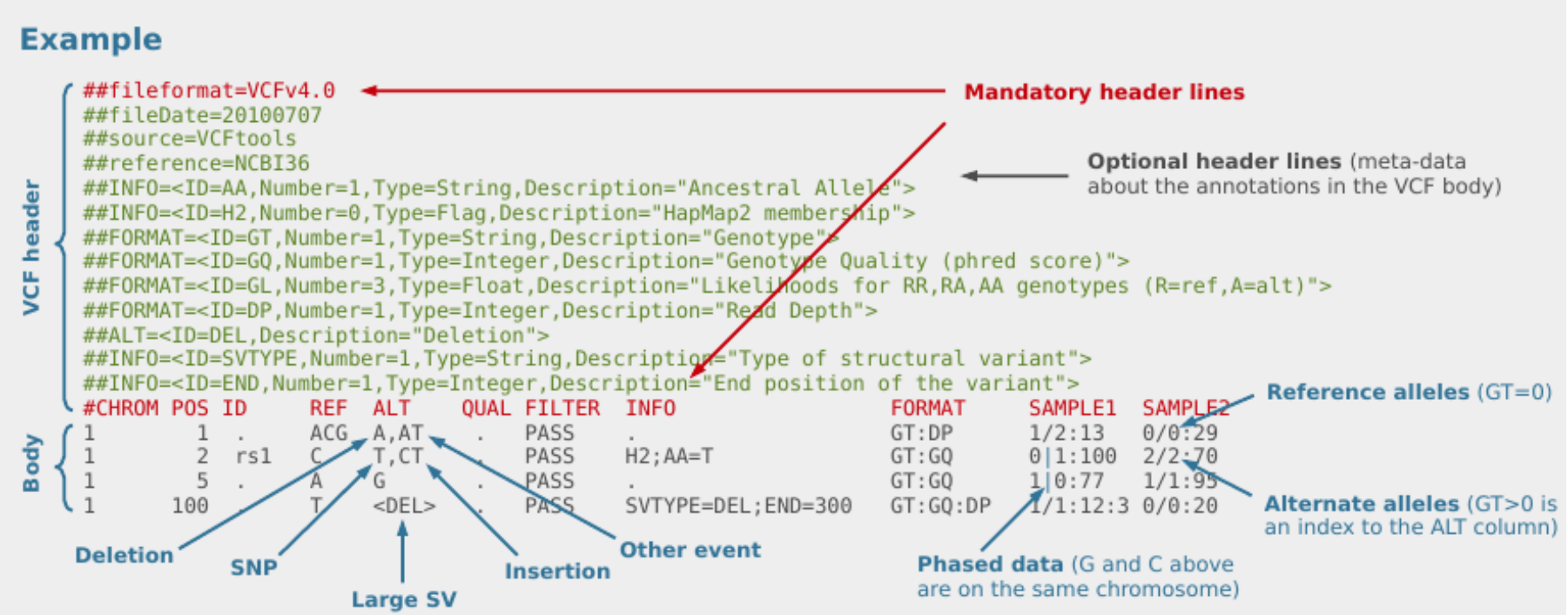


Figure : VCF file info from `http://vcftools.sourceforge.net/VCF-poster.pdf`

Phased alleles are on the same chromosome strand

Differential gene expression analysis

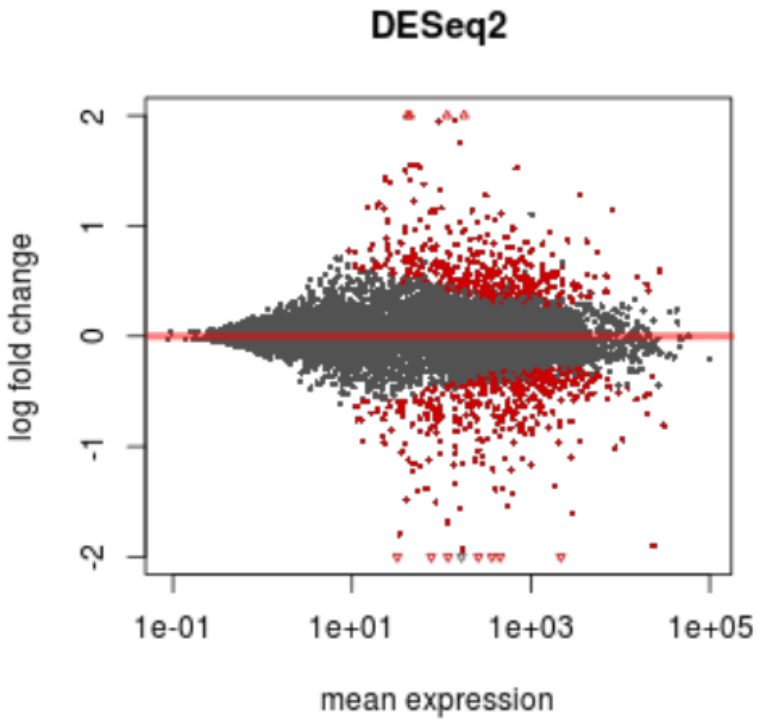


Figure : Log2 fold-change of expression over the mean of counts normalized by size factors. Differentially expressed genes (p<0.1) are red.

From the DESeq2 R package documentation

Clustering

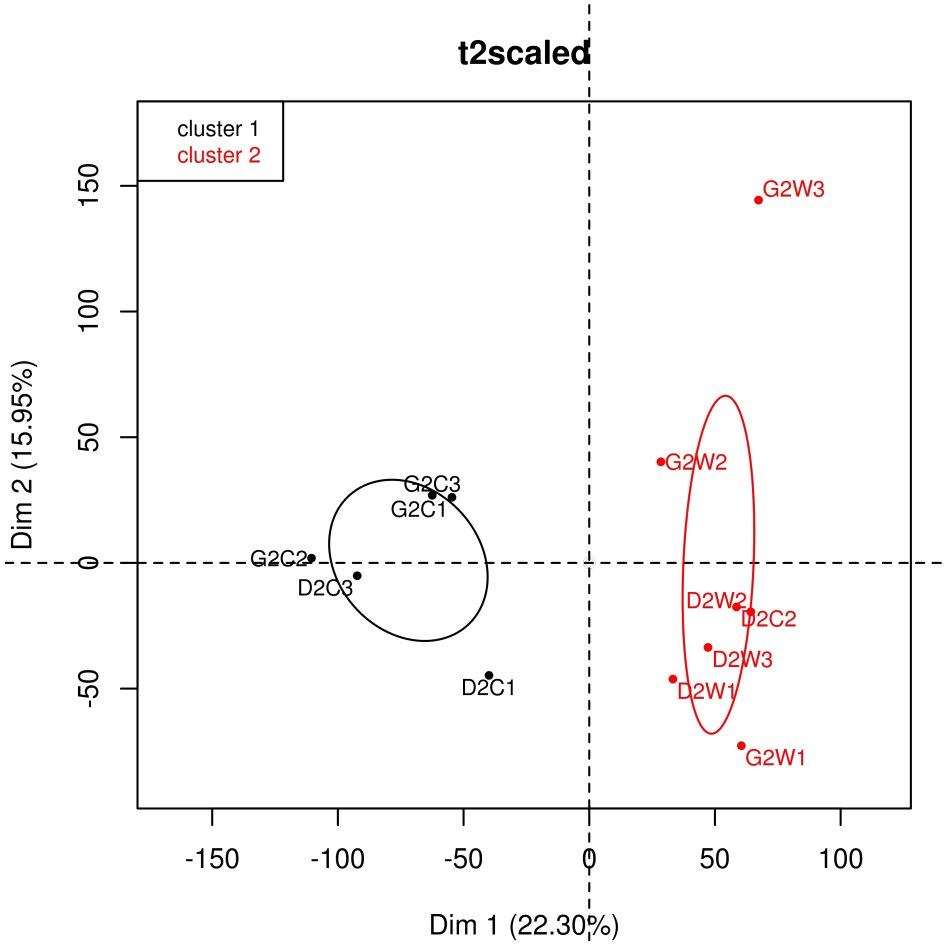


Figure : Multivariate grouping of stressed (W) and control (C) seagrass samples. Most variation is explained by the first principle component

Visualizing differential expression

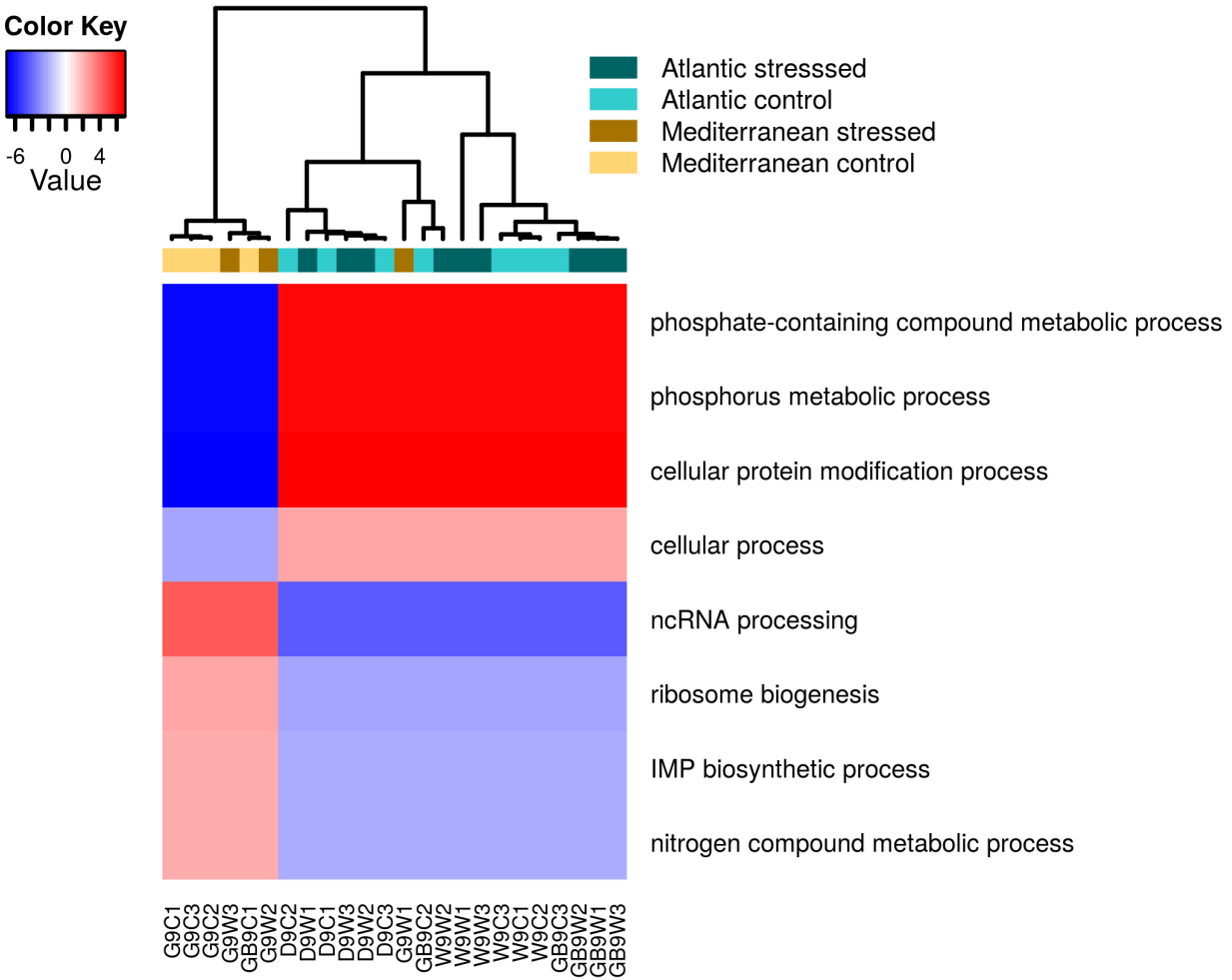
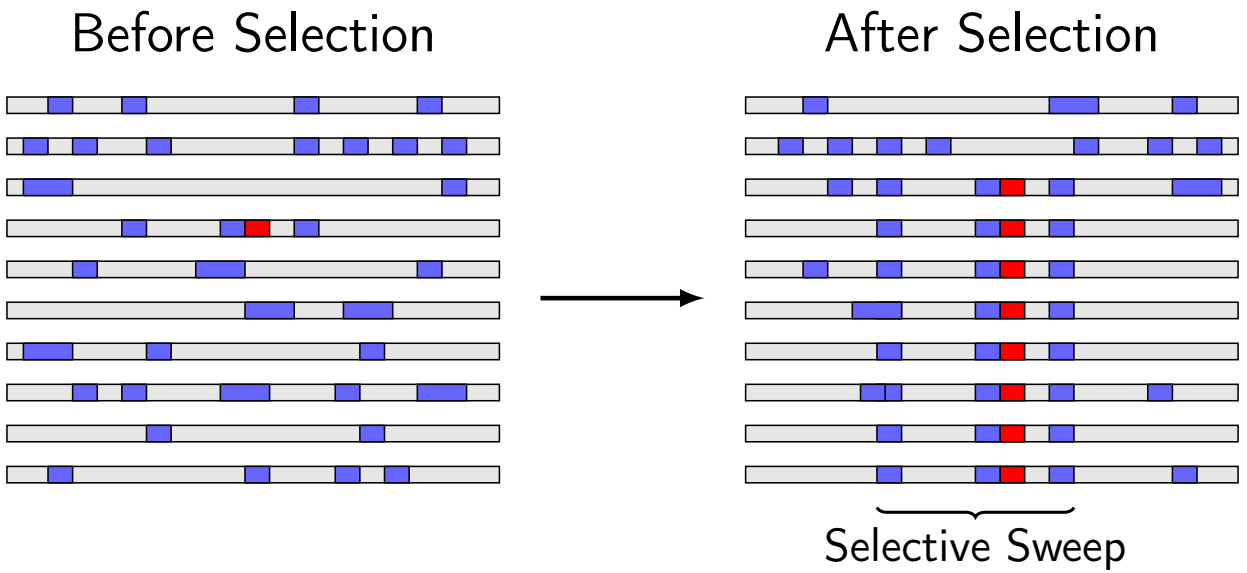


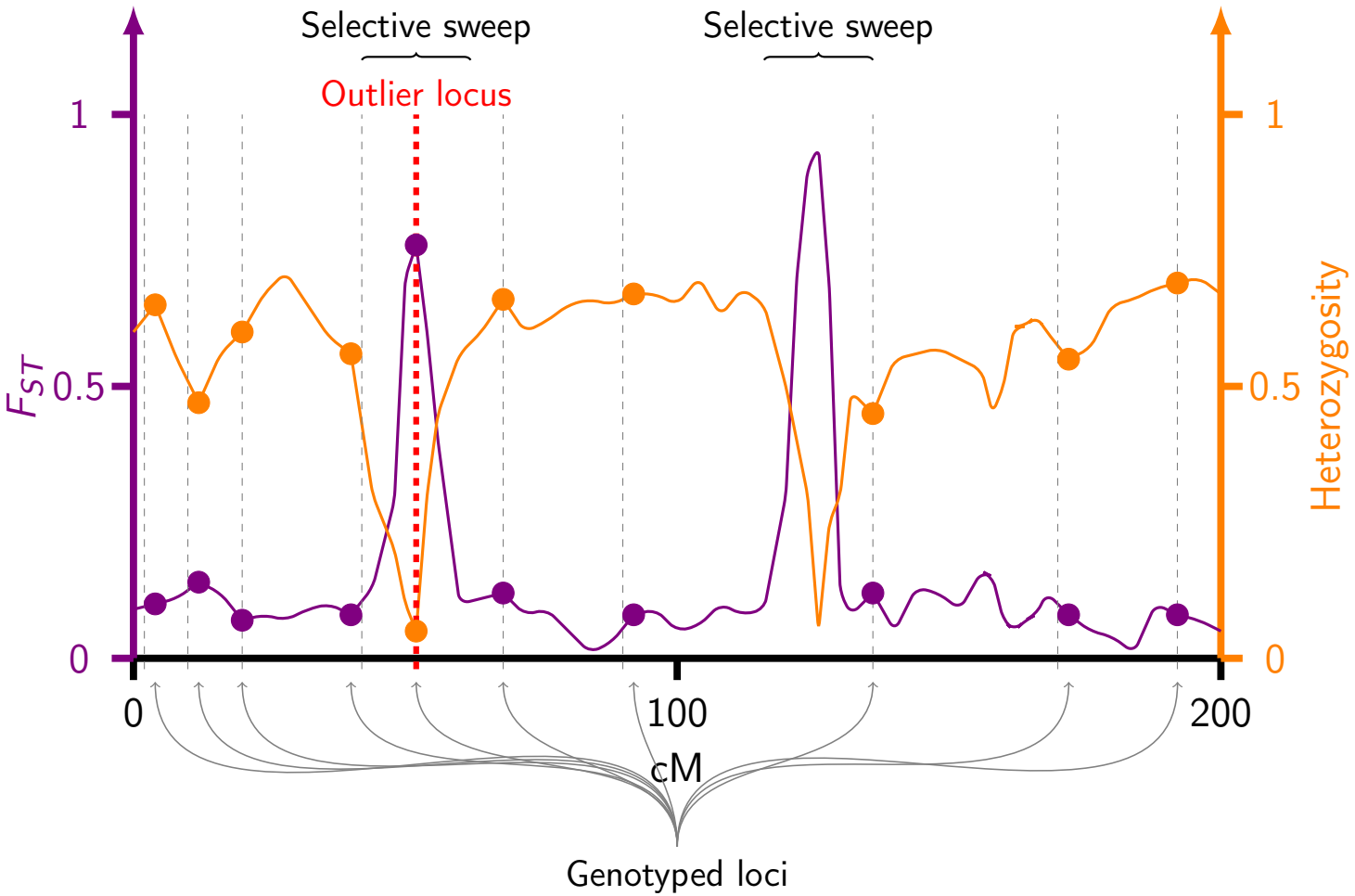
Figure : Heatmap of functions that were differentially expressed between Atlantic and Mediterranean seagrass samples.

Outlier analysis



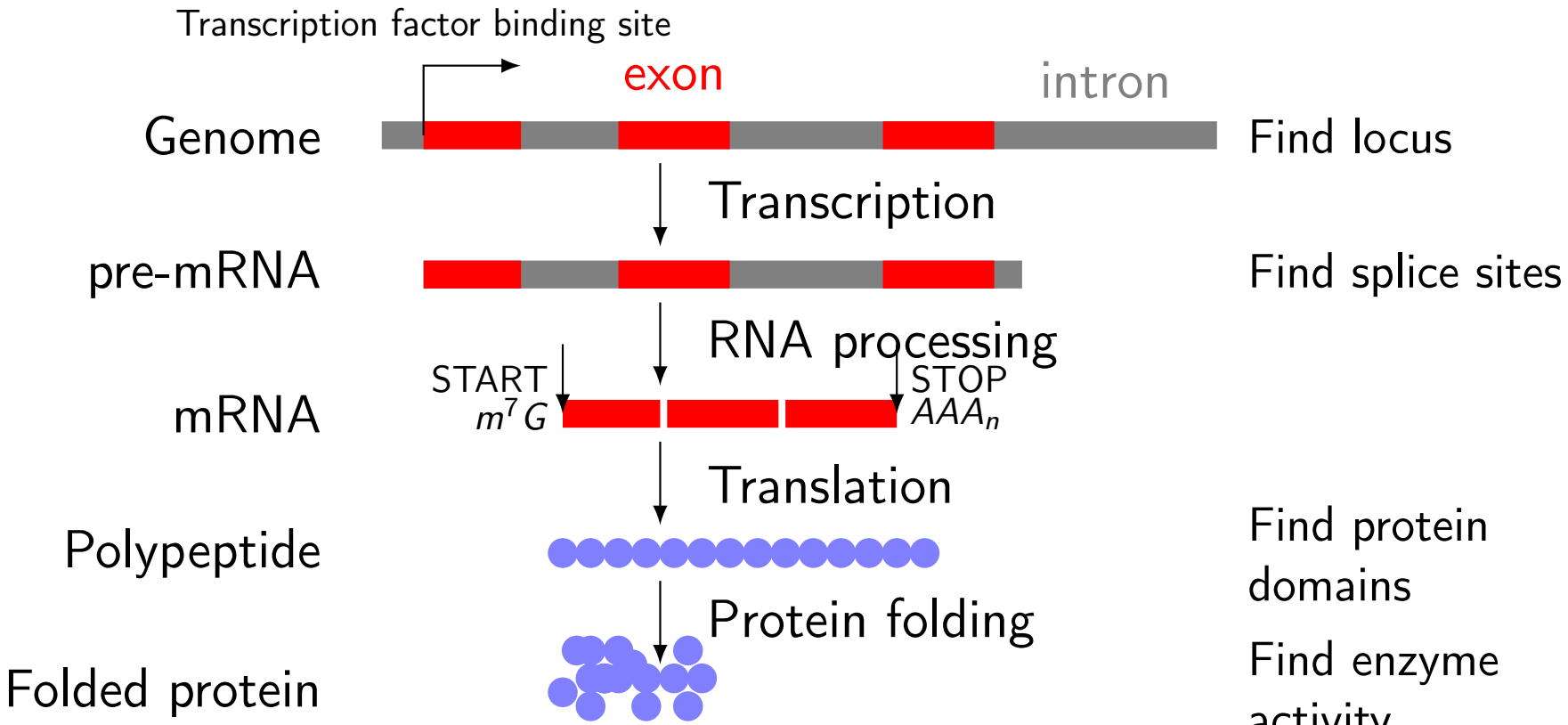
Based on Vitti et al. (2012)

Outlier detection



Eukaryote genome annotation

Identify the strcuture and functional role



Gene ontologies

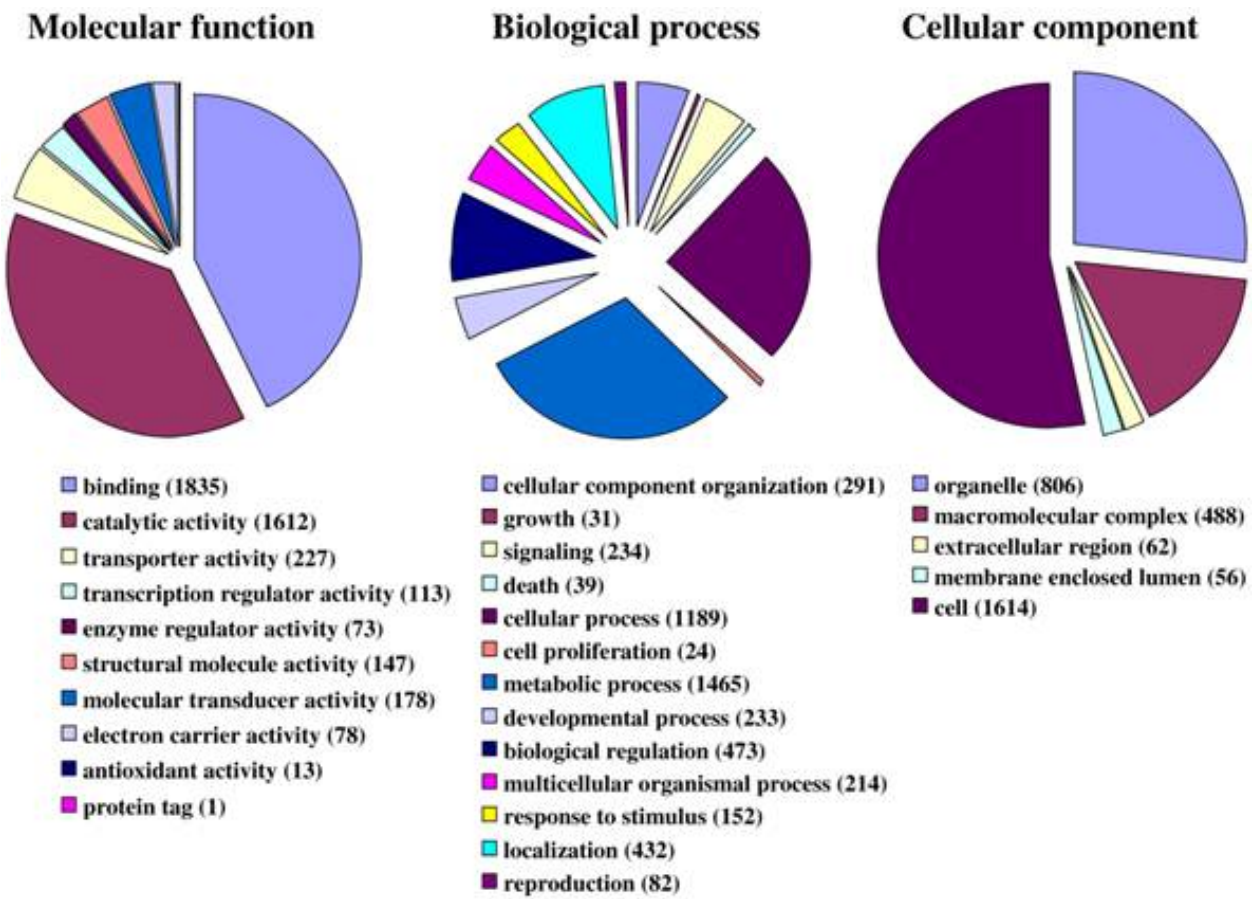


Figure : GO terms of unigenes in a moth genome

(Jacquin-Joly et al., 2012)

Functional enrichment of GO terms

	GO.ID	Term	Annotated	Significant	Expected	Rank in classicFisher	classicFisher
1	GO:0007067	mitotic nuclear division	175	17	25.97	932	0.9988
2	GO:0051301	cell division	162	18	24.04	887	0.9819
3	GO:0045931	positive regulation of mitotic cell cycl...	44	5	6.53	657	0.8222
4	GO:0000910	cytokinesis	15	2	2.23	534	0.6821
5	GO:0002757	immune response-activating signal transd...	14	7	2.08	32	0.0016
6	GO:0033077	T cell differentiation in thymus	10	6	1.48	21	0.0010
7	GO:0042108	positive regulation of cytokine biosynth...	18	6	2.67	111	0.0353
8	GO:0090068	positive regulation of cell cycle proces...	37	3	5.49	809	0.9393
9	GO:0048639	positive regulation of developmental gro...	12	3	1.78	298	0.2565
10	GO:0051129	negative regulation of cellular componen...	52	5	7.72	777	0.9215

Figure : Test for enrichment of GO terms with Fisher's exact test in the R package 'topGO'

(Alexa and Rahnenfuhrer, 2010)

Cloud of GO term enrichments

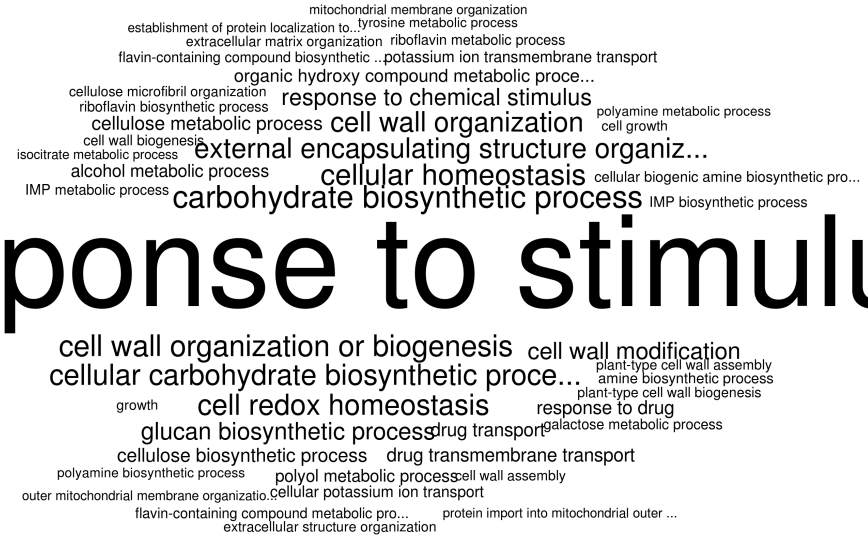


Figure : Term cloud of heat-responsive functions in seagrass

References I

- Alexa, A and J Rahnenfuhrer (2010). *topGO: topGO: Enrichment analysis for Gene Ontology*. R package version 2.16.0.
- Haas, BJ and MC Zody (2010). "Advancing RNA-seq analysis". In: *Nature biotechnology* 28.5, pp. 421–423.
- Hansen, KD, SE Brenner, and S Dudoit (2010). "Biases in Illumina transcriptome sequencing caused by random hexamer priming". In: *Nucleic acids research* 38.12, e131–e131.
- Jacquin-Joly, E, F Legeai, N Montagné, C Monsempes, MC François, J Poulain, et al. (2012). "Candidate chemosensory genes in female antennae of the noctuid moth Spodoptera littoralis". In: *International journal of biological sciences* 8.7, p. 1036.

References II


Kofler, R, P Orozco-terWengel, N De Maio, RV Pandey, V Nolte, A Futschik, et al. (2011). "PoPoolation: A Toolbox for Population Genetic Analysis of Next Generation Sequencing Data from Pooled Individuals". In: *PLoS ONE* 6.1, e15925.


Martin, J and Z Wang (2011). "Next-generation transcriptome assembly". In: *Nature Reviews Genetics*.


Schlötterer, C, R Tobler, R Kofler, and V Nolte (2014). "Sequencing pools of individuals [mdash] mining genome-wide polymorphism data without big funding". In: *Nature Reviews Genetics*.


Vitti, JJ, MK Cho, SA Tishkoff, and PC Sabeti (2012). "Human evolutionary genomics: ethical and interpretive issues". In: *Trends in Genetics* 28.3, pp. 137 –145.