

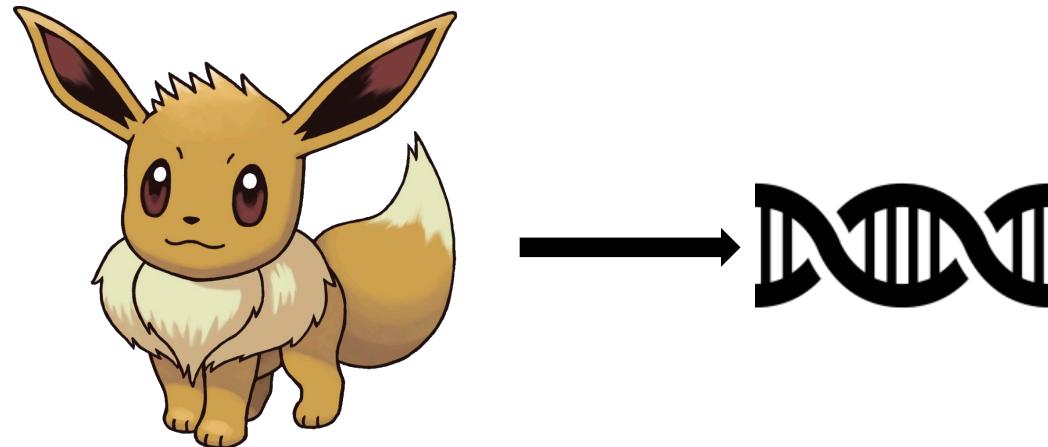
Modern Sequencing and File Formats

Mike Campbell, CSHL

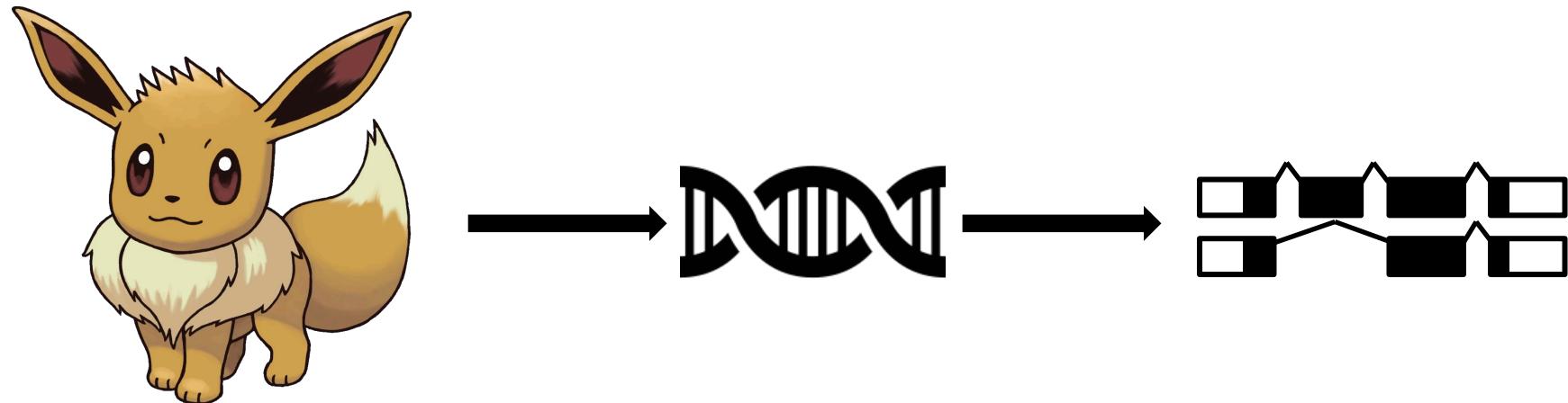
Genome Project Overview



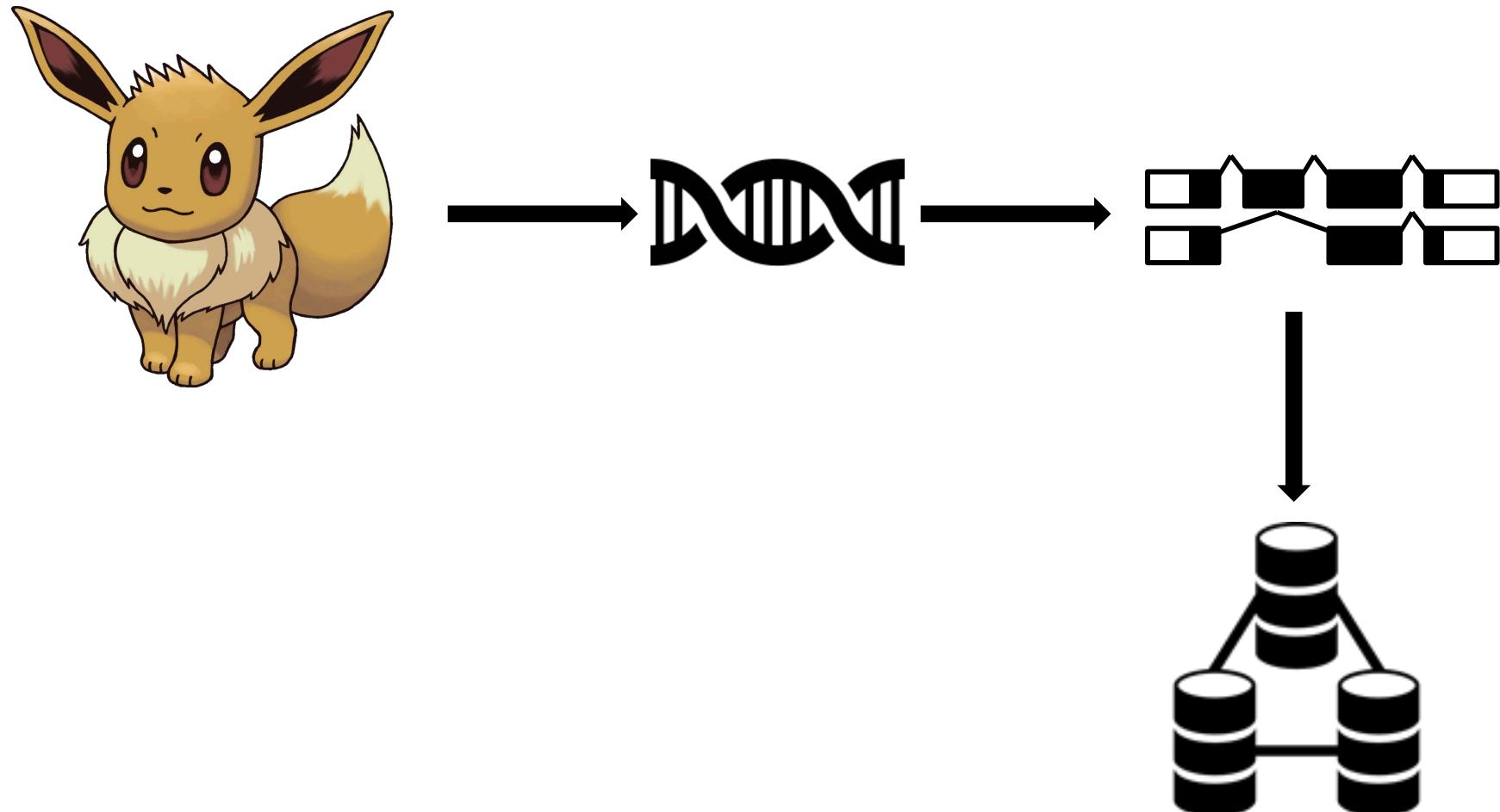
Genome Project Overview



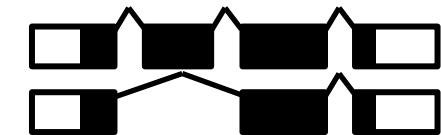
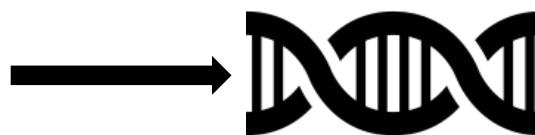
Genome Project Overview



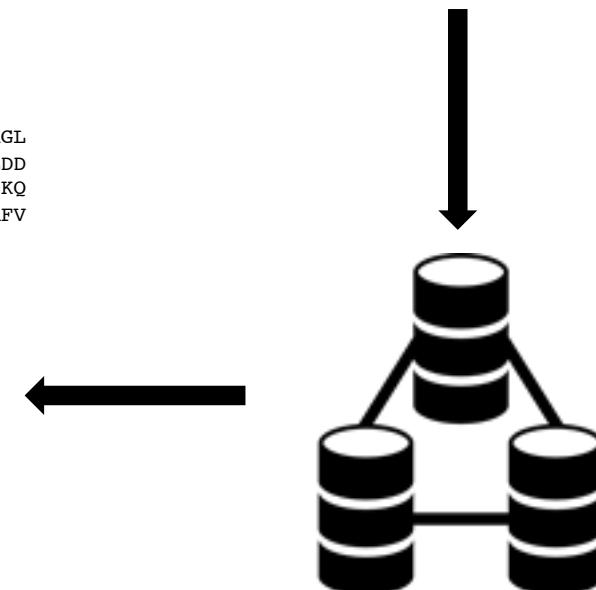
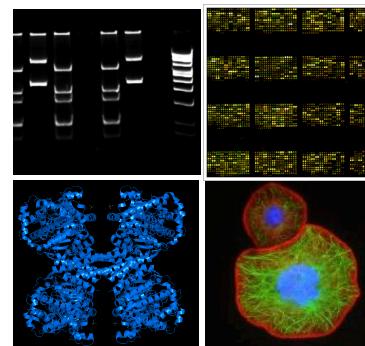
Genome Project Overview



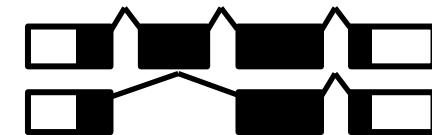
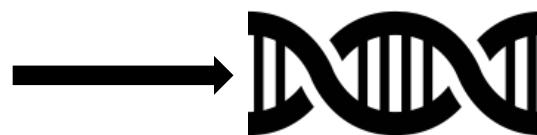
Genome Project Overview



>Smg5
MEVTFSSGGSSNASSECAIDGGTNRCGL
EPNNGTCILSQEVKDLYRSLYTASKQLDD
AKRNVQSVGQLFQHEIEEKRSLLVQLCKQ
IIFKDYQSVGKKVREVMWRRGYYEFAFV



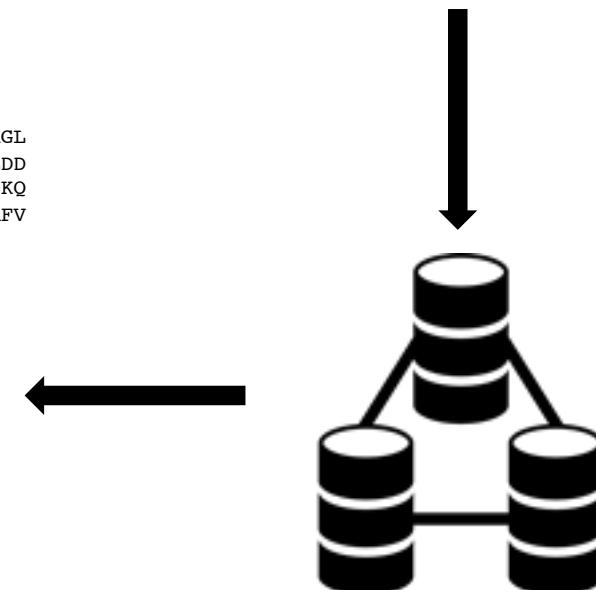
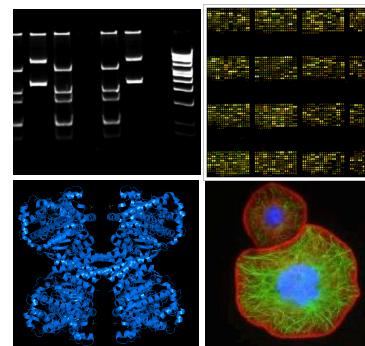
Genome Project Overview



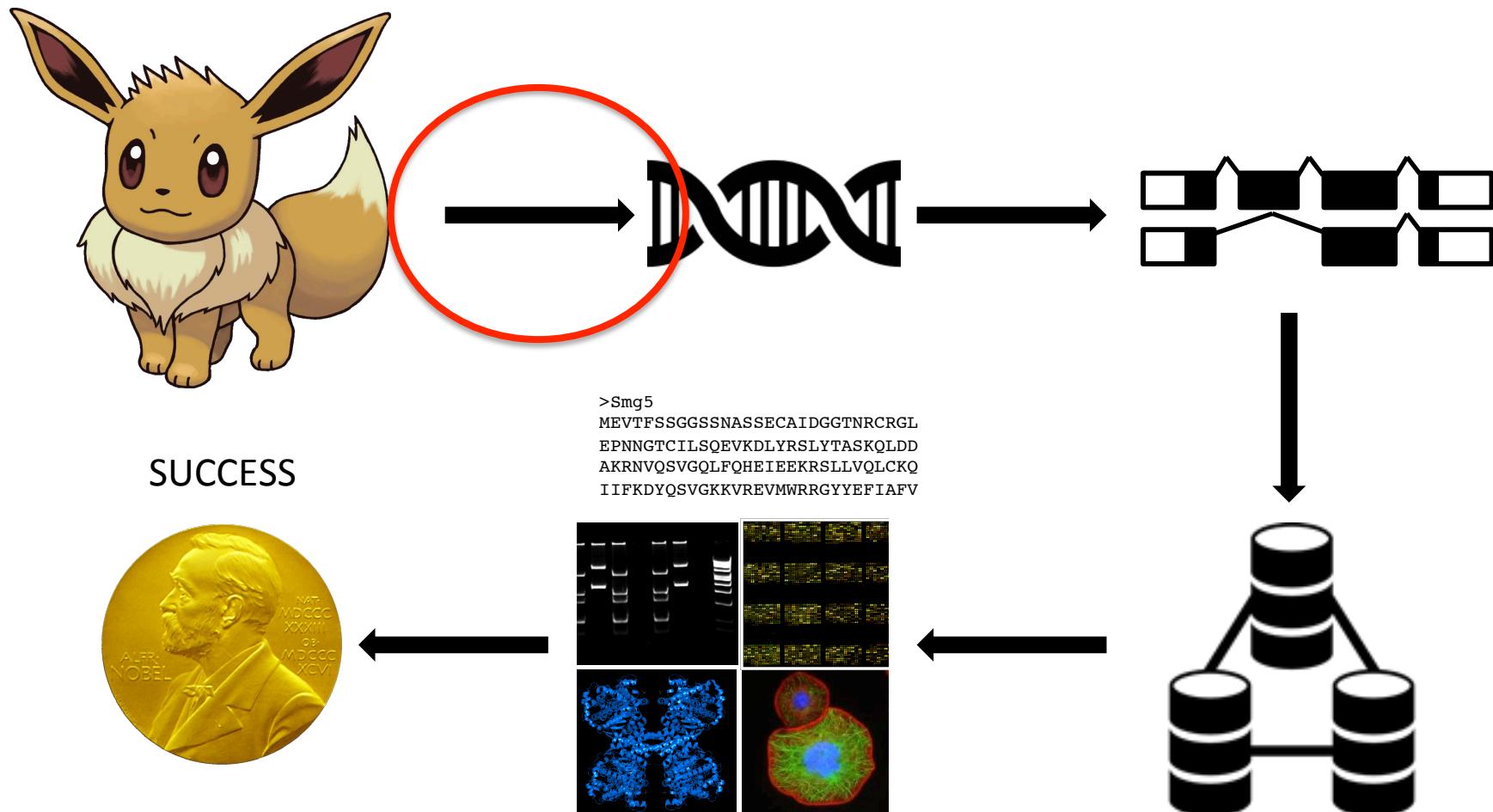
SUCCESS



>Smg5
MEVTFSSGGSSNASSECAIDGGTNRCGL
EPNGTICILSQEVKDLYRSLYTASKQLDD
AKRNVQSVGQLFQHEIEEKRSLLVQLCKQ
IIFKDYQSVGKKVREVMWRRGYYEFAFV



Genome Project Overview



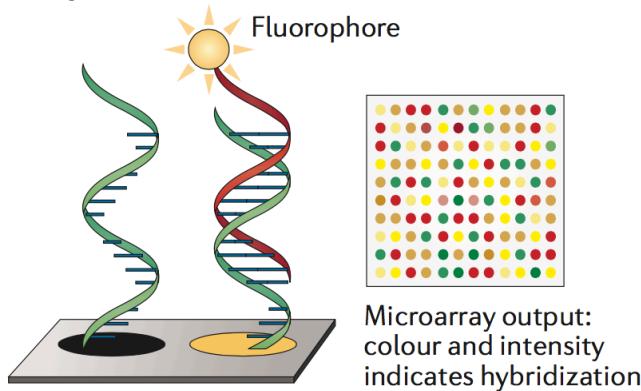


Coming of age: ten years of next-generation sequencing technologies

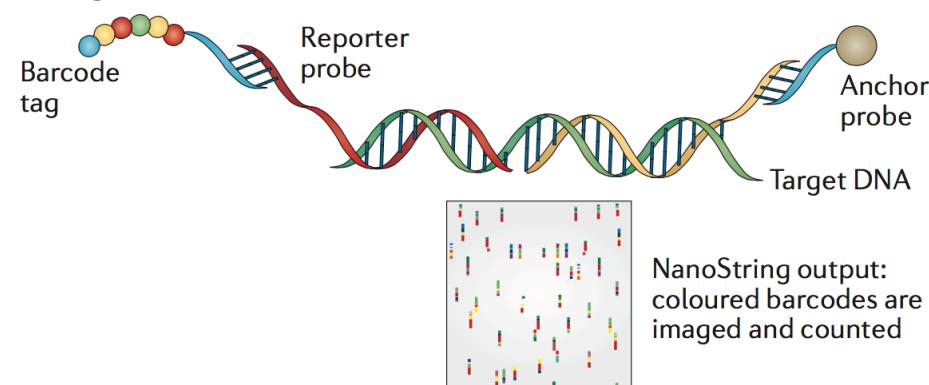
Sara Goodwin¹, John D. McPherson² and W. Richard McCombie¹

What did we do before whole genome sequencing?

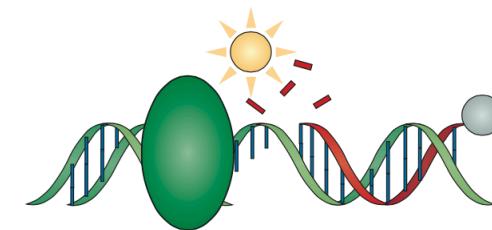
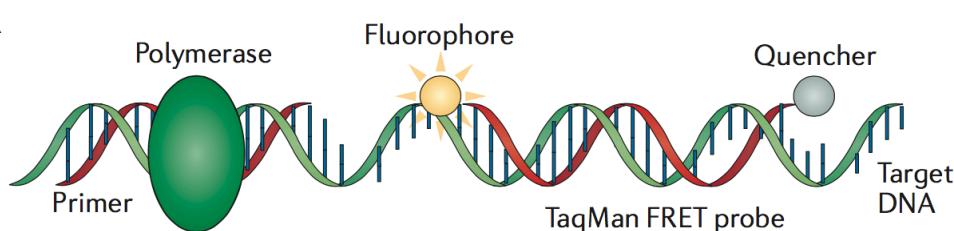
a Microarray



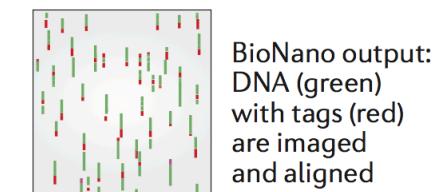
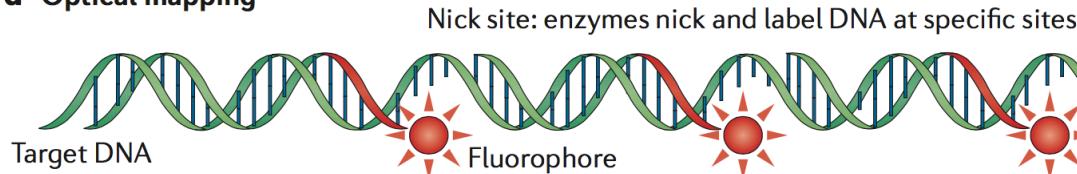
b NanoString



c qPCR



d Optical mapping



BioNano output:
DNA (green)
with tags (red)
are imaged
and aligned

Second Generation Sequencing

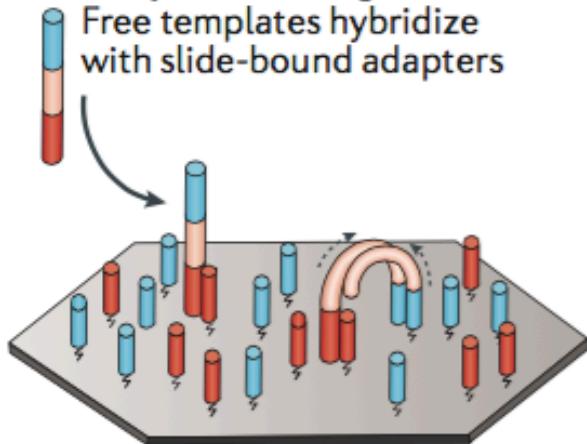
Extract -> amplify -> sequence -> analyze

Illumina

b Solid-phase bridge amplification (Illumina)

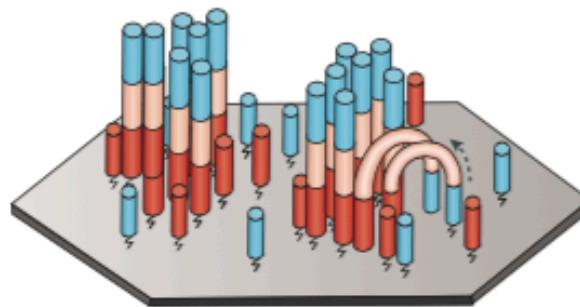
Template binding

Free templates hybridize with slide-bound adapters



Bridge amplification

Distal ends of hybridized templates interact with nearby primers where amplification can take place

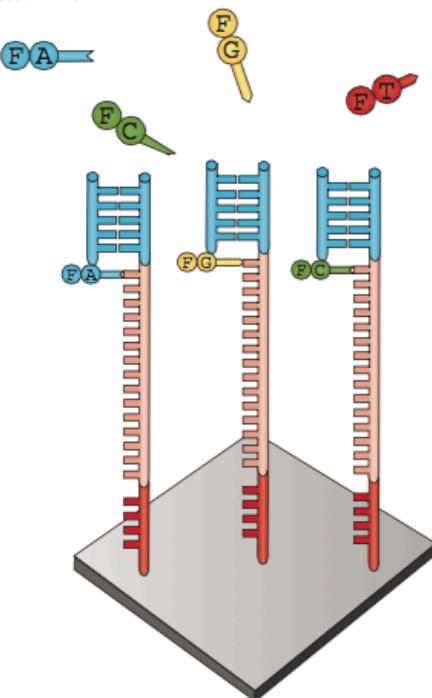


Cluster generation

After several rounds of amplification, 100–200 million clonal clusters are formed

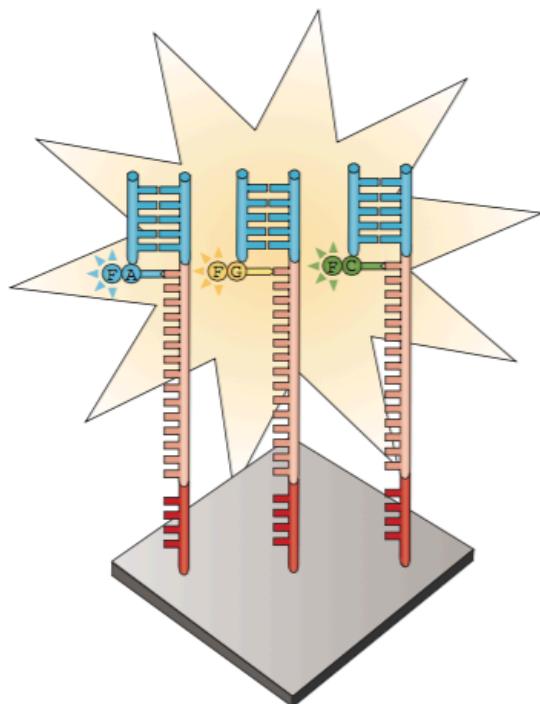
Illumina

a Illumina



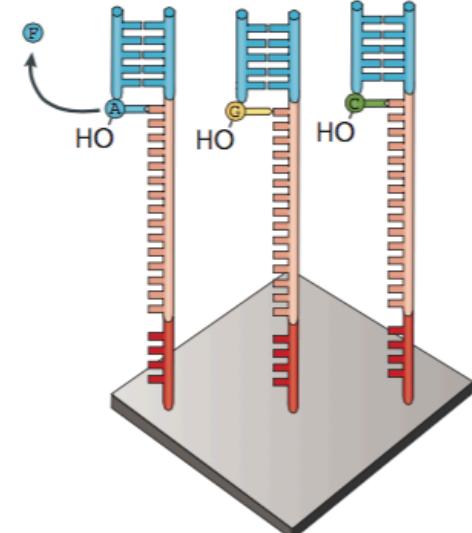
Nucleotide addition

Fluorophore-labelled, terminally blocked nucleotides hybridize to complementary base. Each cluster on a slide can incorporate a different base.



Imaging

Slides are imaged with either two or four laser channels. Each cluster emits a colour corresponding to the base incorporated during this cycle.



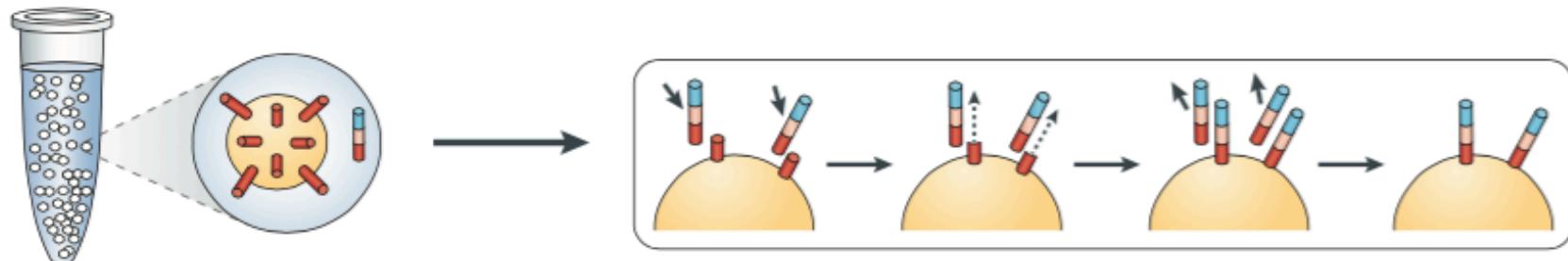
Cleavage

Fluorophores are cleaved and washed from flow cells and the 3'-OH group is regenerated. A new cycle begins with the addition of new nucleotides.

Ion Torrent

a Emulsion PCR

(454 (Roche), SOLiD (Thermo Fisher), GeneReader (Qiagen), Ion Torrent (Thermo Fisher))

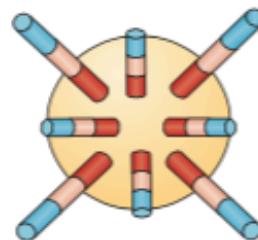


Emulsion

Micelle droplets are loaded with primer, template, dNTPs and polymerase

On-bead amplification

Templates hybridize to bead-bound primers and are amplified; after amplification, the complement strand disassociates, leaving bead-bound ssDNA templates

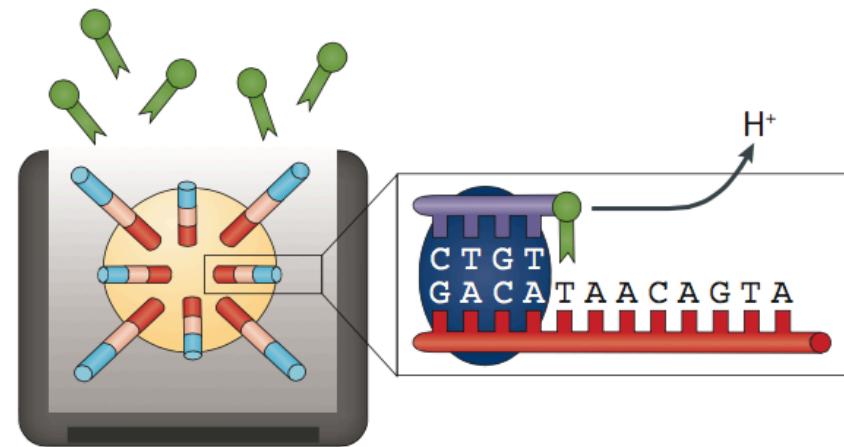


Final product

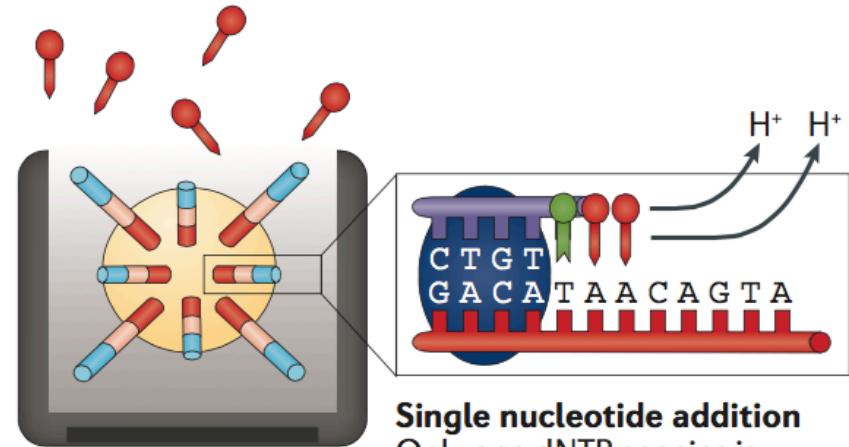
100–200 million beads with thousands of bound template

Ion Torrent

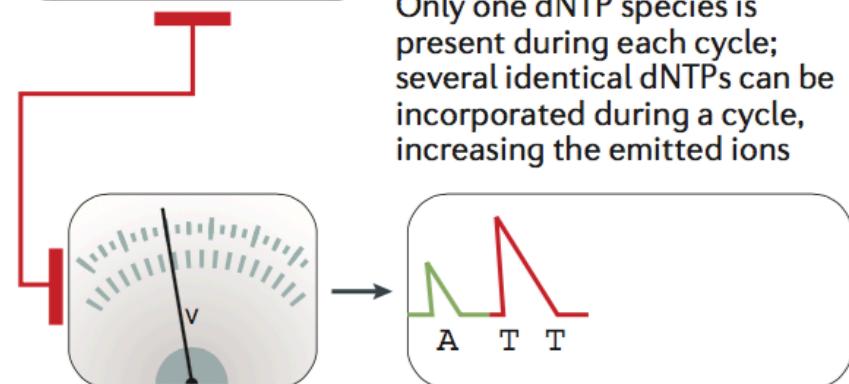
b Ion Torrent
(Thermo Fisher)



Semiconductor sequencing
As a base is incorporated, a single H^+ ion is released, which is detected by a CMOS-ISFET sensor



Single nucleotide addition
Only one dNTP species is present during each cycle; several identical dNTPs can be incorporated during a cycle, increasing the emitted ions



Third generation sequencing

Long molecule sequencing

Pac bio

A Real-time long-read sequencing

Aa Pacific Biosciences

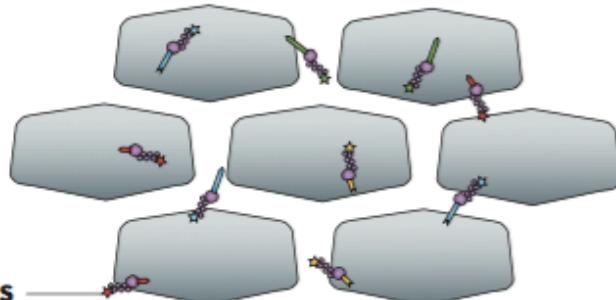
SMRTbell template

Two hairpin adapters allow continuous circular sequencing



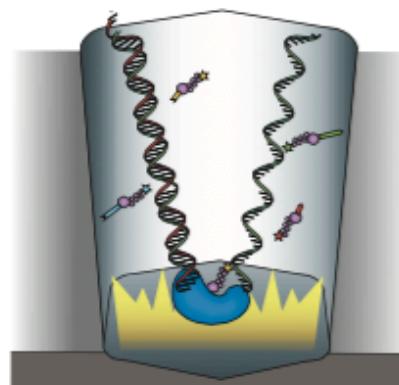
ZMW wells

Sites where sequencing takes place



Labelled nucleotides

All four dNTPs are labelled and available for incorporation



Modified polymerase

As a nucleotide is incorporated by the polymerase, a camera records the emitted light

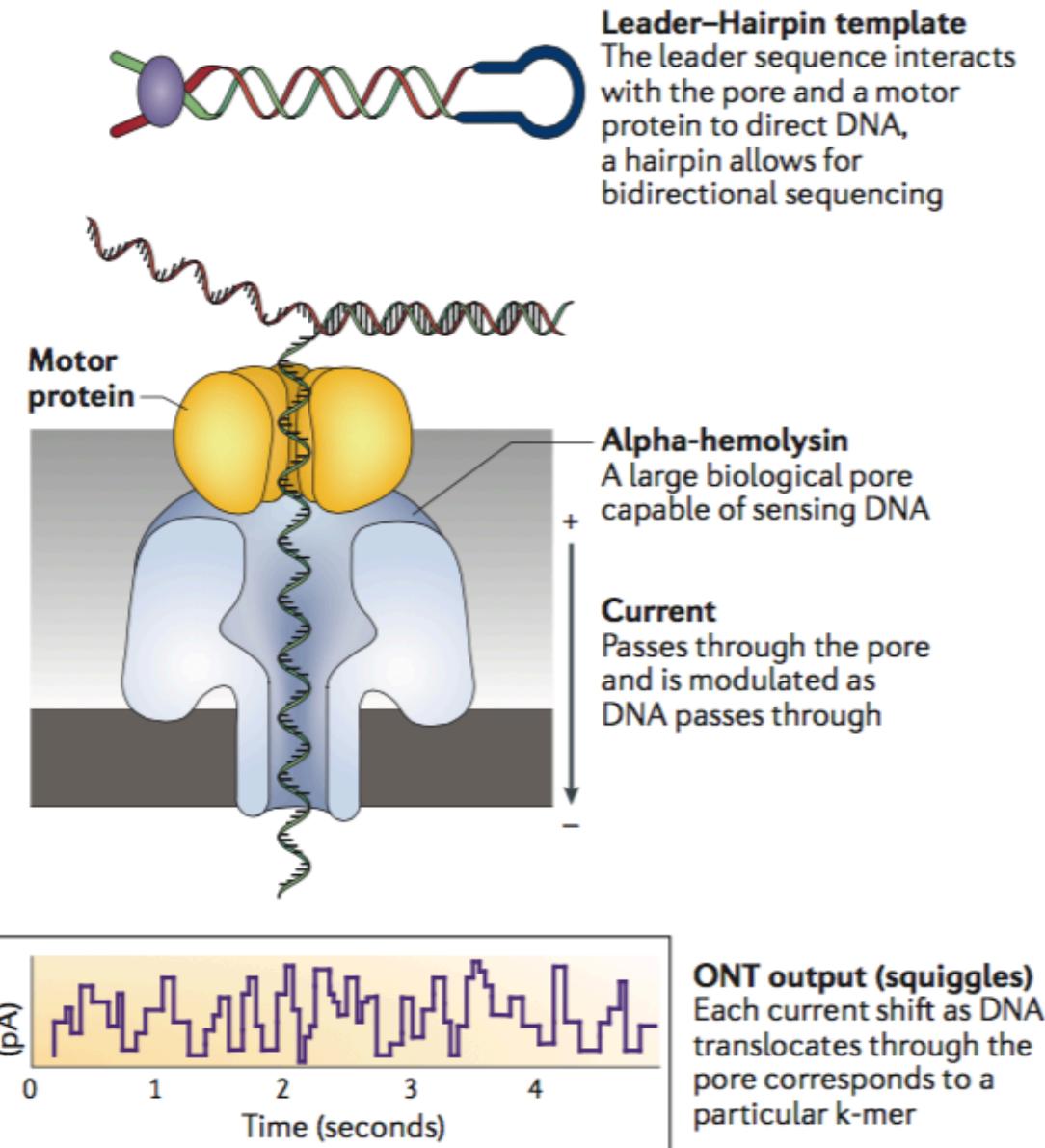
PacBio output

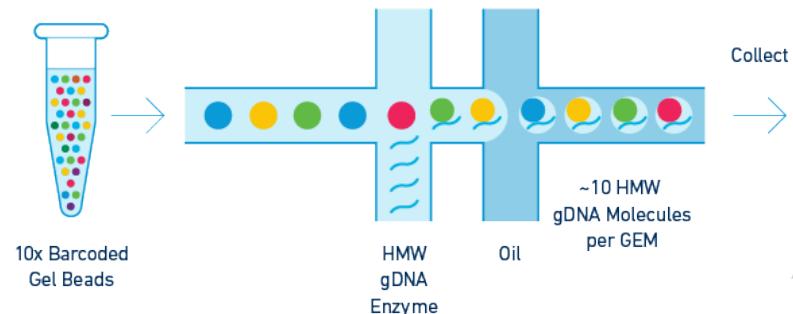
A camera records the changing colours from all ZMWs; each colour change corresponds to one base



Oxford Nanopore

Ab Oxford Nanopore Technologies

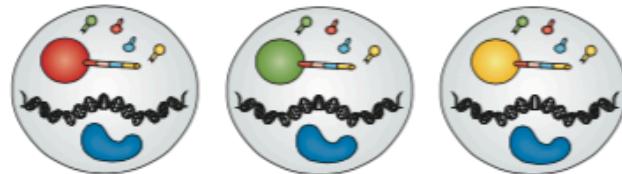




Bb 10X Genomics

Emulsion PCR

Arbitrarily long DNA is mixed with beads loaded with barcoded primers, enzyme and dNTPs



GEMs

Each micelle has 1 barcode out of 750,000

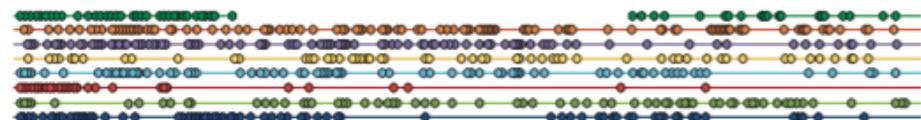
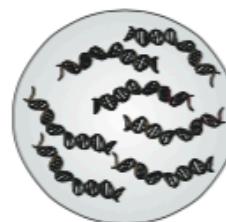
Amplification

Long fragments are amplified such that the product is a barcoded fragment ~350 bp



Pooling

The emulsion is broken and DNA is pooled, then it undergoes a standard library preparation



Linked reads

- All reads from the same GEM derive from the long fragment, thus they are linked
- Reads are dispersed across the long fragment and no GEM achieves full coverage of a fragment
- Stacking of linked reads from the same loci achieves continuous coverage

10X genomics
linked reads:
second generation
sequencing
technology with a
third generation
flavor

Whatever technology you use you get standard file formats back

- What is a file format?

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- What is a file format?
 - A standard way of storing information in a computer file
 - All file formats have specifications some are published others are unpublished

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- Can I tell what kind of file it is by the extension?

Whatever technology you use you get standard file formats back

- What is a file format?
 - A standard way of storing information in a computer file
 - All file formats have specifications some are published others are unpublished
- Can I tell what kind of file it is by the extension?
 - Nope, decent human beings will use an extension that identifies the format, but you can't count on it
 - Changing a file extension doesn't change the format of the file

File formats of interest to biologists

- FASTA
- FASTQ
- SAM/BAM
- GFF
- BED
- VCF

FASTA/Pearson format

[https://blast.ncbi.nlm.nih.gov/Blast.cgi?
CMD=Web&PAGE_TYPE=BlastDocs&DOC_TYPE=BlastHelp](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Web&PAGE_TYPE=BlastDocs&DOC_TYPE=BlastHelp)

```
>P01013 GENE X PROTEIN (OVALBUMIN-RELATED)
QIKDLLVSSSTDLDTTLVLVNAIYFKGMWKTAFNAEDTREMPFHVTKQESKPVQMMCMNNSFNVATLPAE
KMKILELPFASGDLSMLVLLPDEVSDLERIEKTINFEKLTEWTNPNTMEKRRVKVYLPQMKIEEKYNLTS
VLMALGMTDLFIPSANLTGISSAESLKISQAVHGAFMELSEDGIEMAGSTGVIEDIKHSPESEQFRADHP
FLFLIKHNPTNTIVYFGRYWSP
```

FASTQ (added quality scores)

<http://maq.sourceforge.net/fastq.shtml>

```
@EAS54_6_R1_2_1_413_324
CCCTTCTTGTCTTCAGCGTTCTCC
+
;;3;;;;;;7;;;;;88
@EAS54_6_R1_2_1_540_792
TTGGCAGGCCAAGGCCGATGGATCA
+
;;;;;;7;;;;;-;;3;83
@EAS54_6_R1_2_1_443_348
GTTGCTTCTGGCGTGGGTGGGGGGG
+EAS54_6_R1_2_1_443_348
;;;;;;9;7;.7;393333
```

SAM/BAM (Sequence alignment map)

<https://samtools.github.io/hts-specs/SAMv1.pdf>

```
@HD VN:1.5 SO:coordinate
@SQ SN:ref LN:45
r001 99 ref 7 30 8M2I4M1D3M = 37 39 TTAGATAAAAGGATACTG *
r002 0 ref 9 30 3S6M1P1I4M * 0 0 AAAAGATAAGGATA *
r003 0 ref 9 30 5S6M * 0 0 GCCTAAGCTAA * SA:Z:ref,29,-,6H5M,17,0;
r004 0 ref 16 30 6M14N5M * 0 0 ATAGCTTCAGC *
r003 2064 ref 29 17 6H5M * 0 0 TAGGC * SA:Z:ref,9,+,5S6M,30,1;
r001 147 ref 37 30 9M = 7 -39 CAGCGGCAT * NM:i:1
```

VCF (Variant call format)

<http://samtools.github.io/hts-specs/VCFv4.2.pdf>

```
##fileformat=VCFv4.2
##fileDate=20090805
##source=myImputationProgramV3.1
##reference=file:///seq/references/1000GenomesPilot-NCBI36.fasta
##contig=<ID=20,length=62435964,assembly=B36,md5=f126cdf8a6e0c7f379d618ff66beb2da,spe
##phasing=partial
##INFO=<ID=NS,Number=1>Type=Integer>Description="Number of Samples WithData">
##INFO=<ID=DP,Number=1>Type=Integer>Description="Total Depth">
#CHROM POS ID REF ALT QUAL FILTER INFO FORMAT NA00001 NA00002 NA00003
20 14370 rs6054257 G A 29 PASS NS=3;DP=14; GT 0|0 1|0 1/1
20 17330 . T A 3 q10 NS=3;DP=11 GT 0|0 0|1 0/0
20 1110696 rs6040355 A G,T 67 PASS NS=2;DP=10 GT 1|2 2|1 2/2
20 1230237 . T . 47 PASS NS=3 GT 0|0 0|0 0/0
20 1234567 microsat1 GTC G,GTCT 50 PASS NS=3;DP=9 GT 0/1 0/2 1/1
```

BED (Browser Extensible Data)

- <https://genome.ucsc.edu/FAQ/FAQformat.html#format1>

```
browser position chr7:127471196-127495720
browser hide all
track name="ItemRGBDemo" description="Item RGB demonstration"
visibility=2 itemRgb="On"
chr7    127471196    127472363    Pos1    0    +    127471196    127472363    255,0,0
chr7    127472363    127473530    Pos2    0    +    127472363    127473530    255,0,0
chr7    127473530    127474697    Pos3    0    +    127473530    127474697    255,0,0
chr7    127474697    127475864    Pos4    0    +    127474697    127475864    255,0,0
chr7    127475864    127477031    Neg1    0    -    127475864    127477031    0,0,255
chr7    127477031    127478198    Neg2    0    -    127477031    127478198    0,0,255
chr7    127478198    127479365    Neg3    0    -    127478198    127479365    0,0,255
chr7    127479365    127480532    Pos5    0    +    127479365    127480532    255,0,0
chr7    127480532    127481699    Neg4    0    -    127480532    127481699    0,0,255
```

The first three columns are required

Genome browser view



GFF3 format

<https://github.com/The-Sequence-Ontology/Specifications/blob/master/gff3.md>

```
##gff-version 3
ctg123 . gene          1300  9000  .  +  .  ID=gene0001;Name=sonic;biotype=protein
ctg123 . mRNA          1300  9000  .  +  .  ID=mrna0001;Parent=gene0001;Name=sonic
ctg123 . exon          1300  1500  .  +  .  ID=exon00001;Parent=mrna0001
ctg123 . exon          1050  1500  .  +  .  ID=exon00002;Parent=mrna0001
ctg123 . exon          3000  3902  .  +  .  ID=exon00003;Parent=mrna0001
ctg123 . exon          5000  5500  .  +  .  ID=exon00004;Parent=mrna0001
ctg123 . exon          7000  9000  .  +  .  ID=exon00005;Parent=mrna0001
```

FASTQ (added quality scores)

<http://maq.sourceforge.net/fastq.shtml>

```
@EAS54_6_R1_2_1_413_324
CCCTTCTTGTCTTCAGCGTTCTCC
+
;;3;;;;;;7;;;;;88
@EAS54_6_R1_2_1_540_792
TTGGCAGGCCAAGGCCGATGGATCA
+
;;;;;;7;;;;;-;;3;83
@EAS54_6_R1_2_1_443_348
GTTGCTTCTGGCGTGGGTGGGGGGG
+EAS54_6_R1_2_1_443_348
;;;;;;9;7;.7;393333
```

Day to day applications: Quality control

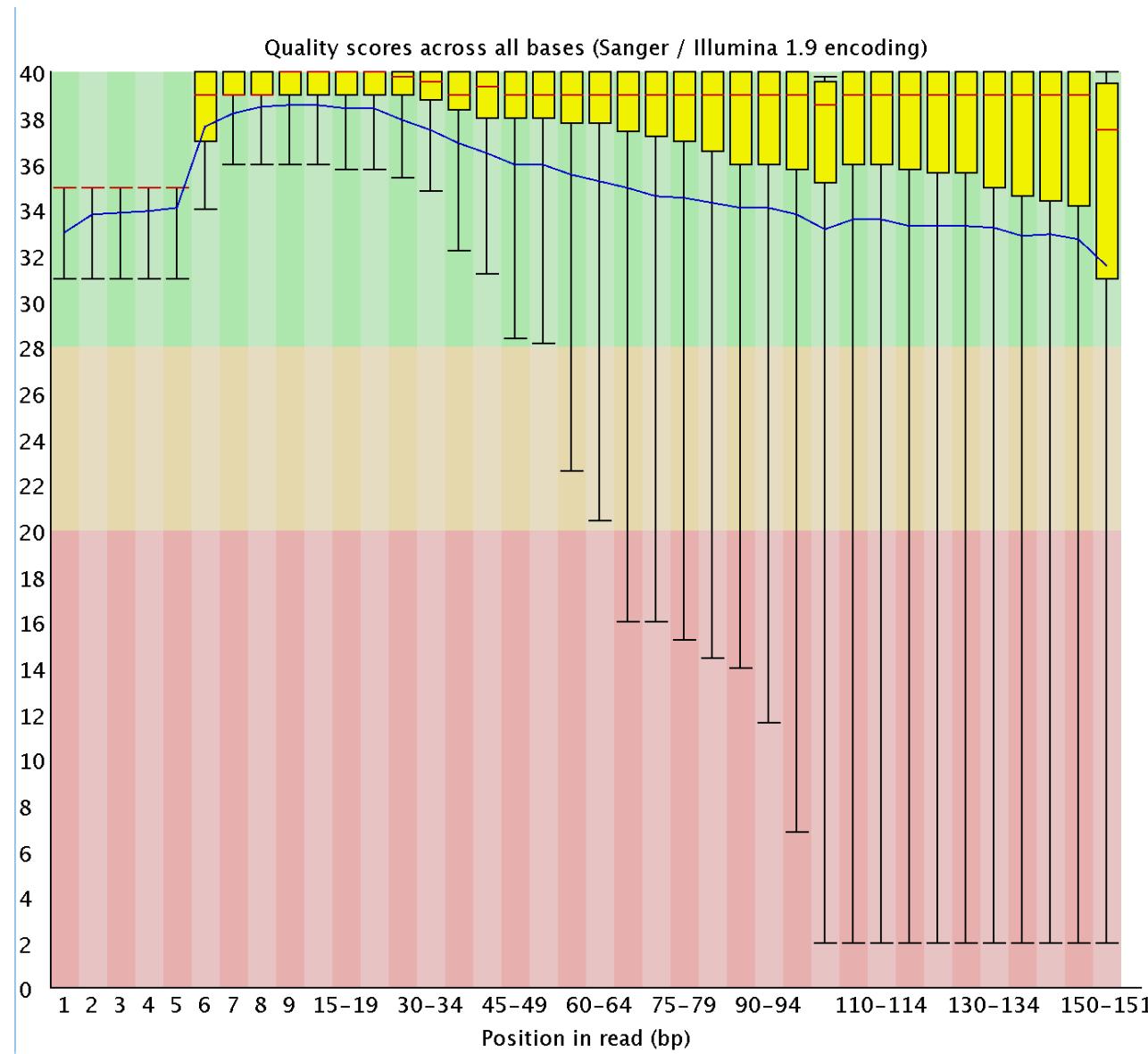
$$Q = -10\log_{10}(E)$$

Where E = estimated probability of the base call being wrong

Q	Probability of incorrect base call	Inferred base call accuracy
10	1 in 10	90%
20	1 in 100	99%
30	1 in 1000	99.9%

Quality scores are platform dependent

FASTQC for looking at base quality

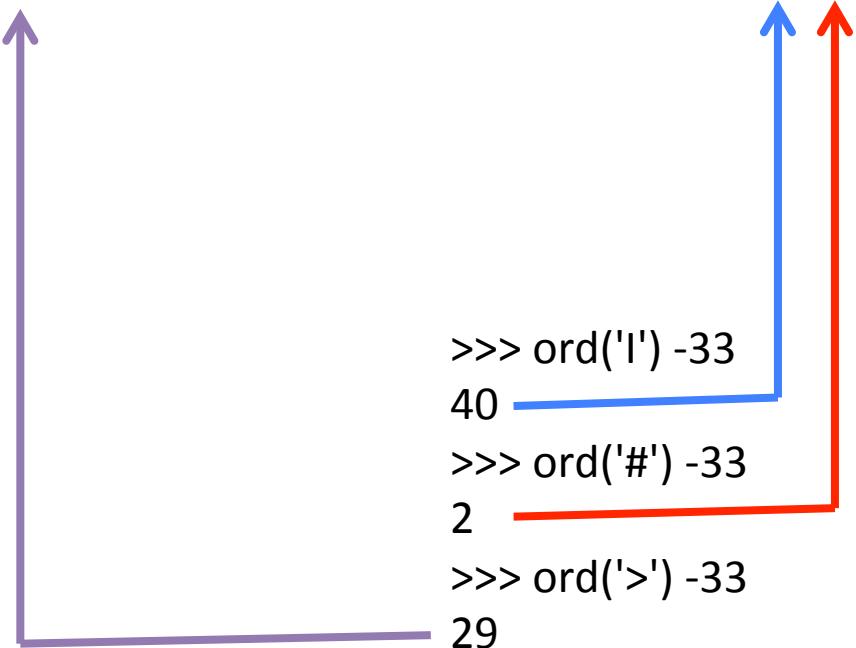


Quality trimming

@D00777:109:HFCWVBCXY:1:1103:1477:2081 1:N:0

GGCTAGCATTAGGCGATAGAGAATTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

+



Day to day applications: Fixing files

FASTA

```
>000263F_quiver
AATGGCAGTTGTGCTGTCACATGATGCCCTTGATGGTTGTAAATGGGTTTGCAGCCTGCATGATCACGTACAT
GGTGCAAAATCCTCAAAGGTGTAGCCTTGCAATCCAATGAAGGTTCCCTTAAATCAGAACAAATGCGCGCTGTAGGC
CACCATGGATGCGTGTGCTATGTTGGCTGTTGTGCTATTTTCGAGAATTAAATGGCAGAGTGGGTCCTCATGATG
CAAGTCTGCATAATGGTGTAGTAGTGGGAATGATAATCTGGTGGTATAGGGTAGGGTGGCAGTGGTAGCATGGTGGTT
ATGGCTATGAGATTGCGGTAGTGGCGATCATGGTGATGAAGGGTGGCGTCATGAATGGCTAGTGGAGGTATGGAGGCG
ACCATGATGGTGCAACAGGGTGGTAGAGACTGGCGGTGGACGACGGTGCTGATAGTAACCACGATTTACGCAGCGGAAAT
AAATCATGATGAAACAAGCATGGAGACAAGCCAAATCATATGAAAAGACTGACCTTTCTTGTGAAAACGCCAC
AATCTCCTACAATCTTCTGTTGTTACCTTATCAATTTCGGACTGTAATTCTTAGTGGACAGAAAAAACATAGCTA
GGTTAGTCACTCTTTCTGTTCTAATATATCTCTCGATGGGAAGAAGACCACTTCTAGAAACTCTTTTC
```

GFF3

```
000263F|quiver maker    gene 41412      41819      .      +      .      ID=CASF_028122
000263F|quiver maker    mRNA   41412      41819      .      +      .      ID=CASF_028122-
RA;Parent=CASF_028122;Name=CASF_028122-RA;Alias=augustus_masked-000263F_quiver-processed-
gene-0.9-mRNA-1;_AED=0.20;_QI=0_-1_0_1_-1_1_0_135;_eAED=0.20;
```

Day to day applications: Fixing files

FASTA

```
>000263F_quiver
AATGGCAGTGTGCTGTCACATGATGCCCTTGCATGGTTGTAATGGGTTTGCAGCCTGCATGATCACGTACAT
GGTGCAAAATCCTCAAAGGTGTAGCCTTGCAATCCAATGAAGGTTCCTTAAATCACGAACAATGCGCGCTGTAGGC
CACCATGGATGCGTGTGCTATGTTGGCTGTTGCTATTTCGAGAATTAAATGGCAGAGTGGGTCCTCATGATG
CAAGTCTGCATAATGGTGTAGTAGTGGGAATGATAATCTGGTGGTGATAGGGTAGGGTGGCAGTGGTAGCATGGTGGTT
ATGGCTATGAGATTGCGGTAGTGGCGATCATGGTGATGAAGGGTGGCGTCATGAATGGCTAGTGGAGGTCATGGAGGCG
ACCATGATGGTGCAACAGGGTGGTAGAGACTGGCGGTGGACGACGGTGCTGATAGTAACCACGATTACGCAGCGGAAAT
AAATCATGATGAAACAAGCATGGAGACAAGCCAAATCATATGAAAAGACTGACCTTTCTTGTGAAAACGCCAC
AATCTCCTACAATCTTCTGTTACCTATCAATTTCGGACTGTAATTCTTAGTGGACAGAAAAAACATAGCTA
GGTTAGTCACTCTTTCTGTTCTAATATATCTCTCGATGGGAAGAAGACCACTTCTAGAAACTCTTTT
```

GFF3

000263F|quiver maker gene 41412 41819 . + . ID=CASF_028122
000263F|quiver maker mRNA 41412 41819 . + . ID=CASF_028122-
RA;Parent=CASF_028122;Name=CASF_028122-RA;Alias=augustus_masked-000263F_quiver-processed-
gene-0.9-mRNA-1; AED=0.20; QI=0 -1 0 1 -1 1 1 0 135; eAED=0.20;