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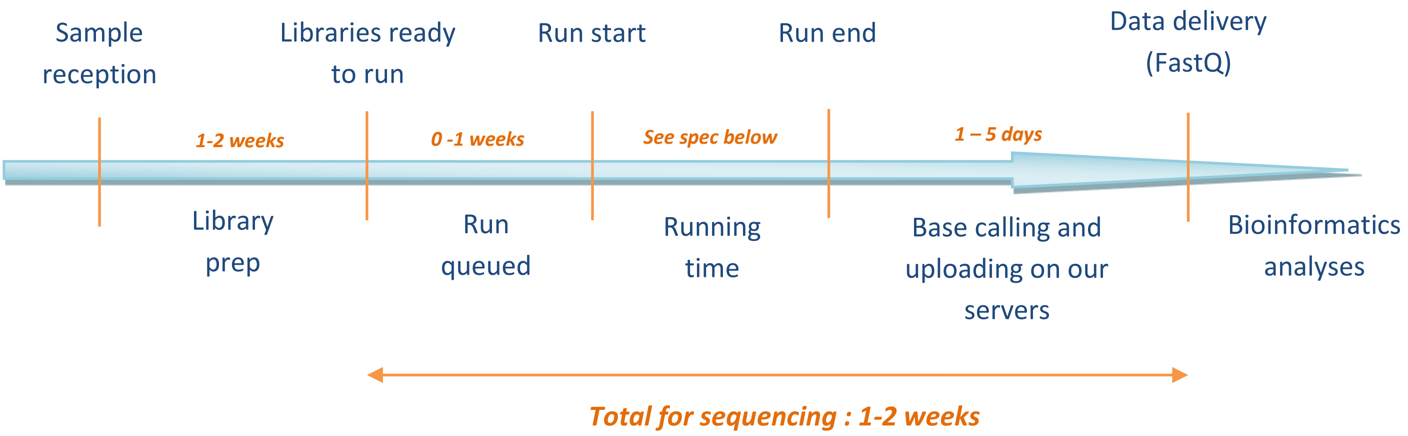
Miseq spec, process and turnaround times

One Single lane & library pool / flow cell (on board clusterisation) – 1 Flow cell / run

Instrument used to sequence small libraries such as targeted sequencing or bacterial genomes, and titrations steps.



Miseq Reagent kits V2 / Miseq Reagent kits V3

Read length	Run time	Output	Read length	Run time	Output
1 × 36 bp	± 4 hrs	540 – 610 Mb	2 × 75 bp	± 21 hrs	3,3 – 3,8 Gb
2 × 25 bp	± 5,5 hrs	750 – 850 Mb	2 × 300 bp	± 56 hrs	13– 15 Gb
2 × 150 bp	± 24 hrs	4,5 – 5,1 Gb			
2 x 250 bp	± 39 hrs	7,8 – 8,5 Gb			

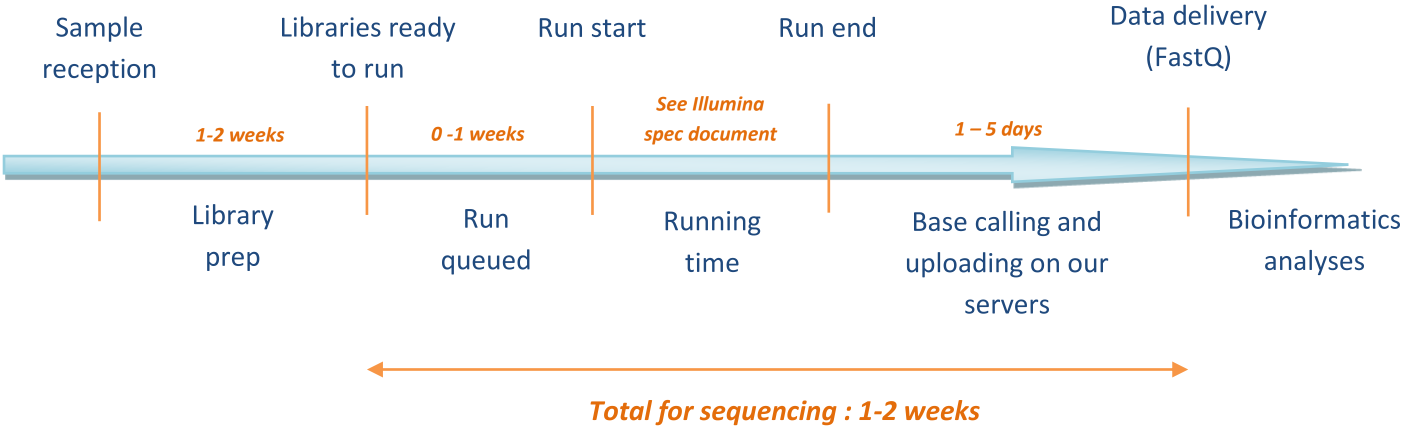
Reads Passing Filter	kits v2	kits v3
Single Reads	12 – 15M	22 – 25M
Paired end reads	24 – 30 M	44 – 50 M

bp = base pairs, Gb = gigabases, M = millions, MO = Mid Output, HO = High Output, hrs = hours

NextSeq500 spec, process and turnaround times

Two Modes : High Output = HO – Mid Output = MO – 4 non-separated lanes = one library pool / flow cell (on board clusterisation) – 1 flow cell / run

Instrument used to sequence medium size libraries such as targeted sequencing or a few RNA and WES (WES: for small projects such as 3-6 captures, to get approx. 100x coverage, we recommend to process 3 libraries with MO mode, 6 libraries with HO mode).


Sample reception
Libraries ready to run
Run start
Run end
Data delivery (FastQ)

1-2 weeks
0 -1 weeks
See Illumina spec document
1 – 5 days

Library prep
Run queued
Running time
Base calling and uploading on our servers
Bioinformatics analyses

Total for sequencing : 1-2 weeks

Nextseq500	HO kit		MO kit	
Read length	**Run time**	**Output**	**Run time**	**Output**
2 x 150 bp	± 29 hrs	100 – 120 Gb	± 26 hrs	32 – 39 Gb
2 × 75 bp	± 18 hrs	50 - 60 Gb	± 15 hrs	16 – 19 Gb
1 × 75 bp	± 11 hrs	25 – 30 Gb		

Reads Passing Filter	HO	MO
Single Reads	Up to 400 M	Up to 130 M
Paired end reads	Up to 800 M	Up to 260 M

bp = base pairs, Gb = gigabases, M = millions, MO = Mid Output, HO = High Output, hrs = hours

NovaSeq6000 spec, process and turnaround times

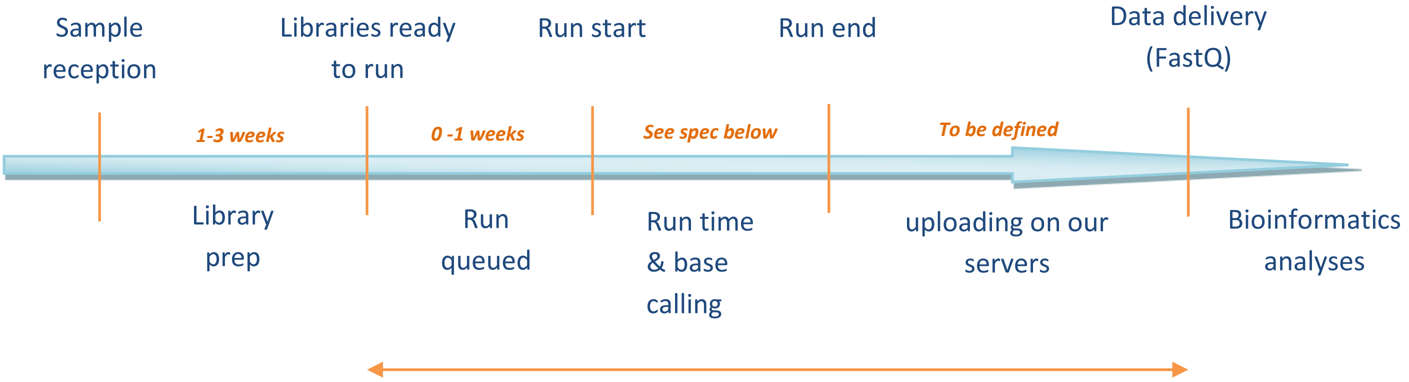
Sequencing modes:

using flow cell S1: up to 2 lanes, and up to 2 flow cell / run

using flow cell S2: up to 2 lanes, and up to 2 flow cell / run

using flow cell S4: up to 4 lanes, and up to 2 flow cell / run

Mode used to sequence large libraries such as human genomes, exomes, transcriptomes.



Total for sequencing : 2 - 4 weeks

S1 Flow Cell Specifications

S2 Flow Cell Specifications

Reads passing filter

Single End Reads	**1,3 – 1,6 – Billion**	**3,3 – 4,1 Billion**
Paired End Reads	**2,6 – 3,2 – Billion**	**6,6 – 8,2 Billion**

Read length	Output	Run time	Output	Run time
2x50 cycles	134 – 167 Gb	13 h	333 - 417 Gb	16h
2x100 cycles	266 – 333 Gb	19 h	667 - 833 Gb	25h
2x150 cycles	400 - 500 Gb	25 h	1000 - 1250 Gb	36h

Run times are based on running 2 flow cells of the same type ; starting two different flow cells will impact run time.

Read length	Quality scores
2x50 cycles	≥ 85%
2x100 cycles	≥ 80%
2x150 cycles	≥ 75%

A quality score (Q-score) is a prediction of the probability of an error in base calling. The percentage of bases > Q30 is averaged across the entire run. Quality scores are based on NovaSeq Reagent Kits run on the NovaSeq 6000 System using an Illumina PhiX control library. Performance may

vary based on library type and quality, insert size, loading concentration, and other experimental factors.
‡ Run time includes cluster generation, sequencing, and base calling.

S4 Flow Cell Specifications

S Prime (SP) flow cell Specifications

Reads passing filter

Single End Reads	**8 – 10 Billion**	**650 – 800 Million**
Paired End Reads	**16 - 20 Billion**	**1,3 – 1,6 Billion**

Read length	Output	Run time	Read length	Output	Run time
2x100 cycles	1600 – 2000 Gb	36h	2x50 cycles	65 – 80 Gb	13h
2x150 cycles	2400 – 3000 Gb	44h	2x150 cycles	200 – 250 Gb	25h
			2x250 cycles	325 – 400 Gb	38h

Performance Specifications of a Dual S2 Flow Cell Run

Read length	Quality scores	Read length	Quality scores
2x150 cycles	≥ 75%	2x50 cycles	≥ 85%
2x100 cycles		2x150 cycles	≥ 75%
		2x250 cycles	≥ 75%

A quality score (Q-score) is a prediction of the probability of an error in base calling. The percentage of bases > Q30 is averaged across the entire run. Quality scores are based on NovaSeq Reagent Kits run on the NovaSeq 6000 System using an Illumina PhiX control library. Performance may vary based on library type and quality, insert size, loading concentration, and other experimental factors.
‡ Run time includes cluster generation, sequencing, and base calling.