NorSeq User survey 2018
Count of 1 of 14. What is your position? (select one alternative)

- Technical position: 7.0%
- PhD student: 8.8%
- PI/prof: 39.5%
- Postdoc/researcher: 44.7%
Count of 2 of 14. What NorSeq node(s) has been used? (multiple alternatives can be selected)

- NorSeq-Tromsø (Geno... 3.5%
- NorSeq-Bergen (UiB Ge... 9.6%
- NorSeq-Oslo (Blindern/... 0.9%
- NorSeq-Oslo (Blindern/... 24.6%
- NorSeq-Oslo (Ullevål/O... 20.2%
- NorSeq-Trondheim (NT... 1.8%
- NorSeq-Oslo (Ullevål/O... 19.3%
- NorSeq-Oslo (Ullevål/O... 14.9%
Count of 3 of 14. How did you get to know about NorSeq (or your local core facility) and our services? (multiple alternative...
Count of 4 of 14. How are you satisfied with the response time on your first request to one of our nodes/core facilities? (select one)

- Very satisfied: 63.2%
- Satisfied: 28.9%
- Neutral: 5.3%
- Dissatisfied/slow: 2.6%
Count of 5 of 14. What type of services have been used? (multiple alternatives can be selected)

- Project consultation, Sequencing only: 14.9%
- Project consultation, Library prep and sequencing: 8.8%
- Library prep and sequencing: 8.8%
- Project consultation, Library prep and sequencing: 4.4%
- Project consultation, Sequencing only: 6.1%
- Project consultation, Library prep and sequencing: 12.3%
- Library prep and sequencing: 3.5%
- Project consultation, Bioinformatics: 0.9%
Count of 6 of 14. If we did project consultation for your project. How satisfied are you with the guidance you received? (select...)

- **Very satisfied**: 43.0%
- **Satisfied**: 27.1%
- **Not applicable**: 23.4%
- **Neutral**: 5.6%
Count of 7 of 14. If we did library prep and sequencing for your project. How satisfied are you with the response/processing ti...
Count of 8 of 14. If we did library prep and sequencing for you project. How satisfied are you with the technical results? (select one)

- Very satisfied: 47.8%
- Satisfied: 31.9%
- Neutral: 7.1%
- Dissatisfied: 2.7%
- Not applicable: 9.7%
Count of 9 of 14. If we did bioinformatics analysis for you project. How satisfied are you with the response/processing time:

- Not applicable: 68.2%
- Very satisfied: 18.2%
- Satisfied: 9.1%
- Dissatisfied/slow: 2.7%
Count of 10 of 14. If we did bioinformatics analysis on your project. How satisfied are you with the way results were reported?

- Not applicable: 68.2%
- Very satisfied: 18.2%
- Neutral: 8.2%
- Satisfied: 3.6%
- Dissatisfied: 0.9%
Count of 11 of 14. Does NorSeq offer the sequencing services you need? (select one alternative)

- Not applicable: 1.8%
- Partly: 15.0%
- Yes: 83.2%
Count of 12 of 14. What do you think about the cost of NorSeq services? (select one alternative)

- **Acceptable:** 55.8%
- **Good value:** 28.3%
- **Not applicable:** 2.7%
- **Too expensive:** 13.3%
13 of 14. Is there any sequencing application that you want NorSeq to establish/offer? (please add free text)

- Attac-seq
- single cell
- HiC, Tissue RNAseq
- Single cell RNAseq sequencing
- Hi-C and/or Optical mapping
- Nanopore GRIDIon, MinION (Oxford Nanopore Technologies)
- Human whole exome sequencing
- Novaseq
- ChIP seq
- Nanopore Sequencing / Long reads
- Nothing in particular, I feel you're coming updated with the new machines so - bra jobb!
- 10 X genomics platform
- Nanopore
- It would be nice to be able to order a fixed amount of Illumina reads/bases. Or perhaps offering a platform with a smaller number of reads (sometimes there are just too many reads with Illumina). Also, offering more varieties of library preps would be nice (e.g. sequencing differently modified RNAs (TSS, degradome...)).
- MinION
- depending on cost: single molecule sequencing
- Long read sequencing when technology is capable of giving good result. This will give better insight into the transcriptome than current short read sequencing technology.
- single cell sequencing
- More options of length reads on the HiSeq without having to do a whole flow cell
- RNA seq on small cell samples; single cell RNA seq
This answer is not included because it names specific people.