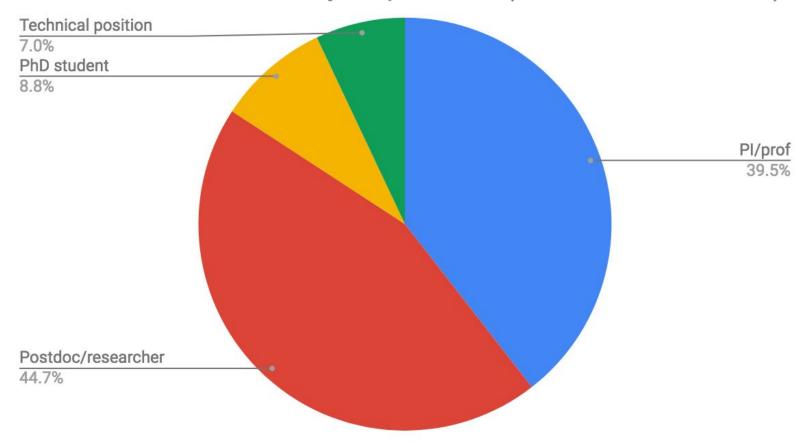
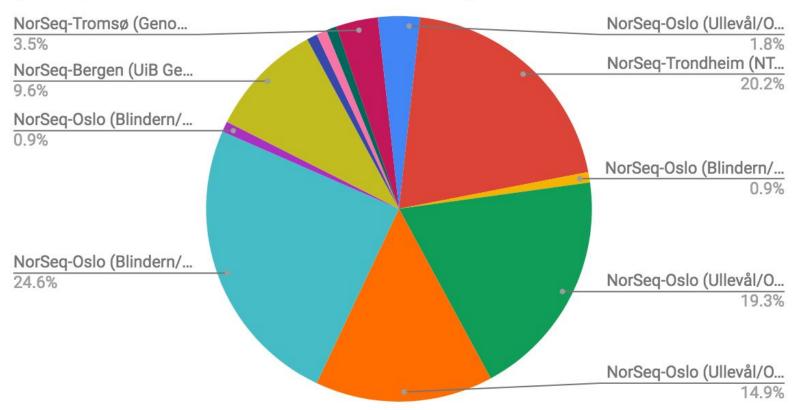
NorSeq User survey 2018

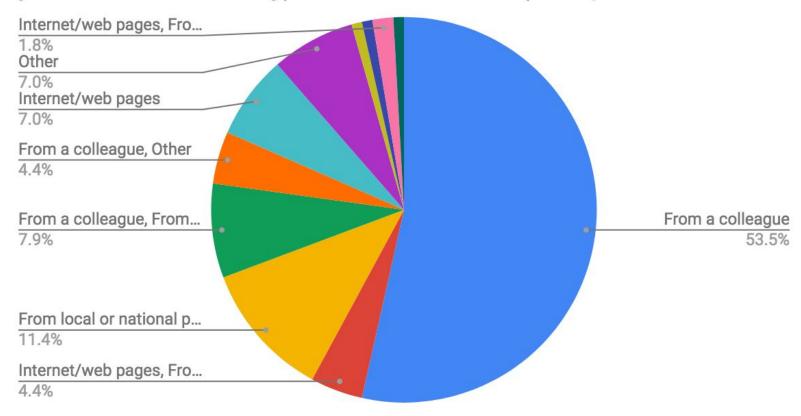
Count of 1 of 14. What is your position? (select one alternative)



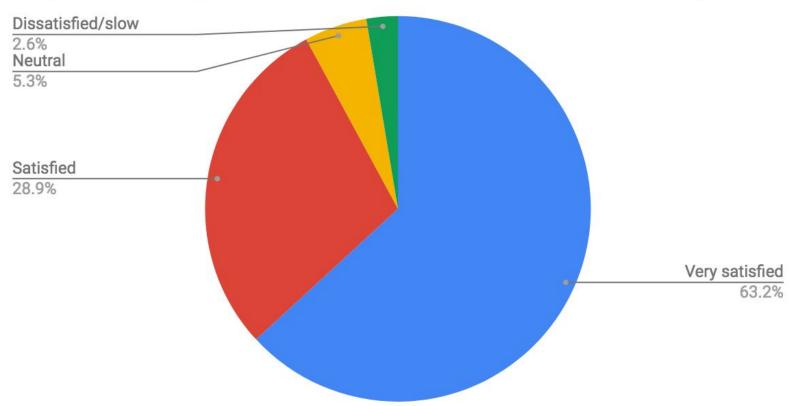
Count of 2 of 14. What NorSeq node(s) has been used? (multiple alternatives can be selected)



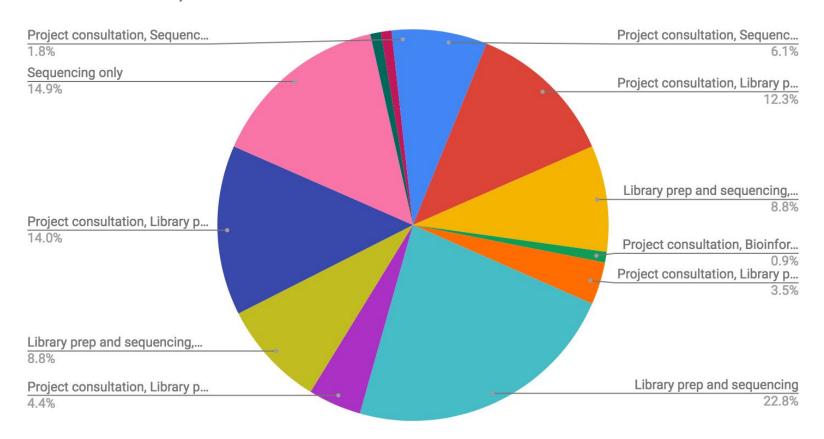
Count of 3 of 14. How did you get to know about NorSeq (or your local core facility) and our services? (multiple alternative...



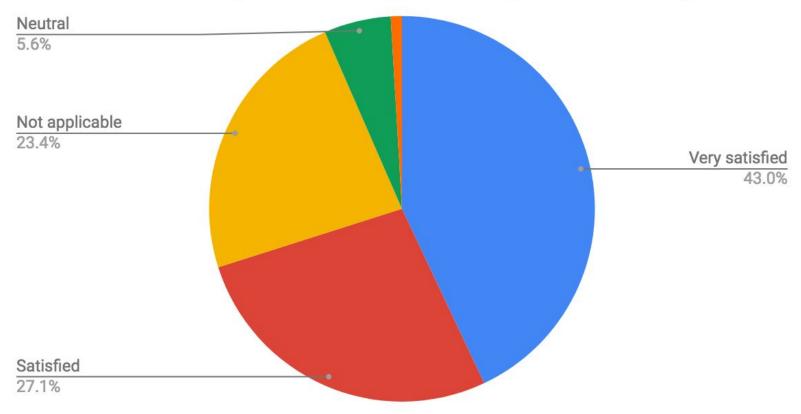
Count of 4 of 14. How are you satisfied with the response time on your first request to one of our nodes/core facilities? (sele...



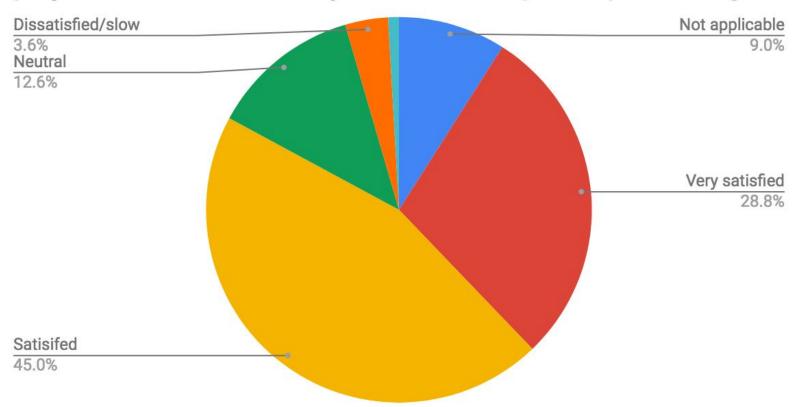
Count of 5 of 14. What type of services have been used? (multiple alternatives can be selected)



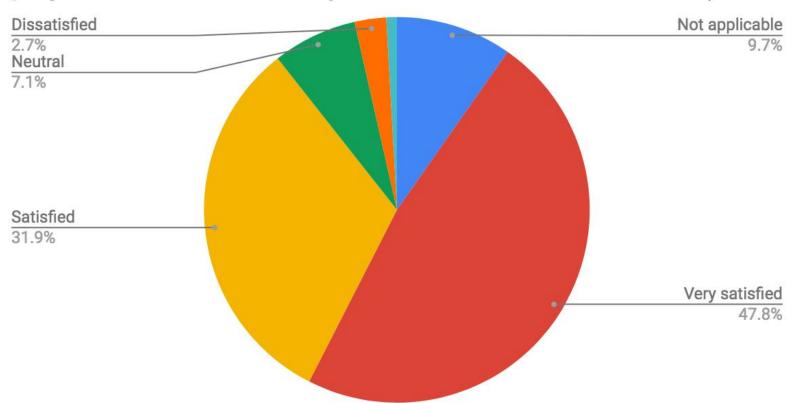
Count of 6 of 14. If we did project consultation for your project. How satisfied are you with the guidance you received? (select...



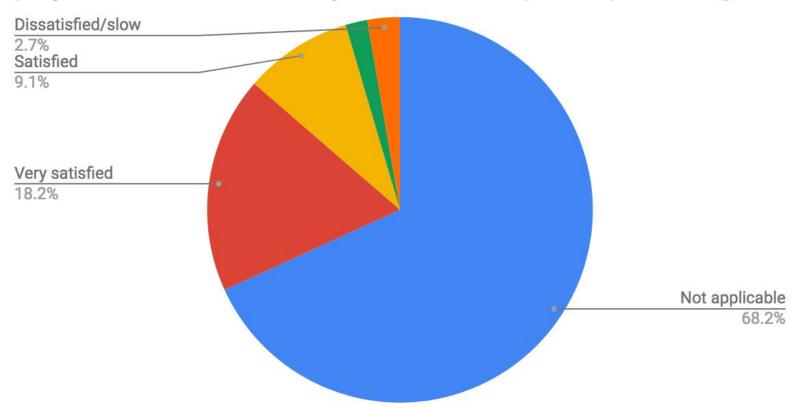
Count of 7 of 14. If we did library prep and sequencing for your project. How satisfied are you with the response/processing ti...



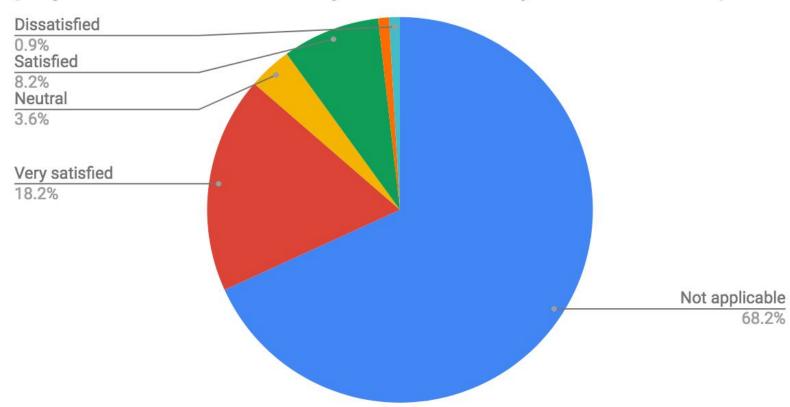
Count of 8 of 14. If we did library prep and sequencing for you project. How satisfied are you with the technical results? (sele...



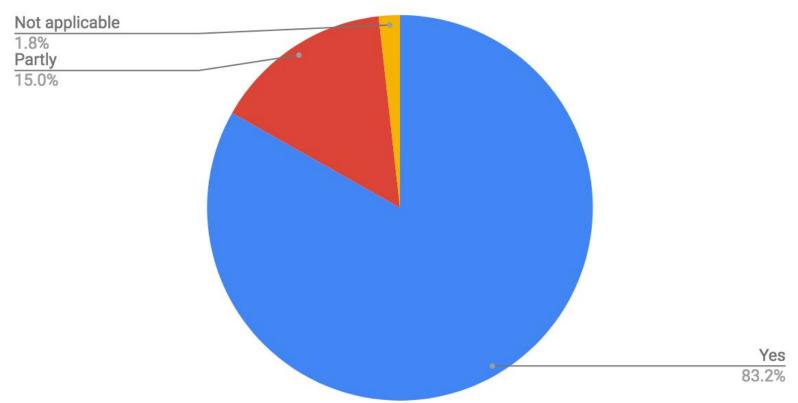
Count of 9 of 14. If we did bioinformatics analysis for you project. How satisfied are you with the response/pocessing ti...



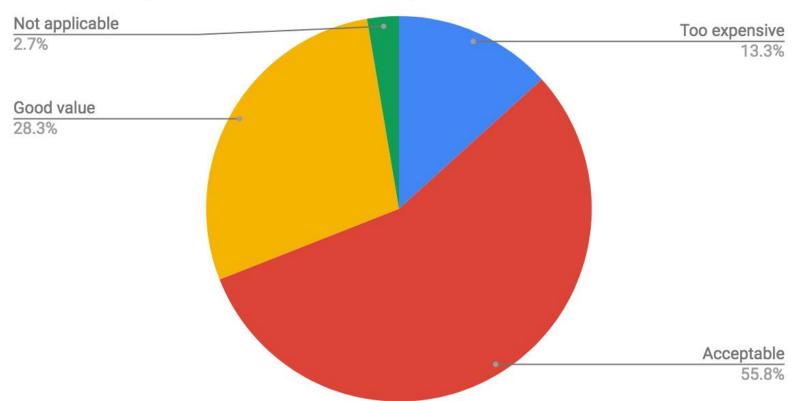
Count of 10 of 14. If we did bioinformatics analysis on your project. How satisfied are you with the way results were repor...



Count of 11 of 14. Does NorSeq offer the sequencing services you need? (select one alternative)



Count of 12 of 14. What do you think about the cost of NorSeq services? (select one alternative)



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

14 of 14. Please feel free to add any comments, that can be useful for us in the evaluation process: (please add free text)

This answer is not included because it names specific people.