ILLUMINA JULY 2014 SURVEY

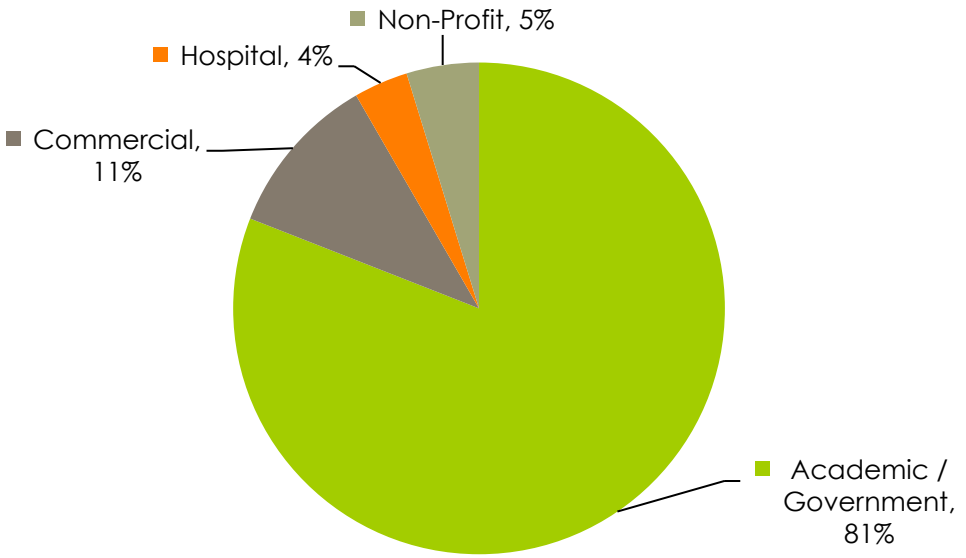
Survey completed July21st, 2014. We surveyed various scientists around the world to determine their lab's current usage of genome sequencing products, with a specific focus on Illumina sequencing products. We also wanted to determine if there is a need to buy additional equipment in the next 12 months, and the direction of budgets.

SURVEY DISTRIBUTION

Number of Surveys
84

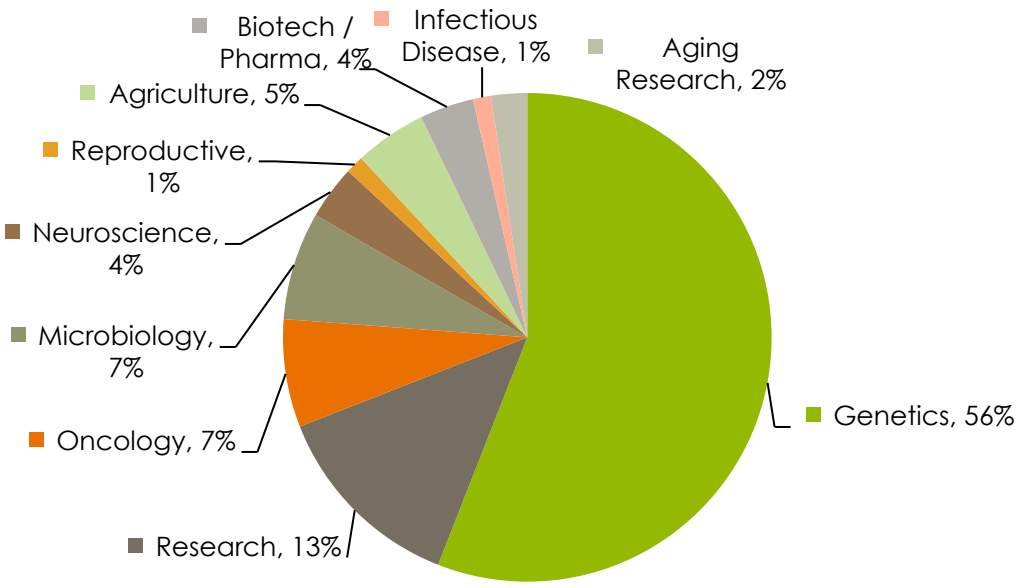
Location	Count	Percentage
Within the US	59	70%
India	6	7%
UK	5	6%
Canada	4	5%
Switzerland	4	5%
Germany	2	2%
Netherlands	2	2%
Austria	1	1%
Israel	1	1%
Total	**84**	**100%**

DISTRIBUTION PER INSTITUTION



Institution Type	Count	Percentage
Academic / Government	68	81%
Commercial	9	11%
Hospital	3	4%
Non-Profit	4	5%
Total	**84**	**100%**

DISTRIBUTION PER LIFE SCIENCE AREA



Life Science Area	Count	Percentage
Genetics	47	56%
Research	11	13%
Oncology	6	7%
Microbiology	6	7%
Neuroscience	3	4%
Reproductive	1	1%
Agriculture	4	5%
Biotech / Pharma	3	4%
Infectious Disease	1	1%
Aging Research	2	2%
Total	**84**	**100%**

Analysis

Utilization:

Utilization of existing Illumina equipment remains high, with the majority (20% of respondents) of labs we spoke with running backlogs of 1 month or more. We also asked about the direction of utilization, and 56% of respondents told us that their lab's genome sequencing usage has increased on a year-over-year basis. We think this implies strong consumables demand ahead, and demand for additional hardware; utilization is something we'd recommend to track on a regular basis to determine directional trends.

Intent to Purchase over the following 12 months:

The IlluminaNextSeq 500 was the most often sited Illumina product to be purchased next year, with 35% citing plans to purchase within the next year. This was followed by interest in the HiSeq 2500Illumina platform, with 24% of respondents citing plans to purchase. Obviously many were uncertain of their purchasing intent, or which model they would ultimately chose, but Illumina was the platform of choice; we'd recommend to track this metric on a regular basis as we approach year-end.

Outsourcing:

Given the high cost of consumables and the high cost of the equipment itself, many of the institutions we spoke with preferred outsourcing their sequencing needs to contractors (such as to BGI, among others). 17% of scientists we spoke with contracted out their sequencing needs to some extent. This is a trend that we'd recommend tracking on a regular basis to see if this shift towards outsourcing grows.

Budget Trajectory:

Our respondents' 2015 budget expectations was certainly a positive for Illumina, with 27% expecting a budget increase in 2015.

Complaints with Illumina products:

The most common complaint we heard from our conversations with scientists was, unsurprisingly, limited read lengths, with 36% citing this is as a complaint. A number of the scientists we spoke with, however, "forgave" Illumina for read

length limitations, as they assumed the technology will eventually catch up in that regard.

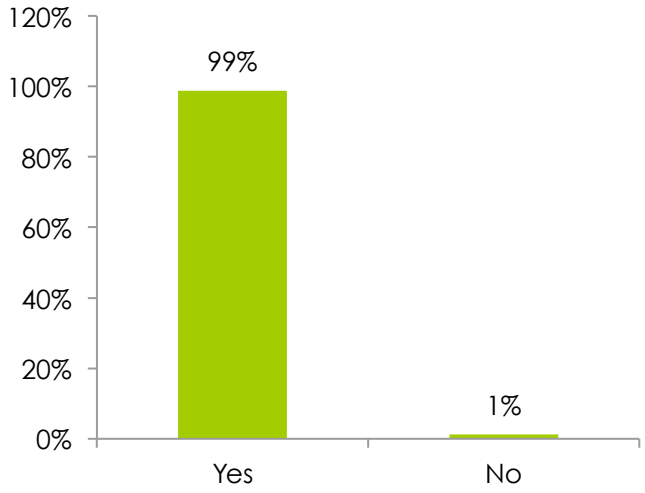
Another frequent complaint was the high cost of reagents, with 16% of scientists citing this is an issue. Some of the labs we spoke with talked about the advantage of outsourcing their genome sequencing needs, given this cost.

Data analysis was another one of the largest complaints among the scientists we contacted – that the analysis of a huge amount of complex data generated from sequencing studies is the biggest roadblock to completing a project, not the sequencing itself. A few labs complained about the lack of bioinformaticists talent (that they can afford to pay) as hampering their productivity. Many of the longer read lengths were too cumbersome for their lab technicians to analyze, given the large amount of data created, and this limits the ability to interpret results properly. Library prep was also sited as difficult to use, and software upgrades were considered difficult.

Other complaints related to high failure rates, and limitation w/ de novo genome assembly (assembly without a reference genome). We even heard of a request for single molecule sequencing from one of the head scientists we spoke with, as a potential solution to high failure rates.

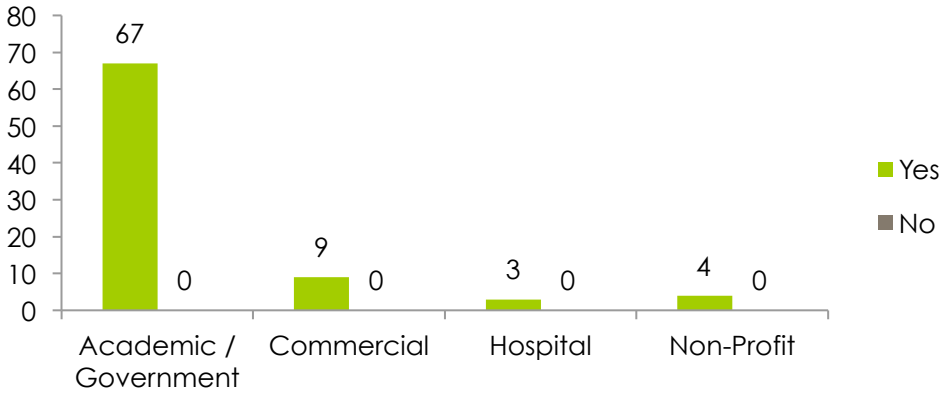
QUESTION 1

Do you (or your facility) currently use next-gen genome sequencing equipment?



Response	Count	Percentage
Yes	83	99%
No	1	1%
Total	**84**	**100%**

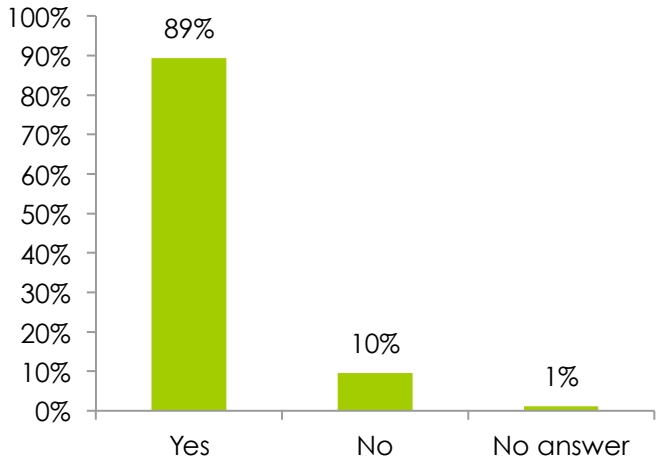
Response by Institution



Response	Academic / Government	Commercial	Hospital	Non-Profit
Yes	67	9	3	4
No	0	0	0	0
Total	**68**	**9**	**3**	**4**

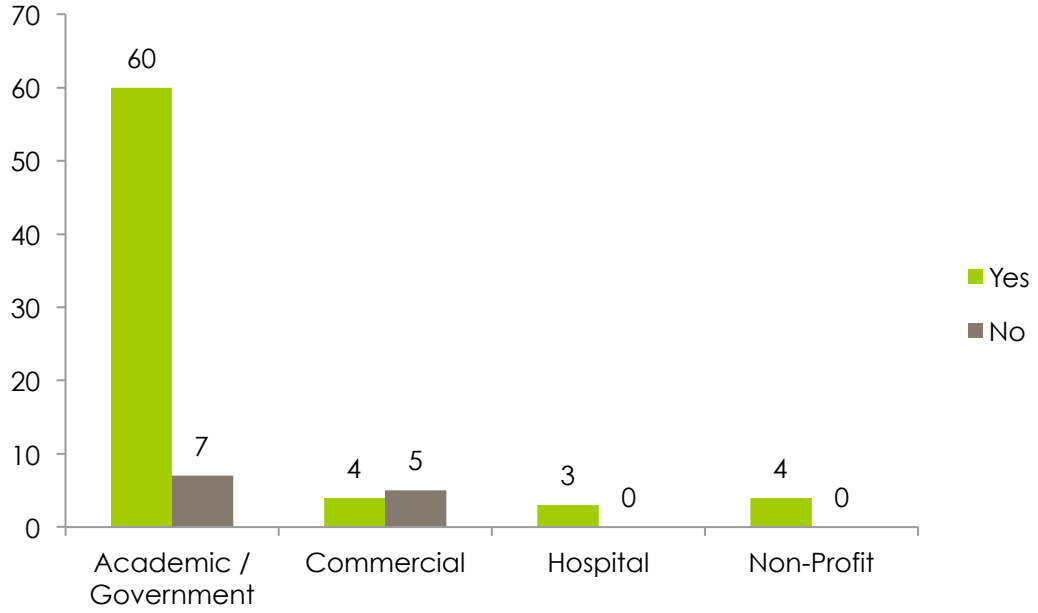
QUESTION 2

Does your facility currently own and use Illumnia equipment for genome sequencing?



Response	Count	Percentage
Yes	75	89%
No	8	10%
No answer	1	1%
Total	**84**	**100%**

Response by Institution



Response	Academic / Government	Commercial	Hospital	Non-Profit
Yes	60	4	3	4
No	7	5	0	0
Total	**67**	**9**	**3**	**4**

Comments:

- Depending on the technology there are different wait times for different technology so it's difficult to answer this question based on general Next Gen sequencing. For 454 there is essentially no wait time and within a week or two you can have your results. But on HiSeq platform we have a wait time of 5 months right now. And with a Pact Bio system it's within a week or 2 again.(Genome Québec Research Institution,Montréal,Canada)

- 1 month of wait time, It varies a lot. If you are using an entire flow cell then you might be able to get on right away but if you are defusing one lane further people to see the lane (Department of Biology, University of Rochester,Rochester,NY,USA)

- No wait time to use the equipment, usually always available, max 2 days. If my sample is ready, I don't have to wait because the pre-processing is there that is Gen extractor and today I start my sequencer and by tomorrow my run is over. (National Centre for Preclinical Reproductive & Genetic Toxicology ,Mumbai, India)

- It's very less for relatively small samples like MiSeq we can definitely get in on incite in 1 week and we also have kind of a co-operative sharing programs where you can do a test run that is less than a full lane and you can get it in a couple of days. Actually you can hop in on someone's lane actually.(The Genome Institute at Washington University, St. Louis, MO, USA)

- 2 weeks to 2 months; it depends on the lab (Center for Functional Genomics University at Albany-Suny,Albany,NY,USA)

- It depends on where we sequence, time of year and backlog. It could be anything from 2 days with MiSeq to 2 weeks for HiSeq equipments(UC Davis Genome Center,Davis,CA,USA)

- No wait time to use the equipment, usually always available, occasionally 1-2 wait period (Scripps Translational Science Institute, La Jolla,CA,USA)

- It depends on as much as the shop has on the equipment(The Genome Institute at Washington University,St. Louis,MO,USA)

- For the MiSeq's its 1-2 weeks and for the HiSeq's is upto a month.(Cornell University Department of MolecularBiology and Genetics,Ithaca,NY,USA)

- Currently contracting and wait times are variable or too long (DNA Reference Laboratory,San Antonio,TX,USA)

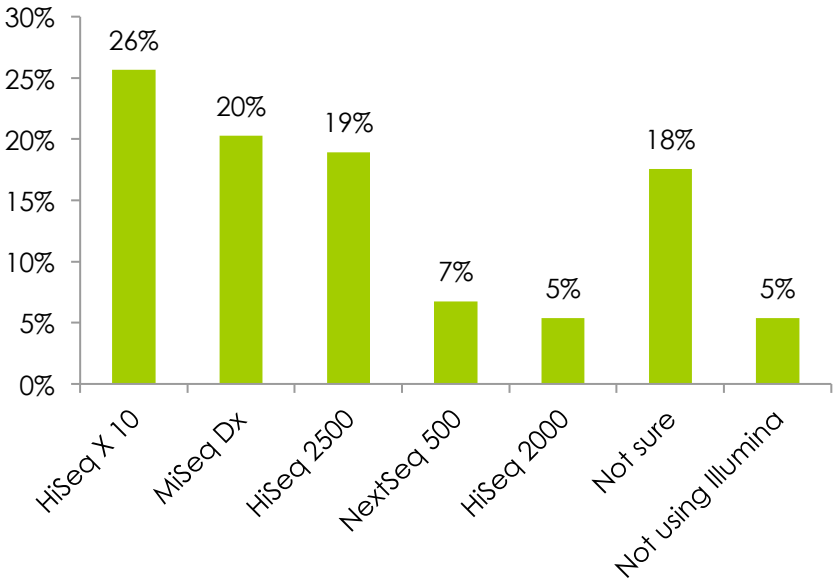
- 2 to 4 weeks of wait time, starting from library preparation, clustering and sequencing takes 2-3 weeks at max.(Forest Genetics and Tree Breeding, Coimbatore,India)

- a few days , we have a straight contract so we exactly know how much we need the equipment per month so no long waiting (Genomic Research Laboratory,Geneva,Switzerland)

- It really depends on what it is and where and our local sequencing facilities can take something between 1 week to a month. Some of the companies can turn it around in few days with less Bioinformatic supporters.(The University of British Columbia,British Columbia,Canada)

QUESTION 3

Which Illumnia products do you use (select as many as apply)?



Response	Count	Percentage
HiSeq X 10	19	26%
MiSeqDx	15	20%
HiSeq 2500	14	19%
NextSeq 500	5	7%
HiSeq 2000	4	5%
Not sure	13	18%
Not using Illumina	4	5%
Total	**74**	**100%**

Comments:

- It fluctuate depends on what one is doing and what samples one has ready to go and things like that (The Genome Institute at Washington University, St. Louis, MO, USA)

- No change, we have downsized a bit, but it does not change our production. We had a big influx with 2 year fellowships, but those are done now. (Cal Berkeley, School of Life Sciences, Berkeley, CA, USA)

- It has been decreasing as of late, but we're gearing up for more. So it's really variable. (Yeshiva U Dept of Genetics, Bronx, New York, USA)

- We have just started to use (The Genome Institute at Washington University, St. Louis, MO, USA)

- Increased as all of my project is based on NGS and it is up by 30-35% (Forest Genetics and Tree Breeding (IFGTB), Coimbatore, India)

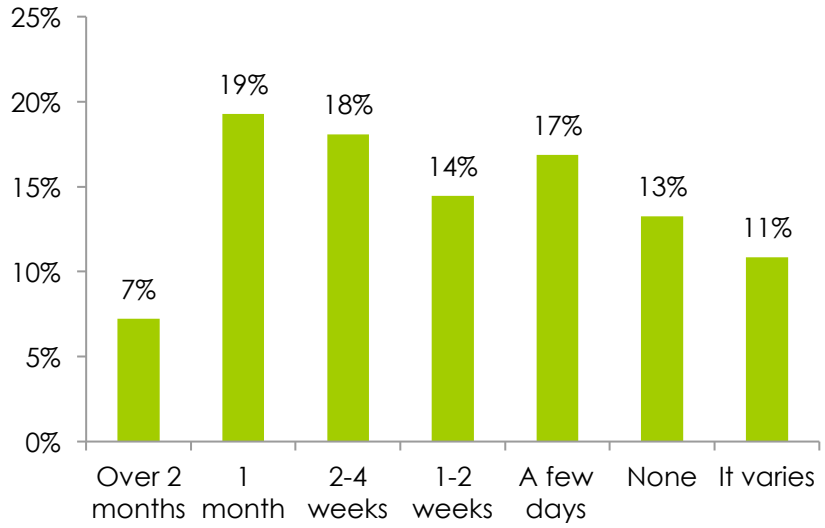
- Increasing, 15-20%. It has increased because in general people have started to use it more and they are trying to tap the facility of NGS more and trying to derive more information out of which the data which is available. (Rajiv Gandhi Centre for Biotechnology, Thiruvananthapuram, Kerala, India)

- Increasing, Our machine is new, but we are doing more of this work than last year. (Active Motiff, Carlsbad, California, USA)

- No change, Due to lack of funding we are not doing much of utilization (The University of British Columbia, British Columbia, Canada)

QUESTION 4

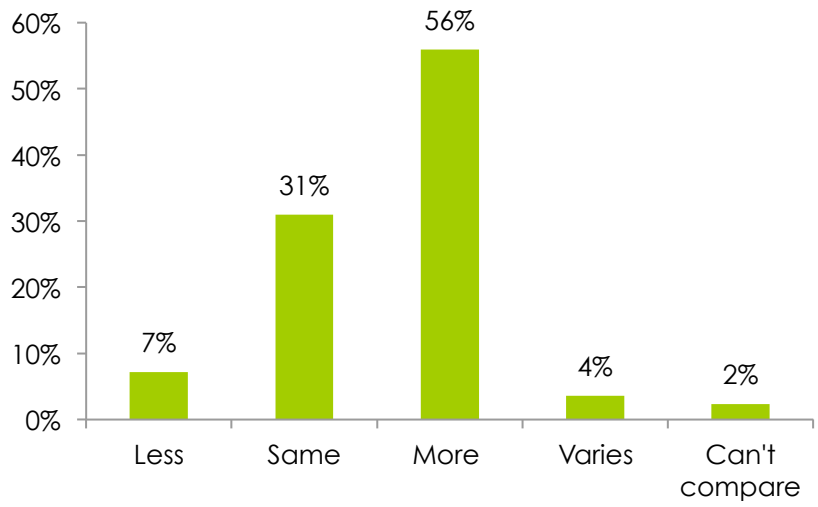
What is the wait time to use the Illumina equipment in your lab?



Response	Count	Percentage
Over 2 months	6	7%
1 month	16	19%
2-4 weeks	15	18%
1-2 weeks	12	14%
A few days	14	17%
None	11	13%
It varies	9	11%
Total	**83**	**100%**

QUESTION 5

Are you utilizing Illumina equipment more or less, relative to last year?



Response	Count	Percentage
Less	6	7%
Same	26	31%
More	47	56%
Varies	3	4%
Can't compare	2	2%
Total	**84**	**100%**

Comments:

- I find it more user friendly for the computational, which is what I do. We have better control of the extent of coverage. (U of North Texas, Fort Worth, Texas, USA)

- I would say the advancement of the services what we are doing is the Bio Informatics Analysis (The Genome Institute at Washington University, St. Louis, MO, USA)

- Different technologies have different pros & cons so it's difficult to give generalized response to this question. If I say ease of preparation of libraries it is ok with Genomic DNA but it's more complex when it comes to capture

technologies even if your end product is on a HiSeq instruments. Different applications requires different things and which in some cases is heavier than other in terms of time, reagents and delays so there is not a single answer. (Genome Québec Research Institution, Montréal, Canada)

- We like the quality of the sequencing and the output--the yield. (U of Illinois High Throughput Sequencing and Genotyping Unit, Urbana, IL, USA)

- The number of reads is very important for us. (Life Sciences, The University of Manchester, Manchester, UK)

- Ability to annotate transcriptase of un-sequenced organisms. (Institute of Integrative Biology, Liverpool, UK)

- It's the volume of the data so we can generate an awful amount of data in a few runs. So that's the real advantage when you try to do big studies (Ophthalmology and Molecular Biology & Genetics Johns Hopkins UniversitySchool of Medicine Institute of Genetic Medicine, Baltimore, MD, USA)

- The error rates are extremely low. The quality, though, is high. The capacity in the machine we use is extremely large. If you have a large library, then you'll have a lower number of duplicates. If you have a small library, then the chance for duplication is greater. There is less chance of duplication with more material. (Translational and Functional Genomics Branch of National Human Genome Research Institute, Rockville, Maryland, USA)

- We only use Illumina. We like their work and really specifically chose it for cost and throughput. They provide some very good tools for analyzing. (Cal Berkeley, School of Life Sciences, Berkeley, CA, USA)

- We have been mutliplexing, so the throughput is wonderful. (Yeshiva U Dept of Genetics, Bronx, New York, USA)

- With next-gen you get huge amount of data relatively quickly and cheaply. I like getting lots of data. (The Genome Institute at Washington University, St. Louis, MO, USA)

- I guess compared to some other sequences we had in the past this one has higher capacity that's what I care high support & better. (The Genome Institute at Washington University, St. Louis, MO, USA)

- Earlier we have been using common mutation for CFTR but with the use of NGS its possible to do the entire Gene home. CFTR there had been lot of issues like compound hit and we get lot of mutation but due to Indian population common mutation is not possible and had lot of restriction. With the sequencing we get lot of rare diseases. (Institute of Human Genetics, Ahmedabad, Ahmedabad, Gujarat, India)

- If the client requests something, then it is usually Illumina. Sometimes the Life Technologies is requested, but no brand is specified. But I don't think it makes much difference. They're pretty much the same. (Center for Functional Genomics University at Albany-Suny, Albany, New York, USA)

- The great thing about Illumina is its combination of no air rates and hi tree port rates so we get a lot of reads and the lower range and are really low (Cold Spring Harbor Laboratory (CSHL), Cold Spring Harbor, NY, USA)

- Accuracy. I probably can't add much else, because accuracy says it all. Yes, we are satisfied with the accuracy we get. We don't worry too much about other items because we leave this part to the experts. We do, thought, some over the sequencing. We still do it manually--the checking. We're very conservative. (Amarantus Bioscience Holdings, Sunnyvale, California, USA)

- The speed. You can get the results out in 2-3 days. (Scripps Translational Science Institute, La Jolla, California, USA)

- Ability to talk to the Bio informative people, its bio-analysis and data. (Institute of Integrative Biology, Liverpool, UK)

- depends if we want to close genome of if we do analyses more useful for projects (Genomic Research Laboratory, Geneva, Switzerland)

- I am not a direct user, but know that reproducibility of Illumina reads for the time it takes to sequence is better than other existing or beta technologies. (New York, USA)

- Exome Sequencing. RNAseq(New York, USA)

- Whole genome approaches. (Ohio, USA)

- One thing I value the most is consumable price that's an important consideration while choosing the contract company. (The Genome Institute at Washington University, St. Louis, MO, USA)

- The biggest factor is always money so its cost per GB pare (per run). The minor things are read lengths especially with MiSeqs and then also ease of use, flexibility. (Cornell university department of molecular biology and genetics, Ithaca, NY, USA)

- 1st thing is Illumina is most popular and commonly used so you can compare results and 2nd is lower cost (Ontario Genomics Institute, Toronto, ON, Canada)

- As a scientist I value the data quality the most at this time. (The Genome Institute at Washington University, St. Louis, MO, USA)

- Swiftech salad system and Gene &Nanopore systems are more experimental than productions. Accuracy is the one thing I like the most (Department of Genetics Harvard Medical School, Boston, MA, USA)

- Illumina provides good depth in sequencing and the cost of Illumina sequencing comparatively is less and that actually fits my budget. My reason for using Illumina is its pretty cost effective in terms of our Indian scientific scenario so we are able to do lot of runs and are able to generate lot of data. The second part is the read depth is very high in Illumina basically when I am doing a target enrichment & re-sequencing. (Forest Genetics and Tree Breeding (IFGTB), Coimbatore, India)"

- Quality, read lengths and the amount of data which we receive. (Rajiv Gandhi Centre for Biotechnology, Thiruvananthapuram, Kerala, India)

- I'd say probably the throughput. It's really a combination of the throughput and the cost. Yes, that is the value. (Washington U Genome Institute, St. Louis, MO, USA)

- It's the newest system that we have in the department, 454 is an old technology. Illumina has high output but read length is short compared to 454. But probably accuracy is higher compared to ion torrent. (Department of Genetics, University of Leicester, Leicester, UK)

- The volume is really good. It's a nice multiplex. The issue is that you have to save up so many samples to run unless you're doing something large. The old Sanger was really better. But you can still do about 900 reads--maybe a 1000 reads with an average quality value of 30. The disadvantage though, is low throughput. (J Craig Venter Institute, Rockville, Maryland, USA)

- We knew we needed a lot of coverage. We need 50 million reads per sample. We like that the Illumina does multiplexing. (Active Motiff, Carlsbad, California, USA)

- the equipment itself is great and useful (Institute of Integrative Biology, Zurich, Switzerland)

- I just like the turnaround time. Nothing though really sticks out for anything else. (ActivX Biosciences, La Jolla, California, USA)

- Ease of use, quality of sequence data (Massachusetts, USA)

- Reliability, reproducibility, throughput, service &support (New Mexico, USA)

- I like that I can send out a piece of DNA and they clean it up and send it back. (Agdia, Elkhart, IN, USA)

- I like the maximum reads. Get can get about a million off one chip. And actually, we can get up to 18,000,000 reads depending on the chip. (Base Pair Technologies, Houston, Texas, USA)

- Very user-friendly modules for the next-seq, such as better flowcells. (Massachusetts, USA)

- Low error rate, low cost, well established pipelines within our institution (California, USA)

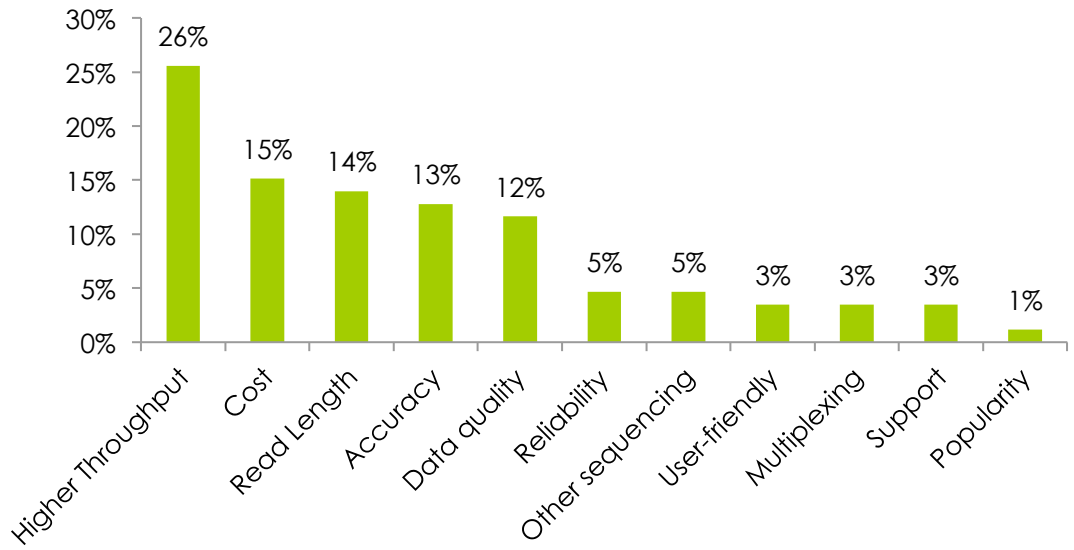
- We like the reliability of the results. What we use is high quality. (National Institute of Mental Health, Bethesda, Maryland, USA)

- Yes I think the amount of data which we get in Roche is not something as good as illumina. Because Illumina gives us more data for our research. (Institute of Genomics and Integrative Biology Metagenomics, India)

- shorter rapid read mode run times (Rotterdam, The Netherlands)

QUESTION 6

What features of your lab's Illumina equipment do you personally value the most?



Response	Count	Percentage
Higher Throughput	22	26%
Cost	13	15%
Read Length	12	14%
Accuracy	11	13%
Data quality	10	12%
Reliability	4	5%
Other sequencing abilities	4	5%
User-friendly	3	3%
Multiplexing	3	3%
Support	3	3%
Popularity	1	1%
Total	**86**	**100%**

Comments:

- We prefer to have a little more validation in this proprietary software. This is in the context of mitochondrial sequencing. Not all of the variance has an equal signal. So we need to have a significant number of coverage so that we can differentiate between the signals. (U of North Texas, Fort Worth, Texas, USA)

- BioInformatics was the only thing that could be improved. Yes other things I feel is longer reads and etc but that's a technology that that will happen. (The Genome Institute at Washington University, St. Louis, MO, USA)

- It's very technology dependent. The HiSeq instruments will provide 100 to 150 base spares reads where the Roche 454 technologies allows you to go to 800 and the Pact pile allows you to go to 10 KB so clearly different technology providers have developed their own niche so in a way, it depends on what you want to do. If you want to do a Bacterial Genome then the Pact pile system is the best technology to use for that reason. If you want to do Human genomic DNA to be sequenced Pact pile is not the best technology because it doesn't have the depth regardless of the read lengths so different technologies have different applications. (Genome Québec Research Institution, Montréal, Canada)

- The MiSeq can be unreliable. These machines we have are old for what we do. That's why we might look into something more updated. We're looking at the NextSeq 500. (U of Virginia School of Medicine, Charlottesville, VA, USA)

- Read length is really the limitation of all the next gen equipments and other than some of the thing which are just coming up in the market. Its less an issue with the pact pile instruments. Real problem is when you are trying to put genome sequences it is a problem when short read lengths and I do feel like having a read length of couple of thousand base lengths but that's not possible with the equipment's. Though there are some ways around it and we will be testing it with the technology that's been released with Illumina. (Ophthalmology and Molecular Biology & Genetics Johns Hopkins University School of Medicine Institute of Genetic Medicine, Baltimore, MD, USA)

- The reagent cost is very high, the failure rate is larger than I would like and the documentation is, in many cases, poor. (Washington, USA)

- The run time is two weeks, but that is too long. The entire process is 4-6 weeks, but run time is two. We'd actually like to get that down to a couple of days. (U of Illinois High Throughput Sequencing and Genotyping Unit, Urbana, Illinois, USA)

- Next generation sequencing is very good but the cost factor is there. For every sample is a long sequencing and hence, huge data is generated and its good for high throughput study also but eventually we don't have experts in our lab who will manage the data maximize the sense and that is what we are lacking. For short sequences we can manage with the help of our technicians. (National Centre for Preclinical Reproductive & Genetic Toxicology , Mumbai, Mumbai, India)

- The polymerases are not optimized for doing out of box sequencing. What that means is--it has to do with finishing. You have to recheck the sequencing and refine to eliminate the mistakes and close gaps. You might see something two or three times and that's not correct. (Translational and Functional Genomics Branch of National Human Genome Research Institute, Rockville, Maryland, USA)

- We don't generate a lot on our own, but are happy with what we do and the equipment. When we do the computational, we have to rely on those people. My impression is that the people who do this are happy with the process. (Cal Berkeley, School of Life Sciences, Berkeley, CA, USA)

- The biggest block is the bioinformatcis. There are not enough talented bioinformaticists that we can hire--that we can pay. You then end up waiting a long time for data analysis. Then it's not what you wanted. So it's not the sequencing equipment itself that is the roadblock. (Yeshiva U Dept of Genetics, Bronx, New York, USA)

- I think longer reads would help just because of getting more information/data helps. (National Human Genome Research Institute, Bethesda, MD, USA)

- We have a very specific kind of limited usage and it's like a right up the alley what we are trying to optimize all the time so relatively short reads, I know longer reads are better but they are pretty long for us now and they are getting cheaper and getting more reads per lane all the time so it seems to be a nice resource and adequate what we need right now. (The Genome Institute at Washington University, St. Louis, MO, USA)

- If Illumina can become more pact file and give us 2KB reads that will be fantastic. But the air rates of those reads are so awful right now. (Cold Spring Harbor Laboratory (CSHL), Cold Spring Harbor, NY, USA)

- I would love to see the Improved Analysis Softwares(The University of British Columbia, British Columbia, Canada, USA)

- Again, I could not really add much because it's accuracy we look at. Accuracy, accuracy, accuracy. And they do a good job with that. (Amarantus Bioscience Holdings, Sunnyvale, California, USA)

- Longer read lengths as that's the problem with the research we face; it's not the technology to improve but a need to improve to work more efficiently. (Associate Professor, UC Davis Genome Center, Davis, CA, USA)

- Capacity. We'd like to generate more data with initial information that is fed in. Also, the Read Lengths. These machines have a specific setting that can't be adjusted. We want to be able to look at less little pieces. Illumina is coming out with machines that allow you to look at longer strands. They combine the pieces for the longer Read Lengths. (Scripps Translational Science Institute, La Jolla, California, USA)

- maybe reduce the cost , decreasing a lot the error rate, could reduce the length of the read (Genomic Research Laboratory, Geneva, Switzerland)
- Actually I'll be the worst person to recommend. As far as I know, library prep should be simplified, but no idea how can the equipment be improved. (New York, USA)

- Reliability. Our machine often breaks down. (Ohio, USA)

- Less consumable price (The Genome Institute at Washington University, St. Louis, MO, USA)

- Longer read lengths and lesser cost for the instrumentation. To upgrade the instruments they are very expensive to upgrade (Cornell university department of molecular biology and genetics, Ithaca, NY, USA)

- I would like to see single molecule sequencing. It kind of technical feature but right now there are many copies of same molecule generated prior to the sequencing process and then you actually are getting the redials of each of these copies trying to guess what the original copy looks like so called consensus sequencing and I will like to look at the true single molecule sequencing where you are not making any copies ahead of time you are just reading directly from whatever DNA was put in to the machine that would be one thing which I think will be very helpful. (The Genome Institute at Washington University, St. Louis, MO, USA)

- If the cost will come down it will be better as we can do more but the technology is good. If it can be like 300 base, it's easier to find out the diffusers. (Department of Genetics, University of Madras, Madras, India)

- They do not use the equipment directly, but the wait times need to be really reduced. (DNA Reference Laboratory, San Antonio, TX, USA)

- Longer read will be easy to handle to data because with a short read sometimes when we do the Denovo lots of artifacts are coming. So one problem with Illumina when it comes to Denovo assembly we do face some problems because of the short read length and we do go wrong in our assembly. (Forest Genetics and Tree Breeding (IFGTB), Coimbatore, India)

- One thing I would like to point out is because of which we do lot of running around is awareness of Statistical application and software. We at our end do not get timely update regarding the latest version of software which will go well with the equipments we have so its lack of information at our end and I request that the equipment manufacturers should keep updating all the institution about the same in a timely manner. (Rajiv Gandhi Centre for Biotechnology, Thiruvananthapuram, Kerala, India)

- None really. We really looked into this and did our homework. We used the HiSeq 2500 with our company that we outsourced from, but that cost was just too much for us since we're a new company. We got the NextSeq because it was sort of in-between among the offerings. (Active Motiff, Carlsbad, California, USA)

- The protocols can be sometimes incomplete some small error can destroy a whole cartridge and that's annoying and bad (Institute of Integrative Biology, Zurich, Switzerland)

- Reagent cost (New Mexico, USA)

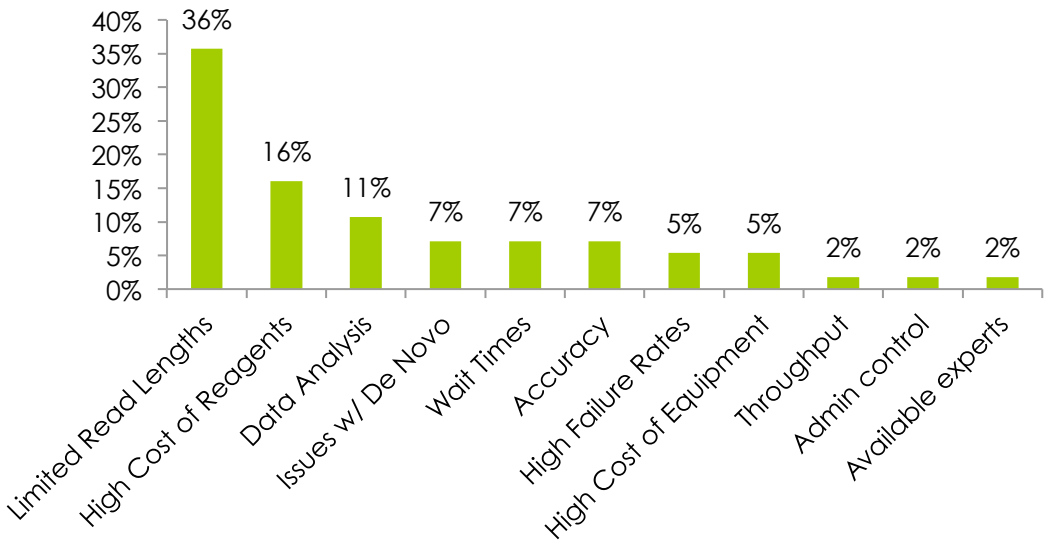
- The cluster numbers are always hard to hit right. FFPE material routine would be nice. (New York, USA)

- Have a system where the administrator has more control over the users' usage (Massachusetts, USA)

- We'd like even better quality. But that is more the internal lab and there isn't much we can do about that. Sometimes there might be duplication, like the read is the in the same place twice or three times. It's just that we can't verify ourselves. (National Institute of Mental Health, Bethesda, Maryland, USA)

QUESTION 7

What features of your lab's Illumina equipment do you personally think could use improvement?



Response	Count	Percentage
Limited Read Lengths	20	36%
High Cost of Reagents	9	16%
Data Analysis	6	11%
Issues w/ De Novo Genome Assembly	4	7%
Wait Times	4	7%
Accuracy	4	7%
High Failure Rates	3	5%
High Cost of Equipment	3	5%
Throughput	1	2%
Admin control	1	2%
Available experts	1	2%
Total	**56**	**100%**

Comments:

- I would say in the Canadian environment right now for the major funding agencies the funding has not increased it been the same. (Genome Québec Research Institution, Montréal, Canada)

- Overall it's got decreased from last year for all our service 5-10% down as a net ball park. Sequencing is up but everything else which makes overall the budget is down. (Ophthalmology and Molecular Biology & Genetics Johns Hopkins University School of Medicine Institute of Genetic Medicine, Baltimore, MD, USA)

- Up 5% (But it depends on funding). Recently we bought 20 Lacks Instrument i.e, Bio chemical Analyzer. (Institute of Human Genetics, Ahmedabad, Ahmedabad, Gujarat, India)

- Up 50%. Our budget was not great last year. It was sort of an abnormal year, so that's why the increase. (Amarantus Bioscience Holdings, Sunnyvale, California, USA)

- It is all depended on our grant funding. Overall its down but for us its up by 200% (Associate Professor, UC Davis Genome Center, Davis, CA, USA)

- For my lab we have been very successful so our budgets have increased. Technically speaking, a year ago, I had 0 grants and now I have 3 and half grants. That has happened in the past year. I am a new investigator so things have been scaling up. (The Genome Institute at Washington University, St. Louis, MO, USA)

- Last year it was down due to the government problem and this year it's getting better. It's on the rise. (Department of Genetics, University of Madras, Madras, India)

- It depends on funding from Government of India and to do NGS we have asked for 30% increase for 2 years continuously. (Forest Genetics and Tree Breeding (IFGTB), Coimbatore, India)

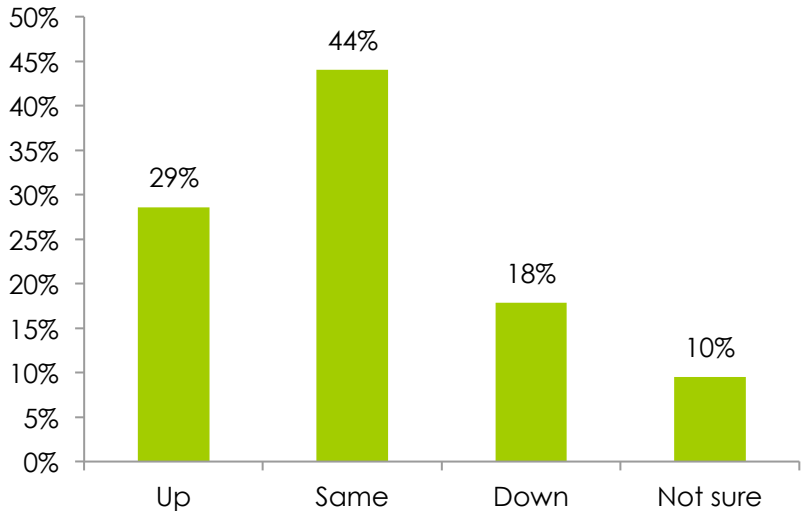
- Flat. This year we are still waiting to get an update about the funding but I am sure its at least same what we had last year. (Rajiv Gandhi Centre for Biotechnology, Thiruvananthapuram, Kerala, India)

- It's just more difficult to get funded. It's down, but I don't know how much. (J Craig Venter Institute, Rockville, Maryland, USA)

- Budgets are higher by (50%) but that's coming from last year's almost nothing, so still not a lot (The University of British Columbia, British Columbia, Canada)

QUESTION 8

Did your research budget increase or decrease in 2014?



Response	Count	Percentage
Up	24	29%
Same	37	44%
Down	15	18%
Not sure	8	10%
Total	**84**	
Average		**10.30%**

Comments:

- Could be down 25%, but it is significant. *(U of North Texas, Fort Worth, Texas, USA)*

- It may drop by 10% because the Government's in power right now in Canada & Quebec seems to give priority to other area besides research. *(Genome Québec Research Institution, Montréal, Canada)*

- I think it will be flat and it depends a lot with what happens with Congress the CNHI budget. *(Ophthalmology and Molecular Biology & Genetics Johns Hopkins University School of Medicine Institute of Genetic Medicine, Baltimore, MD, USA)*

- Same. We're getting a grant this year, and it's the same one. *(Yeshiva U Dept of Genetics, Bronx, New York, USA)*

- I expect it will be flat for us as we are not a huge user in campus. *(The Genome Institute at Washington University, St. Louis, MO, USA)*

- Yes we are planning to increase 5% *(The Genome Institute at Washington University, St. Louis, MO, USA)*

- Difficult to answer because we are Cost recovery operation so our budget basically breaks even but I think it will go up by 10% *(Cornell university department of molecular biology and genetics, Ithaca, NY, USA)*

- Go up slightly as my appetite for weeding grants are slowing down a little bit now and we have got funded so I am trying to bring highly qualified people to do the work I have been funded to do. So optimistically I think my budget will increase by 10%. *(The Genome Institute at Washington University, St. Louis, MO, USA)*

- Up (50%). This is what I feel because it's a really visionary type of management over there then the budget has to go up for Science. *(Rajiv Gandhi Centre for Biotechnology, Thiruvananthapuram, Kerala, India)*

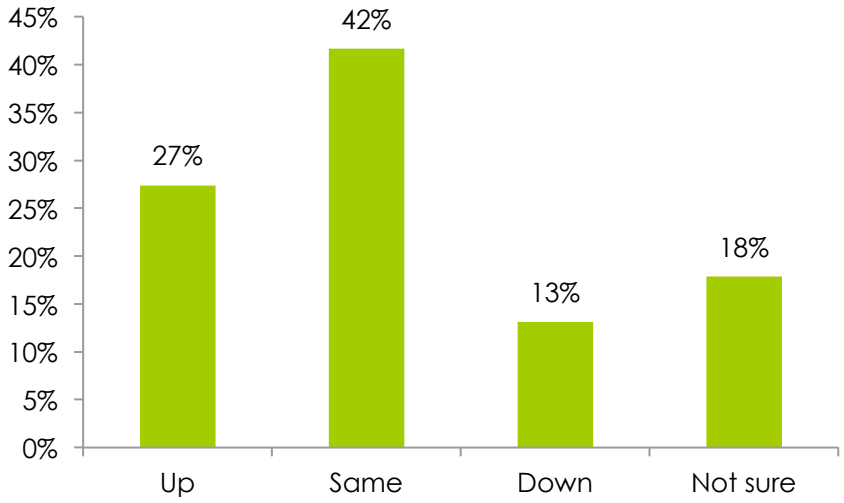
- Grant application has been placed so there could be some expectation of an increase. *(Department of Genetics, University of Leicester, Leicester, UK)*

- At this point it can only go up. *(J Craig Venter Institute, Rockville, Maryland, USA)*

- Hard to say because it will either go up a lot or down a lot depending on the requirement. *(The Genome Institute at Washington University, St. Louis, MO, USA)*

QUESTION 9

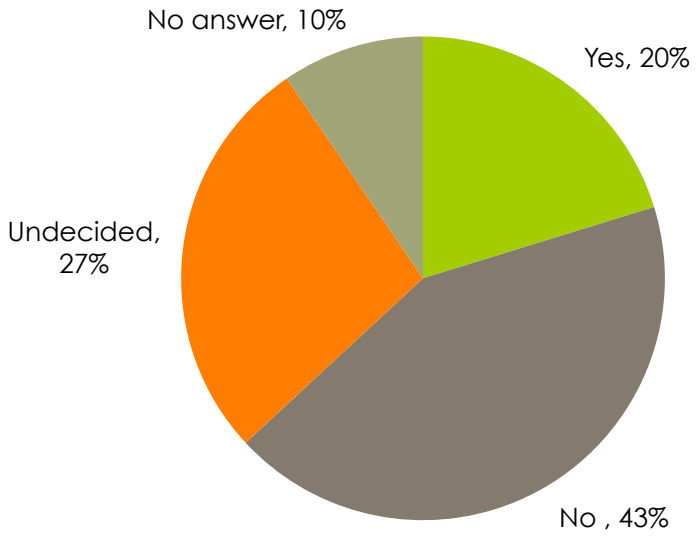
What do you expect for your 2015 budget?



Response	Count	Percentage
Up	23	27%
Same	35	42%
Down	11	13%
Not sure	15	18%
Total	**84**	
Average		**2.34%**

QUESTION 10

Does your facility plan to purchase additional genome sequencing and/or diagnostic equipment over the next 12 months?



Response	Count	Percentage
Yes	17	20%
No	36	43%
Undecided	23	27%
No answer	8	10%
Total	**84**	**100%**

Comments:

- Not really in the next year, but that could change. (U of North Texas, Fort Worth, Texas, USA)

- Yes, we are hope to start up a clinical service so we will be buying equipments dedicated to that use (Ophthalmology and Molecular Biology & Genetics Johns Hopkins University School of Medicine Institute of Genetic Medicine, Baltimore, MD, USA)

- It is decided by CGR, they do everything related to it. (Institute of Integrative Biology, Liverpool, UK)

- Not thinking of buying because of the budget (National Human Genome Research Institute, Bethesda, MD, USA)

- We will not buy one in our lab. Because they core facility they always try to upgrading in they usually have couple of HiSeq running there and MiSeq so I don't know what their plans are but they always kind of keeping up with the latest technology. They also do library preparation but we tend to not use that facility (The Genome Institute at Washington University, St. Louis, MO, USA)

- Yes we are planning because we are running out of capacity. The equipment we still have to decide its up in the air as we are not married to Illumina whatever will be the best we will go for that. (The Genome Institute at Washington University, St. Louis, MO, USA)

- No because we have funding issues and 1 equipment costs 50 Lack to 1 Core. (Institute of Human Genetics, Ahmedabad, Ahmedabad, Gujarat, India)
- No happy with core facility (Cold Spring Harbor Laboratory (CSHL), Cold Spring Harbor, NY, USA)

- No we will be using through a new contract shop (The Genome Institute at Washington University, St. Louis, MO, USA)

- Yes we are trying to if we scrape up the money (Cornell university department of molecular biology and genetics, Ithaca, NY, USA)

- No we will continue using the ones available through our core facility (Weizmann Institute of science Department Genetics, Rehovot, Israel)

- I should mention that fair amount of our research we do is service mode that is what we outsource. So we will either need services or the equipments it doesn't really matter. So sometimes we send thing to china for example so the geographical location doesn't matter. (Department of Genetics Harvard Medical School, Boston, MA, USA)

- No. I would love to own one but right now the issue is maintaining will be a problem and even using that and consumables will also be a problem so I would prefer the outsource service (Department of Genetics, University of Madras, Madras, India)

- We plan to buy, but I don't know the brands or models yet. (Washington U Genome Institute, St. Louis, MO, USA)

- Our Institute is planning on putting a core facility and as far as I know they submitted the quote for Illumina. (The University of British Columbia, British Columbia, Canada)