1. Name (optional)

		Response Count
		17
	answered question	**17**
	skipped question	**7**

2. Email (optional)

		Response Count
		17
	answered question	**17**
	skipped question	**7**

3. Type of delegate

		Response Percent	Response Count
Academic		**70.8%**	**17**
Student		12.5%	3
Corporate		4.2%	1
Other (please specify)		12.5%	3
		answered question	**24**
		skipped question	**0**

4. How did you find out about this course?

	Response Percent	Response Count
From the Australian Bioplatforms website	16.7%	4
Other website (please specify below)	0.0%	0
From an email mailing list (please specify below)	20.8%	5
From a poster (please specify below)	0.0%	0
At a conference (please specify below)	0.0%	0
Word of mouth/recommendation	**62.5%**	**15**
Other (please specify)	12.5%	3
	Other (please specify)	5
	answered question	**24**
	skipped question	**0**

5. What aspect of the workshop/training prompted you to register?

	Response Count
	24
answered question	**24**
skipped question	**0**

6. How useful did you find the following sessions? Please use the text box below to provide specific comments on the programme.

	Not useful (please justify)	Indifferent	Useful	Essential	N/A	Rating Average	Response Count
Next generation sequencing overview	4.2% (1)	4.2% (1)	41.7% (10)	**45.8% (11)**	4.2% (1)	3.35	24
NGS quality control and sequence alignment	0.0% (0)	0.0% (0)	33.3% (8)	**66.7% (16)**	0.0% (0)	3.67	24
Introduction to ChIP-seq	12.5% (3)	8.3% (2)	**41.7% (10)**	29.2% (7)	8.3% (2)	2.95	24
ChIP-seq analysis - peak calling and annotation	8.3% (2)	25.0% (6)	20.8% (5)	**37.5% (9)**	8.3% (2)	2.95	24
ChIP-seq analysis - motif analysis	8.3% (2)	**33.3% (8)**	20.8% (5)	29.2% (7)	8.3% (2)	2.77	24
Introduction to RNA-seq	0.0% (0)	0.0% (0)	33.3% (8)	**66.7% (16)**	0.0% (0)	3.67	24
Alignment and slice junction identification	0.0% (0)	4.2% (1)	33.3% (8)	**62.5% (15)**	0.0% (0)	3.58	24
Transcriptome assembly	0.0% (0)	0.0% (0)	29.2% (7)	**70.8% (17)**	0.0% (0)	3.71	24
Differential expression analysis	0.0% (0)	0.0% (0)	41.7% (10)	**58.3% (14)**	0.0% (0)	3.58	24
Introduction to de novo assembly	0.0% (0)	4.2% (1)	37.5% (9)	**58.3% (14)**	0.0% (0)	3.54	24
De novo assembly using velvet	0.0% (0)	16.7% (4)	29.2% (7)	**54.2% (13)**	0.0% (0)	3.38	24
Review and discussion of Velvet de novo assembly exercises	4.2% (1)	16.7% (4)	29.2% (7)	**45.8% (11)**	4.2% (1)	3.22	24
						Specific comments on topics and the programme	12
						answered question	**24**
						skipped question	**0**

7. What other topics would you like to have seen covered and at what level would you like it to be set?

	Response Count
	24
answered question	**24**
skipped question	**0**

8. Overall organization of the workshop and training

	Response Percent	Response Count
Excellent	**62.5%**	**15**
Good	29.2%	7
Satisfactory	8.3%	2
Poor	0.0%	0
Very poor	0.0%	0
answered question		**24**
skipped question		**0**

9. Programme/format

	Response Percent	Response Count
Excellent	**58.3%**	**14**
Good	33.3%	8
Satisfactory	4.2%	1
Poor	4.2%	1
Very poor	0.0%	0
answered question		**24**
skipped question		**0**

10. Materials provided

	Response Percent	Response Count
Excellent	**58.3%**	**14**
Good	29.2%	7
Satisfactory	12.5%	3
Poor	0.0%	0
Very poor	0.0%	0
	answered question	**24**
	skipped question	**0**

11. Facilities provided

	Response Percent	Response Count
Excellent	33.3%	8
Good	**41.7%**	**10**
Satisfactory	25.0%	6
Poor	0.0%	0
Very poor	0.0%	0
	answered question	**24**
	skipped question	**0**

12. Contents of individual presentation sessions

	Response Percent	Response Count
Excellent	**54.2%**	**13**
Good	29.2%	7
Satisfactory	16.7%	4
Poor	0.0%	0
Very poor	0.0%	0
	answered question	**24**
	skipped question	**0**

13. Clarity of presentations

	Response Percent	Response Count
Excellent	33.3%	8
Good	**37.5%**	**9**
Satisfactory	25.0%	6
Poor	4.2%	1
Very poor	0.0%	0
	answered question	**24**
	skipped question	**0**

14. Knowledge of speakers

	Response Percent	Response Count
Excellent	**87.5%**	**21**
Good	12.5%	3
Satisfactory	0.0%	0
Poor	0.0%	0
Very poor	0.0%	0
	answered question	**24**
	skipped question	**0**

15. Contents of practical sessions

	Response Percent	Response Count
Excellent	41.7%	10
Good	**50.0%**	**12**
Satisfactory	8.3%	2
Poor	0.0%	0
Very poor	0.0%	0
	answered question	**24**
	skipped question	**0**

16. Duration of sessions

	Response Percent	Response Count
Too short	20.8%	5
About right	**75.0%**	**18**
A bit long	4.2%	1
Much too long	0.0%	0
answered question		**24**
skipped question		**0**

17. Level of scientific content in the tutorial

	Response Percent	Response Count
Too general	8.3%	2
About right	**87.5%**	**21**
A little specific	4.2%	1
Much too specific	0.0%	0
answered question		**24**
skipped question		**0**

18. How do you rate tis workshop compared to similar events you have attended previously?

	Response Percent	Response Count
much better	**45.8%**	**11**
better	37.5%	9
average	16.7%	4
poorer	0.0%	0
	please explain	14
	answered question	**24**
	skipped question	**0**

19. How would you rate the practical usefulness of the tutorials as applied to your work?

	Response Percent	Response Count
Not very useful	0.0%	0
Useful	**54.2%**	**13**
Extremely useful	45.8%	11
	answered question	**24**
	skipped question	**0**

20. Would you like further training?

	Response Percent	Response Count
Yes	**100.0%**	**24**
No	0.0%	0
if yes, what would you like to see covered?		19
answered question		**24**
skipped question		**0**

21. Would you recommend this training to colleagues?

	Response Percent	Response Count
Yes	**100.0%**	**24**
No	0.0%	0
answered question		**24**
skipped question		**0**

22. On this course there should have been more opportunities for... because...

	Response Count
	24
answered question	**24**
skipped question	**0**

23. What do you think you will remember most about this course...and why?

	Response Count
	24
answered question	**24**
skipped question	**0**

24. What did you think of the catering?

	Response Count
	20
answered question	**20**
skipped question	**4**

25. Please add any other comments here

	Response Count
	11
answered question	**11**
skipped question	**13**

Page 2, Q4. How did you find out about this course?		
1	via BPA email list	Jul 17, 2012 6:59 AM
2	internal email	Jul 17, 2012 6:59 AM
3	email advertisement from dept	Jul 17, 2012 6:58 AM
4	Via bioinformaticians in CSIRO	Jul 17, 2012 6:58 AM
5	advertised internally in CSIRO via newsletter	Jul 17, 2012 6:58 AM

Page 2, Q5. What aspect of the workshop/training prompted you to register?		
1	RNA-Seq. De Novo Assembly, was interested in learning about ChIP-seq	Jul 17, 2012 7:01 AM
2	Potential new projects involving de-novo transcriptome assembly	Jul 17, 2012 7:01 AM
3	The broad bioinformatics components. As a researcher using 454 NGS I wanted to dvelop my understanding of the languarge and packages around managing NGS data. The professional faccilitators from EMBL and other organisations.	Jul 17, 2012 7:01 AM
4	NGS experiments..........	Jul 17, 2012 6:59 AM
5	It promised to provide an overview of NGS techniques and data analysis at a suitable level for geneticists	Jul 17, 2012 6:59 AM
6	The notion that it started at the beginning and the topics.	Jul 17, 2012 6:59 AM
7	It covered many aspects of the research that I will be doing using NGS data.	Jul 17, 2012 6:58 AM
8	Whole genome sequencing	Jul 17, 2012 6:58 AM
9	RNA-seq and ChIP-seq	Jul 17, 2012 6:58 AM
10	Improving rna-seq analytical skills	Jul 17, 2012 6:58 AM
11	De novo assembly; working with NGS data in general.	Jul 17, 2012 6:58 AM
12	Coverage of ChIPseq and RNAseq data	Jul 17, 2012 6:58 AM
13	De novo assembly, RNA-seq analysis.	Jul 17, 2012 6:58 AM
14	NGS - hands on learning.	Jul 17, 2012 6:58 AM
15	All of the things delivered in this workshop.	Jul 17, 2012 6:58 AM
16	RNA-seq and De novo assembly	Jul 17, 2012 6:58 AM
17	The explanation of the basics of running velvet and de novo assembly.	Jul 17, 2012 6:57 AM
18	I am about to do some bioinformatics work and thought it would be useful.	Jul 17, 2012 6:57 AM
19	Hands-on Next Generation Sequencing training	Jul 17, 2012 6:26 AM
20	Introduction to NGS	Jul 17, 2012 6:17 AM
21	The workshop approach with a small group and focus on ChIP-seq and RNA-seq	Jul 17, 2012 6:13 AM
22	basic NGS analysis with range of tools. the fact that it was aimed at people with little or no bioinformatic skills	Jul 17, 2012 6:06 AM
23	basic training	Jul 17, 2012 6:05 AM
24	course content - specifically hands on training component - course location	Jul 17, 2012 5:32 AM

Page 3, Q6. How useful did you find the following sessions? Please use the text box below to provide specific comments on the programme.

1	The program covered a large amount of content. For my research interests and current work I won't use ChIP-seq but I am very much interested in RNA-seq and De novo. I would have liked more time on RNA seq so perhaps next time you run the course you could split the content or split into groups into interest areas? Then go into more detail. The speakers were great and the diversity of skill sets from faccilitators and experts was amazing.	Jul 17, 2012 7:07 AM
2	Hawkeye loaded very slowly making it difficult to gain full benefit of differential expression analyis module.	Jul 17, 2012 7:06 AM
3	A huge amount of work and preparation has obviously gone into the programme. The introduction to each session was excellent and the excercises were well planned to ensure that we were able to trial them with our own hands. I learned so much from all aspects of the two days including optimal experimental design, recommended programs, quality control,.....to be afraid!!!	Jul 17, 2012 7:06 AM
4	The answers above reflect my research interests, overall the course was a reasonable compromise in the areas covered. It would have been good to have had more time to get a deeper coverage of the topics	Jul 17, 2012 7:03 AM
5	I clear flow chart of the procedures would be great. Ie. what each step does, and what it means. A little more biological releveance would also help.	Jul 17, 2012 7:03 AM
6	I thought that the genome section could have had a more real life example to be a bit more interesting.	Jul 17, 2012 7:02 AM
7	ChIP-seq not particularly useful for non-model organisms (but interesting); More time spent on de novo assembly would have been useful (too much information packed into too little time).	Jul 17, 2012 7:02 AM
8	Great work!	Jul 17, 2012 7:02 AM
9	The parts in ChIP and RNA seq were particularly relevent to my wotk and left me ready - I hope - to go back to work and start analysing my data. So these topics were very relevant for me.	Jul 17, 2012 6:58 AM
10	I have missed Monday afternoon due to other work commitment but the course runs very well. I am surprised that the scripts and sequence assembly runs so well on the cloud. The backup solution (local VM) also ran ok for the transcriptome assembly workshop, albiet slow. I still managed to run all the scripts within time. It will be great, if possible, to have the output file already computed.	Jul 17, 2012 6:33 AM
11	The topics fulfilled my expectations. Although I have a Bioinformatics background, it was very useful.	Jul 17, 2012 6:22 AM
12	ChIP-seq not relevant to my field of study hence "not useful" - it was not due to the presentation of the course at all. I did get some useful practice working in the terminal window The de novo assembly section was extremely informative and useful but needed much more time I am writing this before the final discussion	Jul 17, 2012 6:12 AM

Page 3, Q7. What other topics would you like to have seen covered and at what level would you like it to be set?		
1	a discussion of a recent real world project and how it was achieved including problems and the approach taken may have been usefull but probably too specific	Jul 17, 2012 7:07 AM
2	Metagenomic	Jul 17, 2012 7:07 AM
3	Time prevented long read length assembly	Jul 17, 2012 7:06 AM
4	The RNA Seq and NGS sections could have been expanded to two whole days each! To be able to trial larger datasets over a longer time frame would be excellent, including the opportunity to input users' own data.	Jul 17, 2012 7:06 AM
5	Bisulphite sequencing (methyl C) and SNP calling. At the same or slightly deeper level than in this course	Jul 17, 2012 7:03 AM
6	The topics were great, however, some type of amplicon work would have been great. The level was perfect, challanging but realistic.	Jul 17, 2012 7:03 AM
7	introduction to metagenomics	Jul 17, 2012 7:03 AM
8	Peak calling and aligning assembled genome to a ref- just a brief intro.	Jul 17, 2012 7:02 AM
9	More on de novo assembly.	Jul 17, 2012 7:02 AM
10	I could have used more information on aspects of bioinformatics of NGS data in non-model organisms (those w/o a draft genome).	Jul 17, 2012 7:02 AM
11	Sample preparation and experiemntal skill improvment	Jul 17, 2012 7:01 AM
12	Statistical analysis SNP arrays CNV GWAS	Jul 17, 2012 7:01 AM
13	I think this workshop provided sufficient coverage of the basics. Thank you	Jul 17, 2012 7:01 AM
14	It would be great if the best parameters used for different situations can be shared.	Jul 17, 2012 7:01 AM
15	How to deal with non-model organisms during RNA seq analysis	Jul 17, 2012 7:01 AM
16	Longer, better planned classes	Jul 17, 2012 7:00 AM
17	Differential expression using other programs such as DEGseq	Jul 17, 2012 7:00 AM
18	perhaps more time to work on velvet stuff.	Jul 17, 2012 6:59 AM
19	I think given the time we have for the course it would be hard to add much more. I would be interesed in some training in analysis and interpretation of the data and how to integrate different types of data, eg ChIP-seq + RNA-seq + DNA methlyation + metabolic data - ie what approaches are used to interpret these sorts of data together and to leverage the multiple levels of data	Jul 17, 2012 6:58 AM
20	I guess the next logical step could possibly be SNPs variant calling and analysis of DNA methylation. However, I think the course is set at a good introductory level and I wouldn't expect more.	Jul 17, 2012 6:33 AM
21	If there was an extra day, I would suggest variant calling.	Jul 17, 2012 6:22 AM

Page 3, Q7. What other topics would you like to have seen covered and at what level would you like it to be set?		
22	SNP detection - beginners	Jul 17, 2012 6:12 AM
23	Data from different platforms	Jul 17, 2012 6:08 AM
24	i was interested in RNA-seq so my requirements have been met	Jul 17, 2012 5:34 AM

Page 3, Q18. How do you rate tis workshop compared to similar events you have attended previously?		
1	this workshop was the 1st of its type that I have attended	Jul 17, 2012 7:07 AM
2	Fast moving, exciting, challenging	Jul 17, 2012 7:06 AM
3	it was perfectly tailored with a good level of assumed knowledge but also each step was really well explained	Jul 17, 2012 7:06 AM
4	I haven't done anything similar to this course for a long time, but it was good to have plenty of hands on tuition and very good ratio of trainers to students	Jul 17, 2012 7:03 AM
5	Far better than a previous course run at Syd U.	Jul 17, 2012 7:03 AM
6	Have not attended similar events.	Jul 17, 2012 7:02 AM
7	I have not really attended anythis like this before.	Jul 17, 2012 7:02 AM
8	Most events are good and useful	Jul 17, 2012 7:01 AM
9	I havent been to any other similar workshops but this was run very well	Jul 17, 2012 7:01 AM
10	It ran smoothly with little interruption. Lots of help available - was nice	Jul 17, 2012 7:00 AM
11	the practical hands on approach is much more useful that other courses I have been to based on lectures	Jul 17, 2012 6:58 AM
12	I have learned much more thanks to the hands on exercises.	Jul 17, 2012 6:22 AM
13	lots of people to answer questions, very organised but relaxed, good mix of practical and presentation	Jul 17, 2012 6:12 AM
14	only attened winer school in mathematical and computational biology which had no hands on component	Jul 17, 2012 5:34 AM

Page 4, Q20. Would you like further training?		
1	Have to absorb and apply what I've learnt here before ansering this	Jul 17, 2012 7:09 AM
2	See - expanded RNA-seq and NGS assembly sections	Jul 17, 2012 7:09 AM
3	Deeper coverage of RNAseq, ChIPseq with opportunity to analyse own datasets	Jul 17, 2012 7:05 AM
4	Metagenomics	Jul 17, 2012 7:05 AM
5	Metagenomics	Jul 17, 2012 7:05 AM
6	More directed work in a couple of months using individuals data	Jul 17, 2012 7:04 AM
7	Statistical bioinformatics	Jul 17, 2012 7:04 AM
8	More on de novo assembly and working with non-model organisms.	Jul 17, 2012 7:04 AM
9	More on de novo assembly; analysis of RNA-seq data from non-model organisms.	Jul 17, 2012 7:04 AM
10	Advanced	Jul 17, 2012 7:04 AM
11	NGS data analysis	Jul 17, 2012 7:03 AM
12	RNA seq	Jul 17, 2012 7:03 AM
13	Differential expression	Jul 17, 2012 7:01 AM
14	Velvet optimizer perhaps	Jul 17, 2012 7:01 AM
15	SNPs variant calling, analysis of DNA methylation	Jul 17, 2012 6:36 AM
16	Variant/SNP calling, advanced pipelines (meta-data integration, network)	Jul 17, 2012 6:26 AM
17	more de novo and snp detection	Jul 17, 2012 6:20 AM
18	transcriptome assembly without reference or annotations	Jul 17, 2012 6:18 AM
19	not sure yet need to hit road blocks first to see where I get stuck	Jul 17, 2012 5:36 AM

Page 4, Q22. On this course there should have been more opportunities for... because...		
1	n/a	Jul 17, 2012 7:09 AM
2	the practicals	Jul 17, 2012 7:09 AM
3	NGS de novo - trailoring it for different group requirements	Jul 17, 2012 7:09 AM
4	no	Jul 17, 2012 7:08 AM
5	Discussion of more details about how methods work	Jul 17, 2012 7:05 AM
6	Putting things into biological context.	Jul 17, 2012 7:05 AM
7	Getting started on own data because that would make it possible to ask more specific questions	Jul 17, 2012 7:05 AM
8	repeating excercises	Jul 17, 2012 7:05 AM
9	What does this mean?	Jul 17, 2012 7:04 AM
10	Real life problems with specific examination of the biological research questions so the use of the applications is more grounded in real life examples.	Jul 17, 2012 7:04 AM
11	More time (especially on the de novo assembly section) to run through the exercises and understand them before moving on.	Jul 17, 2012 7:04 AM
12	Time to discuss the content with fellow students.	Jul 17, 2012 7:04 AM
13	The format is just right.	Jul 17, 2012 7:04 AM
14	For practices, because my computer frozed at the last two practices, and I couldn't finish them.	Jul 17, 2012 7:04 AM
15	Questions.	Jul 17, 2012 7:03 AM
16	I think the de-novo assembly workshop was too long with too little context.	Jul 17, 2012 7:03 AM
17	Data analysis	Jul 17, 2012 7:02 AM
18	n/a	Jul 17, 2012 7:01 AM
19	more oppourtunities to complete the tasks provided as it felt a bit rushed towards the end.	Jul 17, 2012 7:01 AM
20	I come from a bioinformatics background, I think the course is set at the right level.	Jul 17, 2012 6:36 AM
21	Advanced analysis (if time permits).	Jul 17, 2012 6:26 AM
22	i would have liked more time on the de novo stuff. partly because it's what i'm doing but also because there was so much to cover in such a short time. with more time we could have asked more questions and got a lot more out of it. it was a stark contrast in pace from the exercises from the previous day and even the rna-seq morning.	Jul 17, 2012 6:20 AM
23	usefulness of the different platforms, dealing with complex data (ie whole genome data from plants - large genomes) delaing with large datasets - storage issues	Jul 17, 2012 6:18 AM

Page 4, Q22. On this course there should have been more opportunities for... because...		
24	no comment	Jul 17, 2012 5:36 AM

Page 4, Q23. What do you think you will remember most about this course...and why?

1	The intellectual excitement it generated	Jul 17, 2012 7:09 AM
2	The software packages and general rules for NGS data handling	Jul 17, 2012 7:09 AM
3	hopefully everything! but particularly the quality control section.	Jul 17, 2012 7:09 AM
4	my brain hurts	Jul 17, 2012 7:08 AM
5	Methods for ChipSeq and RNAsea	Jul 17, 2012 7:05 AM
6	The people and the condifence to use Unix.	Jul 17, 2012 7:05 AM
7	The trainers because of their overwhelming knowledge	Jul 17, 2012 7:05 AM
8	Hopefully how to use the command line to manipulate ChIP-seq and RNA-seq data. Also the enthusiasm and quality of the instructors.	Jul 17, 2012 7:05 AM
9	RNA -seq Coverage better	Jul 17, 2012 7:04 AM
10	Practical exercises. Good, step-by-step process through the commands.	Jul 17, 2012 7:04 AM
11	Where to find the coffee.	Jul 17, 2012 7:04 AM
12	Drawing pigs.	Jul 17, 2012 7:04 AM
13	RNA-Seq and ChIP-Seq. This is key to my research at the present moment.	Jul 17, 2012 7:04 AM
14	I have better understanding about the analysis of NGS, and I would apply them to my work more easily.	Jul 17, 2012 7:04 AM
15	The RNA seq section was very well presented.	Jul 17, 2012 7:03 AM
16	Quality control instructions, because they are essential for bioinformatics work.	Jul 17, 2012 7:03 AM
17	Chip-seq data analysis	Jul 17, 2012 7:02 AM
18	Data quality analysis	Jul 17, 2012 7:01 AM
19	the pigs.	Jul 17, 2012 7:01 AM
20	Getting to know the the command line aspect of the work a bit more.	Jul 17, 2012 6:36 AM
21	I was impressed how such a complex pipeline such as NGS data analysis was easily explained by teh instructors. They made all these difficult concepts very accessible without loosing accuracy.	Jul 17, 2012 6:26 AM
22	simple terminal comands that are extremely useful - getting around the terminal enough to understand how to troubleshoot commands that don't run lots of available tools for analysis and where to find them.	Jul 17, 2012 6:20 AM
23	names of available software and many new terminal commands. I hope that I'll remember a lot ! the course was great. Most fo all it was a good platform to build on.	Jul 17, 2012 6:18 AM
24	no comment	Jul 17, 2012 5:36 AM

Page 4, Q24. What did you think of the catering?		
1	good	Jul 17, 2012 7:08 AM
2	Fine	Jul 17, 2012 7:05 AM
3	Great,	Jul 17, 2012 7:05 AM
4	Ok	Jul 17, 2012 7:05 AM
5	very nice	Jul 17, 2012 7:05 AM
6	OK.	Jul 17, 2012 7:04 AM
7	Average	Jul 17, 2012 7:04 AM
8	Good food, mediocre coffee.	Jul 17, 2012 7:04 AM
9	Excellent. The quality of the coffee could have been better, though.	Jul 17, 2012 7:04 AM
10	Serving of fruit would have been nice during the tea breaks.	Jul 17, 2012 7:04 AM
11	Excellent.	Jul 17, 2012 7:04 AM
12	Ok.	Jul 17, 2012 7:03 AM
13	Good	Jul 17, 2012 7:03 AM
14	It was OK, not fantastic. The 2nd day was better. Also, there needed to be more drink options. Beer would certainly improve everything	Jul 17, 2012 7:01 AM
15	could have been better. needed more juice.	Jul 17, 2012 7:01 AM
16	Ok.	Jul 17, 2012 6:36 AM
17	ok.	Jul 17, 2012 6:26 AM
18	good - thanks :)	Jul 17, 2012 6:20 AM
19	good - we did not expect food for the price of the workshop! thes andwiches on both days were fresh and good. bowl or fruit at afternoon tea could help coffee was bad, only chocolate cakes available on the first afternoon tea (probably a good thing :-)	Jul 17, 2012 6:18 AM
20	coffee could be stronger	Jul 17, 2012 5:36 AM

Page 4, Q25. Please add any other comments here

1	the trainers were amazing and we are so grateful for their knowledge!	Jul 17, 2012 7:09 AM
2	Brilliant course, well organised and fantastic staff. Really happy with the experience. I hope that there are follow-up coarses, and that these will start in the not too distant to maximise the experience.	Jul 17, 2012 7:05 AM
3	Overall I think the course was really great and I am sure that all of my lab based colleagues would benefit from similar training. Obviously such a course draws on significant resources, but it is so relevant to many fields of biology that an investment in more courses like this seems well spent.	Jul 17, 2012 7:05 AM
4	I thnk you need to make sure of the expectations of the group. You need to have an eduactionalist look at the approach to teaching. The tutors were knowledgeable, but the delivery was often poor and more thought needs to go into structure of each presentation and of the overall course. In some cases there was poor outlines given. The speed increased when everyone got tired	Jul 17, 2012 7:04 AM
5	Please print updated version of manual in future. But very interesting!	Jul 17, 2012 7:04 AM
6	Please add page numbers to the manual next time. It would help in cross-referencing.	Jul 17, 2012 7:04 AM
7	I think that the first 2h of day one were a bit wasted with group activities.	Jul 17, 2012 7:01 AM
8	I think it will be great if the results are already computed to speed up the course, or help people catch-up if they fall behind. It can possibly be a case of telling the participants not to use these results unless you fall behind.	Jul 17, 2012 6:36 AM
9	I also appreciated the number of other trainers available to assist us during the workshop.	Jul 17, 2012 6:26 AM
10	The room was not ideal. Background noise made it difficult to hear at times. Overall I thought the course was great. I learnt a lot and had the opportunity to ask lots of questions about things that were and that weren't covered. thanks very much.	Jul 17, 2012 6:20 AM
11	The course could be split in two: for people with reference genomes available and for these without reference genomes available. Chip seq session was slow for the ammount of information while the RNA-seq and de novo sessions were really full. More time could be allocated to the latter. Over all it was a great introduction a follow up would be wonderful. It was really good to be able to talk to the instructors during the practical sessions and breaks about specific problems and issues. This has already provided us with several thing sto explore in order to analyse our data.	Jul 17, 2012 6:18 AM