Brisbane

1. Name (optional)

	Response Count
	8
answered question	**8**
skipped question	**12**

2. Email (optional)

	Response Count
	7
answered question	**7**
skipped question	**13**

3. Type of delegate

		Response Percent	Response Count
Academic		35.0%	7
Student		**40.0%**	**8**
Corporate		10.0%	2
Other (please specify)		15.0%	3
	answered question		**20**
	skipped question		**0**

4. How did you find out about this course?

	Response Percent	Response Count
From the Australian Bioplatforms website	10.0%	2
Other website (please specify below)	0.0%	0
From an email mailing list (please specify below)	30.0%	6
From a poster (please specify below)	5.0%	1
At a conference (please specify below)	0.0%	0
Word of mouth/recommendation	**45.0%**	**9**
Other (please specify)	20.0%	4
	Other (please specify)	9
	answered question	**20**
	skipped question	**0**

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

	Response Count
	20
answered question	**20**
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	0.0% (0)	10.0% (2)	**65.0% (13)**	25.0% (5)	0.0% (0)	3.15	20
NGS quality control and sequence alignment	0.0% (0)	0.0% (0)	45.0% (9)	**55.0% (11)**	0.0% (0)	3.55	20
Introduction to ChIP-seq	5.0% (1)	15.0% (3)	**75.0% (15)**	0.0% (0)	5.0% (1)	2.74	20
ChIP-seq analysis - peak calling and annotation	10.0% (2)	25.0% (5)	**55.0% (11)**	5.0% (1)	5.0% (1)	2.58	20
ChIP-seq analysis - motif analysis	5.0% (1)	30.0% (6)	**55.0% (11)**	5.0% (1)	5.0% (1)	2.63	20
Introduction to RNA-seq	0.0% (0)	10.0% (2)	**45.0% (9)**	**45.0% (9)**	0.0% (0)	3.35	20
Alignment and slice junction identification	0.0% (0)	15.0% (3)	35.0% (7)	**50.0% (10)**	0.0% (0)	3.35	20
Transcriptome assembly	0.0% (0)	10.0% (2)	30.0% (6)	**60.0% (12)**	0.0% (0)	3.50	20
Differential expression analysis	0.0% (0)	0.0% (0)	40.0% (8)	**60.0% (12)**	0.0% (0)	3.60	20
Introduction to de novo assembly	0.0% (0)	15.0% (3)	**50.0% (10)**	35.0% (7)	0.0% (0)	3.20	20
De novo assembly using velvet	0.0% (0)	15.0% (3)	**45.0% (9)**	35.0% (7)	5.0% (1)	3.21	20
Review and discussion of Velvet de novo assembly exercises	0.0% (0)	20.0% (4)	**45.0% (9)**	30.0% (6)	5.0% (1)	3.11	20
Specific comments on topics and the programme							9
answered question							**20**
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
	20
answered question	**20**
skipped question	**0**

8. Overall organization of the workshop and training

	Response Percent	Response Count
Excellent	35.0%	7
Good	**55.0%**	**11**
Satisfactory	10.0%	2
Poor	0.0%	0
Very poor	0.0%	0
answered question		**20**
skipped question		**0**

9. Programme/format

	Response Percent	Response Count
Excellent	35.0%	7
Good	**50.0%**	**10**
Satisfactory	15.0%	3
Poor	0.0%	0
Very poor	0.0%	0
answered question		**20**
skipped question		**0**

10. Materials provided

	Response Percent	Response Count
Excellent	40.0%	8
Good	**50.0%**	**10**
Satisfactory	5.0%	1
Poor	5.0%	1
Very poor	0.0%	0
answered question		**20**
skipped question		**0**

11. Facilities provided

	Response Percent	Response Count
Excellent	30.0%	6
Good	**60.0%**	**12**
Satisfactory	10.0%	2
Poor	0.0%	0
Very poor	0.0%	0
answered question		**20**
skipped question		**0**

12. Contents of individual presentation sessions

	Response Percent	Response Count
Excellent	35.0%	7
Good	**45.0%**	**9**
Satisfactory	15.0%	3
Poor	5.0%	1
Very poor	0.0%	0
	answered question	**20**
	skipped question	**0**

13. Clarity of presentations

	Response Percent	Response Count
Excellent	20.0%	4
Good	**50.0%**	**10**
Satisfactory	25.0%	5
Poor	5.0%	1
Very poor	0.0%	0
	answered question	**20**
	skipped question	**0**

14. Knowledge of speakers

	Response Percent	Response Count
Excellent	**55.0%**	**11**
Good	35.0%	7
Satisfactory	10.0%	2
Poor	0.0%	0
Very poor	0.0%	0
	answered question	**20**
	skipped question	**0**

15. Contents of practical sessions

	Response Percent	Response Count
Excellent	35.0%	7
Good	**50.0%**	**10**
Satisfactory	15.0%	3
Poor	0.0%	0
Very poor	0.0%	0
	answered question	**20**
	skipped question	**0**

16. Duration of sessions

	Response Percent	Response Count
Too short	40.0%	8
About right	**55.0%**	**11**
A bit long	5.0%	1
Much too long	0.0%	0
	answered question	**20**
	skipped question	**0**

17. Level of scientific content in the tutorial

	Response Percent	Response Count
Too general	5.0%	1
About right	**85.0%**	**17**
A little specific	5.0%	1
Much too specific	5.0%	1
	answered question	**20**
	skipped question	**0**

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

	Response Percent	Response Count
much better	15.0%	3
better	**55.0%**	**11**
average	30.0%	6
poorer	0.0%	0
	please explain	7
	answered question	**20**
	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	5.0%	1
Useful	**50.0%**	**10**
Extremely useful	45.0%	9
	answered question	**20**
	skipped question	**0**

20. Would you like further training?

	Response Percent	Response Count
Yes	**90.0%**	**18**
No	10.0%	2
	if yes, what would you like to see covered?	12
	answered question	**20**
	skipped question	**0**

21. Would you recommend this training to colleagues?

	Response Percent	Response Count
Yes	**95.0%**	**19**
No	5.0%	1
	answered question	**20**
	skipped question	**0**

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

	Response Count
	20
answered question	**20**
skipped question	**0**

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

	Response Count
	20
answered question	**20**
skipped question	**0**

24. What did you think of the catering?

	Response Count
	17
answered question	**17**
skipped question	**3**

25. Please add any other comments here

	Response Count
	12
answered question	**12**
skipped question	**8**

Page 2, Q4. How did you find out about this course?

1	forwarded to me by a colleague	Nov 14, 2012 6:55 AM
2	direct email from supervisor	Nov 14, 2012 6:54 AM
3	Internal CSIRO email	Nov 14, 2012 6:49 AM
4	In the lift at work	Nov 14, 2012 6:48 AM
5	from a friend	Nov 14, 2012 6:46 AM
6	not sure which list. Was in my UQ email account	Nov 14, 2012 6:31 AM
7	Google	Nov 14, 2012 6:29 AM
8	ctcb@qut.edu.au	Nov 14, 2012 6:26 AM
9	institute for molecular bioscience	Nov 14, 2012 6:26 AM

Page 2, Q5. What aspect of the workshop/training prompted you to register?		
1	learn data analysis tools and skills	Nov 14, 2012 7:15 AM
2	RNAseq	Nov 14, 2012 7:08 AM
3	It was a basic course with hands-on experience and access to expert bioinformaticians. Based at the nearest capital city to my Institute (North QLD).	Nov 14, 2012 7:02 AM
4	hands on training i use NGS data and that was the topic	Nov 14, 2012 7:00 AM
5	depth of coverage across the NGS bioinformatics and a need to communicate with bioinformactics specialists on projects	Nov 14, 2012 7:00 AM
6	Incentive to understand the data generated from NGS platforms	Nov 14, 2012 6:55 AM
7	hands on training	Nov 14, 2012 6:54 AM
8	hands-on component	Nov 14, 2012 6:54 AM
9	A chance to have hands-on instruction in cmd line based NGS analysis.	Nov 14, 2012 6:49 AM
10	Introductory nature of the workshop	Nov 14, 2012 6:48 AM
11	The need to come to terms with NGS data analysis and the charter of the workshop to cover this topic.	Nov 14, 2012 6:48 AM
12	De Novo Assembly	Nov 14, 2012 6:46 AM
13	learn about next generation sequencing data analysis	Nov 14, 2012 6:46 AM
14	NGS, RNA-seq	Nov 14, 2012 6:34 AM
15	handson and lectures for the NGS data handling	Nov 14, 2012 6:31 AM
16	The opportunity to get a more detailed knowledge of Bioinformatics and the pipelines used by bioinformaticians to get the results they come up with	Nov 14, 2012 6:31 AM
17	General NGS analysis: RNA-Seq, genome assembly	Nov 14, 2012 6:30 AM
18	Due to it covering a no. of different aspects of NGS technology	Nov 14, 2012 6:29 AM
19	NGS data analysis software	Nov 14, 2012 6:26 AM
20	Next gen seq data analysis (RNA -seq)	Nov 14, 2012 6:26 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	More about differential expression analysis	Nov 14, 2012 7:20 AM
2	*the tools for chip-seq were really useful but the actual topic seemed irrelevant *a bit more time spent on the reasons for selecting tools and techniques would be great, ie enable better decision making for participants *insufficient time on the genome assembly-should be whole day on this	Nov 14, 2012 7:08 AM
3	De novo analysis was probably the only part of the workshop which i did not take back much from. It was a fairly complicated.	Nov 14, 2012 7:04 AM
4	Topics were good. Would have appreciated less 'copy, paste, execute' time and a more extended focus (via the intro type presentations) about what we were visualizing and what we could get out of it.	Nov 14, 2012 7:03 AM
5	understanding the parameters of the processing and the impacts on the handling of the data was essential to my educational outcomes.	Nov 14, 2012 6:58 AM
6	Course was good but required more attention on larger genomes.	Nov 14, 2012 6:57 AM
7	Great work guys, well structured and delivered	Nov 14, 2012 6:51 AM
8	I would like to have been shown how to upload tracks to UCSC browser (required file types etc)	Nov 14, 2012 6:47 AM
9	Should be a week broken up into seminars day 1, full day chipseq, next day RNA seq, then de novo, with options to have a go at using if available attendees own data. The final day should be a recap and problem solving. This will give more of a more in depth about what each analysis is used for i.e. giving a laymenZ guide.	Nov 14, 2012 6:38 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	microRNA analysis	Nov 14, 2012 7:20 AM
2	More coverage of what a "beginner" needs to consider when undertaking these experiments - i.e. choice of software, types of analysis, design of experiments (replicates etc), sample preparation (i.e. for RNAseq - total RNA or not etc).	Nov 14, 2012 7:12 AM
3	*could set some review papers as reading for before workshop *comparisons between current platforms *selection of sequencing amount ie how much data do you want	Nov 14, 2012 7:08 AM
4	None	Nov 14, 2012 7:06 AM
5	It would be great to have a next steps course to go the next level now that we have the basics	Nov 14, 2012 7:04 AM
6	Statistics	Nov 14, 2012 7:04 AM
7	None	Nov 14, 2012 7:03 AM
8	adapter trimming, micro-RNA.	Nov 14, 2012 6:58 AM
9	statistics for differential expression at a pretty basic level	Nov 14, 2012 6:57 AM
10	More on typical workflows for RNA-seq and also de novo assembly of transcript data.	Nov 14, 2012 6:57 AM
11	No other topics, but perhaps more time spent on each section, especially the ChiP-Seq and RNA-Seq analysis.	Nov 14, 2012 6:52 AM
12	development of genetic markers	Nov 14, 2012 6:51 AM
13	Na	Nov 14, 2012 6:50 AM
14	?	Nov 14, 2012 6:47 AM
15	variant calling	Nov 14, 2012 6:44 AM
16	An thorough introduction into Bioinformatics and NGS platforms. Too fast coverage for novices	Nov 14, 2012 6:38 AM
17	SNP calling, whole genome seq analysis, gene discovery, mutation detection	Nov 14, 2012 6:37 AM
18	SNP discovery/analysis	Nov 14, 2012 6:34 AM
19	Metagenomics	Nov 14, 2012 6:34 AM
20	Adequate coverage, maybe scale down instead	Nov 14, 2012 6:30 AM

Page 3, Q18. How do you rate tis workshop compared to similar events you have attended previously?

1	needed to be "more general" - for beginners with NO knowledge	Nov 14, 2012 7:12 AM
2	haven't been to any other similar events	Nov 14, 2012 7:06 AM
3	The workshop was informative for a biologist like myself without any NGS experience without being overwhelming. I was skeptical regarding the command line interface used for the workshop, but i think i have gained a fair bit from the workshop and hope i can apply it when at my own computer with the help of all the bioinformaticians who were very helpful during the workshop.	Nov 14, 2012 7:04 AM
4	As indicated above, would have appreciated a bigger focus on interpreting the outputs rather than executing the commands	Nov 14, 2012 7:03 AM
5	good combination of talks, hand-on and well staffed	Nov 14, 2012 6:58 AM
6	The hands-on aspect was essential. Other courses were lecture-only and not as good.	Nov 14, 2012 6:57 AM
7	Others were too command line intense	Nov 14, 2012 6:47 AM

Page 4, Q20. Would you like further training?		
1	microRNA analysis	Nov 14, 2012 7:21 AM
2	intermediate training	Nov 14, 2012 7:10 AM
3	but would really like this with own data	Nov 14, 2012 7:09 AM
4	Statistics	Nov 14, 2012 7:08 AM
5	Use of CLC workbench	Nov 14, 2012 7:02 AM
6	More in-depth on larger data sets	Nov 14, 2012 7:01 AM
7	not sure! more detailed chIP-seq examples?	Nov 14, 2012 6:47 AM
8	advance RNA-seq data analysis	Nov 14, 2012 6:45 AM
9	gene discovery, analysis, anotation of whole genome seq	Nov 14, 2012 6:42 AM
10	more detailed course on specific aspects of NGS applications	Nov 14, 2012 6:37 AM
11	SNPs	Nov 14, 2012 6:36 AM
12	Transcriptome	Nov 14, 2012 6:33 AM

Page 4, Q22. On this course there should have been more opportunities for... because...		
1	microRNA analysis because it is an important part for expression study that NGS can study very well	Nov 14, 2012 7:21 AM
2	Maybe splitting off into groups to ask questions and for more background info - i.e. so people interested in RNAseq can ask questions/discuss what people say focusing on ChIP analysis might not be too fussed on hearing etc.	Nov 14, 2012 7:15 AM
3	to complete the tutorials	Nov 14, 2012 7:15 AM
4	a bit more down time to interact with the trainers. An extra half day may assist	Nov 14, 2012 7:11 AM
5	N/A	Nov 14, 2012 7:10 AM
6	Questions/discussions about the outputs	Nov 14, 2012 7:09 AM
7	no comment	Nov 14, 2012 7:08 AM
8	Sharing a computer... working together with a partner naturally happened and we got more done	Nov 14, 2012 7:02 AM
9	practice with the data viewers and an opportunity to gain greater understanding of their features.	Nov 14, 2012 7:01 AM
10	doing the tutorials and covering more clearly what was being done. The pace of tutorials and knowledge gained from them was quite advanced for newcomers to this area. Perhaps the course needs to be run as a beginners version allowing a bit more questioning and discussion and paced by presenters to keep everyone at same point and then followed up with a more advanced version.	Nov 14, 2012 7:01 AM
11	networking maybe	Nov 14, 2012 7:00 AM
12	social interactions - build collaborative relationships	Nov 14, 2012 7:00 AM
13	na	Nov 14, 2012 6:51 AM
14	-	Nov 14, 2012 6:47 AM
15	more hands on and less presentation	Nov 14, 2012 6:45 AM
16	time limitation	Nov 14, 2012 6:42 AM
17	Review and overview of the current technologies. Barely covered would like to see details of NGS things like ion torrent, SOAP other large genome assemblies	Nov 14, 2012 6:42 AM
18	NA	Nov 14, 2012 6:37 AM
19	SNP analysis Common tool	Nov 14, 2012 6:36 AM
20	Networking with various groups	Nov 14, 2012 6:33 AM

Page 4, Q23. What do you think you will remember most about this course...and why?		
1	commands, programs, workflow	Nov 14, 2012 7:21 AM
2	RNAseq general intro and practical	Nov 14, 2012 7:15 AM
3	the calmness and clarity of the presenters and their material - really really really great	Nov 14, 2012 7:15 AM
4	the opportunity to interact with bioinformatics who work in the field provided a great depth of knowledge than you may have otherwise obtained from a trainer not working in the field all the time. Varied background of the trainers was also beneficial.	Nov 14, 2012 7:11 AM
5	types of programmes required for transcriptome assembly	Nov 14, 2012 7:10 AM
6	That i will still need the input of a bioinformatician	Nov 14, 2012 7:09 AM
7	My first step into the world of bio informatics. It was a good start. And not as overwhelming as i thought it would be. Most definitely not a expert RNA seq analyst but i have more information i started with. I think it will help a long way in understanding my data better. Interactive environment with all the bio informaticians was very very useful.	Nov 14, 2012 7:08 AM
8	QC of data. It all begins with good data. Command line computing. I prefer graphic interfaces.	Nov 14, 2012 7:02 AM
9	The RNA-seq content because it is the most relevant to my current data analyses.	Nov 14, 2012 7:01 AM
10	A good introduction and elucidation of a number of analysis packages and their application. There is a gap to bridge for GUI based Biologists to this next level of Command line analysis.	Nov 14, 2012 7:01 AM
11	using command lines in general	Nov 14, 2012 7:00 AM
12	friendly helpful staff	Nov 14, 2012 7:00 AM
13	na	Nov 14, 2012 6:51 AM
14	Analysis workflows for the different datasets	Nov 14, 2012 6:47 AM
15	workflows	Nov 14, 2012 6:45 AM
16	practicals	Nov 14, 2012 6:42 AM
17	Quality control checks of outsourced data	Nov 14, 2012 6:42 AM
18	I will have a general background knowledge of NGS applications	Nov 14, 2012 6:37 AM
19	RNA-seq analysis. Currently aquiring RNA-seq data.	Nov 14, 2012 6:36 AM
20	NGS because its my first such analysis training	Nov 14, 2012 6:33 AM

Page 4, Q24. What did you think of the catering?		
1	Brilliant	Nov 14, 2012 7:15 AM
2	good	Nov 14, 2012 7:15 AM
3	Brilliant for the dietary restricted	Nov 14, 2012 7:11 AM
4	Awesome!	Nov 14, 2012 7:10 AM
5	Excellent	Nov 14, 2012 7:09 AM
6	very good	Nov 14, 2012 7:08 AM
7	Outstanding!	Nov 14, 2012 7:02 AM
8	Very good!	Nov 14, 2012 7:01 AM
9	very good	Nov 14, 2012 7:01 AM
10	excellent	Nov 14, 2012 7:00 AM
11	fantastic	Nov 14, 2012 7:00 AM
12	ok	Nov 14, 2012 6:51 AM
13	Excellent, however if I had to find a fault, the tea break snacks were a little too sweet	Nov 14, 2012 6:47 AM
14	ok	Nov 14, 2012 6:45 AM
15	Scrumptious, was well organised.	Nov 14, 2012 6:42 AM
16	Great.	Nov 14, 2012 6:36 AM
17	Satisfactory	Nov 14, 2012 6:33 AM

Page 4, Q25. Please add any other comments here		
1	thanks its about time Australia had something like this	Nov 14, 2012 7:15 AM
2	Thank you I got far more out of the course than I expected to. The ability to do hands on with the tutors and their patience was exceptional	Nov 14, 2012 7:11 AM
3	Perhaps it would be useful to run workshops focusing on individual topics e.g. just de novo genome assembly or just RNA-seq experimental design and data analysis so a more in-depth appreciation of a given topic could be gained. I felt quite rushed through the de novo assembly part of the programme and in fact that was my main area of interest. I would appreciate a course just focusing on that.	Nov 14, 2012 7:09 AM
4	Thank you to all who helped.	Nov 14, 2012 7:08 AM
5	excellent. thank you. The cloud computing was new.	Nov 14, 2012 7:02 AM
6	On the whole, well done. There were differing levels of understanding amongst the participants and the facilitators were very patient. All presenters need to speak up though - it was difficult to hear at times.	Nov 14, 2012 7:01 AM
7	Thank-you very much for your patience and friendly tutition. A very difficult course to run for a broad ability audience. A very pleasant learning atmosphere maintained by all Instructors. THANK-YOU	Nov 14, 2012 7:01 AM
8	The course on command lines was really useful. If I had not done that before the course I would have been quite lost I think	Nov 14, 2012 7:00 AM
9	na	Nov 14, 2012 6:51 AM
10	more intepretation of the practicals' outputs, sample raw data and transfer of the data to computer etc..	Nov 14, 2012 6:42 AM
11	Please ensure computers are running effectiently. Had to deal with a slow networked comp and mouse that could only scroll up overall good	Nov 14, 2012 6:42 AM
12	Great effort from the facilitators, very well appreciated	Nov 14, 2012 6:33 AM