Melbourne

1. Name (optional)

	Response Count
	14
answered question	**14**
skipped question	**7**

2. Email (optional)

	Response Count
	14
answered question	**14**
skipped question	**7**

3. Type of delegate

	Response Percent	Response Count
Academic	**61.9%**	**13**
Student	19.0%	4
Corporate	0.0%	0
Other (please specify)	19.0%	4
	answered question	**21**
	skipped question	**0**

4. How did you find out about this course?

	Response Percent	Response Count
From the Australian Bioplatforms website	4.8%	1
Other website (please specify below)	0.0%	0
From an email mailing list (please specify below)	**61.9%**	**13**
From a poster (please specify below)	0.0%	0
At a conference (please specify below)	4.8%	1
Word of mouth/recommendation	42.9%	9
Other (please specify)	0.0%	0
	Other (please specify)	6
	answered question	**21**
	skipped question	**0**

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

	Response Count
	21
answered question	**21**
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)	14.3% (3)	19.0% (4)	**66.7% (14)**	0.0% (0)	3.52	21
NGS quality control and sequence alignment	0.0% (0)	4.8% (1)	33.3% (7)	**61.9% (13)**	0.0% (0)	3.57	21
Introduction to ChIP-seq	0.0% (0)	19.0% (4)	28.6% (6)	**47.6% (10)**	4.8% (1)	3.30	21
ChIP-seq analysis - peak calling and annotation	0.0% (0)	28.6% (6)	14.3% (3)	**47.6% (10)**	9.5% (2)	3.21	21
ChIP-seq analysis - motif analysis	0.0% (0)	23.8% (5)	19.0% (4)	**47.6% (10)**	9.5% (2)	3.26	21
Introduction to RNA-seq	0.0% (0)	0.0% (0)	33.3% (7)	**61.9% (13)**	4.8% (1)	3.65	21
Alignment and slice junction identification	0.0% (0)	4.8% (1)	28.6% (6)	**61.9% (13)**	4.8% (1)	3.60	21
Transcriptome assembly	0.0% (0)	4.8% (1)	14.3% (3)	**76.2% (16)**	4.8% (1)	3.75	21
Differential expression analysis	0.0% (0)	0.0% (0)	14.3% (3)	**76.2% (16)**	9.5% (2)	3.84	21
Introduction to de novo assembly	4.8% (1)	14.3% (3)	38.1% (8)	**42.9% (9)**	0.0% (0)	3.19	21
De novo assembly using velvet	9.5% (2)	19.0% (4)	**38.1% (8)**	33.3% (7)	0.0% (0)	2.95	21
Review and discussion of Velvet de novo assembly exercises	9.5% (2)	23.8% (5)	**38.1% (8)**	28.6% (6)	0.0% (0)	2.86	21
						Specific comments on topics and the programme	14
						answered question	**21**
						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
	21
answered question	**21**
skipped question	**0**

8. Overall organization of the workshop and training

	Response Percent	Response Count
Excellent	38.1%	8
Good	**61.9%**	**13**
Satisfactory	0.0%	0
Poor	0.0%	0
Very poor	0.0%	0
	answered question	**21**
	skipped question	**0**

9. Programme/format

	Response Percent	Response Count
Excellent	23.8%	5
Good	**57.1%**	**12**
Satisfactory	19.0%	4
Poor	0.0%	0
Very poor	0.0%	0
	answered question	**21**
	skipped question	**0**

10. Materials provided

	Response Percent	Response Count
Excellent	**52.4%**	**11**
Good	42.9%	9
Satisfactory	4.8%	1
Poor	0.0%	0
Very poor	0.0%	0
	answered question	**21**
	skipped question	**0**

11. Facilities provided

	Response Percent	Response Count
Excellent	**52.4%**	**11**
Good	38.1%	8
Satisfactory	9.5%	2
Poor	0.0%	0
Very poor	0.0%	0
	answered question	**21**
	skipped question	**0**

12. Contents of individual presentation sessions

	Response Percent	Response Count
Excellent	33.3%	7
Good	**66.7%**	**14**
Satisfactory	0.0%	0
Poor	0.0%	0
Very poor	0.0%	0
answered question		**21**
skipped question		**0**

13. Clarity of presentations

	Response Percent	Response Count
Excellent	14.3%	3
Good	**66.7%**	**14**
Satisfactory	19.0%	4
Poor	0.0%	0
Very poor	0.0%	0
answered question		**21**
skipped question		**0**

14. Knowledge of speakers

	Response Percent	Response Count
Excellent	**76.2%**	**16**
Good	23.8%	5
Satisfactory	0.0%	0
Poor	0.0%	0
Very poor	0.0%	0
answered question		**21**
skipped question		**0**

15. Contents of practical sessions

	Response Percent	Response Count
Excellent	28.6%	6
Good	**52.4%**	**11**
Satisfactory	14.3%	3
Poor	0.0%	0
Very poor	4.8%	1
answered question		**21**
skipped question		**0**

16. Duration of sessions

	Response Percent	Response Count
Too short	23.8%	5
About right	**66.7%**	**14**
A bit long	9.5%	2
Much too long	0.0%	0
	answered question	**21**
	skipped question	**0**

17. Level of scientific content in the tutorial

	Response Percent	Response Count
Too general	4.8%	1
About right	**85.7%**	**18**
A little specific	9.5%	2
Much too specific	0.0%	0
	answered question	**21**
	skipped question	**0**

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

	Response Percent	Response Count
much better	23.8%	5
better	**61.9%**	**13**
average	14.3%	3
poorer	0.0%	0
	please explain	7
	answered question	**21**
	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	47.6%	10
Extremely useful	**52.4%**	**11**
	answered question	**21**
	skipped question	**0**

20. Would you like further training?

	Response Percent	Response Count
Yes	**71.4%**	**15**
No	28.6%	6
if yes, what would you like to see covered?		11
answered question		**21**
skipped question		**0**

21. Would you recommend this training to colleagues?

	Response Percent	Response Count
Yes	**100.0%**	**21**
No	0.0%	0
answered question		**21**
skipped question		**0**

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

	Response Count
	21
answered question	**21**
skipped question	**0**

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

	Response Count
	21
answered question	**21**
skipped question	**0**

24. What did you think of the catering?

	Response Count
	17
answered question	**17**
skipped question	**4**

25. Please add any other comments here

	Response Count
	8
answered question	**8**
skipped question	**13**

Page 2, Q4. How did you find out about this course?		
1	Monash Uni mail list	Jul 13, 2012 7:09 AM
2	email sent around institute (ARMI)	Jul 13, 2012 7:07 AM
3	Monash SOBS/ARMI	Jul 13, 2012 7:06 AM
4	Staff newslatter	Jul 13, 2012 7:06 AM
5	ARMI-EMBL Australia	Jul 13, 2012 7:06 AM
6	Ramacotti NextGen mailing list	Jul 13, 2012 7:05 AM

Page 2, Q5. What aspect of the workshop/training prompted you to register?		
1	Currently, I have projects running in this field and all information I can get to help me with data interpretation is welcome. Besides, the course was given by experts in the field that will now serve as a reference for doubts and possibly future collaborations.	Jul 13, 2012 7:09 AM
2	the necessity of understanding the novel apstec of NGS and planed used in the near future of ChIP-seq and RNA-seq in my research projects	Jul 13, 2012 7:08 AM
3	RNAseq analysis primarily	Jul 13, 2012 7:07 AM
4	ChIPSeq and RNASeq	Jul 13, 2012 7:06 AM
5	to familirise myself to chip-seq and RNA-seq with comand line interface	Jul 13, 2012 7:06 AM
6	Chip- andd RNA- seq	Jul 13, 2012 7:06 AM
7	To gain a better understanding of chip seq, so that i can interperate the data and present it in my thesis in a clear and consise manner	Jul 13, 2012 7:06 AM
8	The components on CHIPseq and RNAseq	Jul 13, 2012 7:06 AM
9	Getting a basic knowledge of NGS and the posthoc analysis in order to optimnise project design	Jul 13, 2012 7:06 AM
10	The topics that listed to be covered	Jul 13, 2012 7:05 AM
11	covering topics that I need to understand for planned experiments	Jul 13, 2012 7:05 AM
12	Hands on aspect of it and focus on RNA Seq	Jul 13, 2012 7:05 AM
13	ChiP-seq analysis	Jul 13, 2012 7:05 AM
14	Well-structured, practical involved, small number of seats, experts from EMBL-EBI, etc	Jul 13, 2012 7:05 AM
15	Hands-on training in an area of high interest	Jul 13, 2012 7:05 AM
16	I wanted more information on de novo assembly and RNAseq	Jul 13, 2012 7:05 AM
17	Level: introductory	Jul 13, 2012 7:05 AM
18	The level of workshop	Jul 13, 2012 7:04 AM
19	Learning the basics of bioinformatics	Jul 13, 2012 7:04 AM
20	The ChIP-seq and RNA-seq training	Jul 13, 2012 7:03 AM
21	Low cost, relevant topics	Jul 13, 2012 6:58 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	Apologies Mattias for the not useful comment - Mattias was an excellent presenter and had the correct balance of guided learning and self-learning, I just had very little understanding of the content.	Jul 13, 2012 7:14 AM
2	I am a user more than a developer. Besides, I always purchase a bundle which includes transcriptomics run and bioinfo analysis. Thus, the program language is not that interesting to me, apart of my personal interest for computational processes.	Jul 13, 2012 7:14 AM
3	The first day is extremley well organised and run. Running the 2nd morning interactive is a bit slow and the last afternoon was very hard to follow.	Jul 13, 2012 7:12 AM
4	Overall introduction was pitched a little high. More detail on how NGS works would have been good.	Jul 13, 2012 7:11 AM
5	I found the entire course useful. However, I found the de novo assembly component difficult to follow (perhaps since it's Friday afternoon).	Jul 13, 2012 7:11 AM
6	Would like to see more specialized modules organized seperately. My main interest is ChiP-seq, and some RNA-seq, apart from that I don't have immediate use. Organizing more specialized courses would allow to go more in depth in more relevant topics.	Jul 13, 2012 7:09 AM
7	MOre time required to complete the practical sessions	Jul 13, 2012 7:08 AM
8	More situations where we go though the work as a group	Jul 13, 2012 7:08 AM
9	Interactive practical s work best	Jul 13, 2012 7:07 AM
10	Not enough time given to teh de novo assembly section, it need a full day. Only 1/2 completed exercises	Jul 13, 2012 7:07 AM
11	Covered most of the things I was expecting to be covered. Liked the interactive part.	Jul 13, 2012 7:07 AM
12	The main area that I was interested in was de novo assembly. There was a large amount of content to learn and not enough time. I believe this section should have been an entire day	Jul 13, 2012 7:07 AM
13	De Novo part of the program is not relevent to my work as I only work on ChIP-seq and soon will be doing RNA-seq.	Jul 13, 2012 7:07 AM
14	De novo assembly was most useful for me but unfortunately it felt quite rushed. Personally I would have preferred to omit the ChIP-Seq sessions to sepnd more time on the de novo assembly.	Jul 13, 2012 7:02 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	Coverage was appropriate for a 2 day course	Jul 13, 2012 7:14 AM
2	I would like to explore more of prokaryotic transcriptome projects.	Jul 13, 2012 7:14 AM
3	Statistical analysis and principal component analysis.	Jul 13, 2012 7:12 AM
4	maybe more time tom go over the contructs and maybe a small training in shell	Jul 13, 2012 7:11 AM
5	Intro to whole exome sequencing (not pracs) and other emerging technologies. Maybe a future directions overview.	Jul 13, 2012 7:11 AM
6	I would have like to have seen more on how to prepare data for interpretation. For example, I am particularly interested in using RNAseq to determine how different immune cells are similar or desimilar to each other. Preparing heatmaps to summarise expression differences would have been very helpful. The trainers, however, did indicate that the 'R' program can facilitate this function. This is not a criticism of the RNAseq component which was excellent.	Jul 13, 2012 7:11 AM
7	NO COMMENT	Jul 13, 2012 7:10 AM
8	Would like to see more specialized analysis covered of specific modules (as mentioned above) Also including statistical analysis.	Jul 13, 2012 7:09 AM
9	slightly advanced, having some experiences	Jul 13, 2012 7:09 AM
10	beginners	Jul 13, 2012 7:08 AM
11	SNP detection set a basic/beginners level	Jul 13, 2012 7:08 AM
12	Course topics appropriate	Jul 13, 2012 7:08 AM
13	maybe some science side	Jul 13, 2012 7:08 AM
14	Microarrays - practical analysis	Jul 13, 2012 7:07 AM
15	Topics and level of coverage was fine	Jul 13, 2012 7:07 AM
16	No extra topics, just more time for de novo assembly	Jul 13, 2012 7:07 AM
17	Everything covered More detailed sections will be more helpful	Jul 13, 2012 7:07 AM
18	there was enough covered in the 2 days. If you wanted to cover more, you would need to make the course longer	Jul 13, 2012 7:07 AM
19	More focus on the functional annotation of ChIP-seq and RNA-seq	Jul 13, 2012 7:07 AM
20	Epigenomes, methylation assays	Jul 13, 2012 7:06 AM
21	More on de novo assembly at a slower pace	Jul 13, 2012 7:02 AM

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

1	The number of tutor, their availability and capacity to address issues was outstanding	Jul 13, 2012 7:12 AM
2	Topics covered more relevant and like inclusion of hands on practical sessions	Jul 13, 2012 7:08 AM
3	hands on and practicals	Jul 13, 2012 7:07 AM
4	better organised and workflow was better explained	Jul 13, 2012 7:07 AM
5	More practical sessions than previous courses	Jul 13, 2012 7:07 AM
6	most other events are just presentations without the hands on practicals. The practicals are an excellent idea	Jul 13, 2012 7:07 AM
7	large focus on practicals was excellent	Jul 13, 2012 7:07 AM

Page 4, Q20. Would you like further training?

1	prokaryotes.	Jul 13, 2012 7:15 AM
2	would like to pratice more to analyse CHip seq and RNA seq data	Jul 13, 2012 7:15 AM
3	Principal component analysis	Jul 13, 2012 7:15 AM
4	more time to have specific examples	Jul 13, 2012 7:13 AM
5	RNA-seq data presentation	Jul 13, 2012 7:12 AM
6	more chip seque and rna seq	Jul 13, 2012 7:10 AM
7	Chip-SEQ and statistical analysis	Jul 13, 2012 7:10 AM
8	Single module ie RNA-seq in more depth	Jul 13, 2012 7:09 AM
9	advanced level allowing for more independant analysis	Jul 13, 2012 7:09 AM
10	More detailed de novo assembly	Jul 13, 2012 7:09 AM
11	de novo assembly	Jul 13, 2012 7:09 AM

Page 4, Q22. On this course there should have been more opportunities for... because...		
1	Group work - if we are stuck would be good to work it out together rather than being told the answer (and hopefully remember better this way?)	Jul 13, 2012 7:16 AM
2	To explore prokaryotic transcriptomes.	Jul 13, 2012 7:15 AM
3	N/A	Jul 13, 2012 7:15 AM
4	praticing data analysis... more computing	Jul 13, 2012 7:15 AM
5	Personnal investigation	Jul 13, 2012 7:15 AM
6	discuss and understand the command lines and what they lead to	Jul 13, 2012 7:13 AM
7	Discussion of Experimental design - replicates etc	Jul 13, 2012 7:12 AM
8	see above	Jul 13, 2012 7:12 AM
9	Completing practical session of course because not enough time to do it in.	Jul 13, 2012 7:11 AM
10	RNA-seq, de novo . insufficient time to understand	Jul 13, 2012 7:11 AM
11	asking for help	Jul 13, 2012 7:10 AM
12	More oppertunities to study the basics of cli	Jul 13, 2012 7:10 AM
13	Interactive training, easier to follow.	Jul 13, 2012 7:10 AM
14	Focusing on the technique we will be working on rather than equal coverage for everyone on all techniques	Jul 13, 2012 7:10 AM
15	no comments	Jul 13, 2012 7:09 AM
16	beer	Jul 13, 2012 7:09 AM
17	more time given for teh de noco assemble section with more time to really go over the exercises and answers to the questions, it was really rushed	Jul 13, 2012 7:09 AM
18	Practical aspect since that is more useful	Jul 13, 2012 7:09 AM
19	interaction during de novo assembly. Matthias had to rush through answers that we didn't get to finish becuase we ran out of time	Jul 13, 2012 7:09 AM
20	about right	Jul 13, 2012 7:08 AM
21	Maybe for people to bring their own data to make it more relevant to own work.	Jul 13, 2012 7:04 AM

Page 4, Q23. What do you think you will remember most about this course...and why?		
1	I will definitely try the RNAseq programs. Fantastic lecturers.	Jul 13, 2012 7:16 AM
2	The quality of the presentations, the clarity, specific the data interpretation.	Jul 13, 2012 7:15 AM
3	My first intro to NGS. Willingness/patience of trainers to help.	Jul 13, 2012 7:15 AM
4	Speakers happy face....And my brain smoking...	Jul 13, 2012 7:15 AM
5	How much work is behind genome assembly!	Jul 13, 2012 7:15 AM
6	how to do RNA-seq and ChIP-seq analysis (linked to my line of research)	Jul 13, 2012 7:13 AM
7	complexity of de novo genome assembly....	Jul 13, 2012 7:12 AM
8	Data manipulation and analysis of CHIPseq and RNAseq data	Jul 13, 2012 7:12 AM
9	In depth coverage of areas and trainers - the latter were very good and helpful	Jul 13, 2012 7:11 AM
10	ChIP-seq and RNA-seq as they are directly relevant to my project	Jul 13, 2012 7:11 AM
11	that programs are shit	Jul 13, 2012 7:10 AM
12	Chip-SEQ analysis	Jul 13, 2012 7:10 AM
13	RNA Seq session = was presenetd through interactiv tarining	Jul 13, 2012 7:10 AM
14	The RNA-seq practicals. These were presented the most clearly as the trainer went through them in an interactive way with us	Jul 13, 2012 7:10 AM
15	chip-seq session because it was very clearly explained and it was fun to work with	Jul 13, 2012 7:09 AM
16	relaxed atmosphere, excellent speakers, was great to have so many support staff helping out too. Enjoyed meeting other scientists with similar and not-so-similar interests.	Jul 13, 2012 7:09 AM
17	Gave me a great insight into the work required for the sequence analysis along witht eh tools to look at the data myself	Jul 13, 2012 7:09 AM
18	The interactive aspect of the course	Jul 13, 2012 7:09 AM
19	how to use command line interface	Jul 13, 2012 7:09 AM
20	RNA Seq interactive practical by Myrto was great	Jul 13, 2012 7:08 AM
21	Tutorials were good. Good to be able to take the material away.	Jul 13, 2012 7:04 AM

Page 4, Q24. What did you think of the catering?		
1	average. not enough lunch. no hot water for tea etc.	Jul 13, 2012 7:15 AM
2	Good	Jul 13, 2012 7:15 AM
3	Need more soy milk and less carbs at lunch!	Jul 13, 2012 7:15 AM
4	Good	Jul 13, 2012 7:13 AM
5	OK	Jul 13, 2012 7:12 AM
6	Morning and afternoon coffee sessions were good. Many of us were left hungry after lunch. There was insufficient food for lunch.	Jul 13, 2012 7:12 AM
7	OK	Jul 13, 2012 7:11 AM
8	Just about OK	Jul 13, 2012 7:11 AM
9	great, love free food	Jul 13, 2012 7:10 AM
10	coffee was okay, food minimal	Jul 13, 2012 7:10 AM
11	Good (some fruits would have been a nice addition)	Jul 13, 2012 7:10 AM
12	it was ok	Jul 13, 2012 7:09 AM
13	food was good, coffee was not so good :(	Jul 13, 2012 7:09 AM
14	Alright.	Jul 13, 2012 7:09 AM
15	OK. There was quite a small amount of food for lunch	Jul 13, 2012 7:09 AM
16	1st day - too less amount of food. 2nd day - good	Jul 13, 2012 7:08 AM
17	Not quite enough food at lunch time.	Jul 13, 2012 7:04 AM

Page 4, Q25. Please add any other comments here		
1	Overall excellent course, good quality trainers, good ratio of trainers/students. Found the de novo section tough going. The presentation and pracs tried to cover too much so the overarching messages got lost. THANK YOU!!!!!	Jul 13, 2012 7:15 AM
2	Great experience.... Just think that we would have needed more time on the computer practicing. An extra afternoon would have been usefull to process all we learned. Anyway, thank you very much...	Jul 13, 2012 7:15 AM
3	Excellent course!	Jul 13, 2012 7:12 AM
4	We need more information about how to access cloud	Jul 13, 2012 7:11 AM
5	Many thanks for the enthusiasm and helpfulness (and patience) of the trainers. Brilliant organization! Thanks for an enjoyable course!	Jul 13, 2012 7:10 AM
6	Was very worthwhile and enjoyed my time here.	Jul 13, 2012 7:09 AM
7	Thank you	Jul 13, 2012 7:09 AM
8	May be a 3 day course will be useful with more detailed sessions for each	Jul 13, 2012 7:09 AM