dun can.brian@gmail.com +

44 responses

Summary

Is this a diverse library?



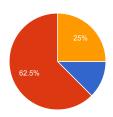
Yes, the vast majority of reads come from sequences which only occur once within the library 38 92.7%

No, this library has a 95% duplication rate 2 4.9%

No, the library sampling is close to saturation 1 2.4%

[Image]

The following 'per base sequence content' plot shows a strange pattern at position 26. What could explain this?



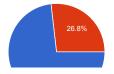
A power failure after 26 minutes 5 12.5%

A mainfold burst in cycle 26 25 62.5%

Nothing. This is the expected pattern of low quality at end of reads 10 25%

[Image]

What could explain this 'Quality per tile' plot?



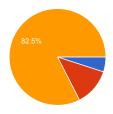
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A transient tile fail, such as a bubble going through the flowcell 30 73.2%

A permanent tile problem 11 26.8%

[Image]

What could explain the following 'per base sequence content' plots?



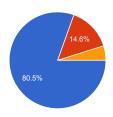
These plots show normal random libraries 2 5%

There might be adapters at the end of the reads 5 12.5%

The evidence of overrepresented sequences in the sample is probably biasing the overall composition of the different bases 33 82.5%

[Image]

What could explain the following 'per base sequence content' plot?



Double adapters at the beginning of the reads 33 80.5%

The sequencer was unable to make a base call 6 14.6%

This shows a normal random library 2 4.9%

[Image]

The presence of a spike around 40% indicates that sequences with 40% GC-content are over-represented in our sample. Why could that be?



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The plot shows a selection bias in around the first 12bp of each run 1 2.4%	The plot shows a sele	ction bias in arou	nd the first 12bi	o of each run	1	2.4%
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Because this is probably a RRBS sample 6 14.6%

Because there are overrepresented sequences in the sample that consist of repeated runs of "AGAGA" – which has 40% GC-content 34 82.9%

[Image]

What could explain the following plots?



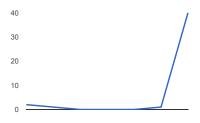
The sequencer was unable to make a base call with sufficient confidence (cycles 15-19) 36 87.8%

The plot shows adapter contamination 2 4.9%

Loss in quality of a subset of sequences 3 7.3%

[Image]

Number of daily responses



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