



ABERYSTWYTH UNIVERSITY

COMPUTER SCIENCE AND STATISTICS (GG34)

CS396: MINOR PROJECT

Application of Machine Learning Techniques to Next Generation Sequencing Quality Control

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Declaration

I certify that except where indicated, all material in this thesis is the result of my own investigation and references used in preparation of the text have been cited. The work has not previously been submitted as part of any other assessed module, or submitted for any other degree or diploma.

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Abstract

Over the past few years advances in genetic sequencing hardware have introduced the concept of massively parallel DNA sequencing; allowing potentially billions of chemical reactions to occur simultaneously, reducing both time and cost required to perform genetic analysis[3]. However, these "next-generation" processes are complex and open to error[2], thus quality control is an essential step to assure confidence in any downstream analyses performed.

During sample sequencing a large number of quality control metrics are generated to determine the quality of the reads from the sequencing hardware itself. At the Wellcome Trust Sanger Institute, the automated QC system currently relies on hard thresholds to make such quality control decisions with individual hard-coded values on particular metrics determining whether a lane has reached a level that requires a warning, or has exceeded the threshold and failed entirely. Whilst this does catch most of the very poor quality lanes, a large number of lanes are flagged for manual inspection at the warning level; a time consuming task which invites inefficiency and error.

In practise most of these manual decisions are based on inspecting a range of diagnostic plots which suggests that a machine learning classifier could potentially be trained on the combinations of quality control statistics available to make these conclusions without the need for much human intervention.

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Chapter 1

Introduction

Over the past few years advances in genetic sequencing hardware have introduced the concept of massively parallel DNA sequencing; allowing potentially billions of chemical reactions to occur simultaneously, reducing both time and cost required to perform genetic analysis[3]. However, these "next-generation" processes are complex and open to error[2], thus quality control is an essential step to assure confidence in any downstream analyses performed.

1.1 Project Aims

The project consists of two sub-projects;

- Analysis of a current quality control system in place
- Identification of quantifiable sample properties that affect downstream analysis

1.1.1 Analysis of Current System

With the support of the Wellcome Trust Sanger Institute in Cambridge, this project works with the Human Genetics Informatics team to investigate **auto_qc**, the institute's current automated quality control tool.

During genetic sequencing a large number of metrics are generated to determine the quality of the data read from the sequencing hardware itself. As part of the current vertebrate sequencing pipeline[1] at the institute, **auto_qc** is responsible for applying quality control to samples within the pipeline by comparing a modest subset of these metrics to simple hard-coded hard thresholds; determining whether a particular sample has reached a level that requires a warning, or has exceeded the threshold and failed entirely. Whilst this does catch most of the very poor quality outputs, a large number of samples are flagged for manual inspection at the warning level; a time consuming task which invites both inefficiency and error.

In practise most of these manual decisions are based on inspecting a range of diagnostic plots which suggests that a machine learning classifier could potentially be trained on the combinations of quality control statistics available to make these conclusions without the need for much human intervention.

The first part of the project aims to apply machine learning techniques to replicate the current **auto_qc** rule set by training a decision tree classifier on a large set of these quality metrics. The idea is to investigate whether these simple threshold based rules can be recovered from such data, or whether a new classifier would produce different rules entirely. During this analysis it is hoped the classifier may be able to identify currently unused quality metrics that improve labelling accuracy. An investigation on the possibility of aggregating or otherwise reducing the dimensions of some of the more detailed quality statistics to create new parameters will also be conducted.

The goal is to improve efficiency of quality control classification, whether by improving accuracy of pass and fail predictions over the current system or merely being able to provide additional information to a lab technician inspecting samples labelled with a warning to reduce arbitrary decisions.

1.1.2 Identification of Properties that affect Downstream Analysis

The other half of this project is motivated by the question "What *is* good and bad in terms of quality?"

To be able to classify samples as a pass or a fail with understanding, we need an idea of what actually constitutes a good or bad quality sample and must look at the effects quality has on analysis performed downstream from sequencing. An example of such is **variant calling** — the process of identifying differences between a DNA sample (such as your own) and a known reference sequence.

Given two high quality data sources where DNA sequences from individuals were identified in two different ways (one of which being next-generation sequencing) it would be possible to measure the difference between each corresponding pair. Using this, we could investigate the effect of leaving out part of the next-generation sample during the variant calling process. If we were to leave a part of a sample out of the variant calling pipeline would the variants found be more (or less) accurate than if it had been included? Would they agree more (or less) with the variants called after using the non next-generation sequencing method?

Having identified such sub-samples, can quality control metrics from the previous part be found in common? If so, such parameters would identify "good" or "bad" samples straight out of the machine! Samples that exhibit these quality variables will go on to improve or detriment analysis.

1.2 Project Methodology

Clearly some team-based practices invited by agile methodologies — pair programming immediately comes to mind — are not applicable in a solo project. It is also unreasonable to expect an "on-site" customer for this particular project. In *The Case Against Extreme Programming*, Matt Stephens describes a "self referential safety net" where the perceived traps in each practice are supported and "made safe" by other XP practices. This would seem to rule out XP as a viable methodology for a solo-project as cutting out some of the

processes that allow this form of evolutionary design to work (and flatten that cost-of-change curve) can introduce serious flaws to the management of a project and potentially result in failure. In the same breath it is important to remember that not all agile processes need be discarded just because XP seems incompatible. Indeed, some processes seem like common sense, for example; frequent refactoring, simple design, continuous integration and version control. Test driven development could also prove a useful process to consider as part of a methodology for this project, setting up a framework that allows for quick and frequent testing (before coding) and ensuring that any refactoring has a positive (or at least non-negative) effect on the system could be a worthwhile contribution to efficiency.

Could a more plan driven approach or form of agile-plan hybrid be considered appropriate here? In *Balancing Agility and Discipline*, Boehm and Turner introduce the idea of "homegrounds" for both agile and plan driven approaches; I note here that for projects that require high reliability and feature a non-located "CRACK customer" in fact align with some of these homegrounds for plan driven development. Combined with the thought that the project requirements will also be relatively stable it would seem that there may be no reason to switch to a more agile methodology as its primary feature is the welcoming of change that is not even needed? Perhaps this is the naivety of an optimist!

Personally I think I would approach this with a form of agile-plan hybrid; I like the idea of quick iterations and getting feedback as opposed to leaving acceptance testing until the very end of the project, but I also want a somewhat detailed feedback process. Whilst through Neil Taylor's course *Agile Methodologies* it was suggested that it is dangerous to pick and choose processes (don't anger the Ring of Snakes!) and also merely paying "lip service" to agile must be avoided (otherwise what's the point?), I feel that on this occasion it can be justified by the size of the project itself.

This project will consist of many research steps, each requiring some form of computational process to prepare the data for the next step. Whilst the implementations of the algorithms themselves pose computational complexity, there appears to be little challenge from a planning perspective and in fact a looser overall plan should probably be considered as we must account for unforeseen and unexpected outcomes from each research step.

The most important part of ensuring this project stays on track will be the development of a sensible testing methodology to ensure we are not only moving in the right direction in terms of which algorithm and parameters to use but also in terms of reliably measuring performance over time in a way that allows justification of such design choices.

Despite this trail of thought, given the research grounding this project entails it might be required to look beyond traditional and even modern software development methodologies and investigate a more scientific approach. A simple "scientific method" would involve establishing a null hypothesis that can be proven false by testing (eg: "**auto_qc** classifier is more accurate than the new classifier") and executing experiments that attempt to prove this null hypothesis false in favour of an alternative hypothesis (typically the opposite, eg: "The new classifier is more accurate than the old classifier"). This form of hypothesis testing could essentially become the project's acceptance tests (providing we have an empirical definition of what "more accurate" means in terms of this system) and any modification can be classed as an experiment ("Do these parameters allow us to reject the null hypothesis?"). Although care must be taken not to let this descend into unstructured cycles of mere hack-and-test, code-and-fix style programming.

Overall it is rather difficult to select a methodology for a project such as this, the research element makes it almost impossible to draw on previous personal experience for ideas of what development processes may or may not be effective.

1.2.1 Task and Time Management

Shortly before embarking on this dissertation project, I had written my own todo list web application; **Triage**.

1.2.2 Time Considerations

It must be remembered that this is supposed to be a minor project completed alongside the study of other modules that have their own assignments...

Chapter 2

Analysis of Current System

2.1 Introduction

This part of the project can be outlined as follows:

- Collect data sets on which a machine learning classifier is to be trained
- Construct a program capable of processing and storing such data sets such that required subsets of the data can be quickly and easily returned for further analysis
- Select a suitable machine learning framework to handle the training and validation of a classifier
- Ensure a robust validation methodology exists for assuring quality of our own results
- Set up an environment capable of allowing results from such a classifier to be stored and compared
- Training a suitable classifier on the collected data sets
- Perform experiments by selecting subsets of the variables and observations and measure whether classification accuracy is improved

2.2 Materials and Methods

2.2.1 Input Data and Format

As part of the project I've been granted access to significant data sets at the Sanger Institute, unlocking quality control data for two of the largest studies currently undergoing analysis. A wide array of quality metrics are available for each and every lanelet that forms part of either of the two studies; totalling 13,455 files.

The files are created by **samtools stats** — part of a collection of widely used open-source utilities for post processing and manipulation of large alignments such as those produced by next-generation sequencers that

are released under the umbrella name of "SAMtools" (Sequence Alignment and Map Tools). **samtools stats** collects statistics from sequence data files and produces key-value summary numbers as well as more complex tab delimited dataframes tabulating several metrics over time.

The output of **samtools stats** is then parsed by an in-house tool called **bamcheckr**, named so as **samtools stats** was once known as **bamcheck** and the tool is written in R. **bamcheckr** supplements the summary numbers section of the **samtools stats** output with additional metrics that are later used by **auto_qc** for classification. This process does not change the file other than adding a few additional key-value pairs in the summary numbers section. A truncated example of a "bamcheckr'd" file can be found in Appendix A.

2.2.2 Development Environment

Language

For the language of the program designed to handle this vast array of input data, Python was selected, more out of personal taste rather than a detailed analysis of required performance and features. From previous experience I was happy with the performance of Python when processing large datasets in terms of both I/O file handling operations and storing the data in memory for later use. Python's generous choice of both built-in and third-party libraries have proven useful on many occasions. Due to its concise and flexible nature it is possible to rapidly develop applications and its readability eases ongoing maintenance; useful given the short time-span allocated for this project and the possibility of others wishing to contribute to the project codebase after completion.

Whilst the choice was made primarily on preference, this is not to say other options were not considered: a highly popular Java-based collection of data mining tools, **WEKA** would certainly have provided a framework for building decision tree classifiers but at the same time did not appear to offer any significant features that were unavailable elsewhere, whilst Java itself has the added constraint of requiring a virtual machine to be installed which could be undesirable from a performance or even security standpoint when the application is deployed to servers at the Sanger Institute.

Difficulty was also encountered finding example implementations for **WEKA** with most documentation and tutorials providing information for performing analysis via the graphical "Explorer" interface instead, which would not be appropriate for quickly setting up and repeating experiments automatically.

Given the quality data we'll be using to train a machine learning classifier is output from the previously mentioned R script; **bamcheckr**, it was worth briefly investigating the options available for R itself as the potential of integrating the learning and predicting functions right in to the same process that outputs the data seemed convenient.

...Whilst the **tree** and **rpart** packages are available for constructing decision trees in R but (and actually **RWeka** provides an R interface to **WEKA**)...they did not appear to be as robust as other more well-known frameworks. Putting it politely, the programming paradigm of R is rather different to other languages and can significantly increase development time if one is not very well versed in the patterns and grammar of the language and it seemed best to stick to one's comfort zone.

...C and C++ also a possibility, however **dlib** didn't support tree-based classifiers although **Shark** did, Python chosen in the end for ease of use...

Framework

...Having studied the Machine Learning module in final year the prospect of getting stuck in to the deep of a machine learning algorithm was exciting, however the reality is a lot of time and effort has gone in to proper optimisation of a framework which is unlikely to be surpassed successfully by a short-term one-person project. It is therefore only natural that a library seems a wise investment for the codebase...

...There are numerous machine learning frameworks available in many languages, some described above... however it seemed counter-intuitive to select a framework in another language for the introduction of an additional arbitrary output and input steps to switch between the two environments.

...A mixed bag of such frameworks exist in Python, two in particular **scikit-learn** and **Orange** were main contenders, partly on their recommendation from the project supervisor...

...scikit integrates the "big names" in Python: numpy, scipy and matplotlib ...put off from Orange due to difficulties in reading in data ...it did however later appear to ship with features that were not in scikit (pruning and printing) ...with more time I'd certainly like to investigate using other libraries such as **Orange** or even outside Python and take a look at WEKA or Shark...

Libraries

numpy, scipy... Fast and reliable implementations of mathematical functions... ggplot2 for beautiful graphing...

Testing

Investigated the possibility of using **Jenkins** but just didn't have the time to set up and tweak all the plugins and options of the platform to do what I wanted... Would still have been poor in terms of searching through logs to track what parameters led to improvements in cross validation... ...Quite likely I'd have needed to author a Java or Groovy plugin to keep good track of cross-validation...

Briefly considered online solutions such as **Travis** and **Wercker** which I use for some personal projects, whilst quicker to set up would probably have not been able to handle artifacts such as dot files without some convoluted solution of uploading them to dropbox or adding them to a private git repository from the build node... ...also would have needed to upload a very large quantity of training data repeatedly which would be inefficient (and more than likely against reasonable use of the platform)

Really wanted to write my own solution for this but had to settle for well formatted log files that could be searched and processed with some command line fu...

Additional Tools

Version control is critical, **git**!

2.3 Implementation

2.3.1 Frontier

2.3.2 R Plots

References

- [1] vr-pipe, a generic pipeline system [Github]. [Online]. Available: <https://github.com/wtsi-hgi/vr-pipe/>
- [2] M. Kircher, U. Stenzel and J. Kelso, "Improved base calling for the Illumina Genome Analyzer using machine learning strategies," *Genome Biology*, vol. 10, no. 8, p. R83, 2009.
Useful introduction to relevant Illumina hardware and the errors that can occur during sequencing.
- [3] T. Strachan and A. Read, *Human Molecular Genetics*, 4th ed. Garland Science, 2011, pp. 214–254.
A concise introduction to the processes involved in massively parallel DNA sequencing.

Appendix A

samtools stats example output

```
# Summary Numbers. Use 'grep ^SN | cut -f 2-' to extract this part.
SN      raw total sequences:      41400090
SN      filtered sequences:       0
SN      sequences:                41400090
SN      is paired:                1
SN      is sorted:                1
SN      1st fragments:            20700045
SN      last fragments:           20700045
SN      reads mapped:             41291484
SN      reads unmapped:           108606
SN      reads unpaired:           60000
SN      reads paired:             41231484
SN      reads duplicated:         5756822
SN      reads MQ0:                1038644
SN      reads QC failed:         0
SN      non-primary alignments:    0
SN      total length:             3105006750
SN      bases mapped:             3096861300
SN      bases mapped (cigar):      3090885143
SN      bases trimmed:            0
SN      bases duplicated:         431761650
SN      mismatches:               9107833
SN      error rate:               0.002946675
SN      average length:           75
SN      maximum length:           75
SN      average quality:          36
SN      insert size average:       178.7
SN      insert size standard deviation: 44.1
SN      inward oriented pairs:     20577242
SN      outward oriented pairs:    3140
SN      pairs with other orientation: 3711
SN      pairs on different chromosomes: 31535
SN      fwd percent insertions above baseline: 1.43135383851191
SN      fwd percent insertions below baseline: 0.686265539012562
SN      fwd percent deletions above baseline: 1.38326380878871
SN      fwd percent deletions below baseline: 0.44923551909251
SN      rev percent insertions above baseline: 1.08264446659241
SN      rev percent insertions below baseline: 0.457290262062496
SN      rev percent deletions above baseline: 1.15931214598243
SN      rev percent deletions below baseline: 0.413119424753248
SN      contiguous cycle dropoff count: 36
SN      fwd.percent.insertions.above.baseline: 1.43135383851191
```

```

SN      fwd.percent.insertions.below.baseline:      0.686265539012562
SN      fwd.percent.deletions.above.baseline:       1.38326380878871
SN      fwd.percent.deletions.below.baseline:       0.44923551909251
SN      rev.percent.insertions.above.baseline:       1.08264446659241
SN      rev.percent.insertions.below.baseline:       0.457290262062496
SN      rev.percent.deletions.above.baseline:       1.15931214598243
SN      rev.percent.deletions.below.baseline:       0.413119424753248
SN      quality.dropoff.fwd.high.iqr.start.read.cycle:      0
SN      quality.dropoff.fwd.high.iqr.end.read.cycle:      0
SN      quality.dropoff.fwd.high.iqr.max.contiguous.read.cycles:      0
SN      quality.dropoff.fwd.mean.runmed.decline.start.read.cycle:      20
SN      quality.dropoff.fwd.mean.runmed.decline.end.read.cycle:      51
SN      quality.dropoff.fwd.mean.runmed.decline.max.contiguous.read.cycles:      32
SN      quality.dropoff.fwd.mean.runmed.decline.high.value:      36.9775883578997
SN      quality.dropoff.fwd.mean.runmed.decline.low.value:      36.301749247405
SN      quality.dropoff.rev.high.iqr.start.read.cycle:      0
SN      quality.dropoff.rev.high.iqr.end.read.cycle:      0
SN      quality.dropoff.rev.high.iqr.max.contiguous.read.cycles:      0
SN      quality.dropoff.rev.mean.runmed.decline.start.read.cycle:      18
SN      quality.dropoff.rev.mean.runmed.decline.end.read.cycle:      56
SN      quality.dropoff.rev.mean.runmed.decline.max.contiguous.read.cycles:      39
SN      quality.dropoff.rev.mean.runmed.decline.high.value:      36.1517621338504
SN      quality.dropoff.rev.mean.runmed.decline.low.value:      35.3152133727245
SN      quality.dropoff.high.iqr.threshold:          10
SN      quality.dropoff.runmed.k:                    25
SN      quality.dropoff.ignore.edge.cycles:          3
SN      A.percent.mean.above.baseline:               0.0991164444444441
SN      C.percent.mean.above.baseline:               0.1273795555555556
SN      G.percent.mean.above.baseline:               0.0603679999999997
SN      T.percent.mean.above.baseline:               0.0868000000000005
SN      A.percent.mean.below.baseline:               0.09911644444444451
SN      C.percent.mean.below.baseline:               0.1273795555555555
SN      G.percent.mean.below.baseline:               0.0603680000000002
SN      T.percent.mean.below.baseline:               0.0867999999999993
SN      A.percent.max.above.baseline:                 0.601733333333332
SN      C.percent.max.above.baseline:                 0.394266666666667
SN      G.percent.max.above.baseline:                 0.2956
SN      T.percent.max.above.baseline:                 0.768000000000001
SN      A.percent.max.below.baseline:                 0.318266666666666
SN      C.percent.max.below.baseline:                 0.825733333333332
SN      G.percent.max.below.baseline:                 0.554400000000001
SN      T.percent.max.below.baseline:                 0.251999999999999
SN      A.percent.max.baseline.deviation:             0.601733333333332
SN      C.percent.max.baseline.deviation:             0.825733333333332
SN      G.percent.max.baseline.deviation:             0.554400000000001
SN      T.percent.max.baseline.deviation:             0.768000000000001
SN      A.percent.total.mean.baseline.deviation:       0.198232888888889
SN      C.percent.total.mean.baseline.deviation:       0.254759111111111
SN      G.percent.total.mean.baseline.deviation:       0.120736
SN      T.percent.total.mean.baseline.deviation:       0.1736

```

First Fragment Qualities. Use 'grep ^FFQ | cut -f 2-' to extract this part.

Columns correspond to qualities and rows to cycles. First column is the cycle number.

FFQ	1	8968	3619	9863	747	5094	0	6642	1609	4673	4208	20
FFQ	2	21676	0	0	0	0	0	0	43	1885	0	0
FFQ	3	7	0	177	0	0	0	0	0	0	0	0
FFQ	4	0	0	0	65	0	0	0	272	0	0	14277
FFQ	5	1917	173	1249	0	1890	0	0	0	10874	0	0
[...]												
FFQ	72	4098	0	0	4806	0	0	0	65507	0	0	0
FFQ	73	3894	2	0	0	0	4931	53483	0	0	0	0
FFQ	74	3697	39	0	919	4933	0	0	56866	1524	0	0
FFQ	75	4542	0	0	0	0	4634	77822	0	0	0	0
FFQ	76	0	0	0	0	0	0	0	0	0	0	0

```

# Last Fragment Qualities. Use 'grep ^LFQ | cut -f 2-' to extract this part.
# Columns correspond to qualities and rows to cycles. First column is the cycle number.
LFQ 1 8869 0 0 0 0 0 63 0 0 1156 616 173
LFQ 2 3300 0 0 0 0 0 0 0 0 0 389 0 0
LFQ 3 6816 0 0 0 573 0 83 0 7011 1171 107134 0
LFQ 4 5492 0 0 13 0 66 730 708 8134 2422 84052
LFQ 5 3512 0 0 0 1023 185 0 8653 1995 0 115559
[...]
LFQ 72 5135 166 0 0 2872 13643 0 59649 4249 11351 346
LFQ 73 6025 229 0 86 1042 13417 0 66093 3741 8151 354
LFQ 74 5980 3 91 0 0 1340 9696 72939 4924 304090
LFQ 75 4314 0 0 168 0 848 8591 0 70358 3827 352180
LFQ 76 0 0 0 0 0 0 0 0 0 0 0 0
# Mismatches per cycle and quality. Use 'grep ^MPC | cut -f 2-' to extract this part.
# Columns correspond to qualities, rows to cycles. First column is the cycle number, second
# is the number of N's and the rest is the number of mismatches
MPC 1 14078 0 2594 6777 416 1919 0 2222 352 987 537
MPC 2 21407 0 0 0 0 0 0 0 5 223 19 0
MPC 3 3205 0 0 37 0 43 0 12 0 691 71 6984
MPC 4 1774 0 0 0 2 29 4 65 73 863 192 6749
MPC 5 1913 0 94 885 0 969 23 0 959 213 1203 84
[...]
MPC 72 361 0 13 0 573 276 934 0 16376 426 1066
MPC 73 1005 0 11 0 4 79 777 539 15025 363 699
MPC 74 779 0 3 0 131 440 0 93 7485 6589 387 24
MPC 75 136 0 0 0 3 0 47 704 9302 5886 260 2650
MPC 76 0 0 0 0 0 0 0 0 0 0 0 0
# GC Content of first fragments. Use 'grep ^GCF | cut -f 2-' to extract this part.
GCF 0.5 56
GCF 1.76 60
GCF 3.02 126
GCF 4.27 212
GCF 5.78 347
[...]
GCF 93.72 378
GCF 95.23 186
GCF 96.48 87
GCF 97.74 55
GCF 99.25 17
# GC Content of last fragments. Use 'grep ^GCL | cut -f 2-' to extract this part.
GCL 0.5 118
GCL 1.76 175
GCL 3.02 230
GCL 4.27 354
GCL 5.78 525
[...]
GCL 93.72 613
GCL 95.23 430
GCL 96.48 274
GCL 97.74 185
GCL 99.25 110
# ACGT content per cycle. Use 'grep ^GCC | cut -f 2-' to extract this part. The columns are: cycle, and A,C,G,T counts [%]
GCC 1 26.93 23.09 22.77 27.2
GCC 2 26.78 23.24 22.97 27.02
GCC 3 26.46 23.59 23.3 26.66
GCC 4 26.29 23.79 23.45 26.46
GCC 5 26.47 23.61 23.3 26.62
[...]
GCC 70 26.09 24.26 23.45 26.2
GCC 71 26.07 24.25 23.46 26.22
GCC 72 26.04 24.27 23.49 26.2
GCC 73 26.07 24.25 23.47 26.22
GCC 74 26.08 24.24 23.45 26.23

```

```

GCC      75      26.01      24.31      23.51      26.18
# Insert sizes. Use 'grep ^IS | cut -f 2-' to extract this part. The columns are: pairs total, inward oriented pairs, outward oriented pairs
IS      0      10      0      1      9
IS      1      3      0      3      0
IS      2      4      0      4      0
IS      3      5      0      5      0
IS      4      2      0      2      0
IS      5      3      0      3      0
[...]
IS      110     33952     33952      0      0
IS      111     38433     38433      0      0
IS      112     43373     43370      0      3
IS      113     48160     48159      0      1
IS      114     53175     53171      0      4
IS      115     59504     59502      0      2
IS      116     64668     64668      0      0
IS      117     71107     71105      0      2
IS      118     77157     77156      0      1
IS      119     84044     84044      0      0
IS      120     90116     90110      3      3
[...]
IS      327     6546      6546      0      0
IS      328     6483      6483      0      0
IS      329     6201      6201      0      0
IS      330     6228      6228      0      0
IS      331     5852      5852      0      0
# Read lengths. Use 'grep ^RL | cut -f 2-' to extract this part. The columns are: read length, count
RL      75      41400090
# Indel distribution. Use 'grep ^ID | cut -f 2-' to extract this part. The columns are: length, number of insertions, number of deletions
ID      1      128650     183418
ID      2      26409      39770
ID      3      10213     16046
ID      4      7756      11444
ID      5      1746      3455
[...]
ID      35      0      8
ID      36      0      1
ID      37      0      1
ID      38      0      1
ID      40      0      2
# Indels per cycle. Use 'grep ^IC | cut -f 2-' to extract this part. The columns are: cycle, number of insertions (fwd), .. (rev) , number of deletions
IC      1      0      0      105      97
IC      2      24      15      150      179
IC      3      129      138      441      509
IC      4      253      310      623      829
IC      5      557      724      786      1164
[...]
IC      70      571      710      638      761
IC      71      350      428      309      434
IC      72      154      150      38      45
IC      73      60      61      15      23
IC      74      20      19      11      12
# Coverage distribution. Use 'grep ^COV | cut -f 2-' to extract this part.
COV      [1-1]      1      332980694
COV      [2-2]      2      105004580
COV      [3-3]      3      29112182
COV      [4-4]      4      13415014
COV      [5-5]      5      6716815
[...]
COV      [996-996]      996      2
COV      [997-997]      997      2
COV      [998-998]      998      2
COV      [1000-1000]      1000      4

```

```

COV      [1000<]      1000      116
# GC-depth. Use 'grep ^GCD | cut -f 2-' to extract this part. The columns are: GC%, unique sequence percentiles, 10th, 25th, 50th, 75th and 90th
GCD      0          0.001      0          0          0          0          0
GCD      0.4        0.002      0.101      0.101      0.101      0.101      0.101
GCD      19         0.003      0.049      0.049      0.049      0.049      0.049
GCD      20         0.004      0.06       0.06       0.06       0.06       0.06
GCD      21         0.004      0.045      0.045      0.045      0.045      0.045
[...]
GCD      66         99.99      0.244      2.693      6.746      11.794     15.885
GCD      67         99.994     1.279      1.279      4.305      9.667      11.483
GCD      68         99.997     4.148      4.148      4.463      5.741      7.354
GCD      69         99.999     0.499      0.499      0.499      1.935      1.935
GCD      72         100       0.476      0.476      0.476      1.219      1.219

```