Sequencing QC Report
Based upon: 8,702,061 sequences in 8 data sets
Generated by: sr320
Creation date: Tue Nov 20 14:03:14 PST 2012
Software: CLC Genomics Workbench 5.5.1

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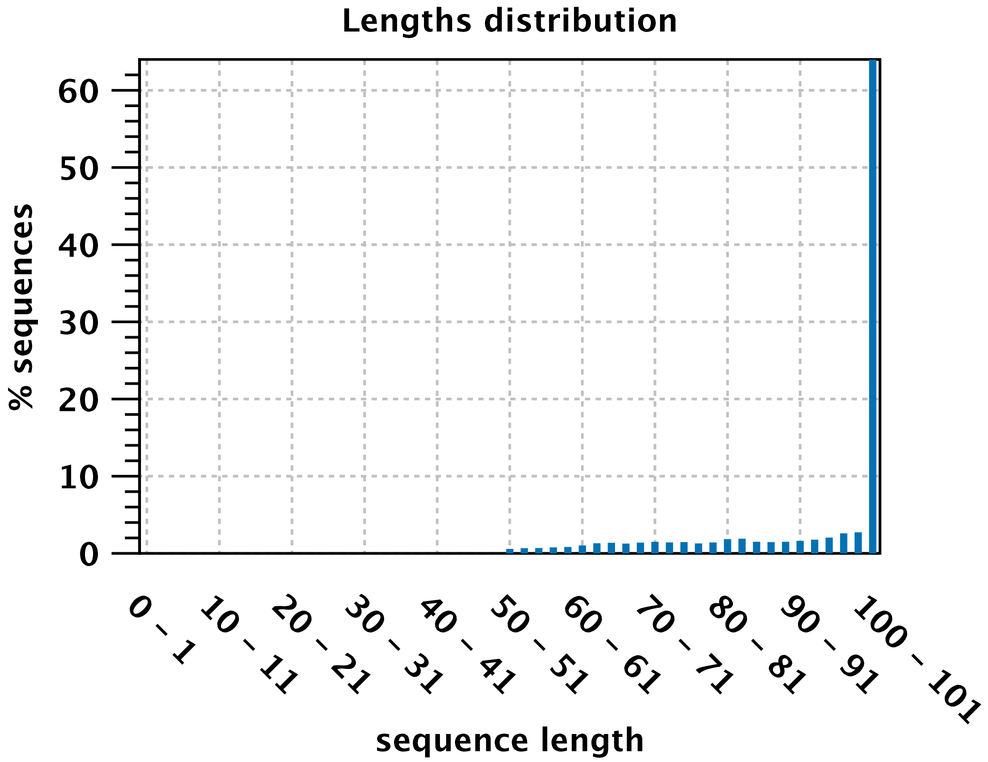
1. Summary

Creation date:	Tue Nov 20 14:03:14 PST 2012
Generated by:	sr320
Software:	CLC Genomics Workbench 5.5.1
Based upon:	8 data sets
EM2A trimmed:	1,321,667 sequences
EM2B trimmed:	1,032,727 sequences
EM2C trimmed:	1,125,488 sequences
EM2D trimmed:	1,384,875 sequences
EM2E trimmed:	742,923 sequences
EM2F trimmed:	1,024,307 sequences
EM2G trimmed:	1,104,480 sequences
EM2H trimmed:	965,594 sequences

2. Per-sequence analysis

2.1 Lengths distribution



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Distribution of sequence lengths. In cases of untrimmed Illumina or SOLiD reads it will ju st contain a single
peak.
x: sequence length in base-pairs
y: number of sequences featuring a particular length normalized to the total number of seq uences
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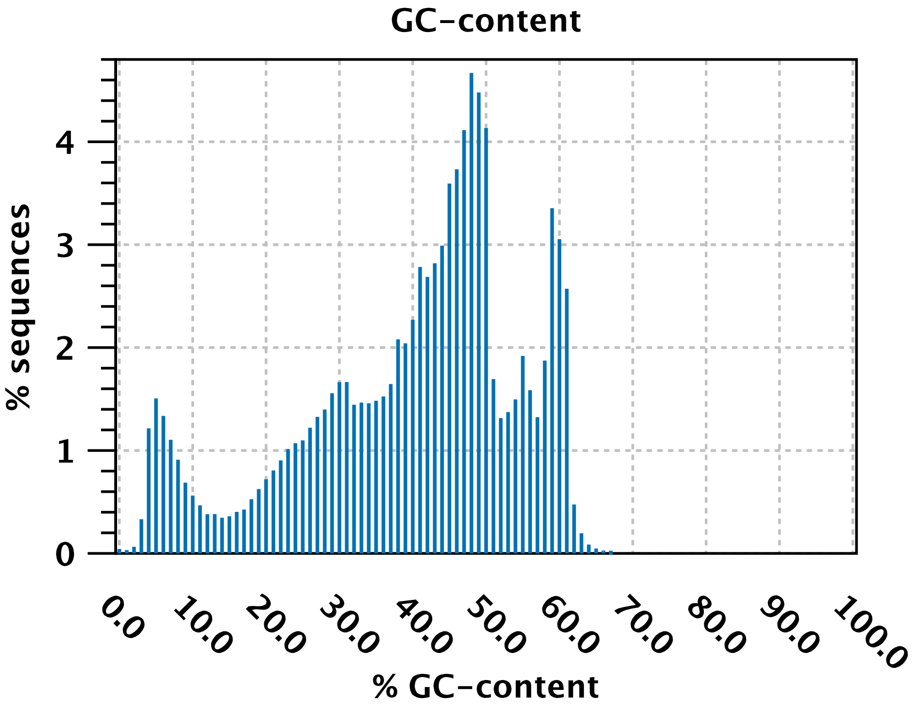
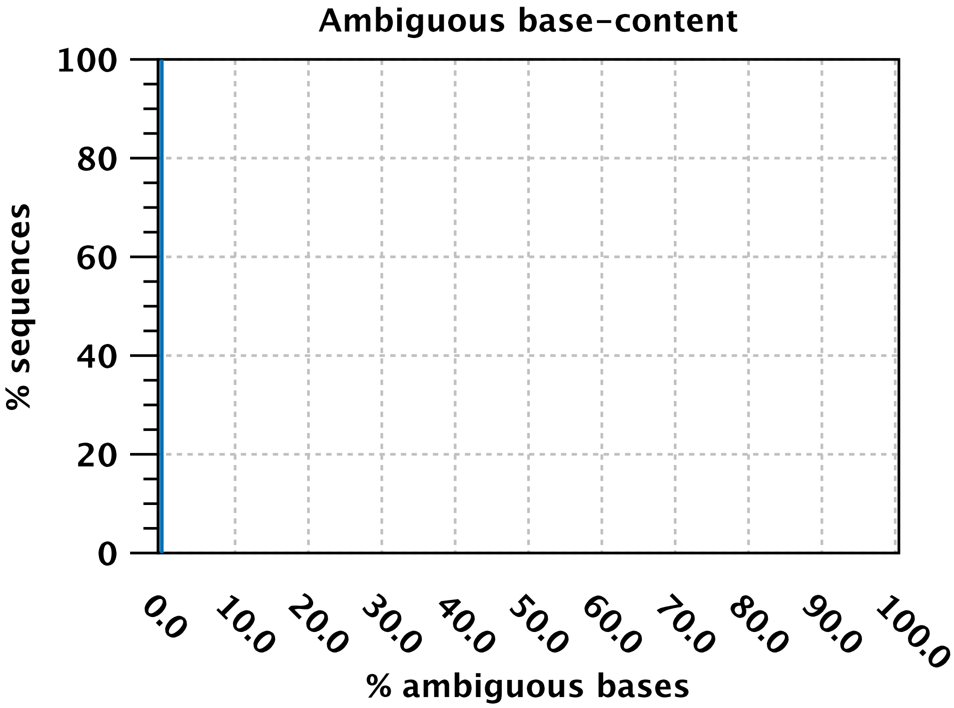
2.2 GC-content



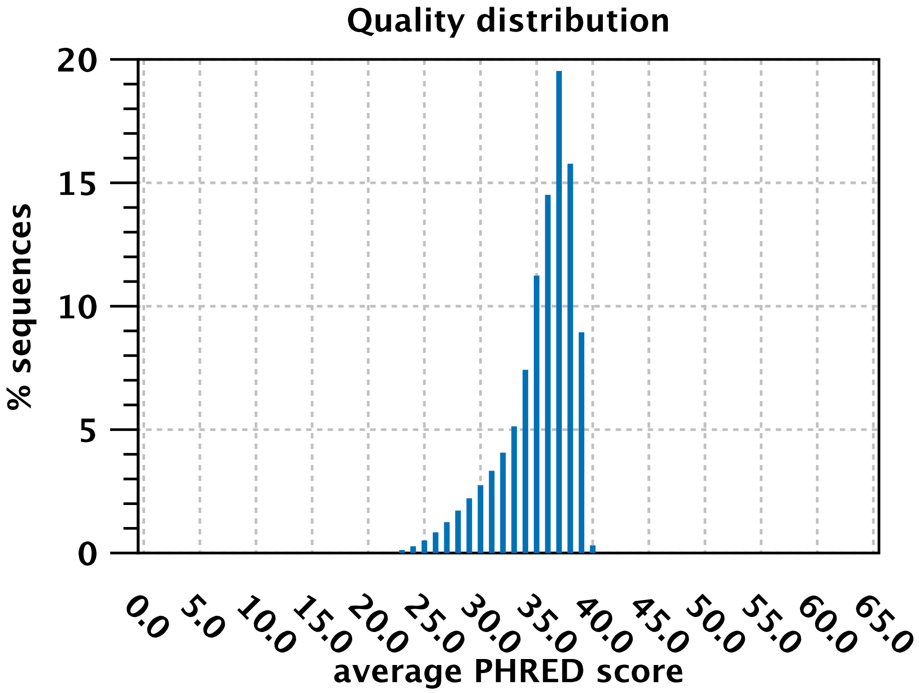
Distribution of GC-contents. The GC-content of a sequence is calculated as the number of G C-bases compared to all bases (including ambiguous bases).
x: relative GC-content of a sequence in percent
y: number of sequences featuring particular GC-percentages normalized to the total number of sequences

2.3 Ambiguous base-content



Distribution of N-contents. The N-content of a sequence is calculated as the number of amb iguous bases compared to all bases.
x: relative N-content of a sequence in percent
y: number of sequences featuring particular N-percentages normalized to the total number o f sequences

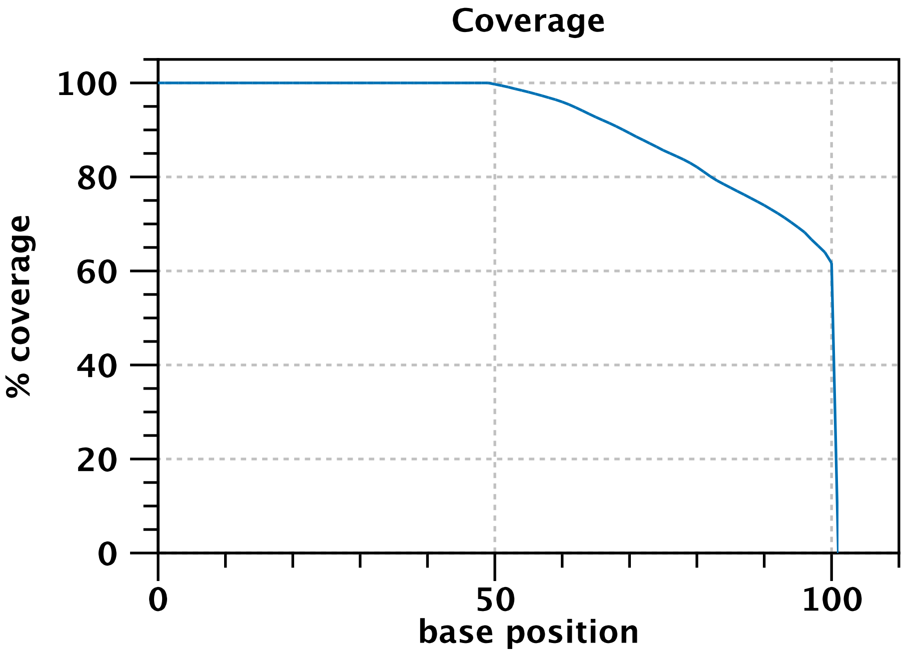
2.4 Quality distribution



Distribution of average sequence qualitie scores. The quality of a sequence is calculated as the arithmetic mean of its base qualities.
x: PHRED-score
y: number of sequences observed at that qual. score normalized to the total number of sequ ences

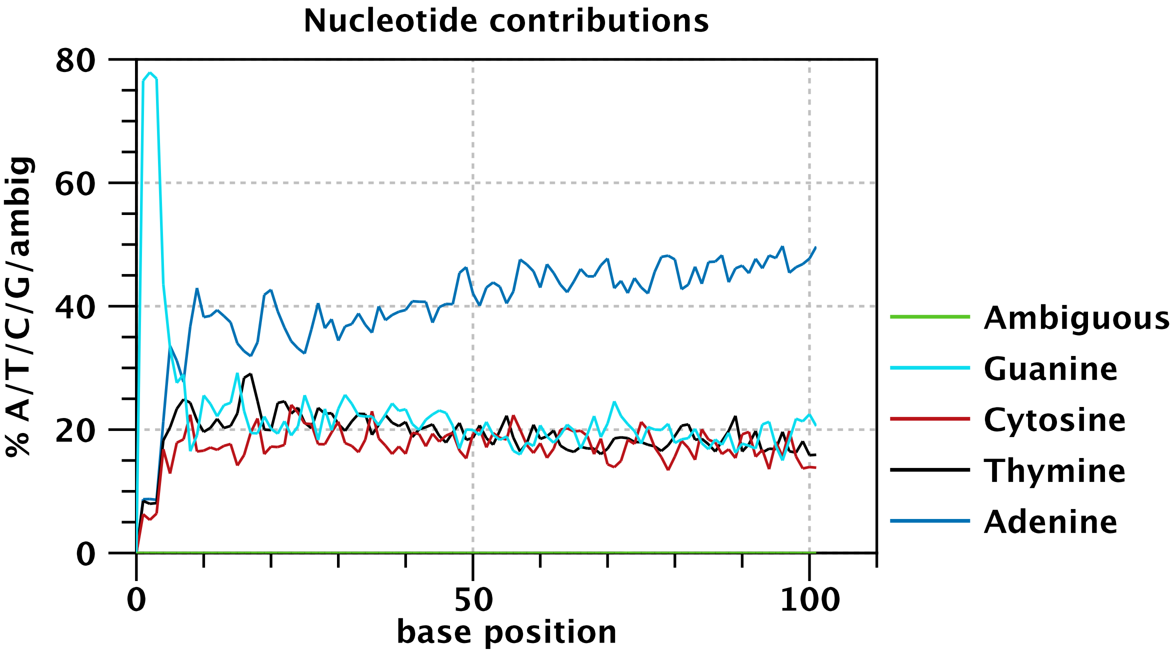
3. Per-base analysis

3.1 Coverage



The number of sequences that support (cover) the individual base positions. In cases of un trimmed Illumina or SOLiD reads it will just contain a rectangle.
x: base position
y: number of sequences covering individual base positions normalized to the total number o f sequences

3.2 Nucleotide contributions



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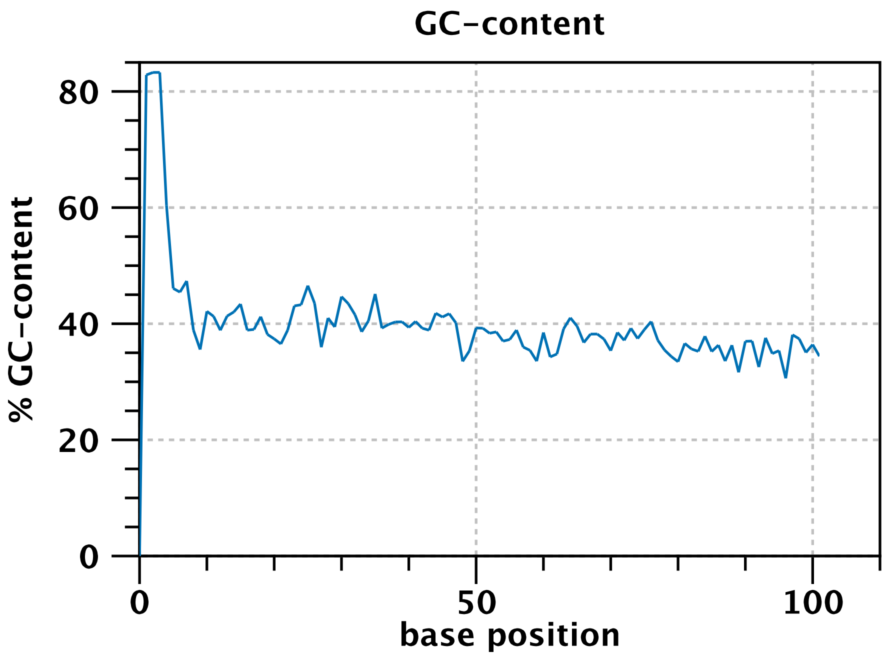
Coverages for the four DNA nucleotides and ambiguous bases.
x: base position
y: number of nucleotides observed per type normalized to the total number of nucleotides o bserved at that
position
```

3.3 GC-content



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Combined coverage of G- and C-bases.
x: base position
y: number of G- and C-bases observed at current position normalized to the total number of  bases observed at that
position
```
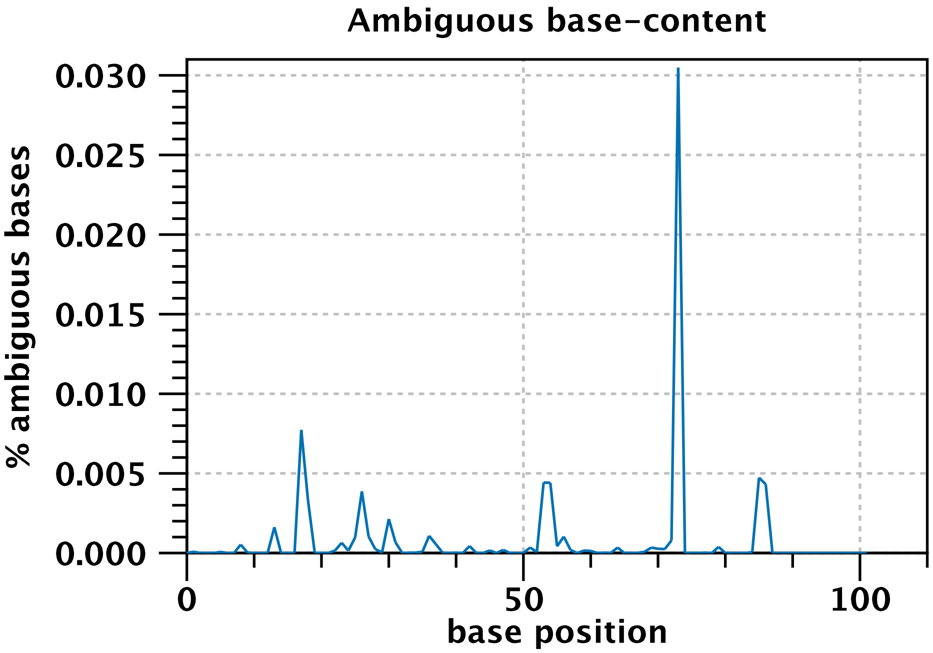
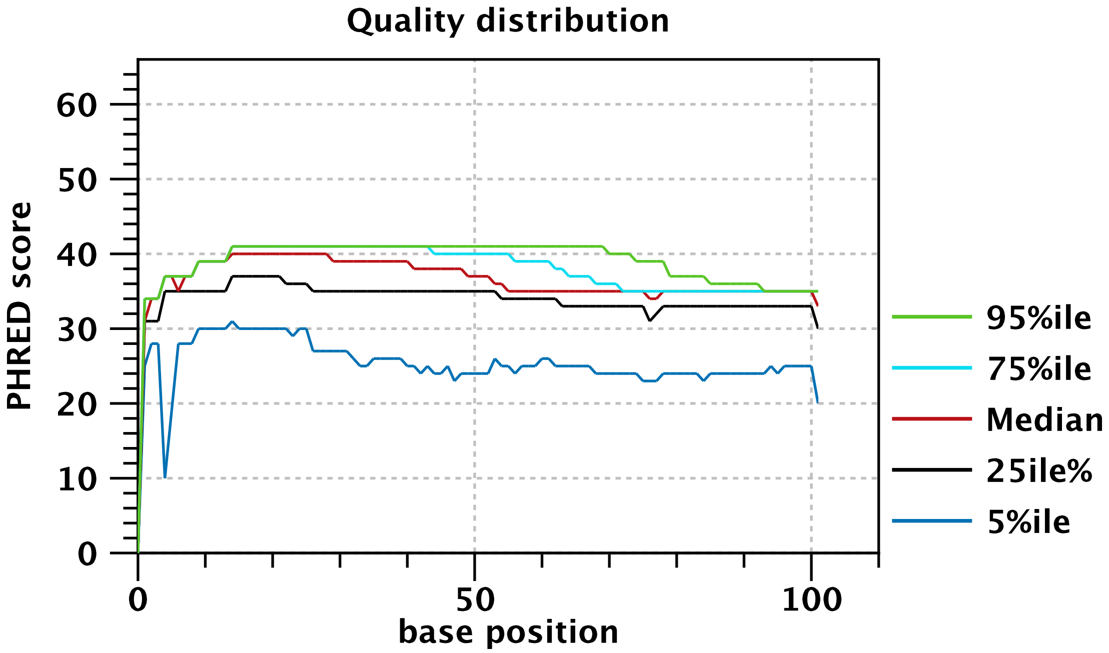

3.4 Ambiguous base-content



Combined coverage of ambiguous bases.
x: base position
y: number of ambiguous bases observed at current position normalized to the total number o f bases observed at that position

3.5 Quality distribution



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Base-quality distribution along the base positions.
x: base position
y: median & percentiles of quality scores observed at that base position
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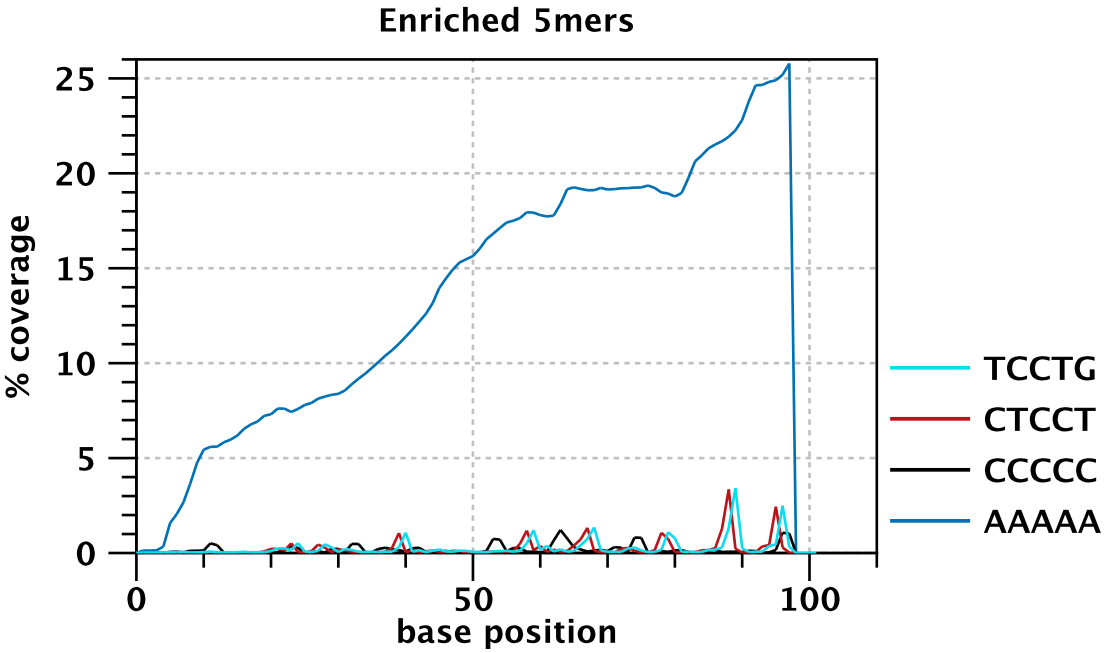
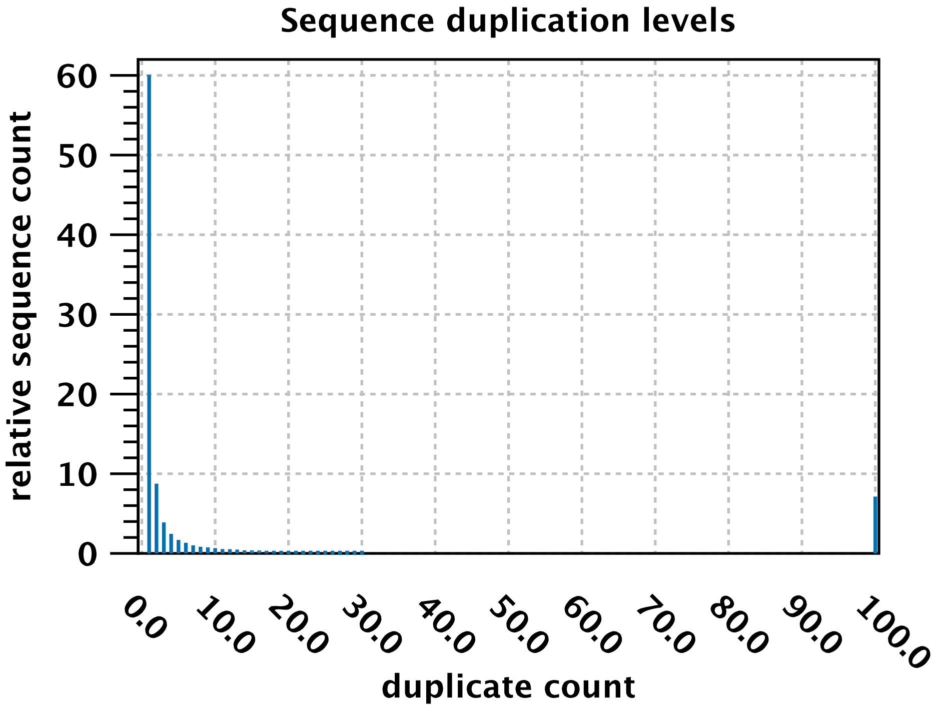
4. Over-representation analyses

4.1 Enriched 5mers



The five most-overrepresented 5mers. The over-representation of a 5mer is calculated as th e ratio of the observed and expected 5mer frequency. The expected frequency is calculated as product of the empirical nucleotide probabilities that make up the 5mer. (5mers that contain ambiguous bases are ignored)
x: base position
y: number of times a 5mer has been observed normalized to all 5mers observed at that posit ion

4.2 Sequence duplication levels



Duplication level distribution. Duplication levels are simply the count of how often a par ticular sequence has been found.
x: duplicate count
y: number of sequences that have been found that many times normalized to the number of un ique sequences

4.3 Duplicated sequences

A table of over-represented sequences is given in the supplementary report