

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:37:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/126
7
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1267 .nodup.bam
Program:	bwa (0.7.17-r1188)
Analyze overlapping paired-end reads:	no
Command line:	bwa mem -M -t 8 -R @RG\tID:\$unit\tPL:Illumina\tLB:LibA\t SM:\$sample /proj/uppstore2018210/Aalpina/data/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_154/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_154_S244_L002 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_154/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_154_S244_L002 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:37:48 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	90,130,955
Mapped reads	83,290,552 / 92.41%
Unmapped reads	6,840,403 / 7.59%
Mapped paired reads	83,290,552 / 92.41%
Mapped reads, first in pair	41,702,061 / 46.27%
Mapped reads, second in pair	41,588,491 / 46.14%
Mapped reads, both in pair	81,341,295 / 90.25%
Mapped reads, singletons	1,949,257 / 2.16%
Read min/max/mean length	30 / 151 / 148.1
Duplicated reads (flagged)	14,840,958 / 16.47%
Clipped reads	18,723,003 / 20.77%

2.2. ACGT Content

Number/percentage of A's	3,569,239,973 / 30.95%
Number/percentage of C's	2,198,100,225 / 19.06%
Number/percentage of T's	3,572,651,185 / 30.98%
Number/percentage of G's	2,193,659,869 / 19.02%
Number/percentage of N's	48,812 / 0%
GC Percentage	38.08%

2.3. Coverage

Mean	37.11
Standard Deviation	279.2643

2.4. Mapping Quality

Mean Mapping Quality	43.93
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2.5. Insert size

Mean	250,288.83
Standard Deviation	2,373,815.38
P25/Median/P75	336 / 440 / 575

2.6. Mismatches and indels

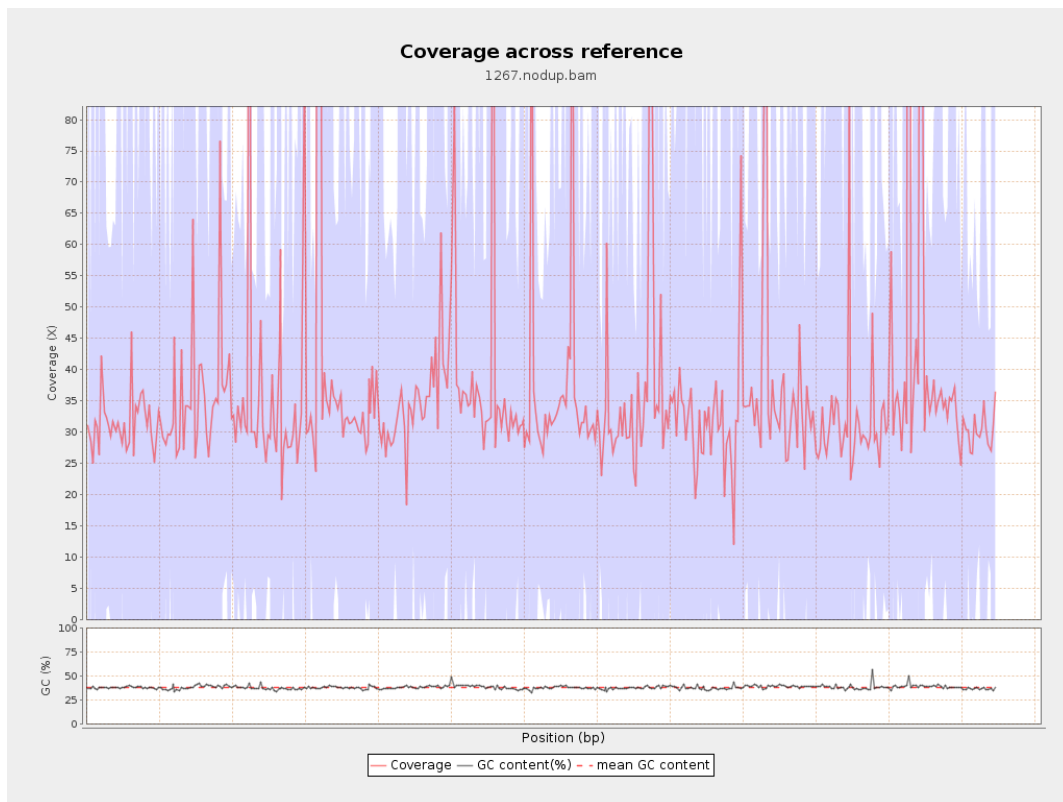
General error rate	2.32%
Mismatches	245,771,337
Insertions	8,041,562
Mapped reads with at least one insertion	8.65%
Deletions	8,169,400
Mapped reads with at least one deletion	8.7%
Homopolymer indels	56.94%

2.7. Chromosome stats

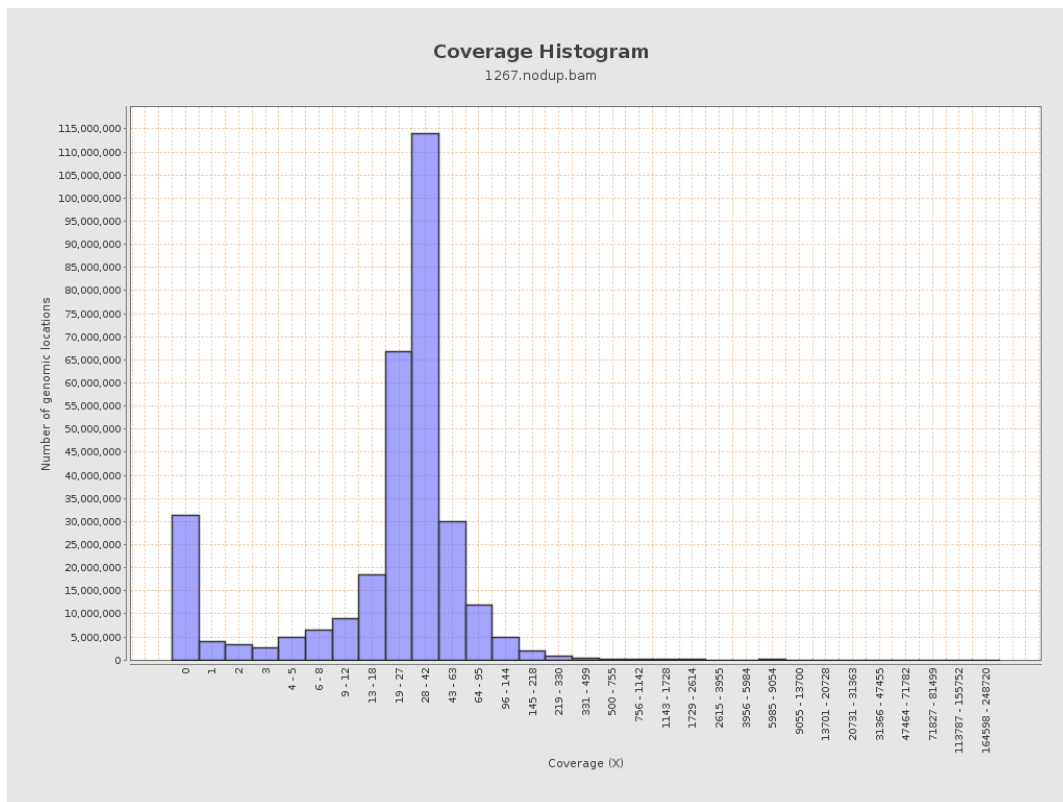
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	927543899	31.2049	86.5808

LT669789.1	36598175	1363570194	37.2579	276.3165
LT669790.1	30422129	1262115978	41.4868	327.4157
LT669791.1	52758100	1940372651	36.7787	247.2399
LT669792.1	28376109	1044861915	36.8219	298.6129
LT669793.1	33388210	1180041110	35.343	264.4319
LT669794.1	50579949	1762026511	34.8365	228.6766
LT669795.1	49795044	2084493943	41.8615	382.5733

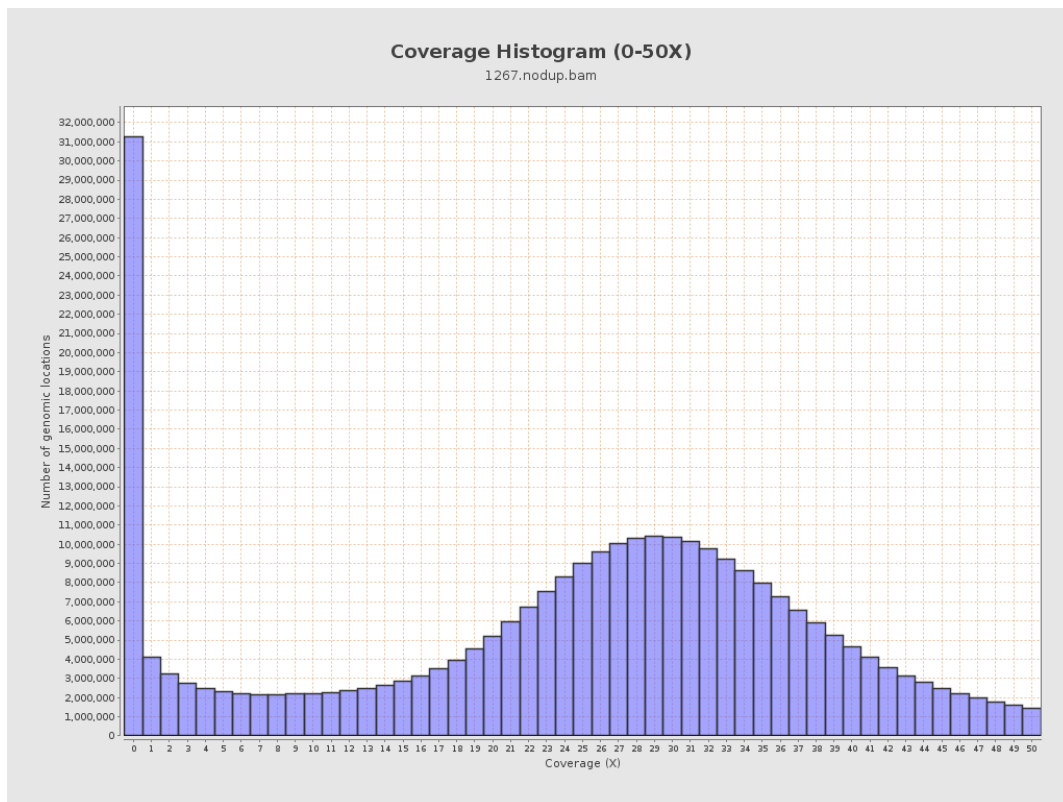
3. Results : Coverage across reference



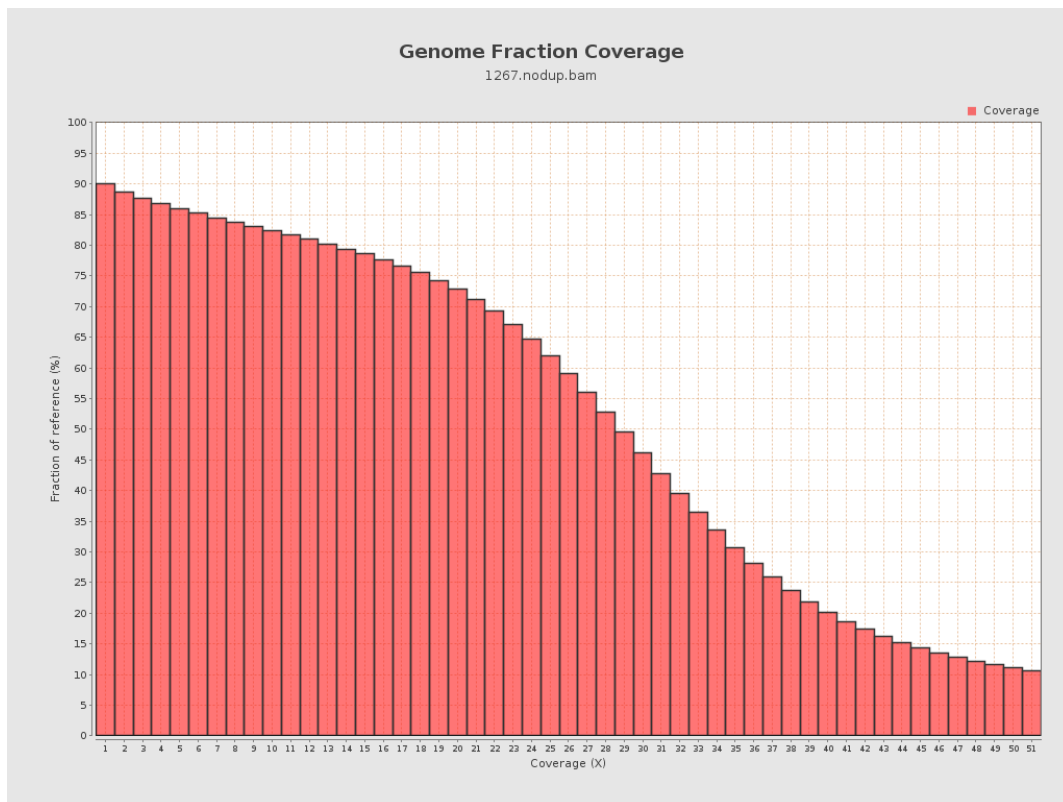
4. Results : Coverage Histogram



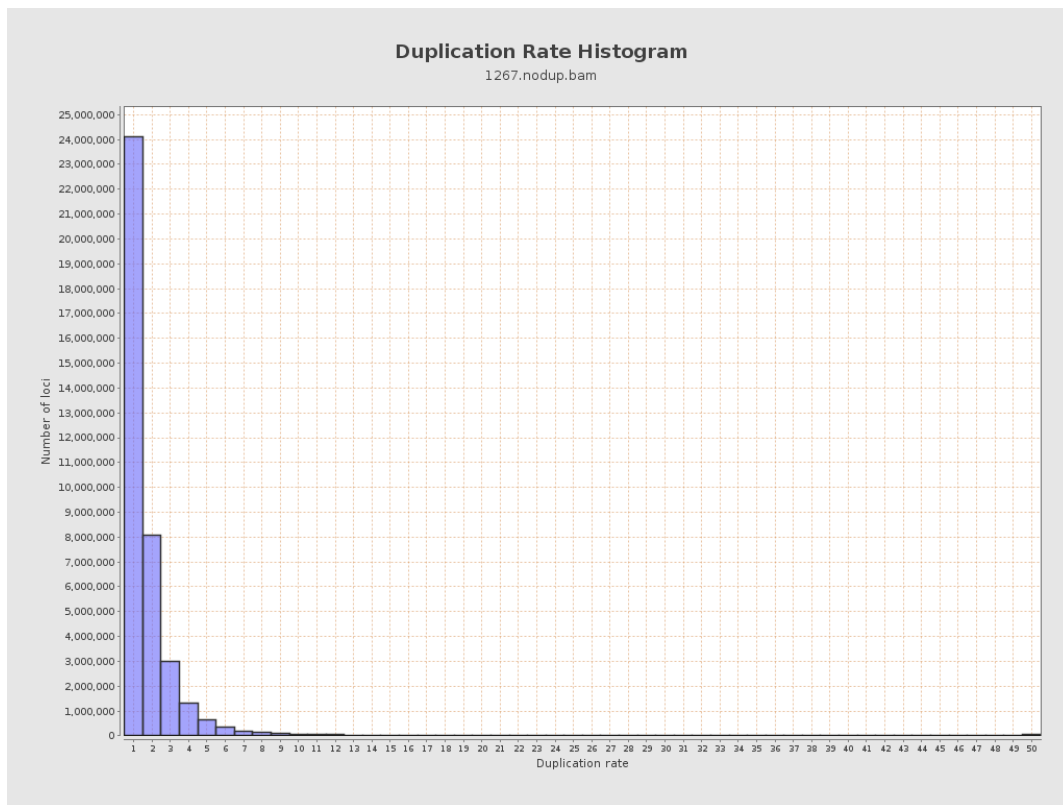
5. Results : Coverage Histogram (0-50X)



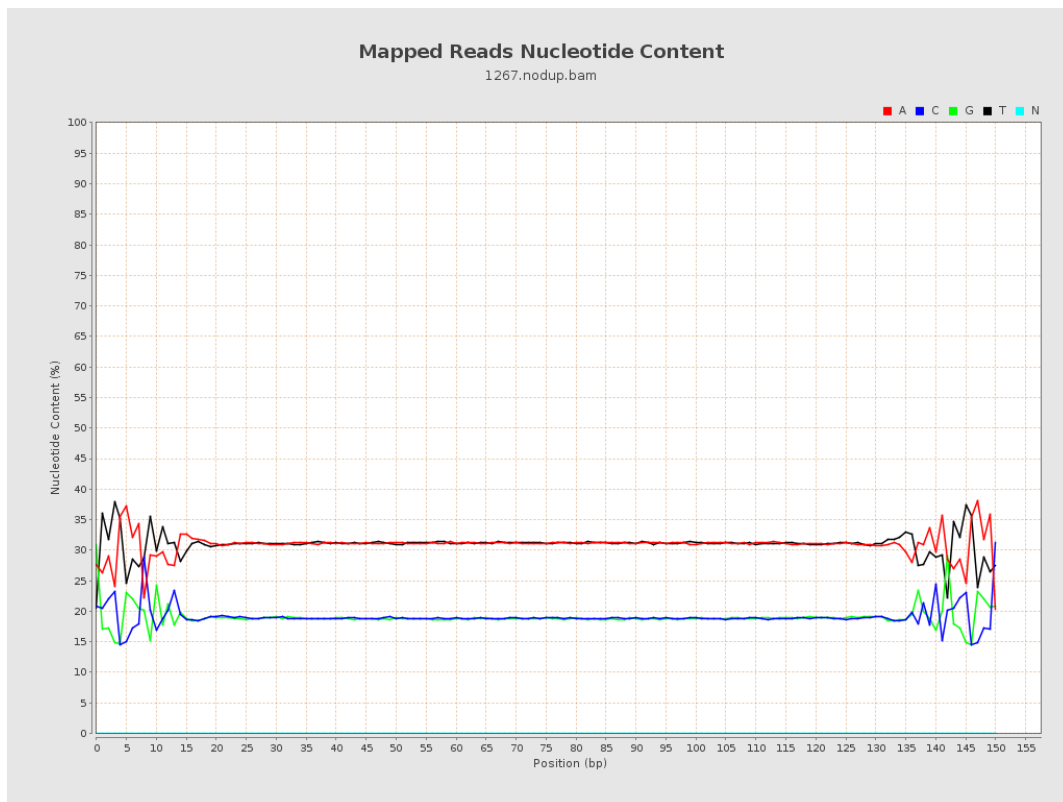
6. Results : Genome Fraction Coverage



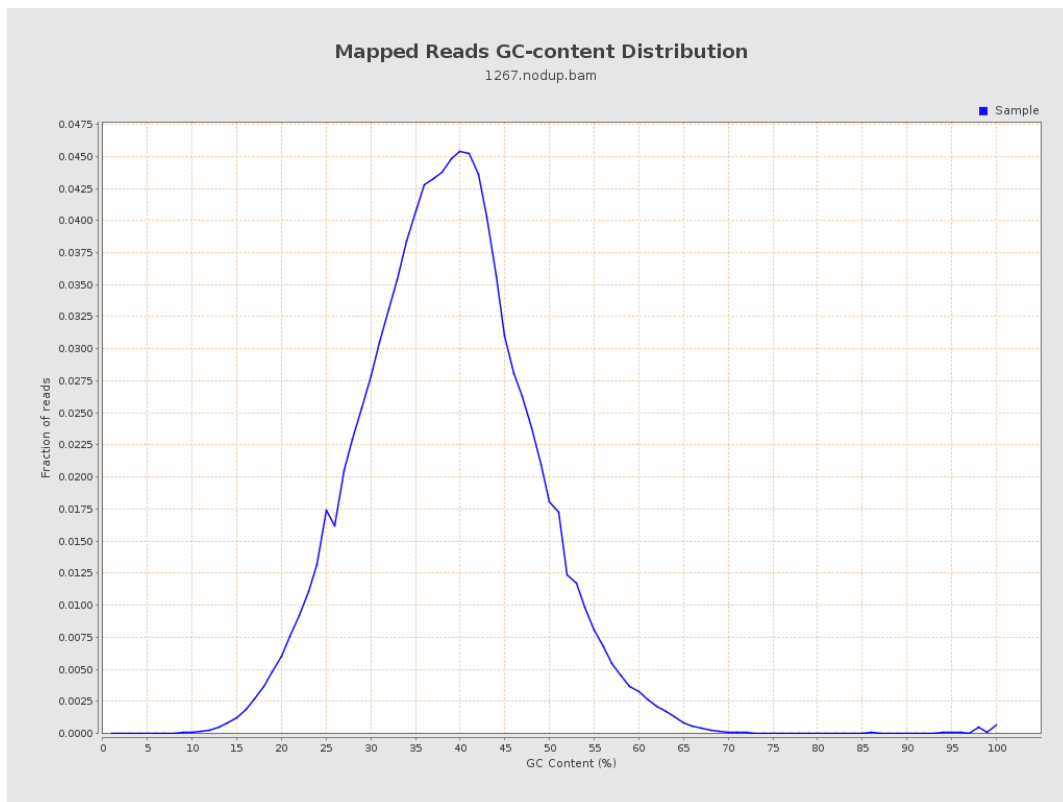
7. Results : Duplication Rate Histogram



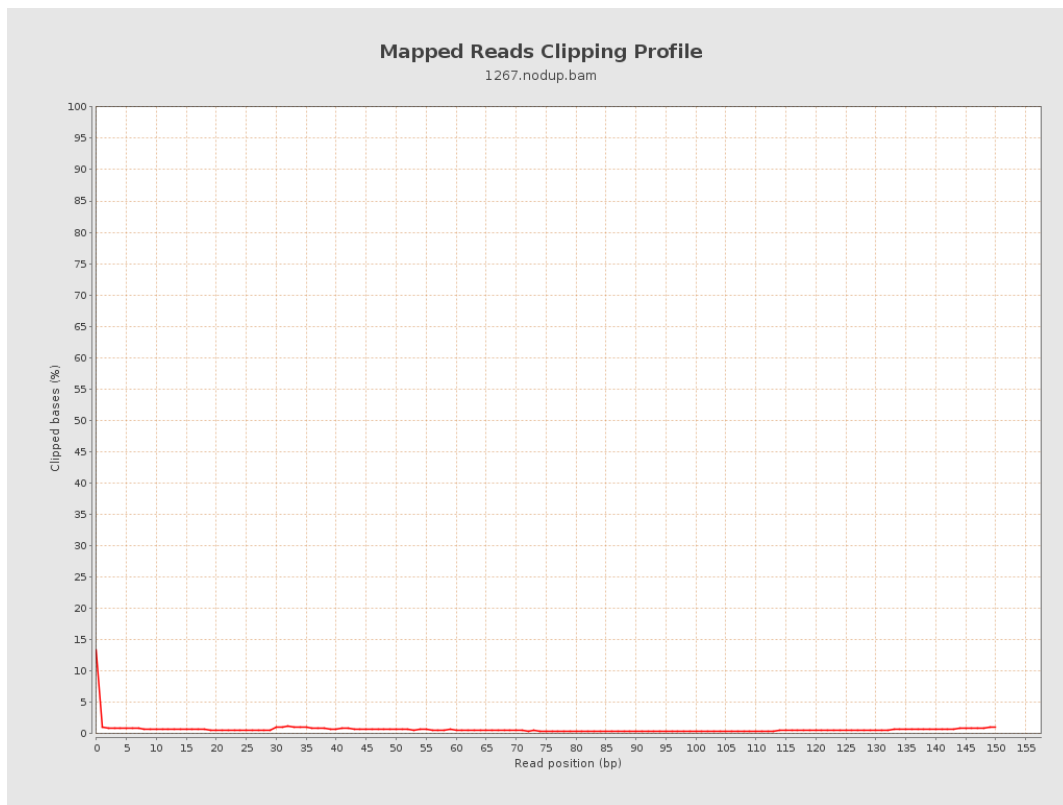
8. Results : Mapped Reads Nucleotide Content



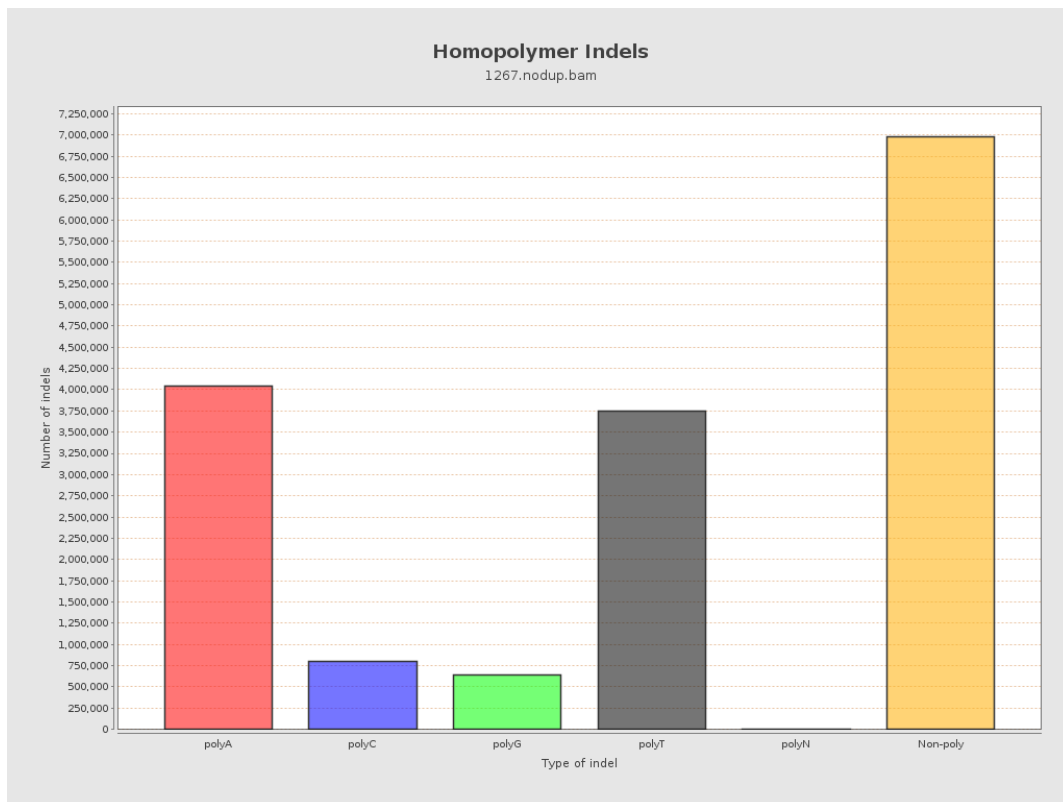
9. Results : Mapped Reads GC-content Distribution



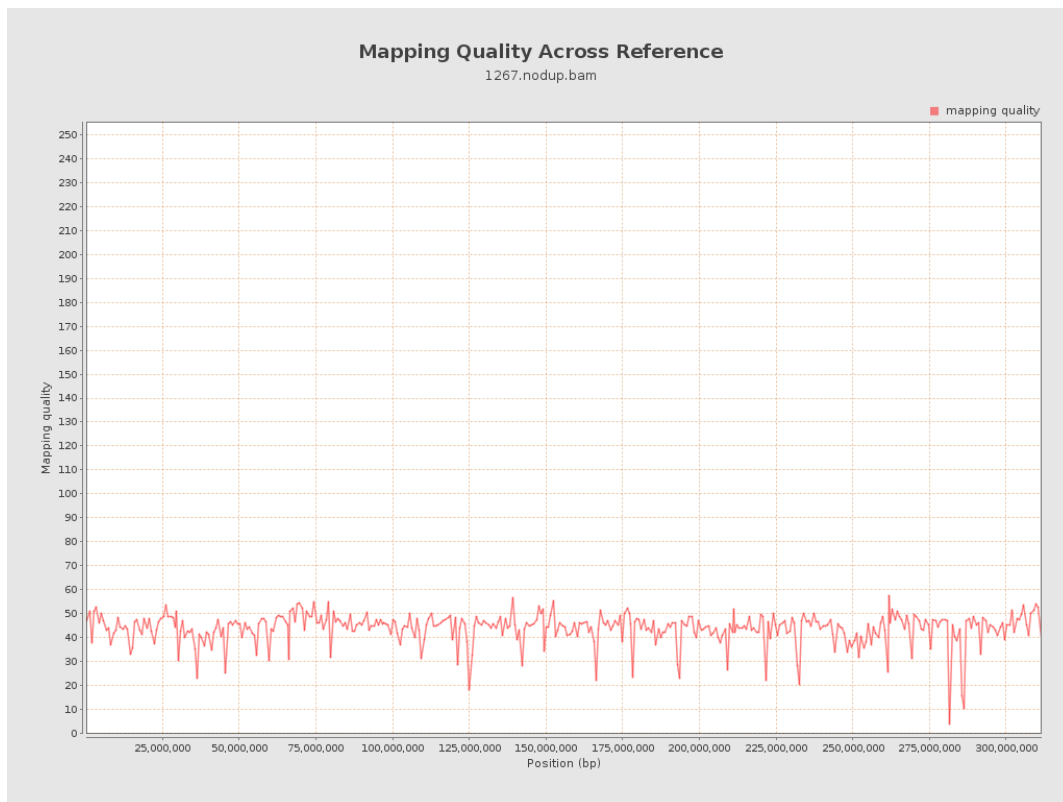
10. Results : Mapped Reads Clipping Profile



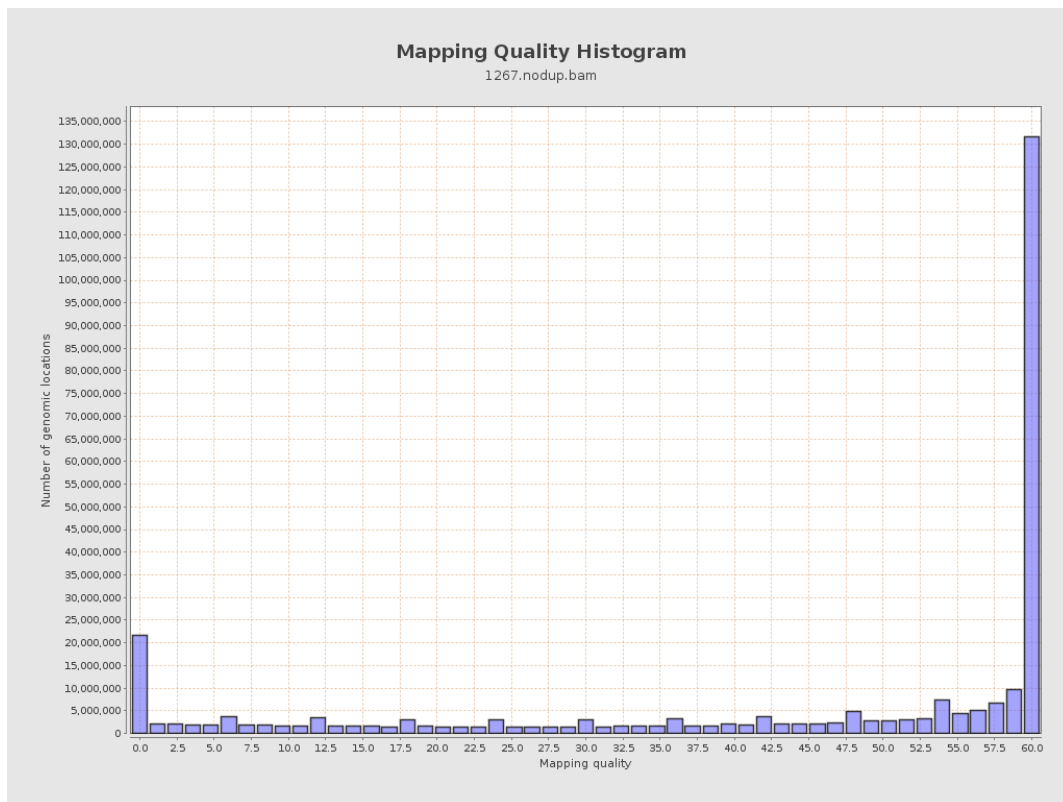
11. Results : Homopolymer Indels



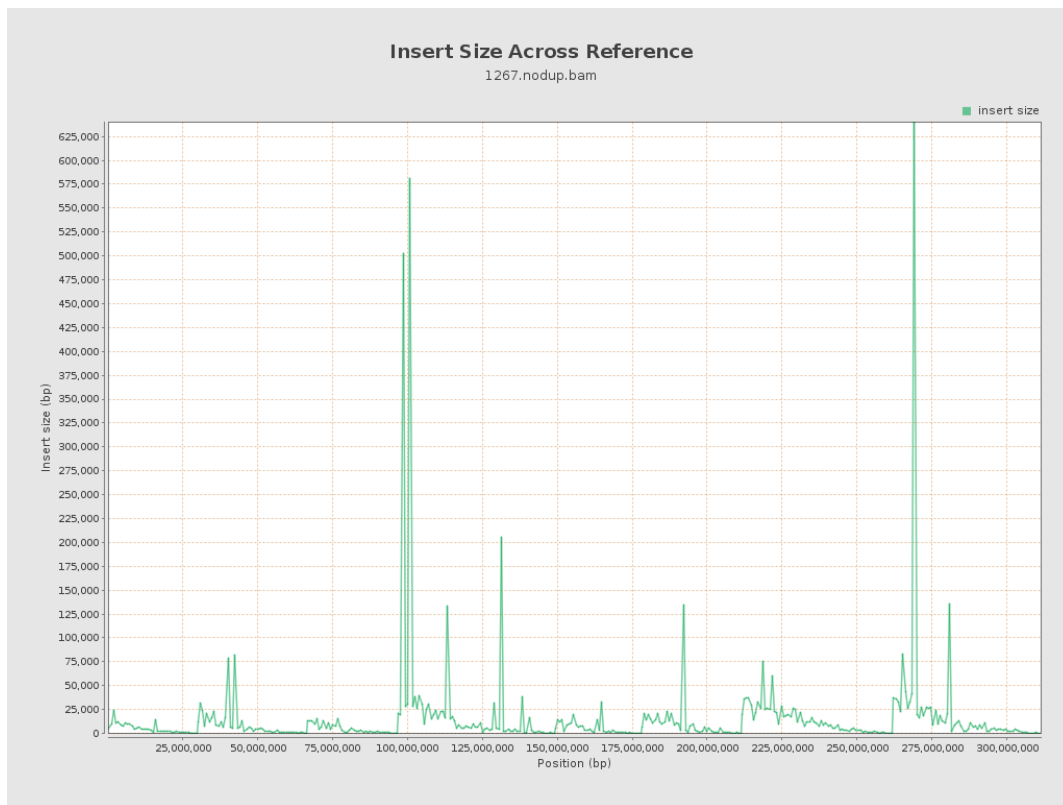
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

