

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/102
9
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1029 .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_554/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_554_S121_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_554/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_554_S121_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:28:04 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	56,796,791
Mapped reads	53,159,647 / 93.6%
Unmapped reads	3,637,144 / 6.4%
Mapped paired reads	53,159,647 / 93.6%
Mapped reads, first in pair	26,694,655 / 47%
Mapped reads, second in pair	26,464,992 / 46.6%
Mapped reads, both in pair	51,933,844 / 91.44%
Mapped reads, singletons	1,225,803 / 2.16%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	7,973,655 / 14.04%
Clipped reads	12,648,952 / 22.27%

2.2. ACGT Content

Number/percentage of A's	2,275,392,048 / 31%
Number/percentage of C's	1,394,960,892 / 19.01%
Number/percentage of T's	2,276,179,672 / 31.01%
Number/percentage of G's	1,392,646,501 / 18.98%
Number/percentage of N's	49,612 / 0%
GC Percentage	37.98%

2.3. Coverage

Mean	23.6101
Standard Deviation	174.7717

2.4. Mapping Quality

Mean Mapping Quality	44.34
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2.5. Insert size

Mean	232,715.35
Standard Deviation	2,297,652.95
P25/Median/P75	348 / 454 / 572

2.6. Mismatches and indels

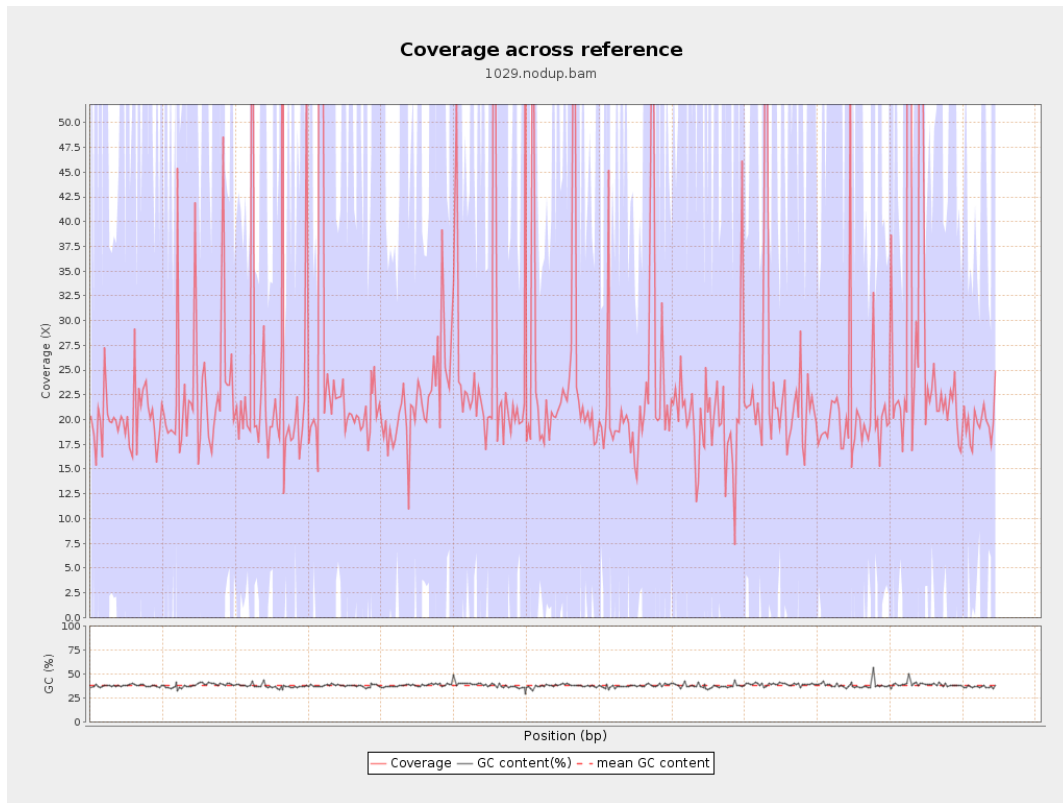
General error rate	2.56%
Mismatches	174,739,917
Insertions	4,896,444
Mapped reads with at least one insertion	8.28%
Deletions	4,944,915
Mapped reads with at least one deletion	8.28%
Homopolymer indels	56.72%

2.7. Chromosome stats

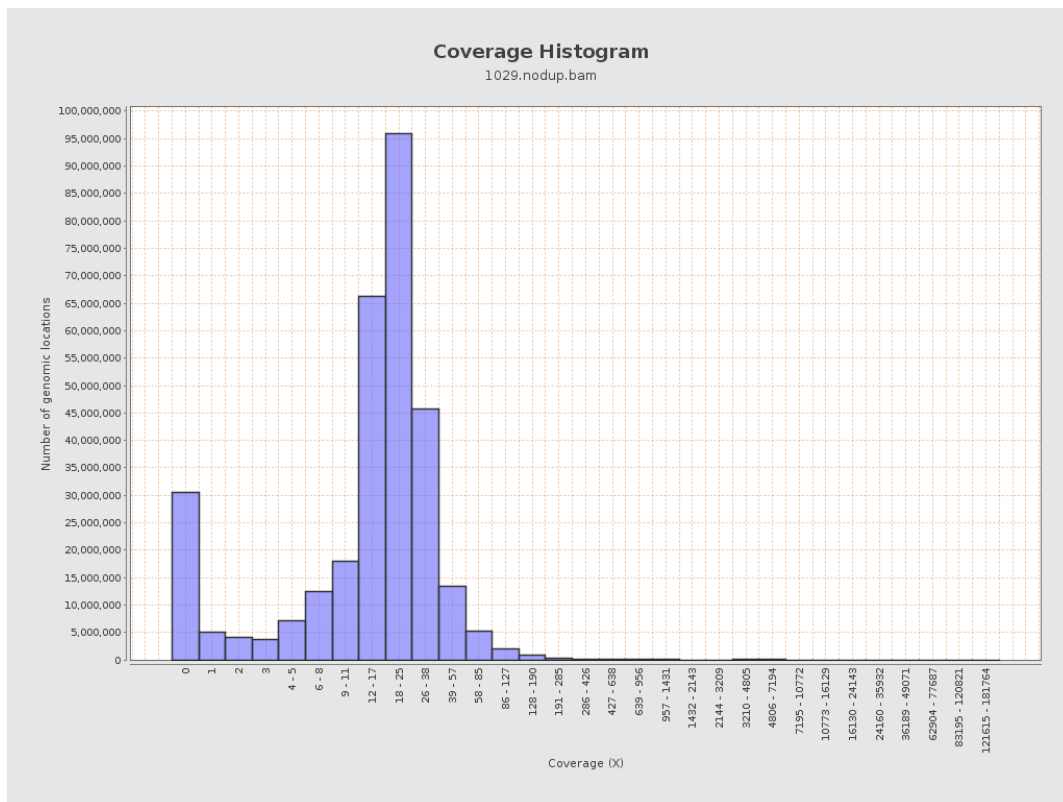
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	594269474	19.9927	53.4509

LT669789.1	36598175	877211276	23.9687	182.884
LT669790.1	30422129	797159990	26.2033	199.4024
LT669791.1	52758100	1219512435	23.1152	151.7526
LT669792.1	28376109	670905685	23.6433	180.7942
LT669793.1	33388210	735370410	22.0249	130.1249
LT669794.1	50579949	1121526263	22.1733	143.3084
LT669795.1	49795044	1341936991	26.9492	255.5763

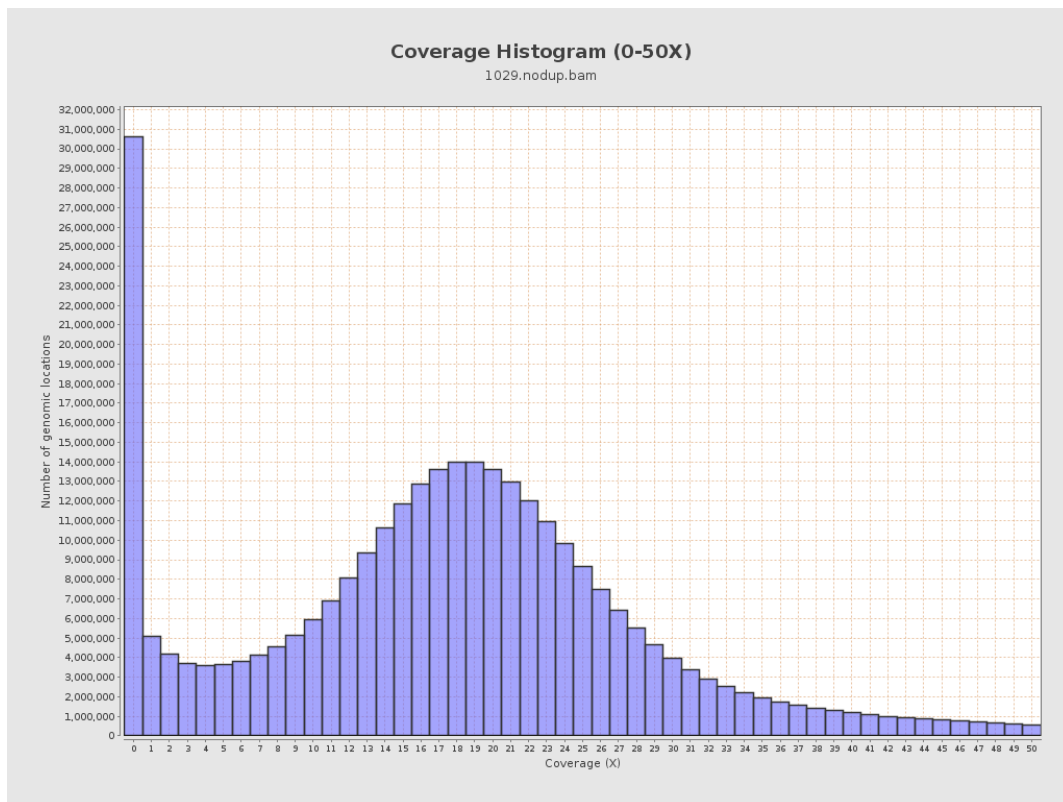
3. Results : Coverage across reference



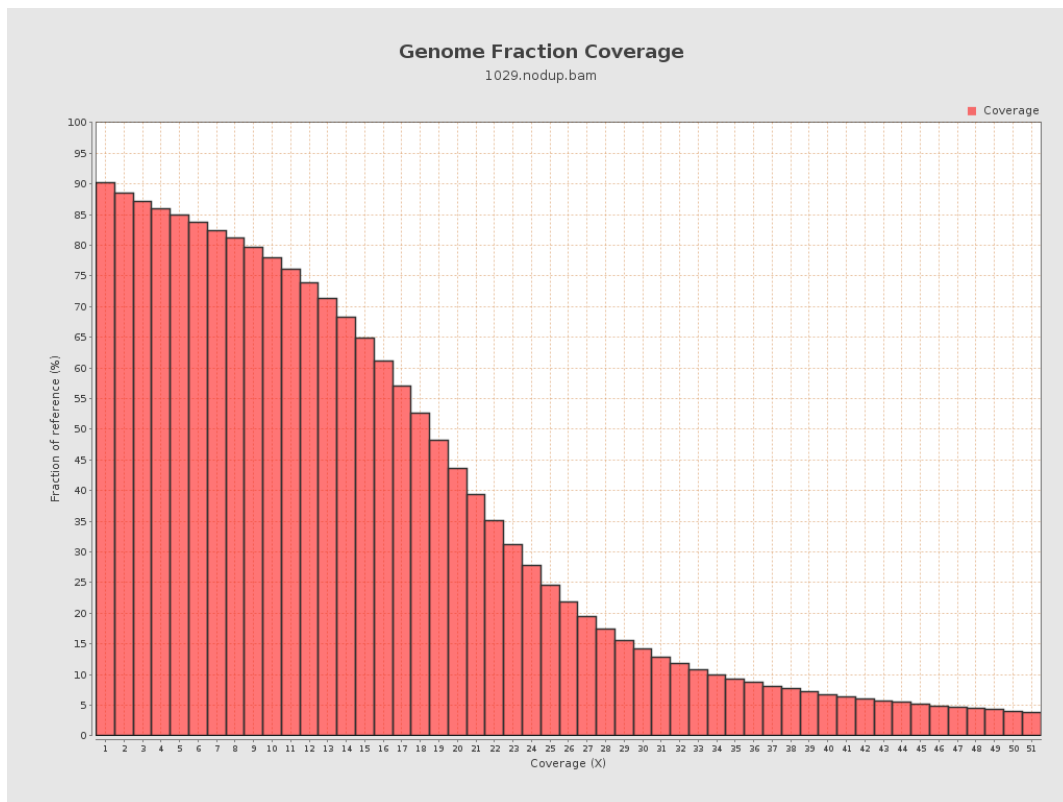
4. Results : Coverage Histogram



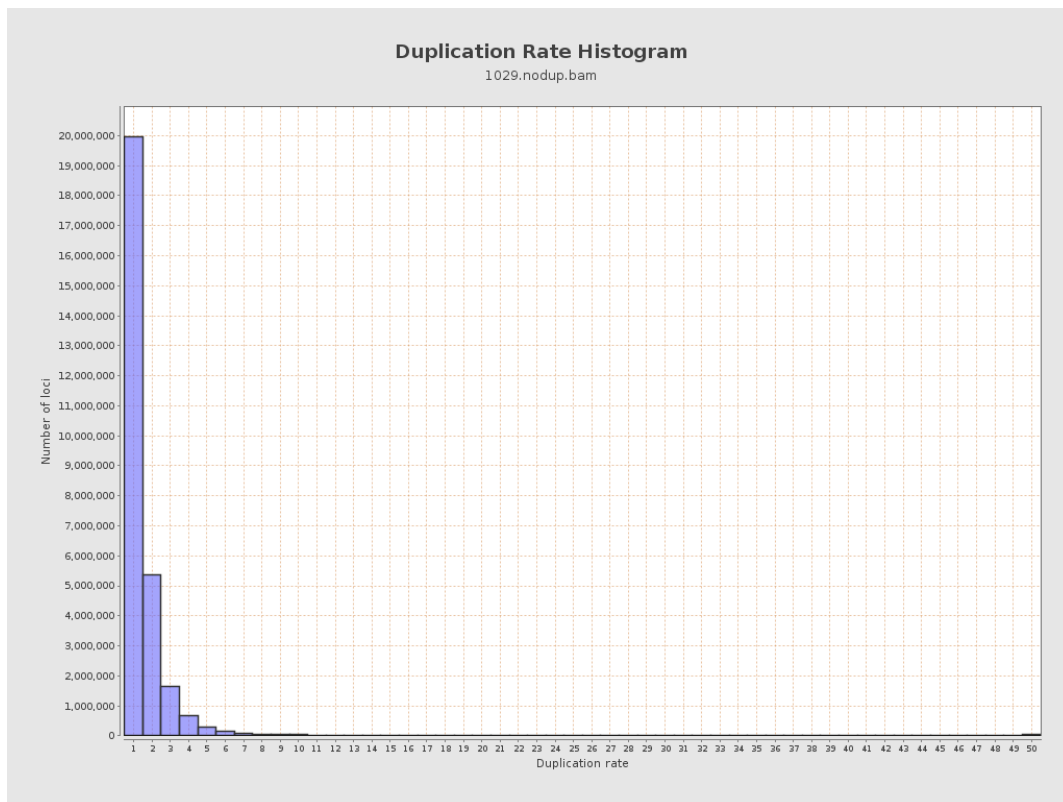
5. Results : Coverage Histogram (0-50X)



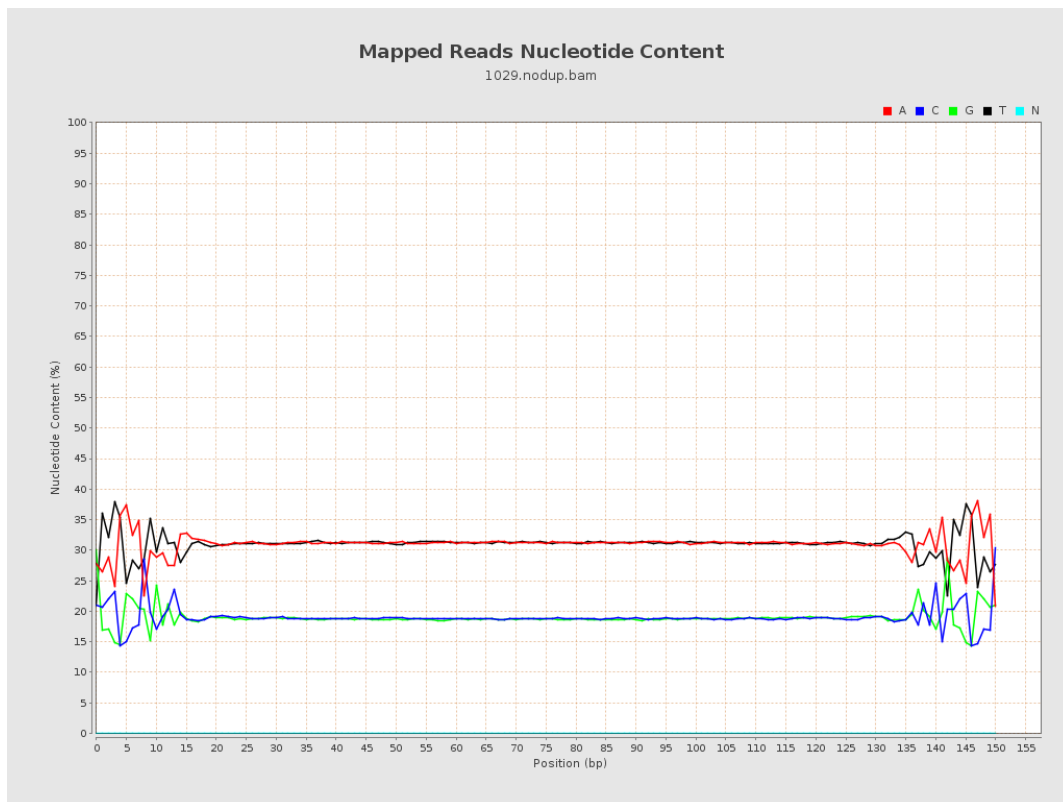
6. Results : Genome Fraction Coverage



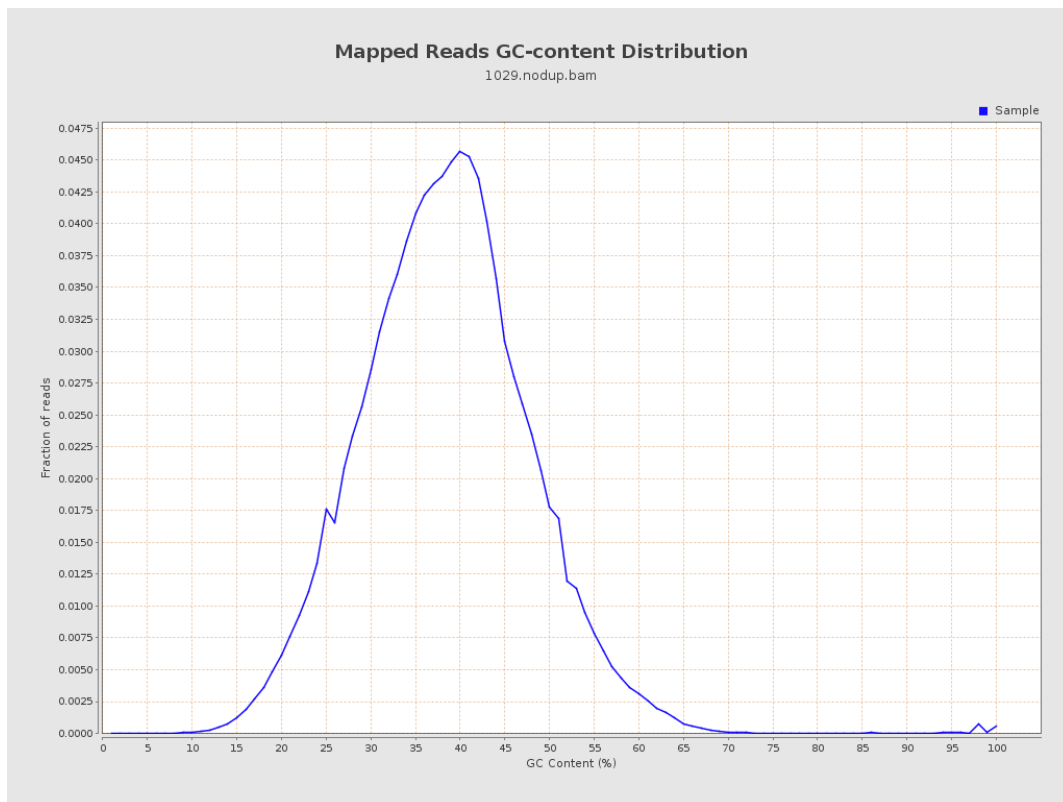
7. Results : Duplication Rate Histogram



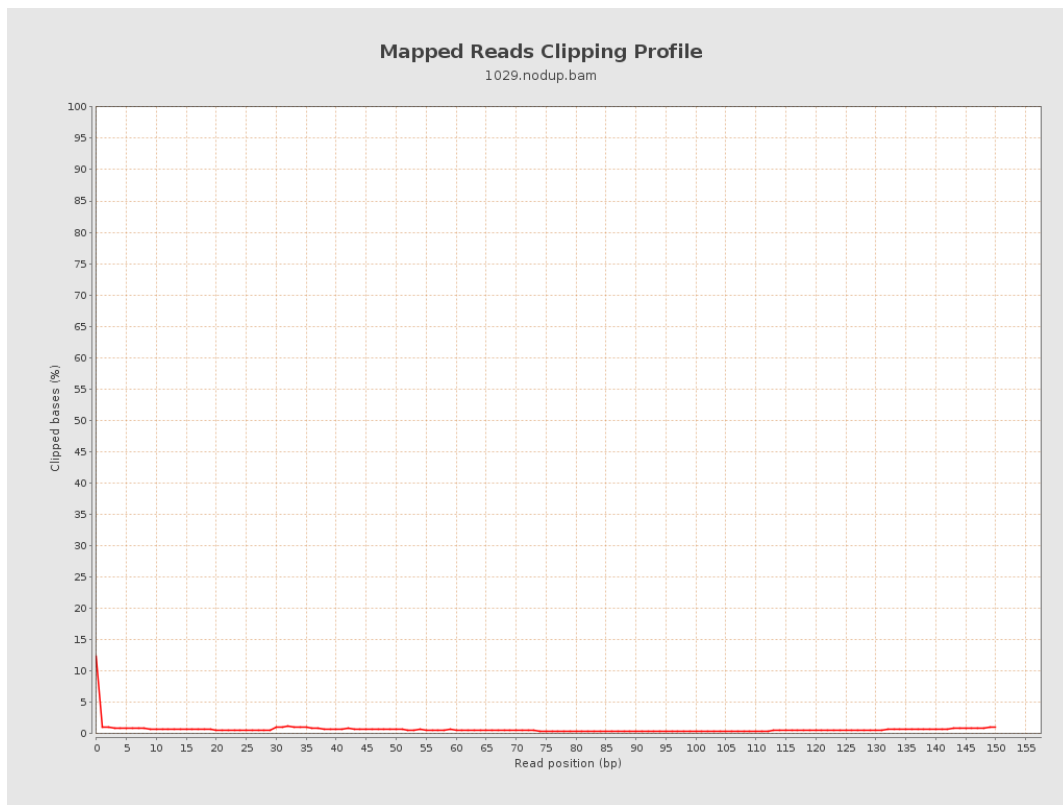
8. Results : Mapped Reads Nucleotide Content



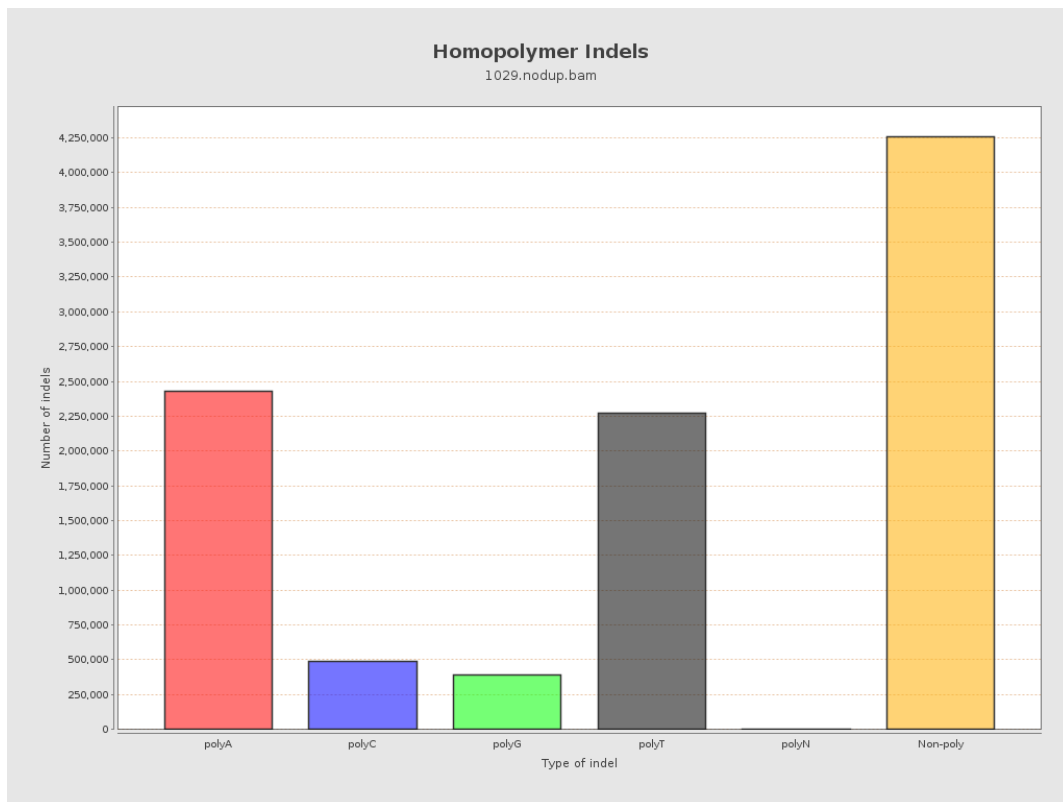
9. Results : Mapped Reads GC-content Distribution



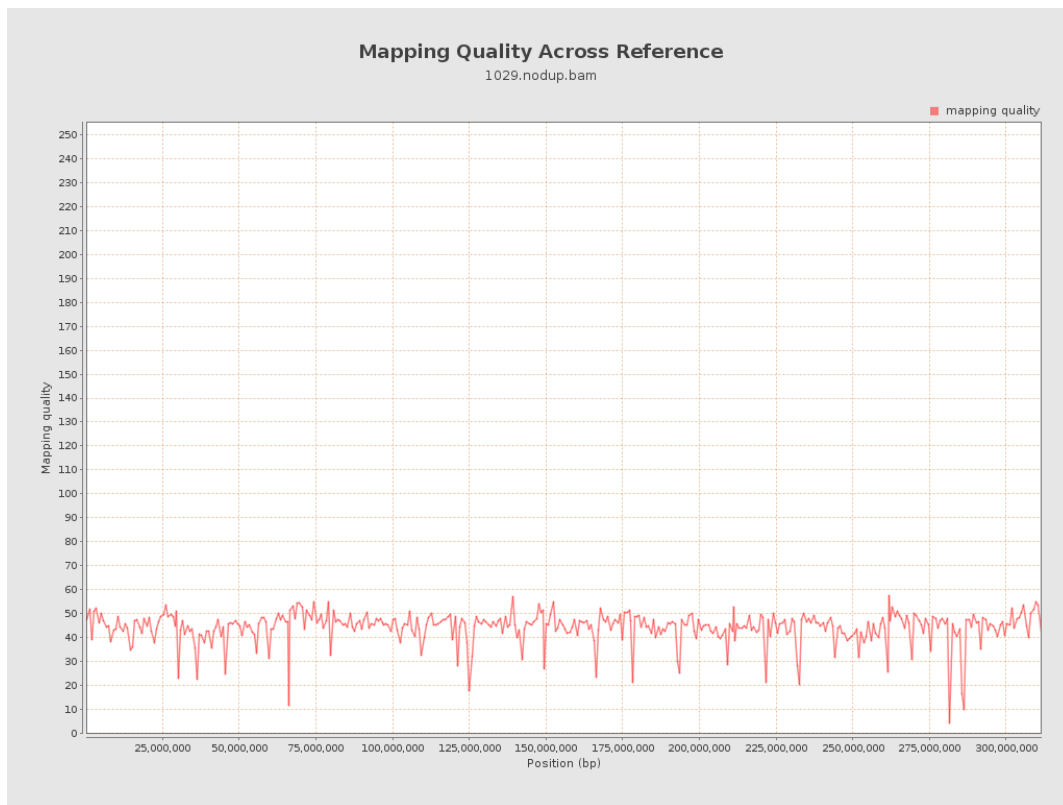
10. Results : Mapped Reads Clipping Profile



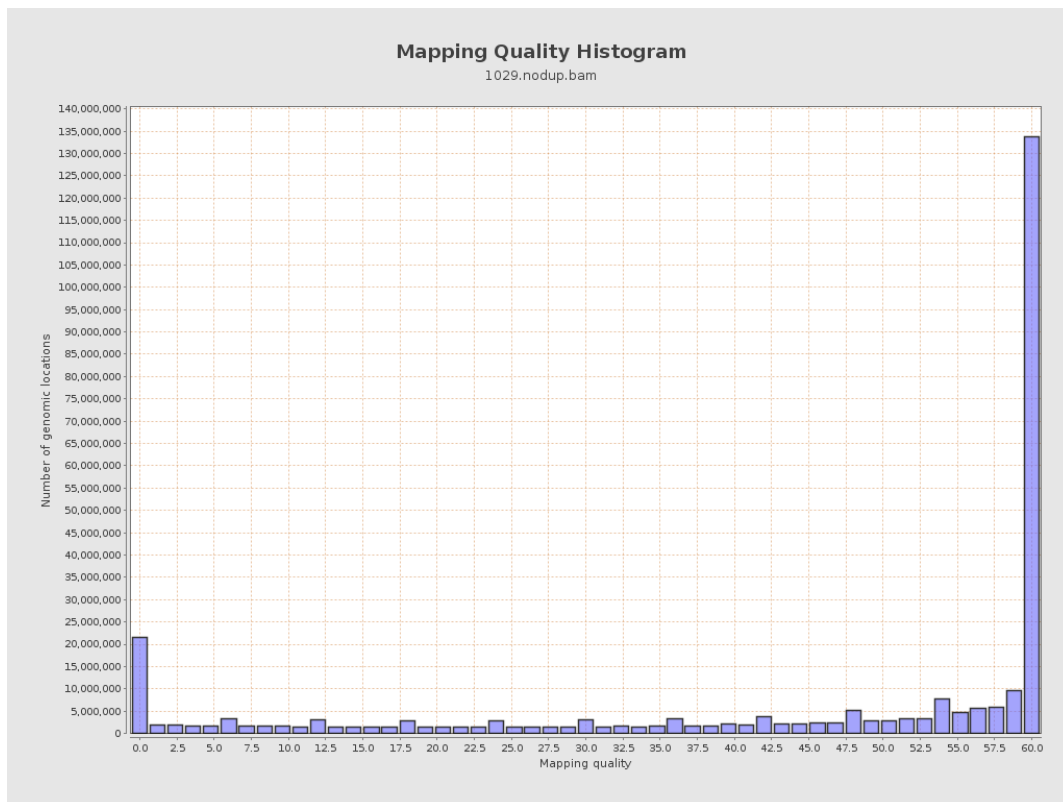
11. Results : Homopolymer Indels



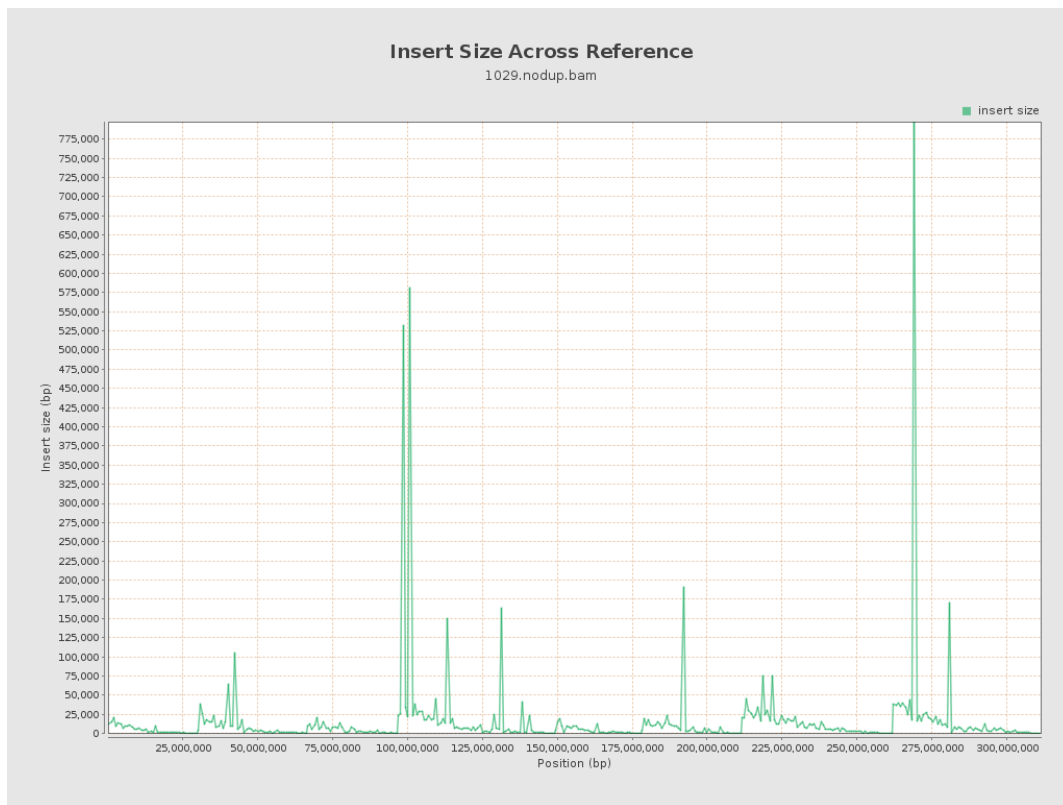
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

