

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/870
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/870 .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\tSM:\$sample /proj/uppstore2018210/Aalpina/data/reference/GCA_900128785.1_MPIPZ.v5_genomic.fa /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_214/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_214_S295_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_214/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_214_S295_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:54 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,774,603
Mapped reads	61,817,110 / 89.88%
Unmapped reads	6,957,493 / 10.12%
Mapped paired reads	61,817,110 / 89.88%
Mapped reads, first in pair	30,984,683 / 45.05%
Mapped reads, second in pair	30,832,427 / 44.83%
Mapped reads, both in pair	59,813,679 / 86.97%
Mapped reads, singletons	2,003,431 / 2.91%
Read min/max/mean length	30 / 151 / 147.93
Duplicated reads (flagged)	10,823,377 / 15.74%
Clipped reads	15,636,160 / 22.74%

2.2. ACGT Content

Number/percentage of A's	2,594,577,662 / 30.85%
Number/percentage of C's	1,608,293,260 / 19.12%
Number/percentage of T's	2,597,250,679 / 30.88%
Number/percentage of G's	1,609,447,248 / 19.14%
Number/percentage of N's	31,175 / 0%
GC Percentage	38.26%

2.3. Coverage

Mean	27.0573
Standard Deviation	275.1756

2.4. Mapping Quality

Mean Mapping Quality	43.68
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2.5. Insert size

Mean	271,869.39
Standard Deviation	2,514,139.92
P25/Median/P75	316 / 418 / 547

2.6. Mismatches and indels

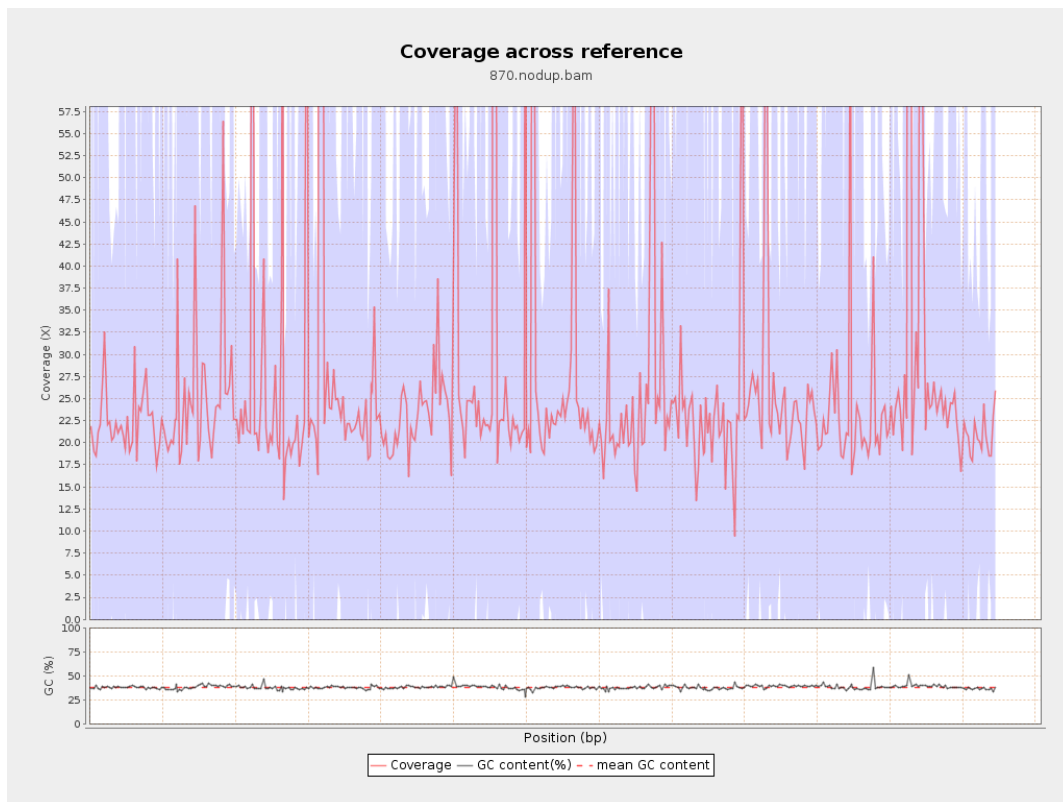
General error rate	2.43%
Mismatches	187,145,648
Insertions	6,318,356
Mapped reads with at least one insertion	9.1%
Deletions	6,034,895
Mapped reads with at least one deletion	8.64%
Homopolymer indels	57.14%

2.7. Chromosome stats

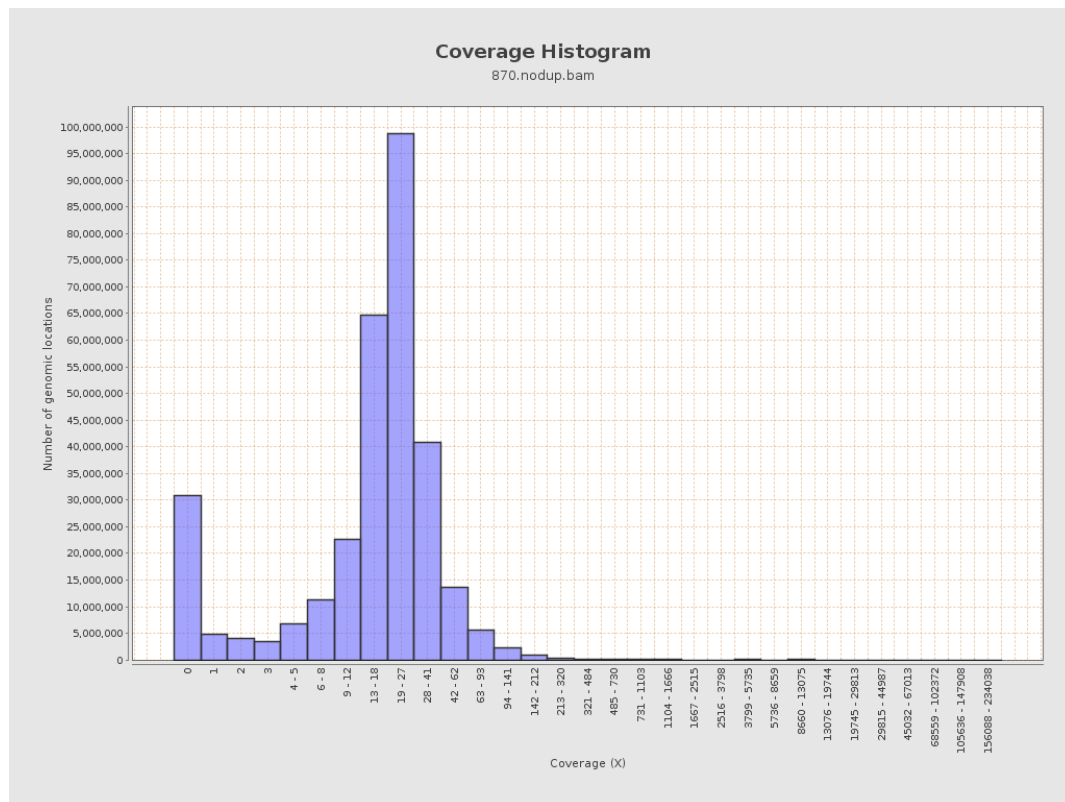
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	656386194	22.0824	115.1117

LT669789.1	36598175	1003543114	27.4206	290.031
LT669790.1	30422129	1027269685	33.7672	393.699
LT669791.1	52758100	1401020818	26.5556	302.787
LT669792.1	28376109	766593410	27.0155	247.2351
LT669793.1	33388210	837092509	25.0715	210.8883
LT669794.1	50579949	1288026437	25.4652	227.7751
LT669795.1	49795044	1452259572	29.1647	308.1119

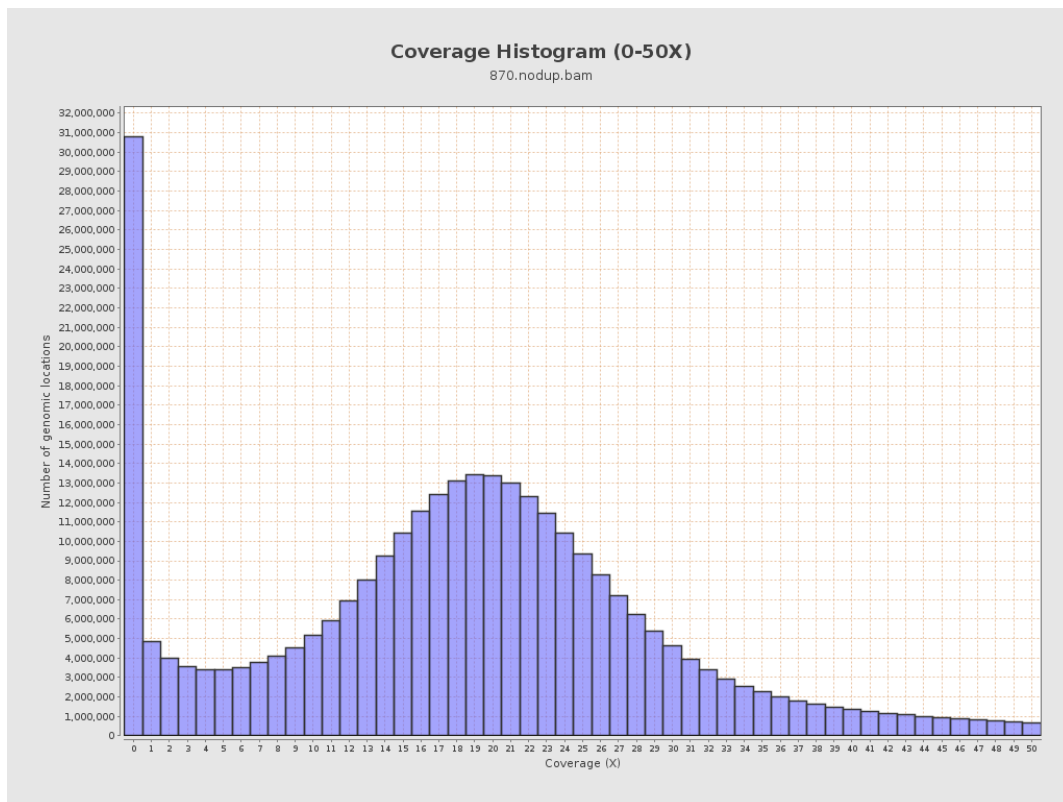
3. Results : Coverage across reference



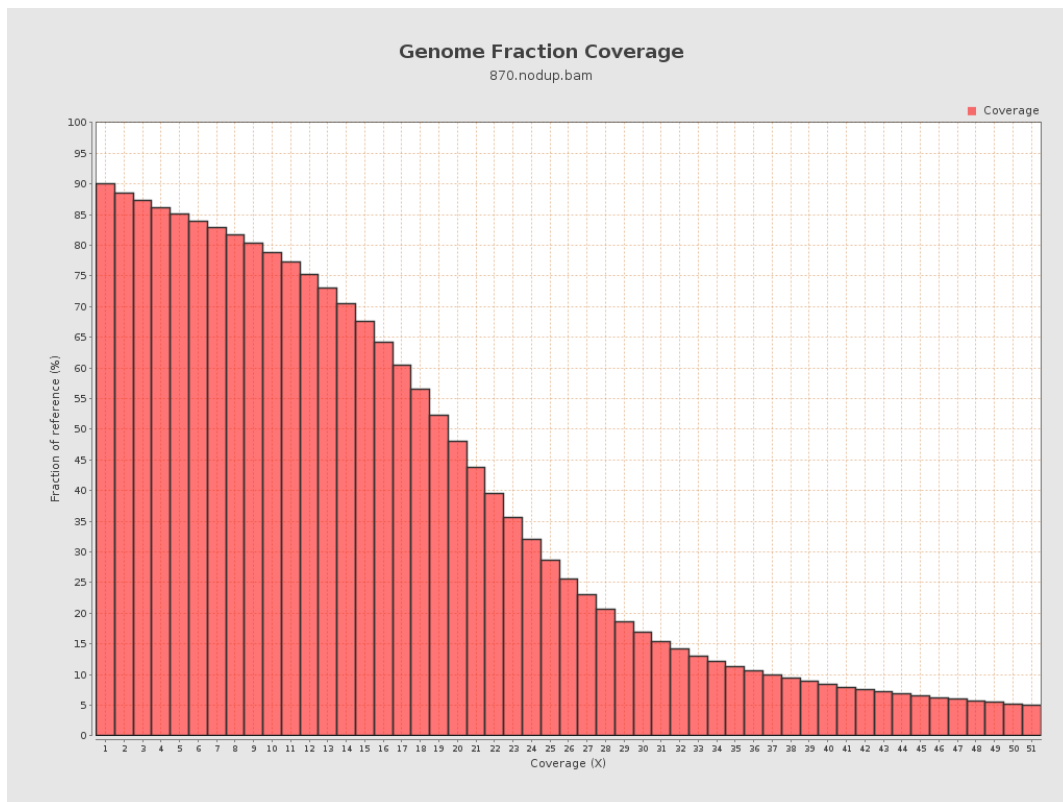
4. Results : Coverage Histogram



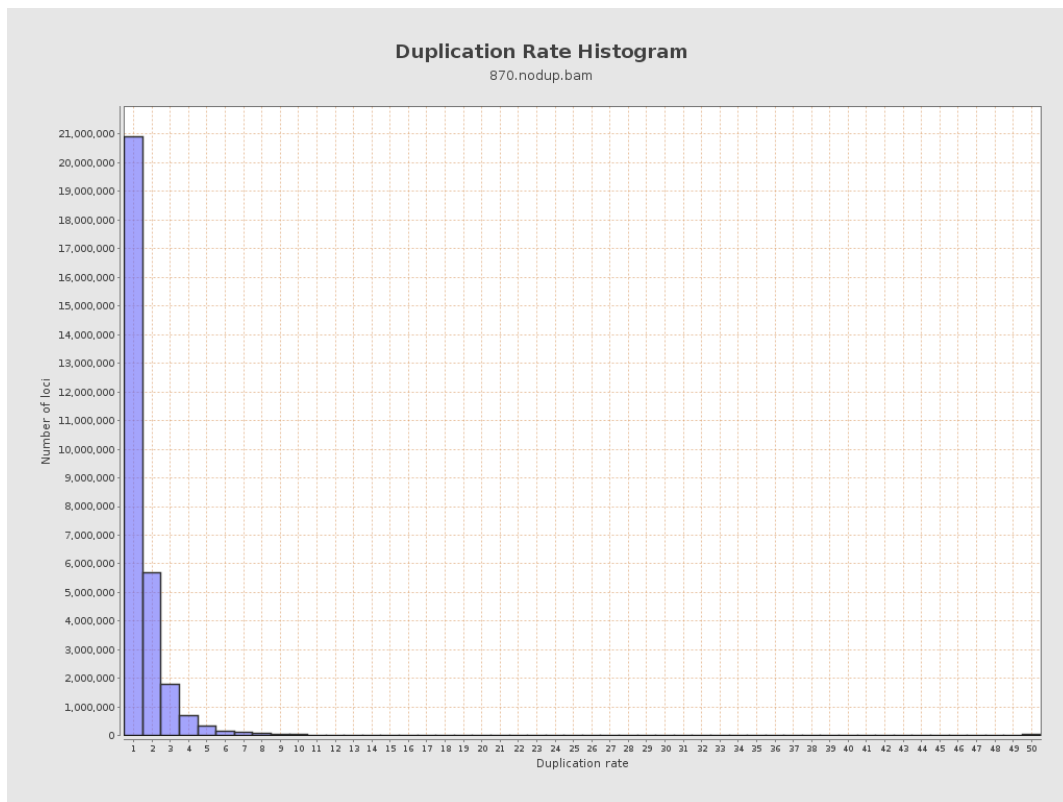
5. Results : Coverage Histogram (0-50X)



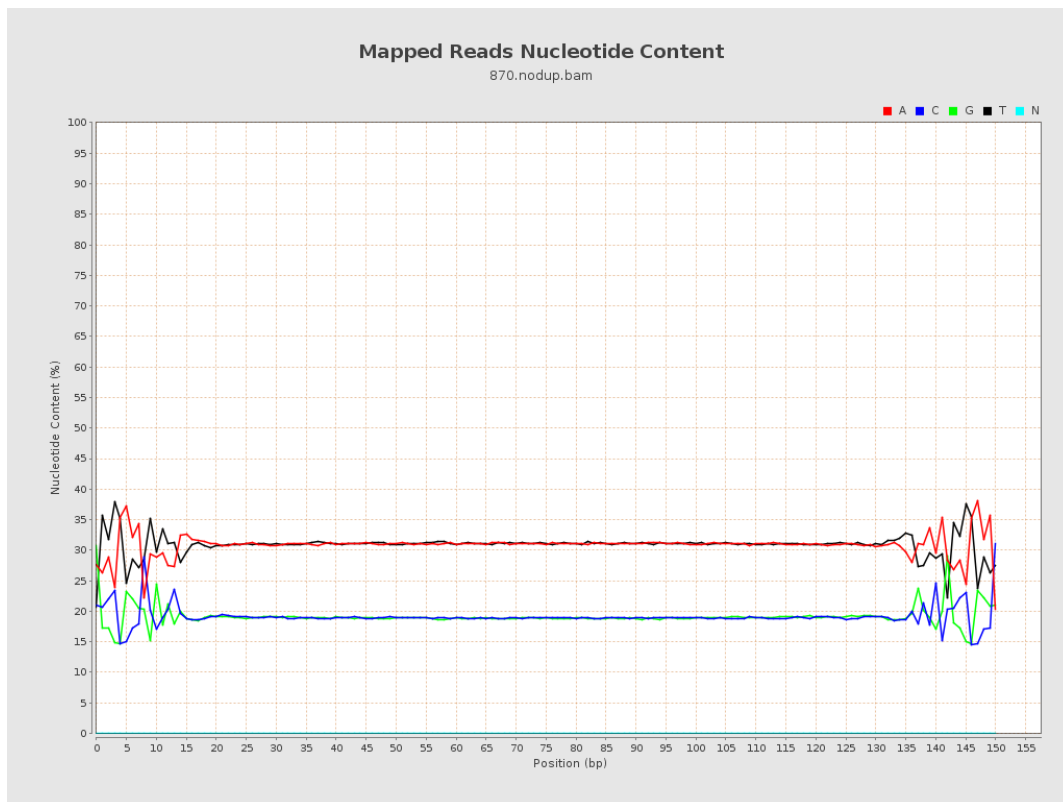
6. Results : Genome Fraction Coverage



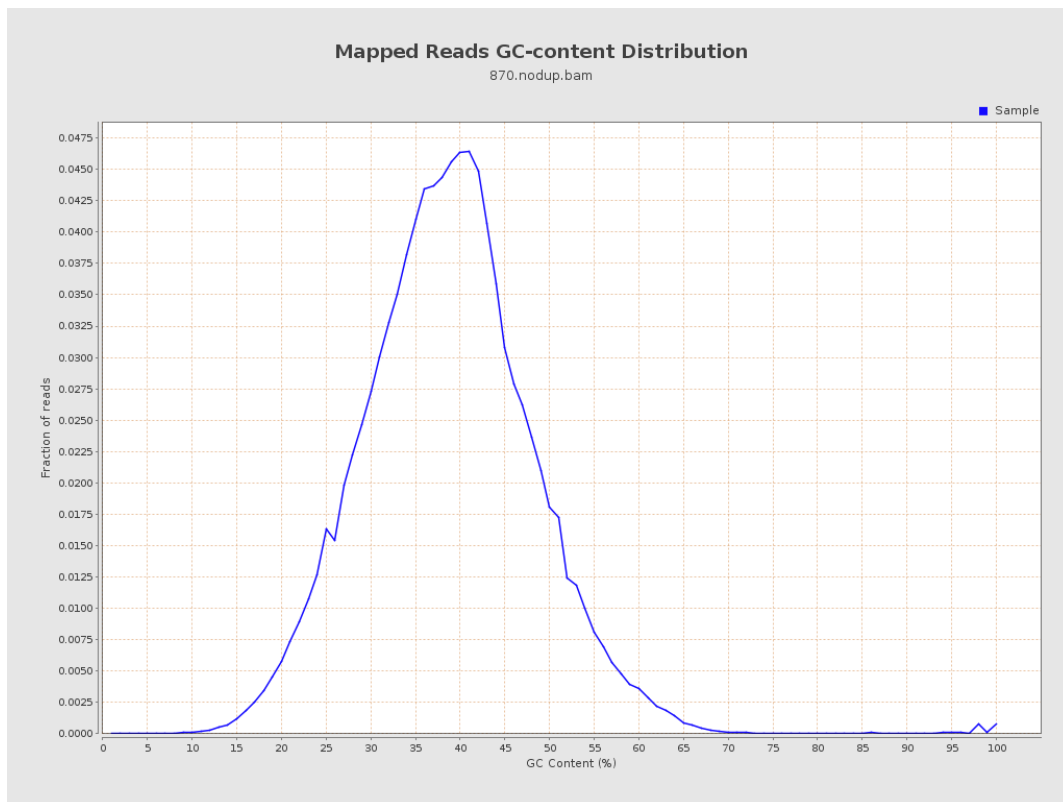
7. Results : Duplication Rate Histogram



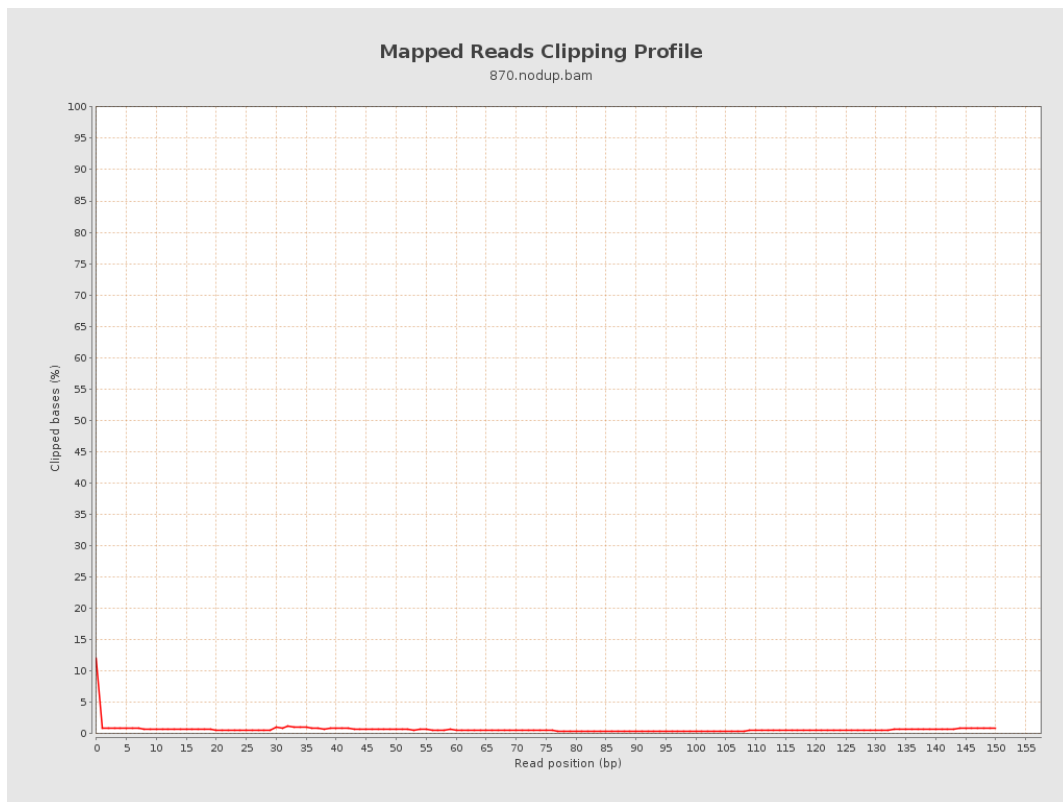
8. Results : Mapped Reads Nucleotide Content



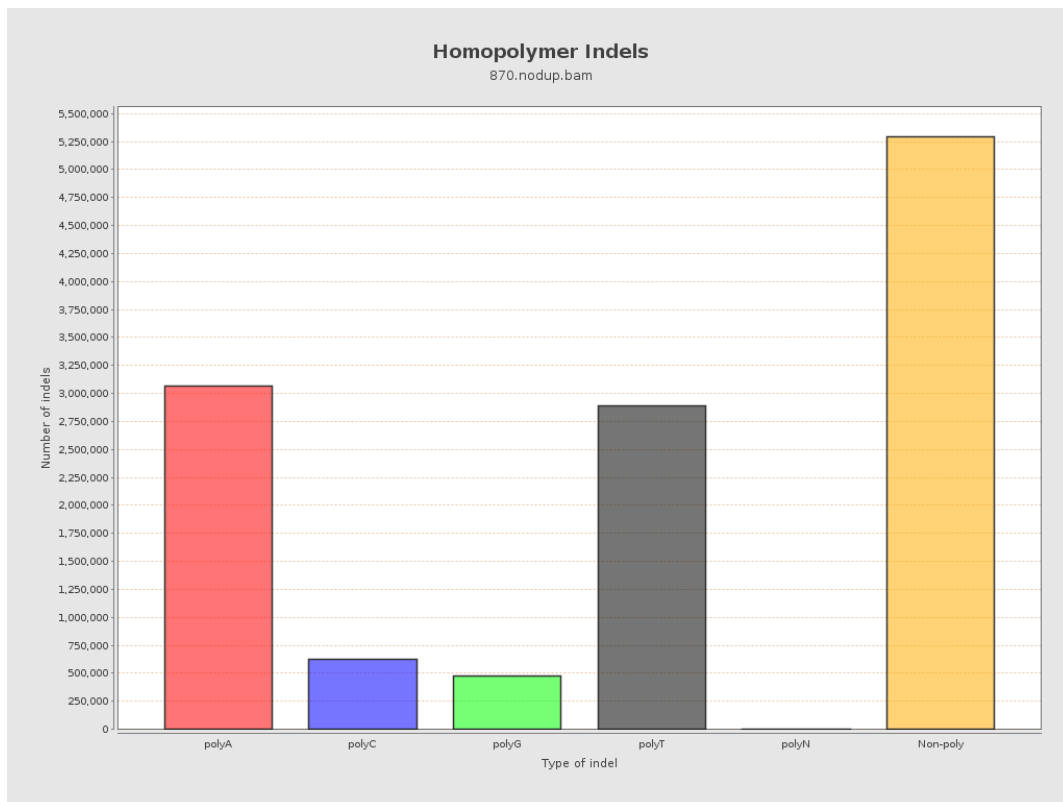
9. Results : Mapped Reads GC-content Distribution



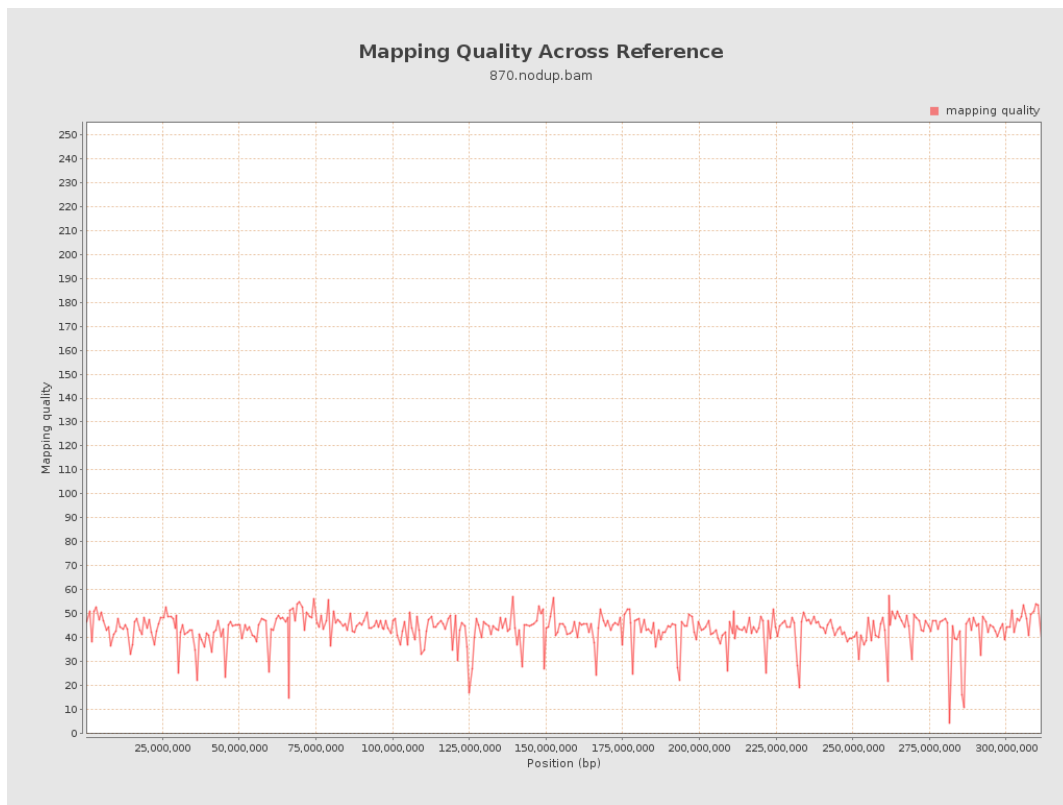
10. Results : Mapped Reads Clipping Profile



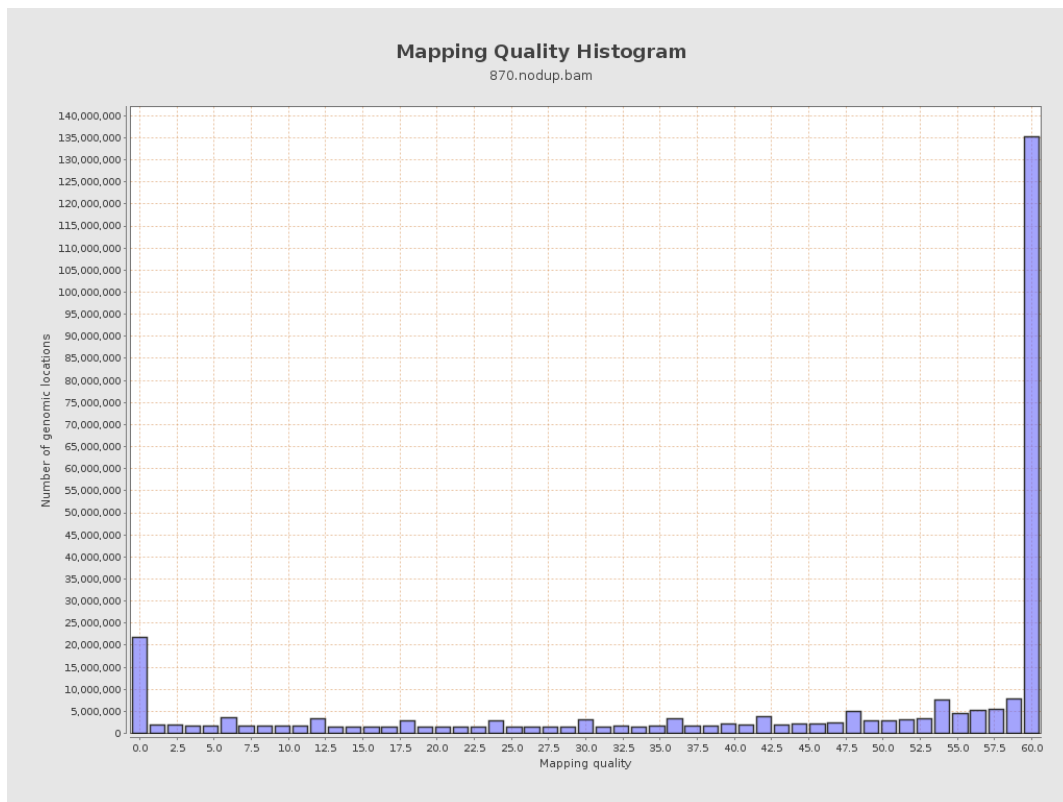
11. Results : Homopolymer Indels



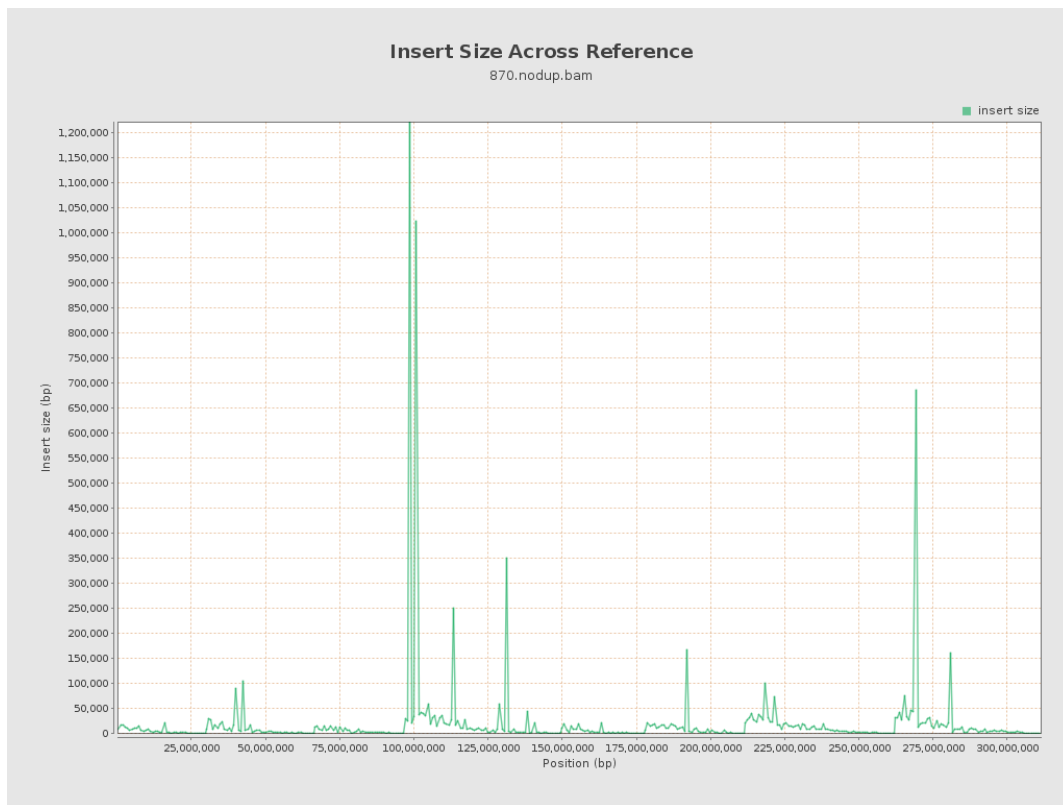
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

