

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/721
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/721.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_114/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_114_S204_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_114/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_114_S204_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:06 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	69,121,015
Mapped reads	63,603,144 / 92.02%
Unmapped reads	5,517,871 / 7.98%
Mapped paired reads	63,603,144 / 92.02%
Mapped reads, first in pair	31,873,311 / 46.11%
Mapped reads, second in pair	31,729,833 / 45.9%
Mapped reads, both in pair	61,809,615 / 89.42%
Mapped reads, singletons	1,793,529 / 2.59%
Read min/max/mean length	30 / 151 / 148.1
Duplicated reads (flagged)	11,434,122 / 16.54%
Clipped reads	14,684,942 / 21.25%

2.2. ACGT Content

Number/percentage of A's	2,712,370,457 / 30.93%
Number/percentage of C's	1,672,607,298 / 19.07%
Number/percentage of T's	2,715,173,161 / 30.96%
Number/percentage of G's	1,670,097,899 / 19.04%
Number/percentage of N's	36,535 / 0%
GC Percentage	38.11%

2.3. Coverage

Mean	28.2179
Standard Deviation	245.2032

2.4. Mapping Quality

Mean Mapping Quality	43.86
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2.5. Insert size

Mean	257,321.5
Standard Deviation	2,433,350.41
P25/Median/P75	330 / 430 / 559

2.6. Mismatches and indels

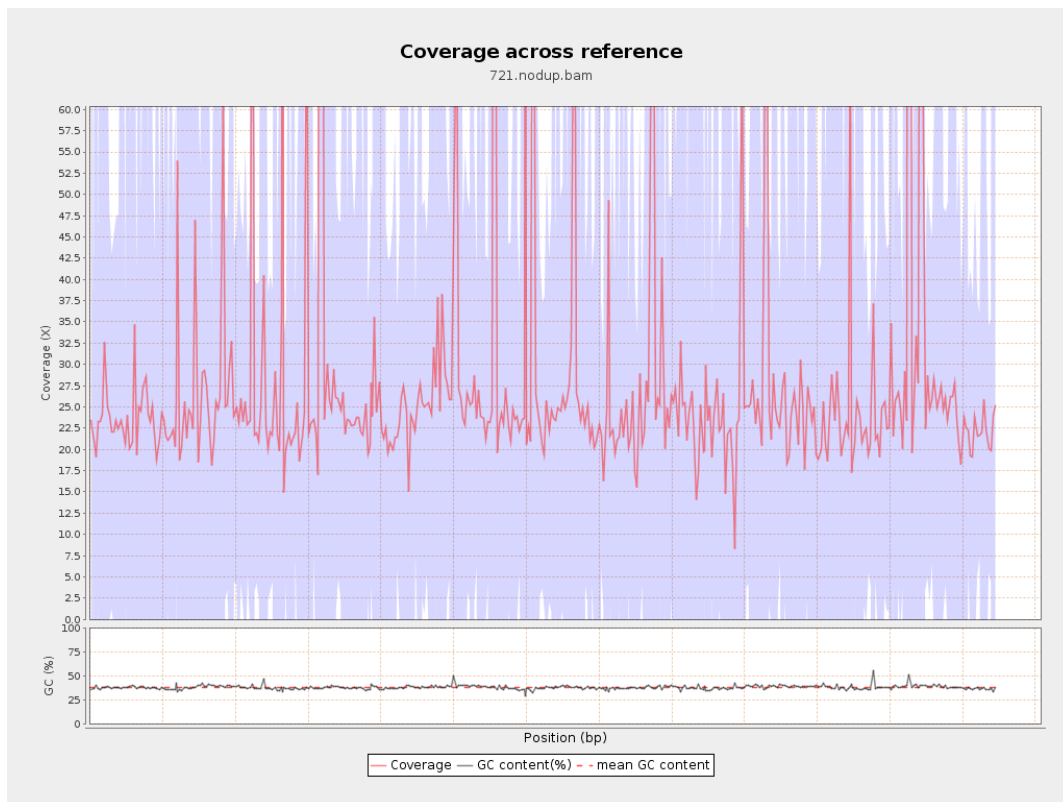
General error rate	2.4%
Mismatches	193,206,180
Insertions	6,328,820
Mapped reads with at least one insertion	8.88%
Deletions	6,226,707
Mapped reads with at least one deletion	8.67%
Homopolymer indels	57.02%

2.7. Chromosome stats

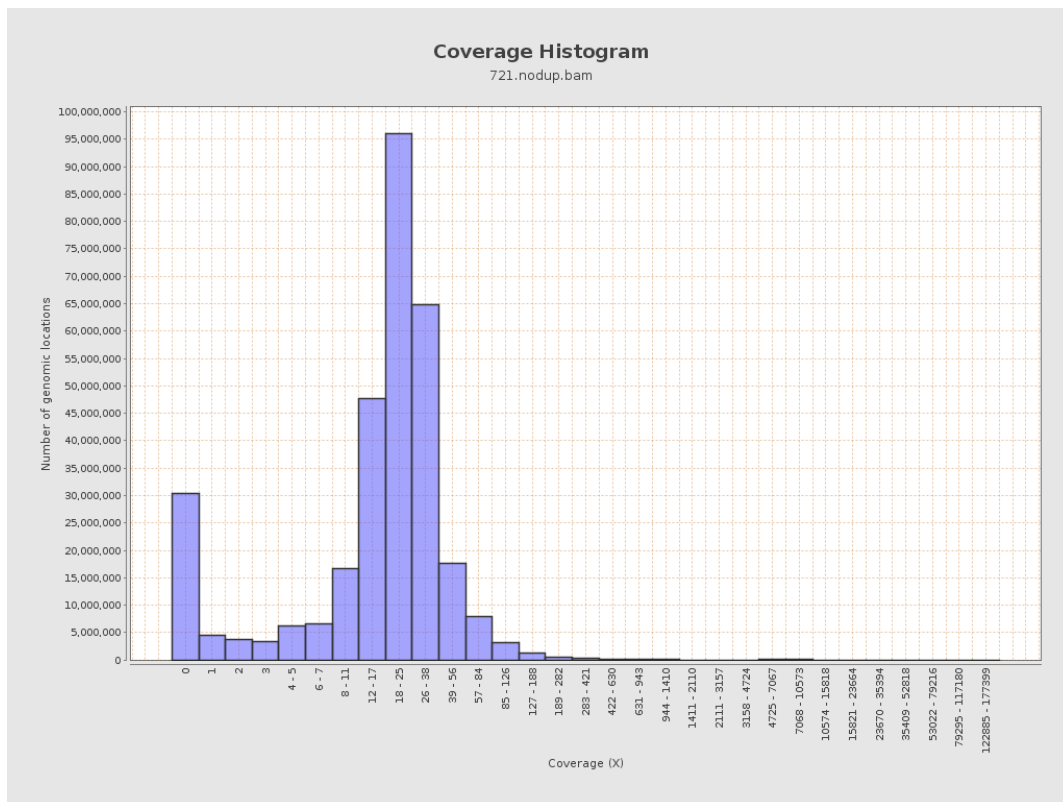
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	693231745	23.322	91.1388

LT669789.1	36598175	1042649554	28.4891	259.5509
LT669790.1	30422129	1013900375	33.3277	330.2852
LT669791.1	52758100	1463392339	27.7378	247.2993
LT669792.1	28376109	796805820	28.0802	240.6875
LT669793.1	33388210	882820570	26.4411	213.6562
LT669794.1	50579949	1330676545	26.3084	202.6228
LT669795.1	49795044	1570413442	31.5375	291.5553

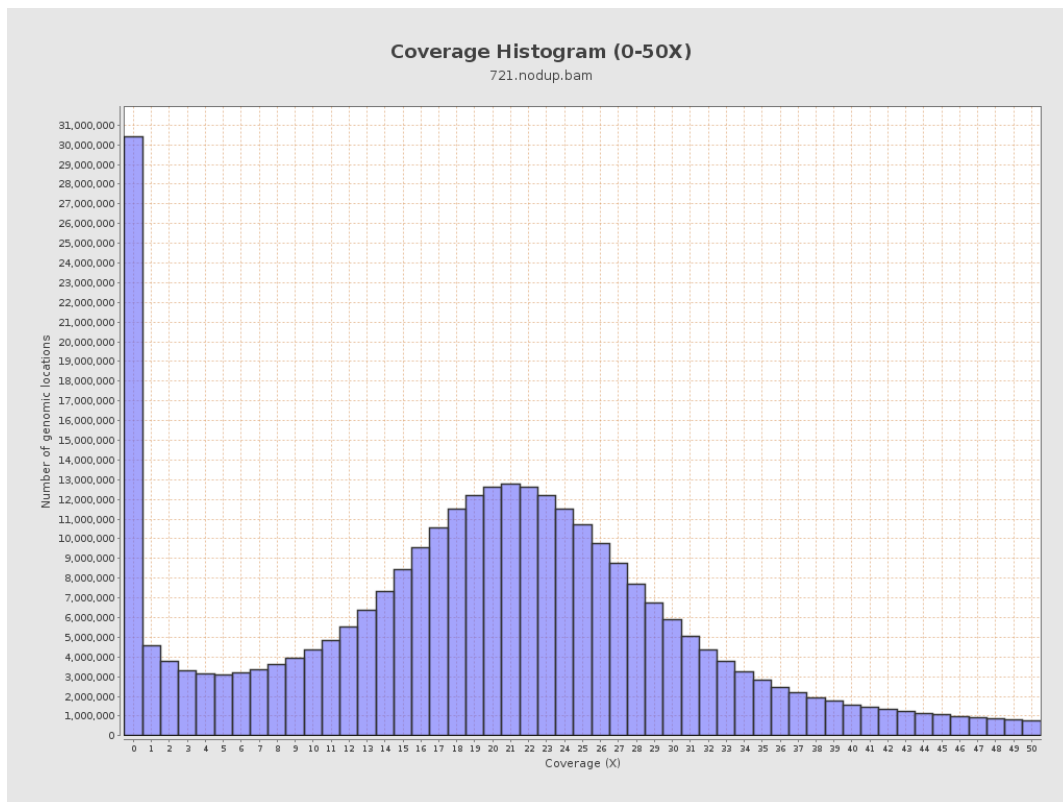
3. Results : Coverage across reference



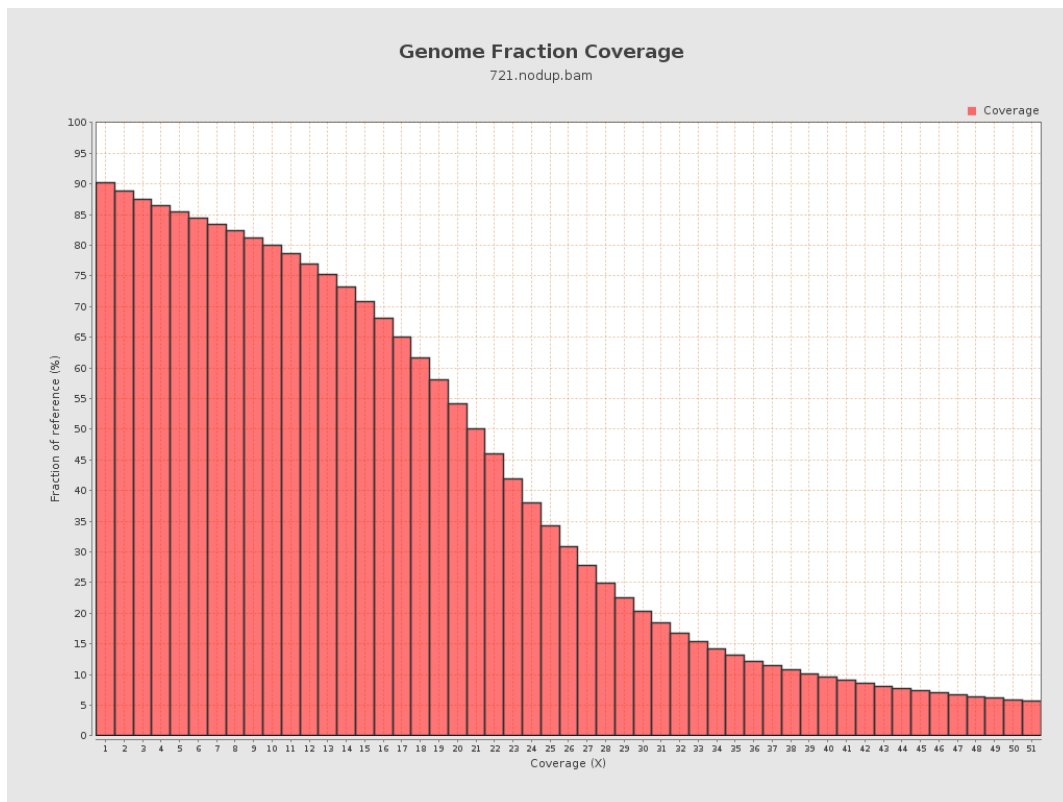
4. Results : Coverage Histogram



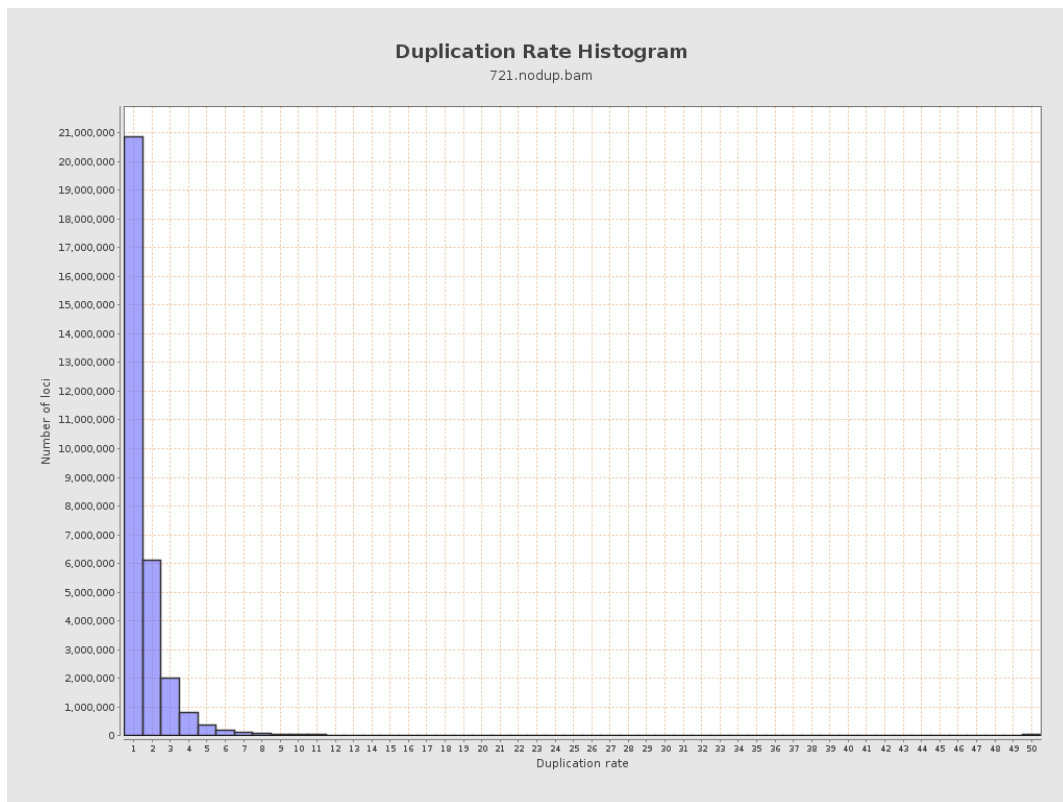
5. Results : Coverage Histogram (0-50X)



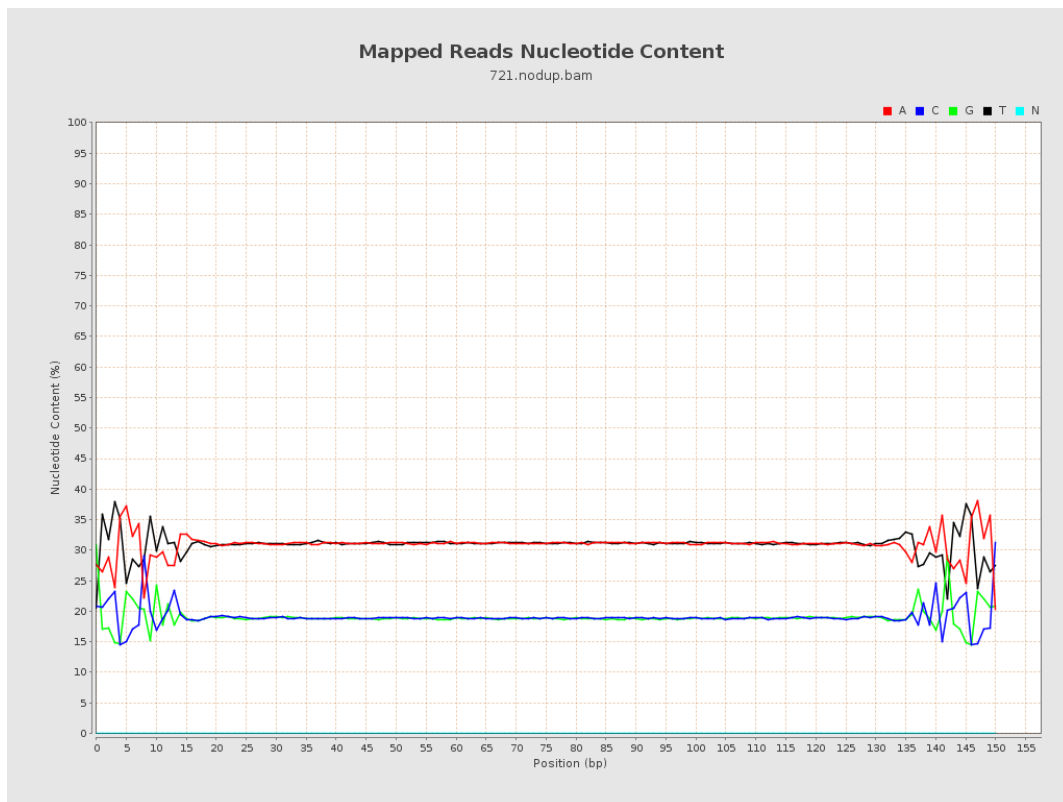
6. Results : Genome Fraction Coverage



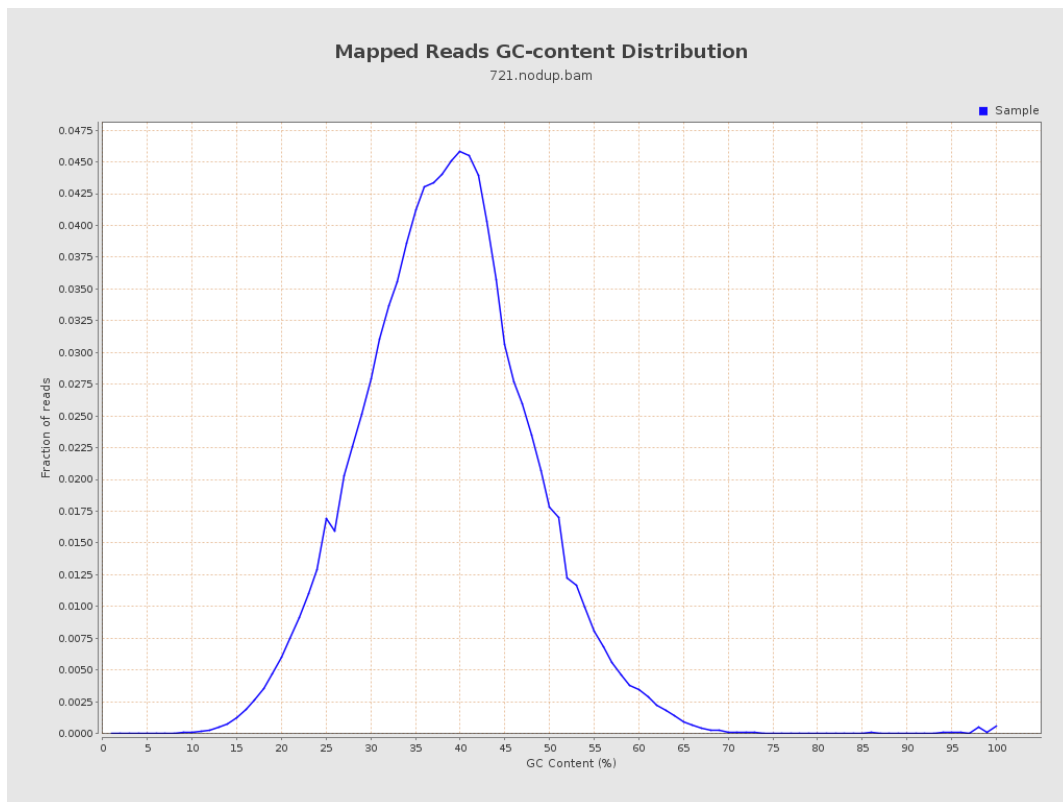
7. Results : Duplication Rate Histogram



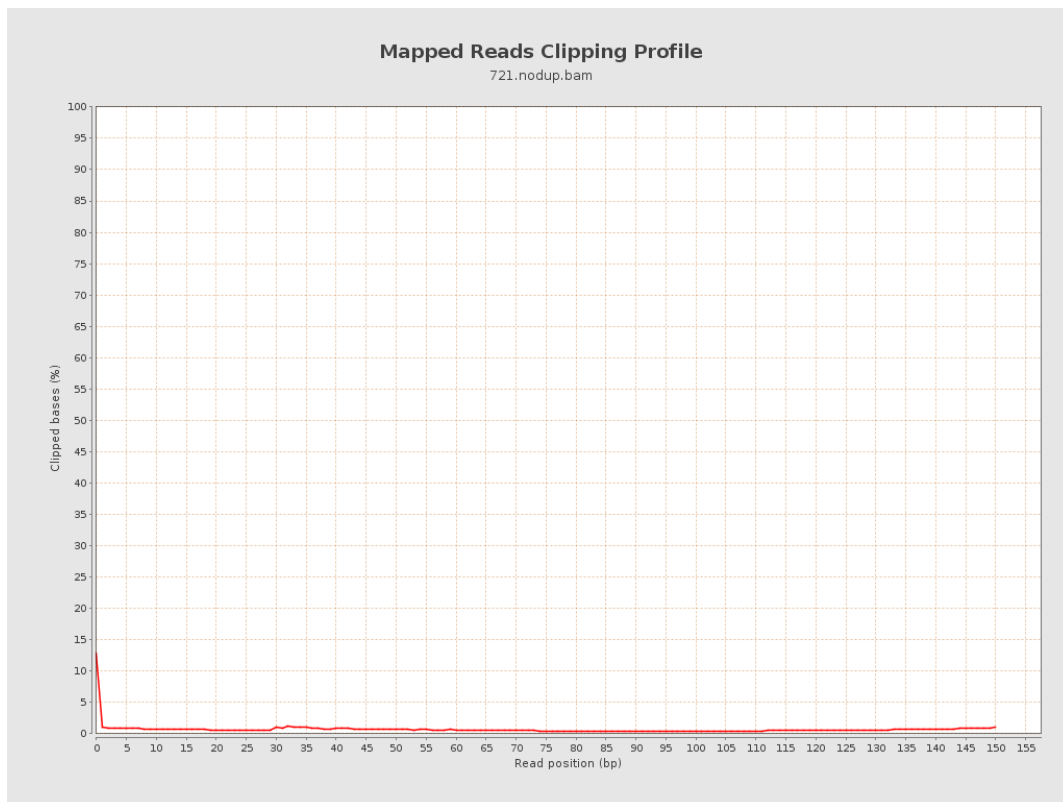
8. Results : Mapped Reads Nucleotide Content



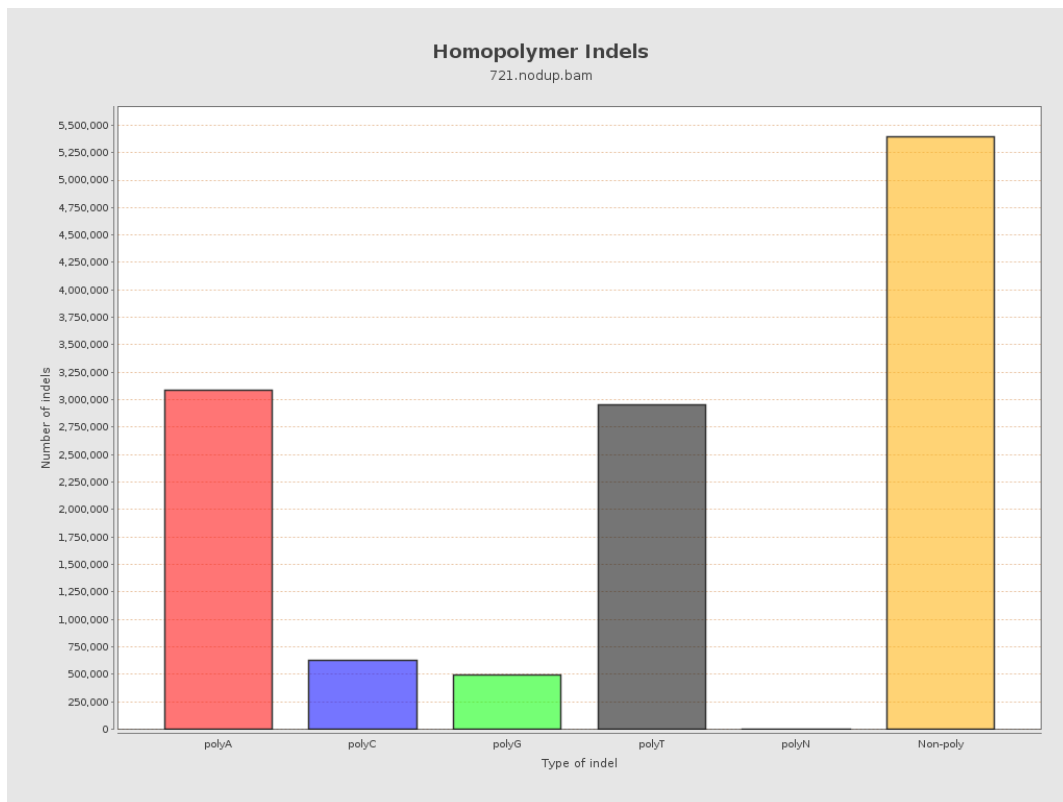
9. Results : Mapped Reads GC-content Distribution



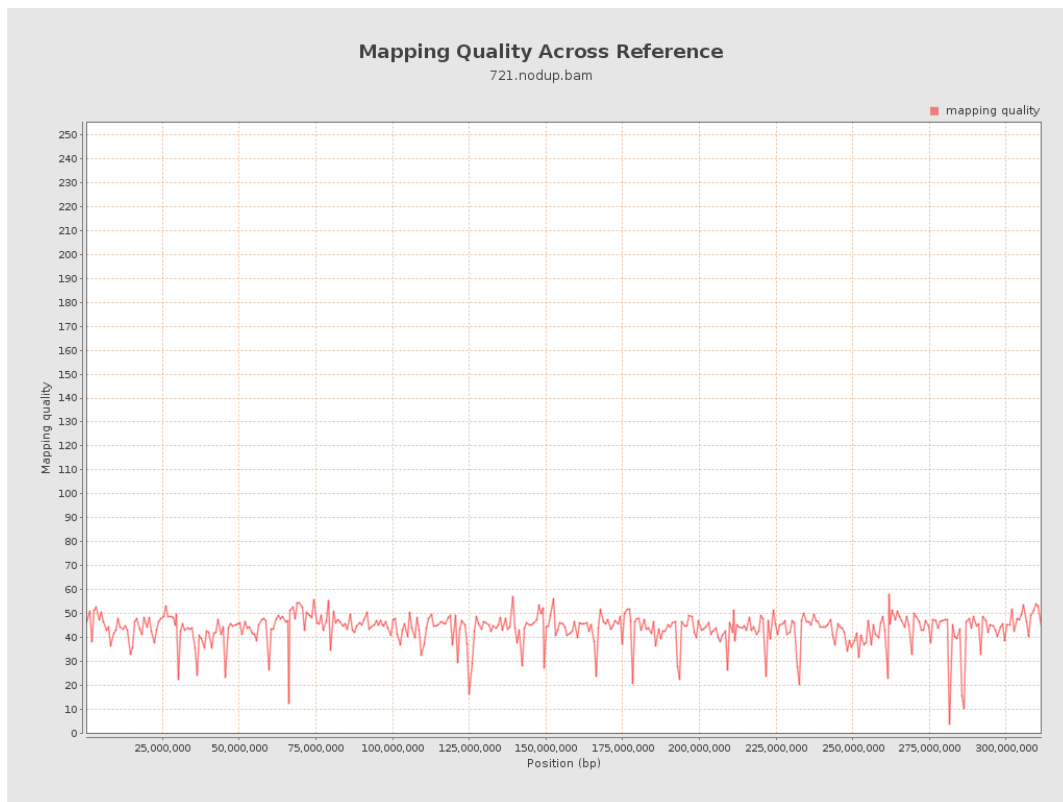
10. Results : Mapped Reads Clipping Profile



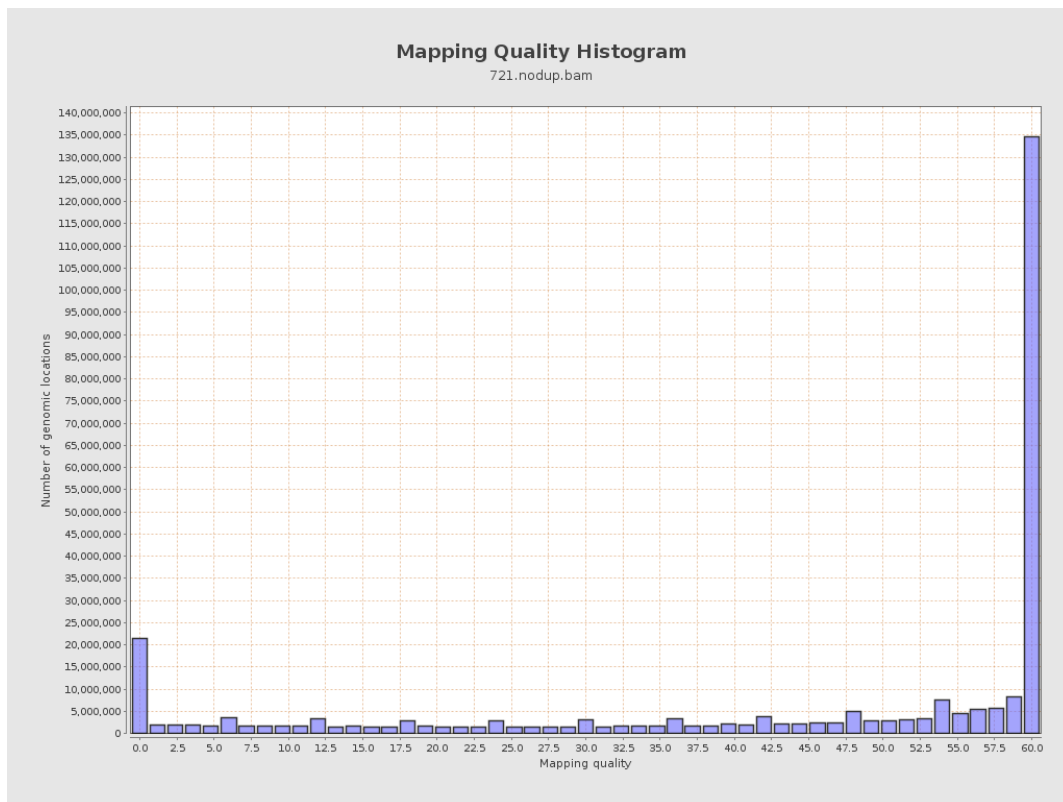
11. Results : Homopolymer Indels



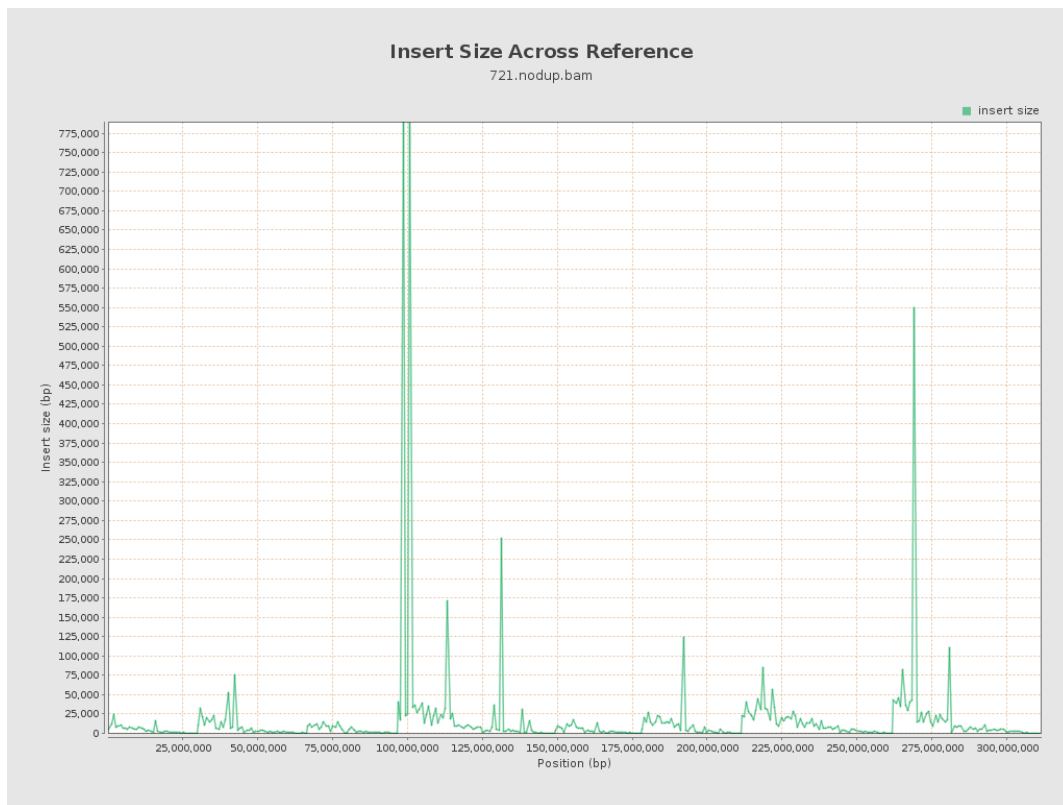
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

