Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:26:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/715.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/715.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/rawdata/P26207/P26207_291/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_291_S372_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_291/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_291_S372_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:26:28 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	54,043,724
Mapped reads	48,974,517 / 90.62%
Unmapped reads	5,069,207 / 9.38%
Mapped paired reads	48,974,517 / 90.62%
Mapped reads, first in pair	24,553,973 / 45.43%
Mapped reads, second in pair	24,420,544 / 45.19%
Mapped reads, both in pair	47,400,392 / 87.71%
Mapped reads, singletons	1,574,125 / 2.91%
Read min/max/mean length	30 / 151 / 147.94
Duplicated reads (flagged)	7,806,446 / 14.44%
Clipped reads	12,404,461 / 22.95%

2.2. ACGT Content

Number/percentage of A's	2,055,949,188 / 30.88%
Number/percentage of C's	1,271,044,302 / 19.09%
Number/percentage of T's	2,059,062,595 / 30.93%
Number/percentage of G's	1,271,951,933 / 19.1%
Number/percentage of N's	24,845 / 0%
GC Percentage	38.19%

2.3. Coverage

Mean	21.421
Standard Deviation	221.0491

2.4. Mapping Quality

Mean Mapping Quality	44.03

2.5. Insert size

Mean	265,444.77
Standard Deviation	2,476,318.05
P25/Median/P75	320 / 423 / 547

2.6. Mismatches and indels

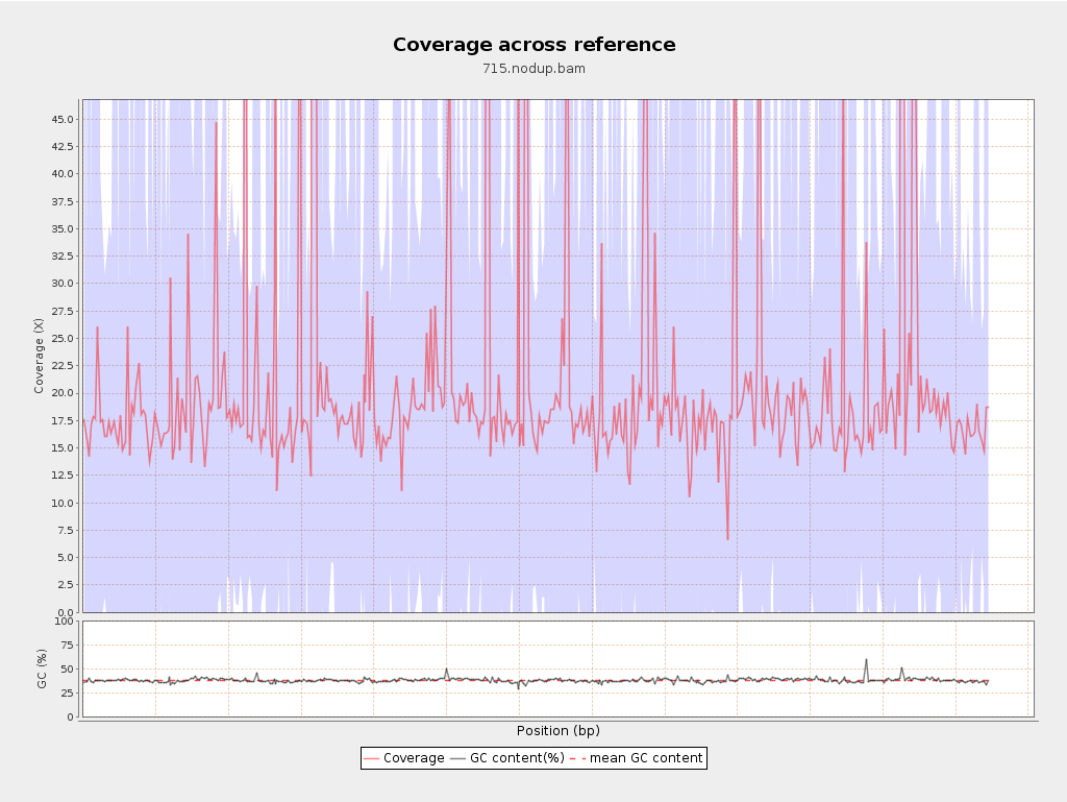
General error rate	2.42%
Mismatches	147,623,567
Insertions	4,965,885
Mapped reads with at least one insertion	9.03%
Deletions	4,700,842
Mapped reads with at least one deletion	8.51%
Homopolymer indels	57.12%

2.7. Chromosome stats

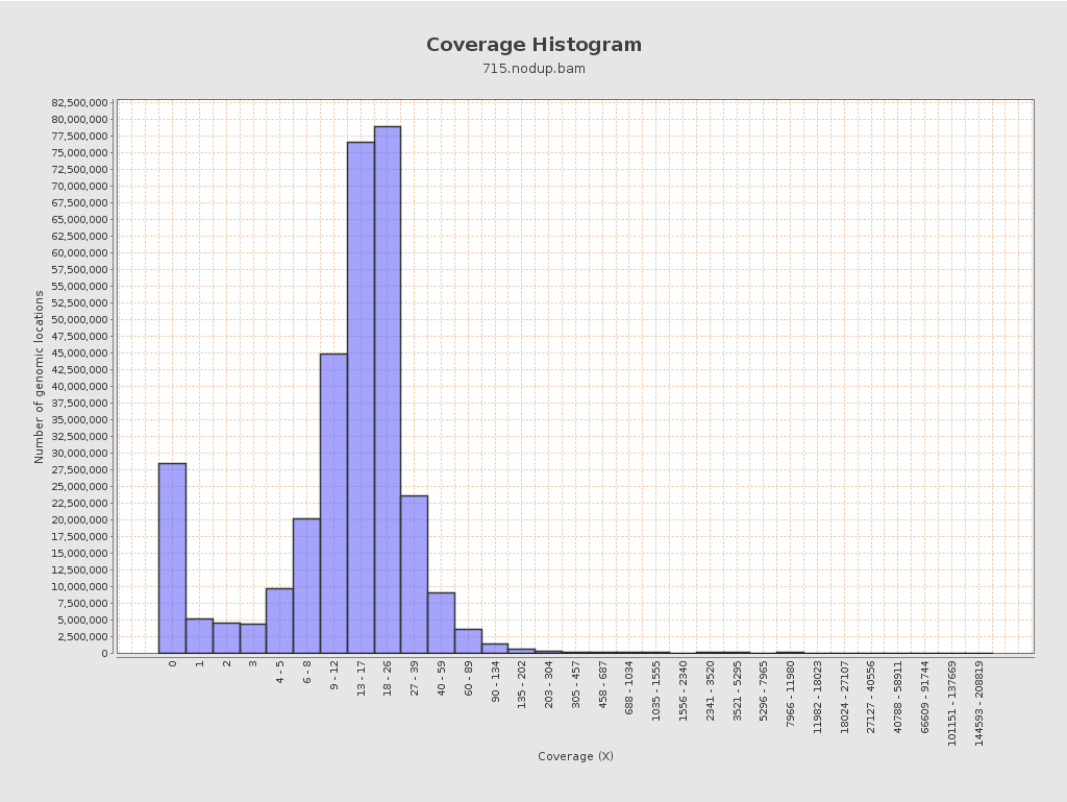
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	517389329	17.4062	86.8267

LT669789.1	36598175	773578253	21.1371	215.9082
LT669790.1	30422129	815217425	26.7969	316.1811
LT669791.1	52758100	1122693232	21.28	238.0682
LT669792.1	28376109	613958148	21.6364	224.1794
LT669793.1	33388210	659210978	19.7438	171.5037
LT669794.1	50579949	1001464042	19.7996	167.0599
LT669795.1	49795044	1172161677	23.5397	263.0075

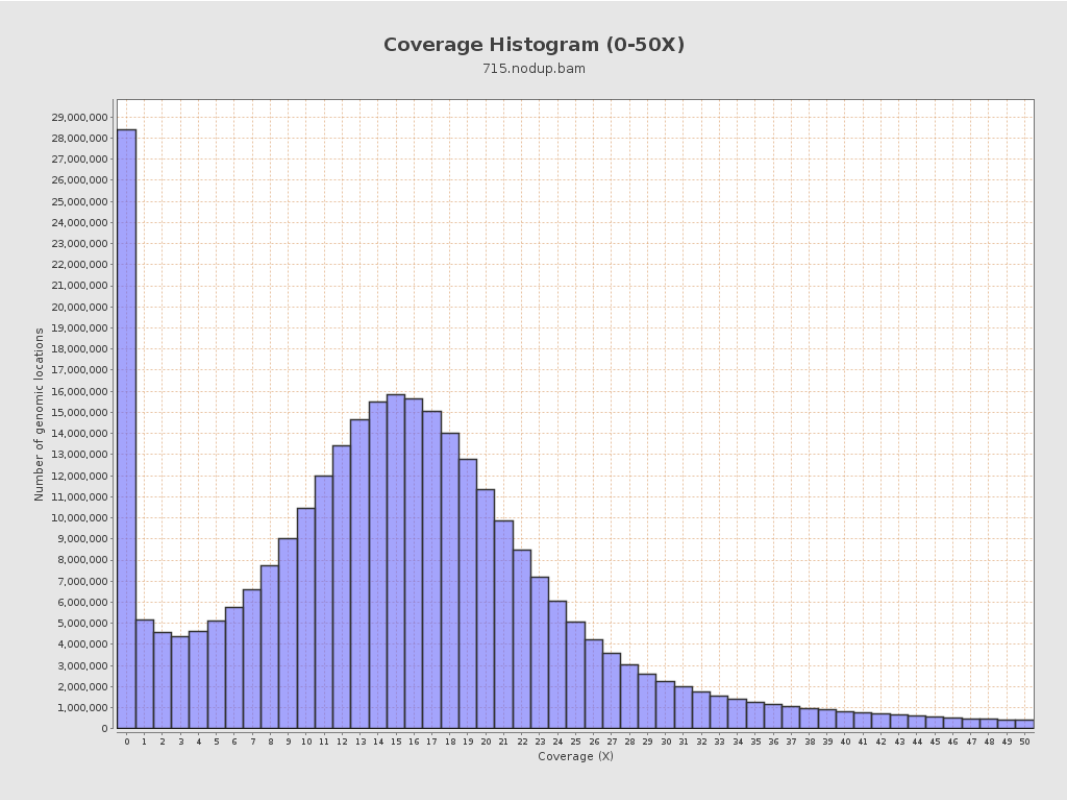
3. Results : Coverage across reference



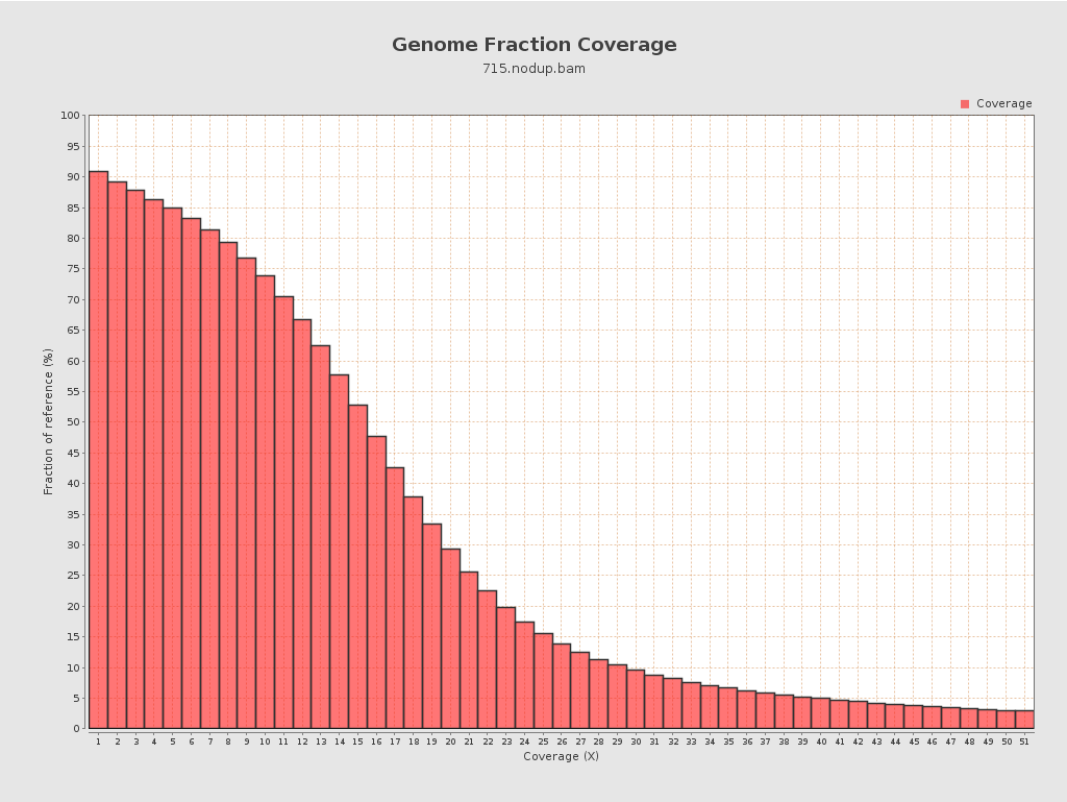
4. Results : Coverage Histogram



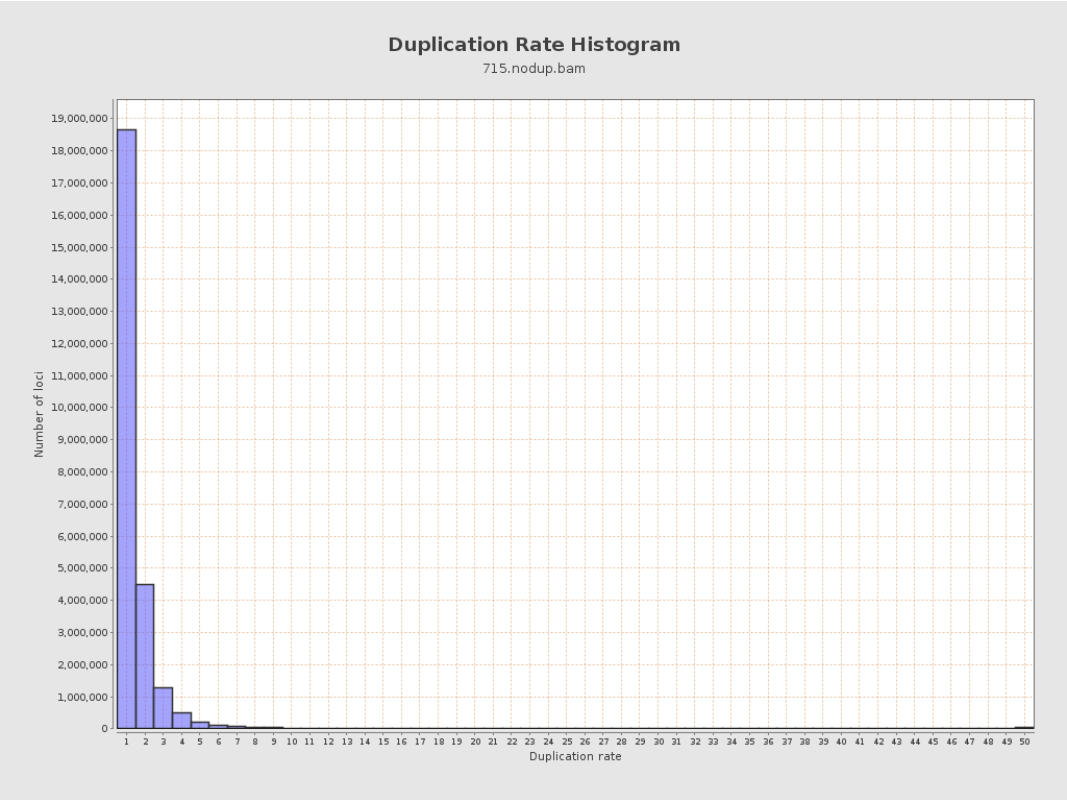
5. Results : Coverage Histogram (0-50X)



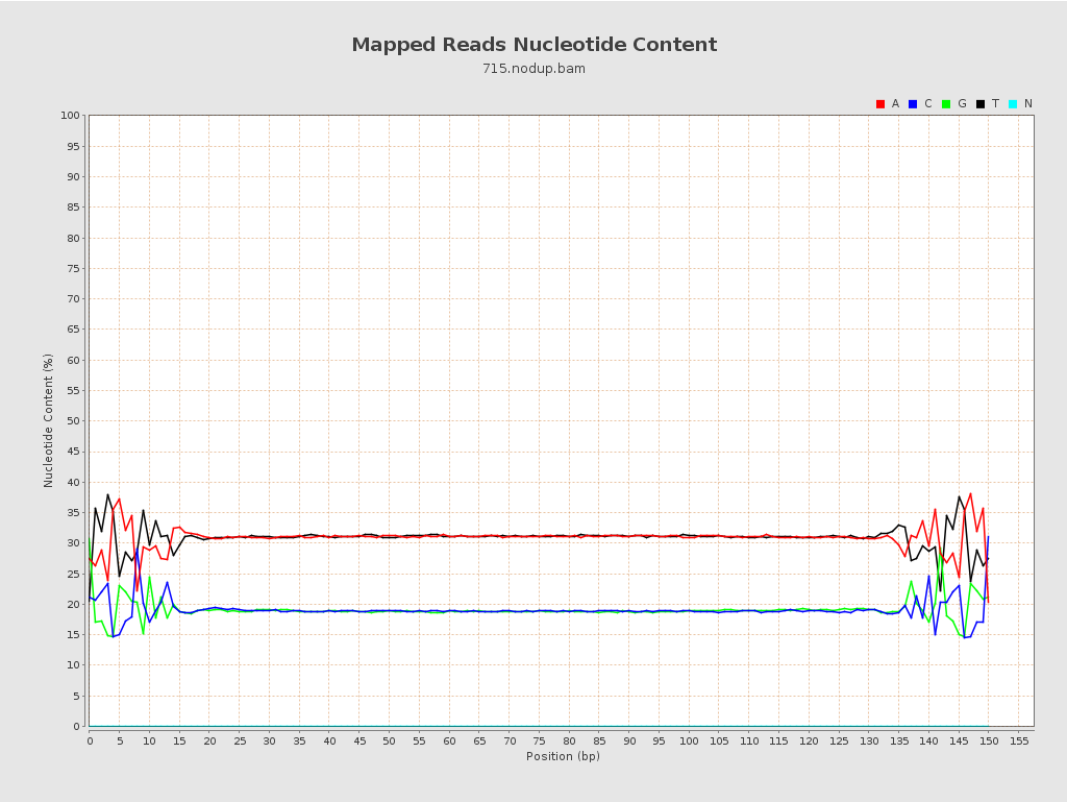
6. Results : Genome Fraction Coverage



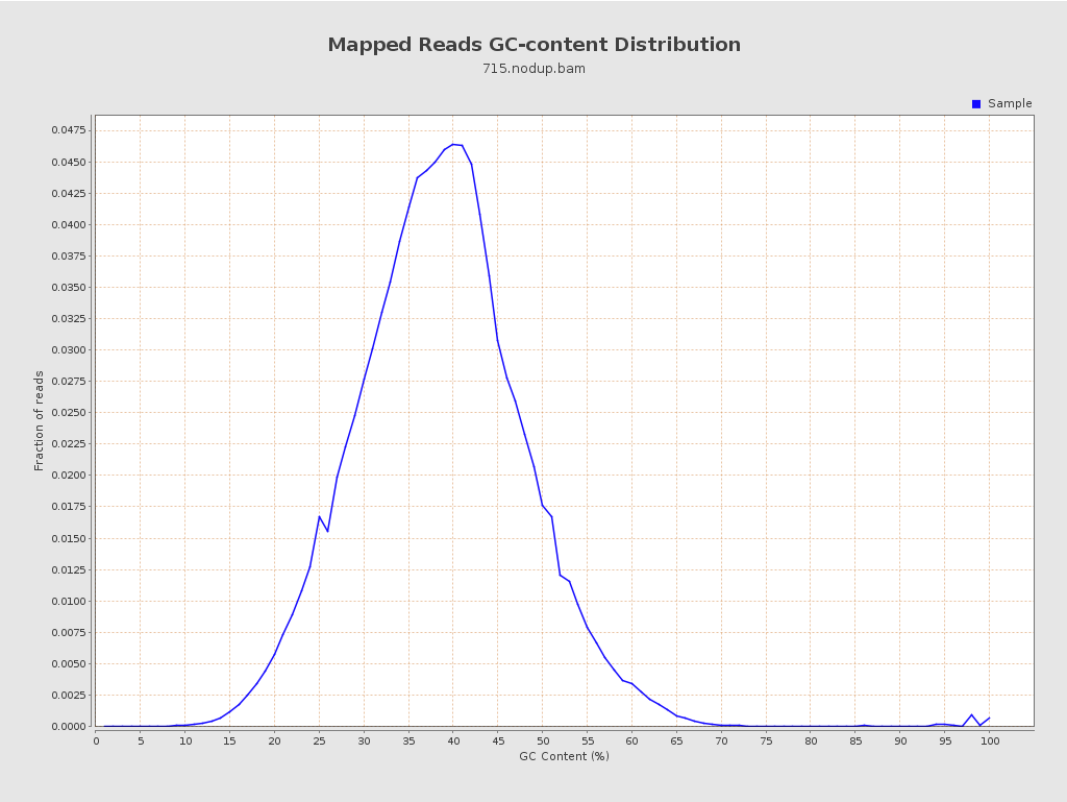
7. Results : Duplication Rate Histogram



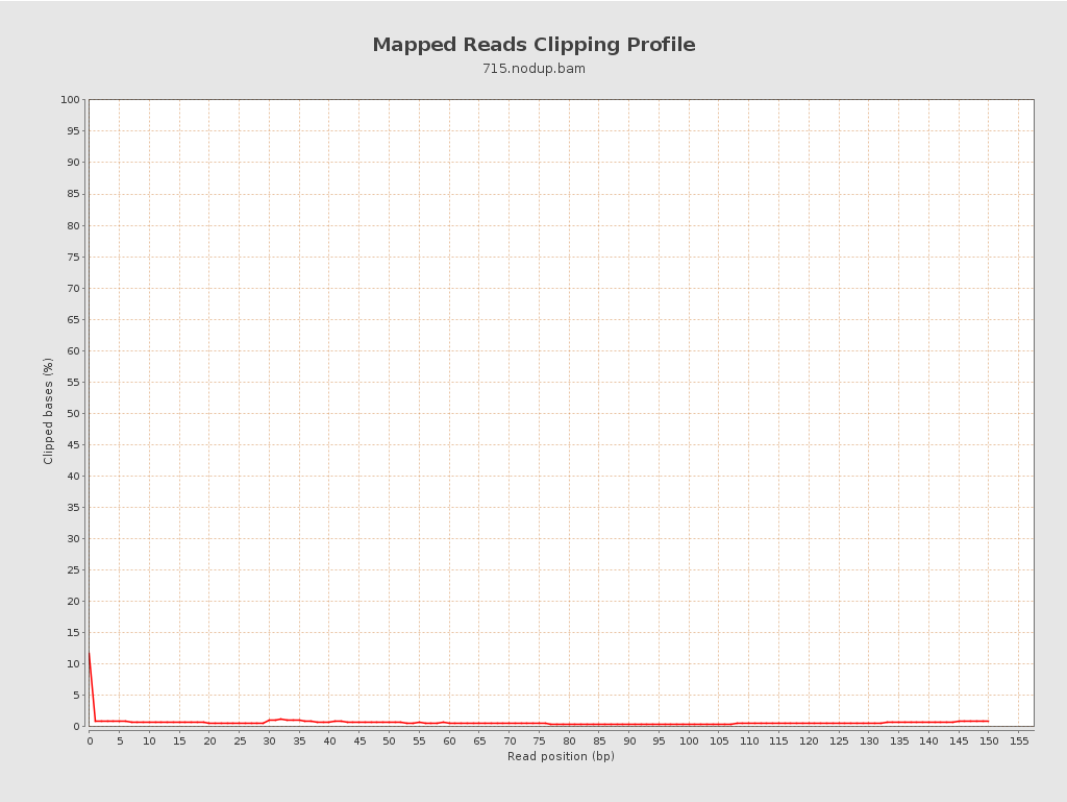
8. Results : Mapped Reads Nucleotide Content



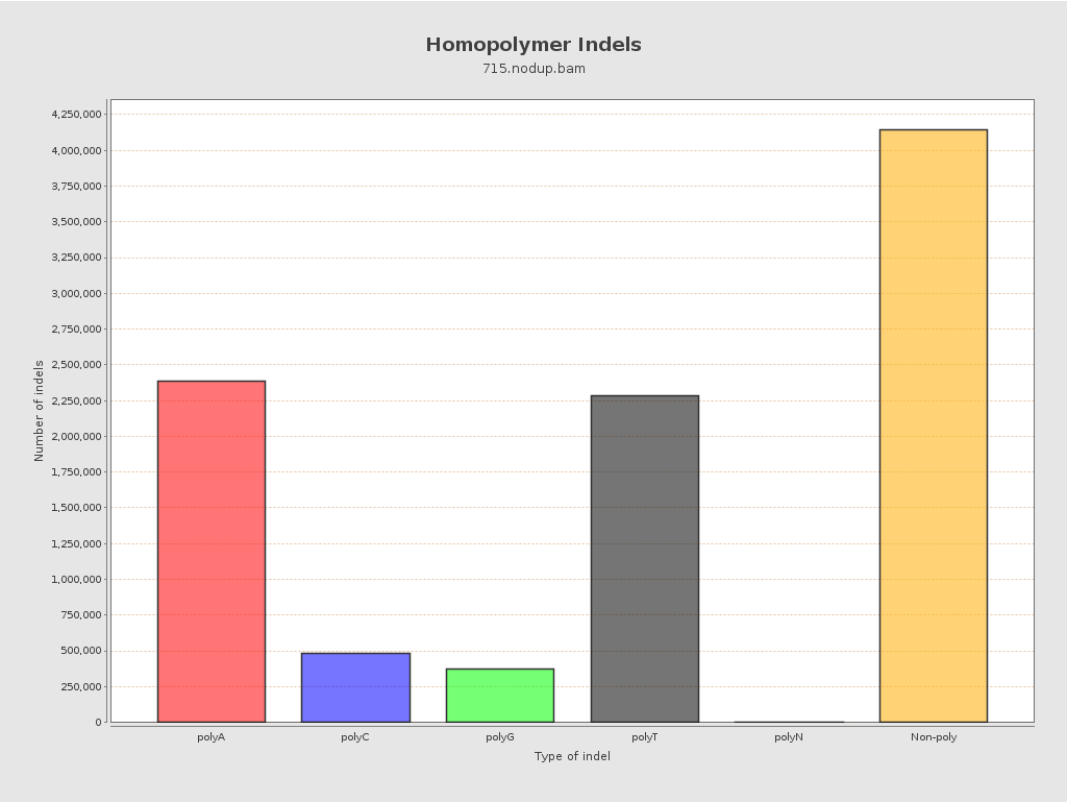
9. Results : Mapped Reads GC-content Distribution



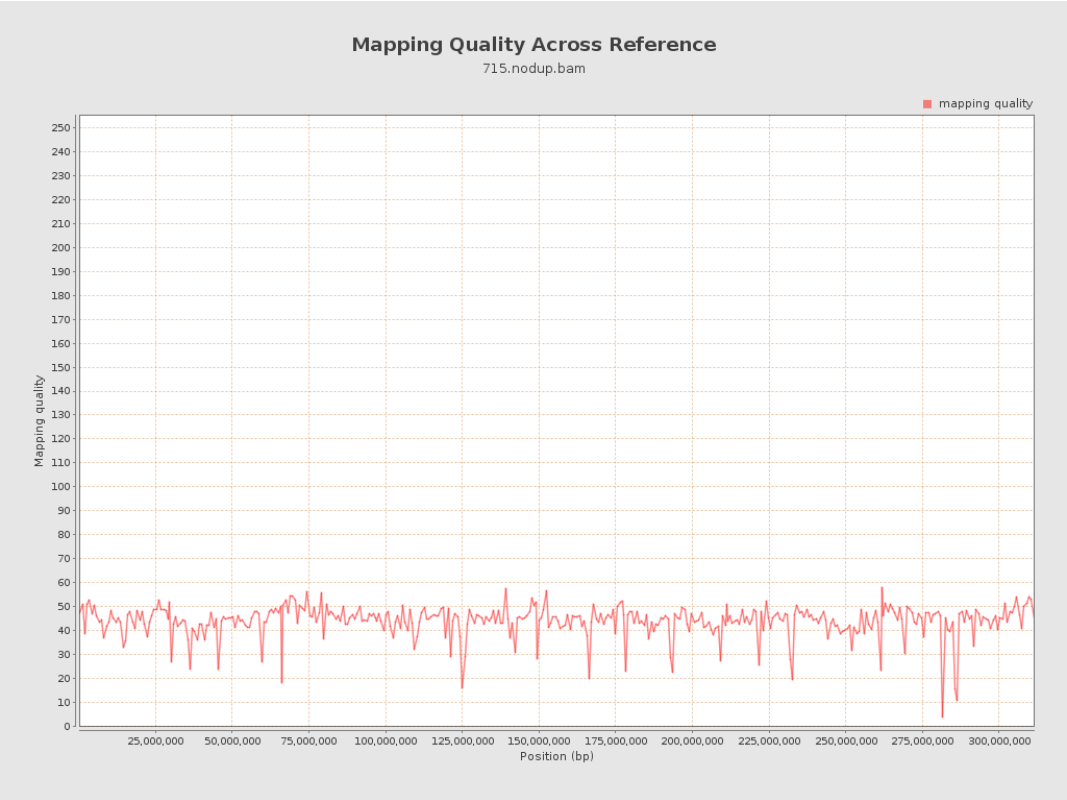
10. Results : Mapped Reads Clipping Profile



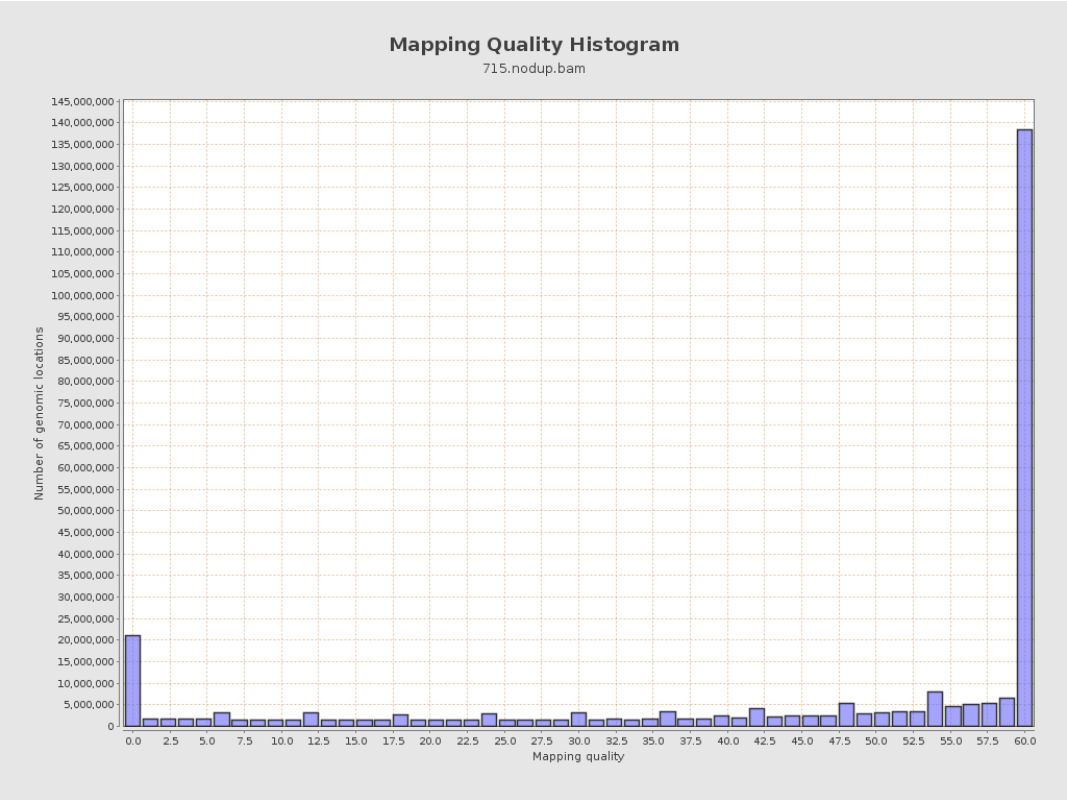
11. Results : Homopolymer Indels



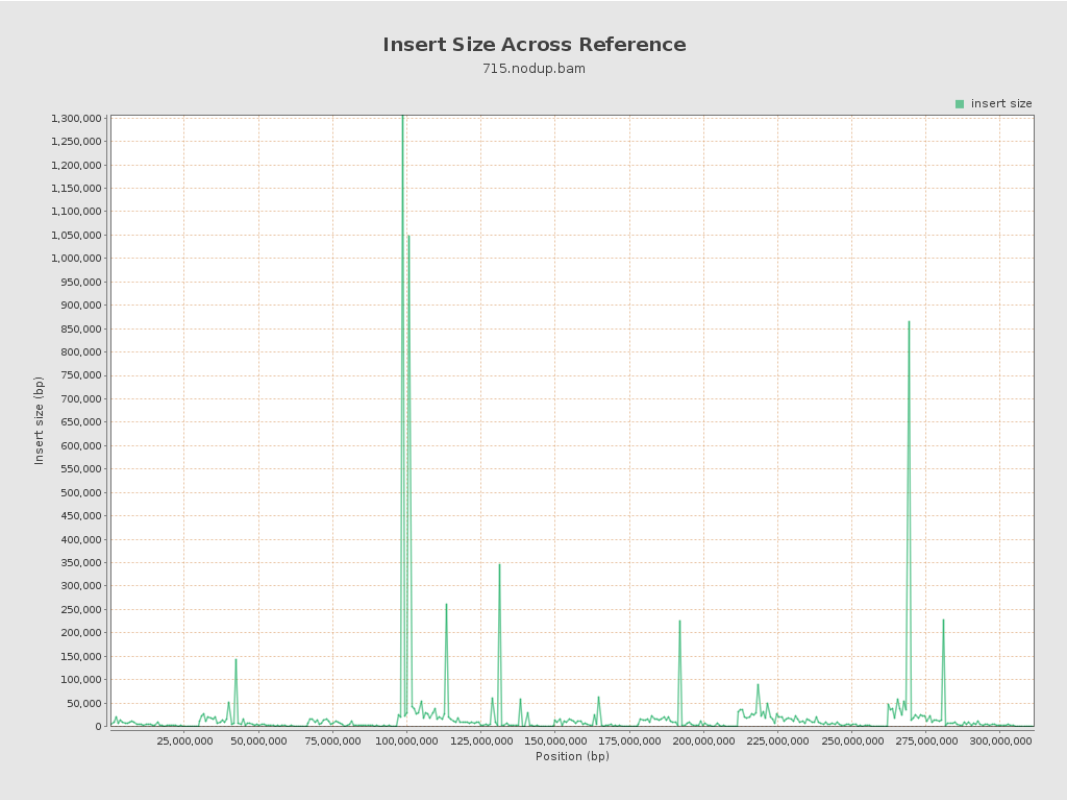
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram