Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/717.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/717.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_165/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_165_S255_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_165/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_165_S255_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:32:28 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	67,925,718
Mapped reads	62,741,763 / 92.37%
Unmapped reads	5,183,955 / 7.63%
Mapped paired reads	62,741,763 / 92.37%
Mapped reads, first in pair	31,425,985 / 46.27%
Mapped reads, second in pair	31,315,778 / 46.1%
Mapped reads, both in pair	61,551,697 / 90.62%
Mapped reads, singletons	1,190,066 / 1.75%
Read min/max/mean length	30 / 151 / 148.35
Duplicated reads (flagged)	9,931,343 / 14.62%
Clipped reads	13,002,932 / 19.14%

2.2. ACGT Content

Number/percentage of A's	2,711,225,309 / 30.93%
Number/percentage of C's	1,672,364,901 / 19.08%
Number/percentage of T's	2,713,234,431 / 30.96%
Number/percentage of G's	1,667,558,127 / 19.03%
Number/percentage of N's	37,232 / 0%
GC Percentage	38.11%

2.3. Coverage

Mean	28.194
Standard Deviation	195.8342

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Insert size

Mean	217,169.39
Standard Deviation	2,212,387.92
P25/Median/P75	333 / 433 / 564

2.6. Mismatches and indels

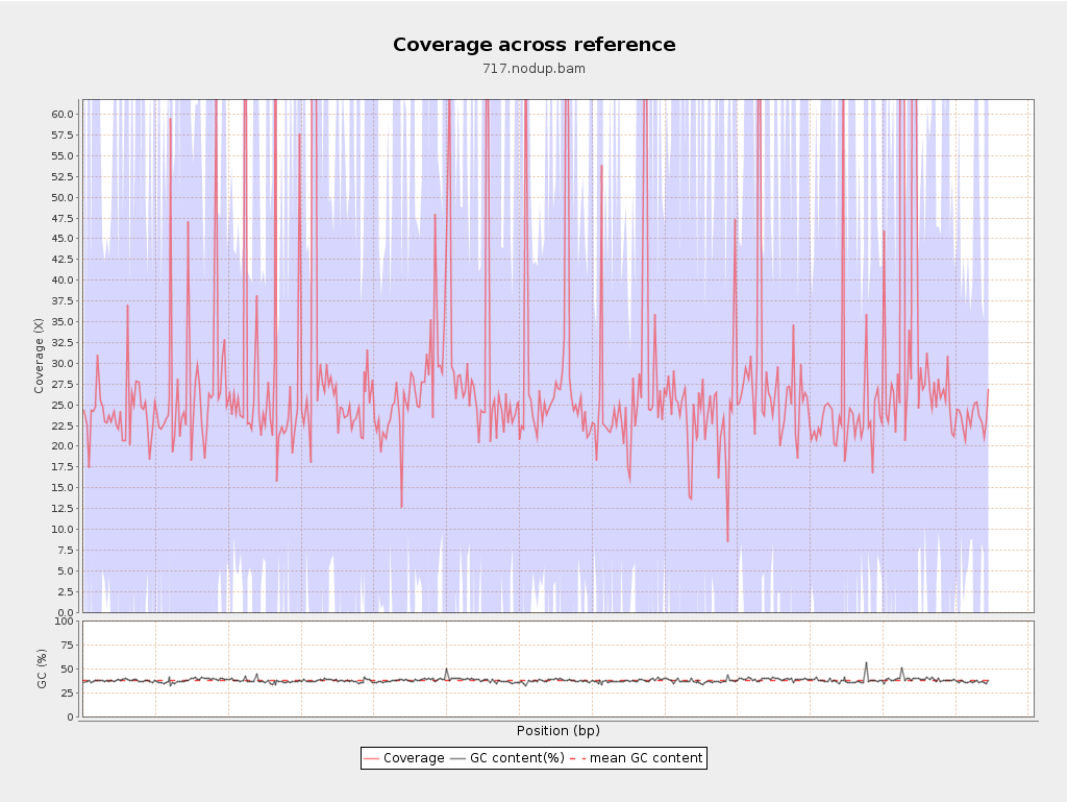
General error rate	2.2%
Mismatches	176,585,005
Insertions	5,656,526
Mapped reads with at least one insertion	8.11%
Deletions	5,800,841
Mapped reads with at least one deletion	8.21%
Homopolymer indels	56.96%

2.7. Chromosome stats

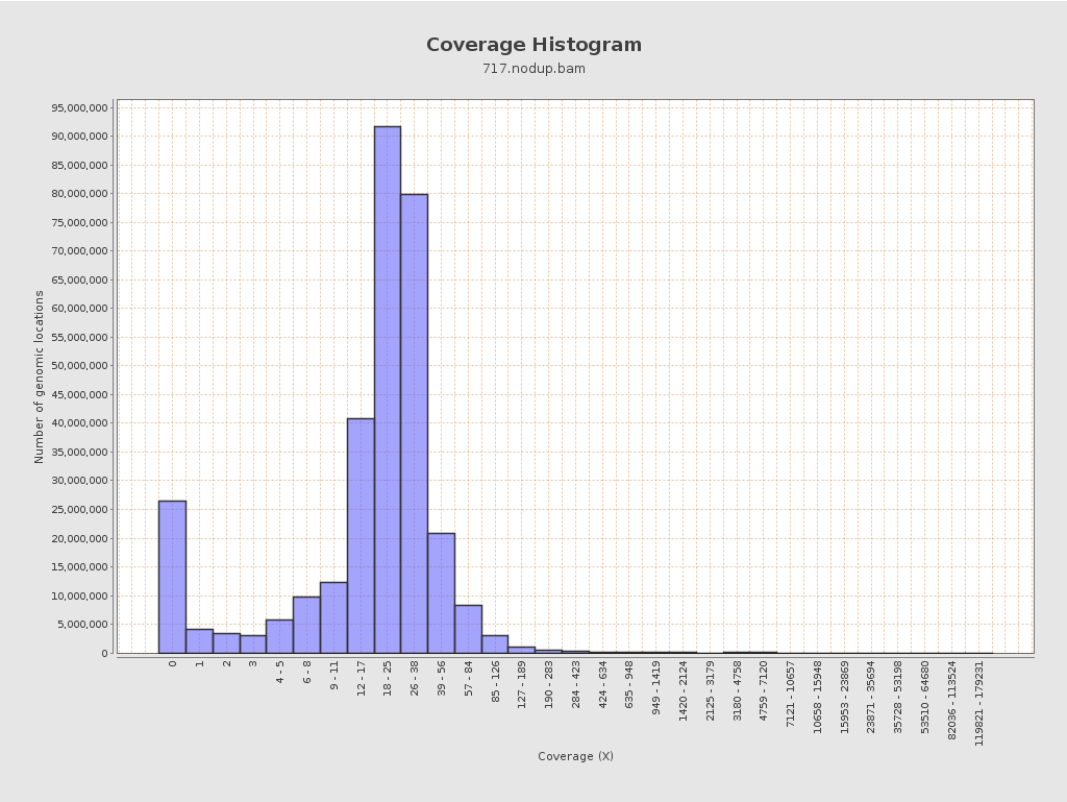
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	712985840	23.9866	60.5561

LT669789.1	36598175	1037261308	28.3419	202.3375
LT669790.1	30422129	926601682	30.4581	202.0786
LT669791.1	52758100	1462791612	27.7264	156.4066
LT669792.1	28376109	786788842	27.7272	209.694
LT669793.1	33388210	879750820	26.3491	144.8294
LT669794.1	50579949	1335425931	26.4023	163.6546
LT669795.1	49795044	1644817770	33.0318	300.8378

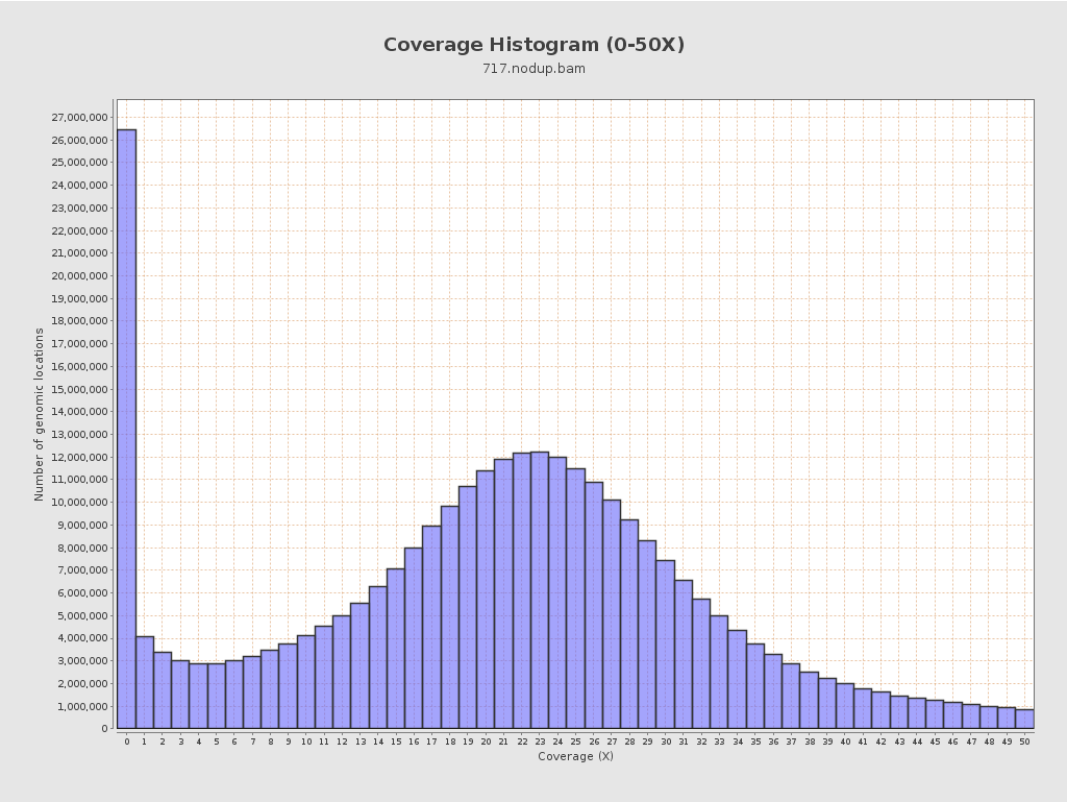
3. Results : Coverage across reference



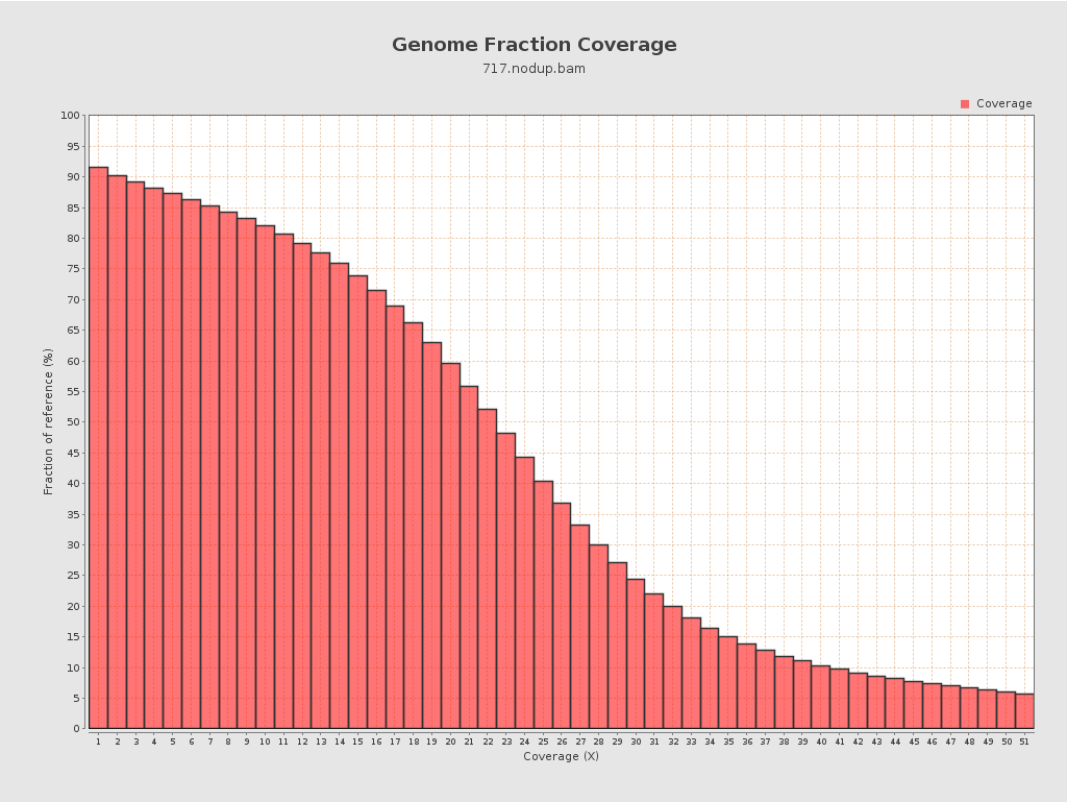
4. Results : Coverage Histogram



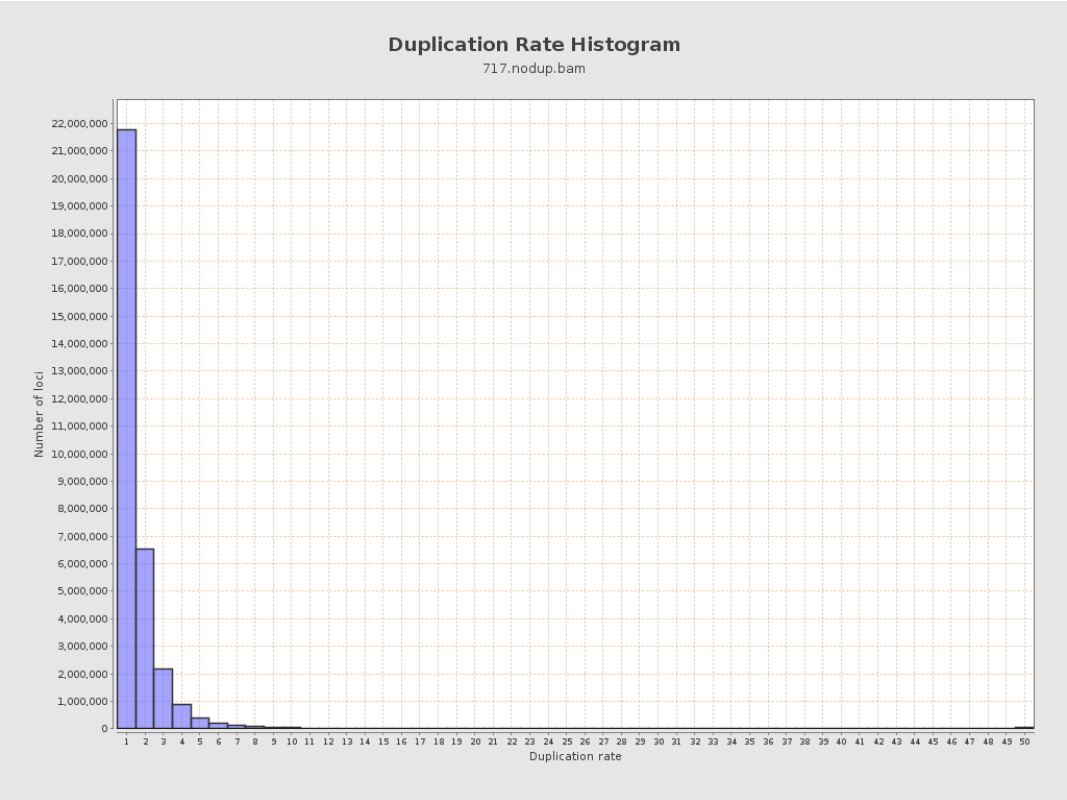
5. Results : Coverage Histogram (0-50X)



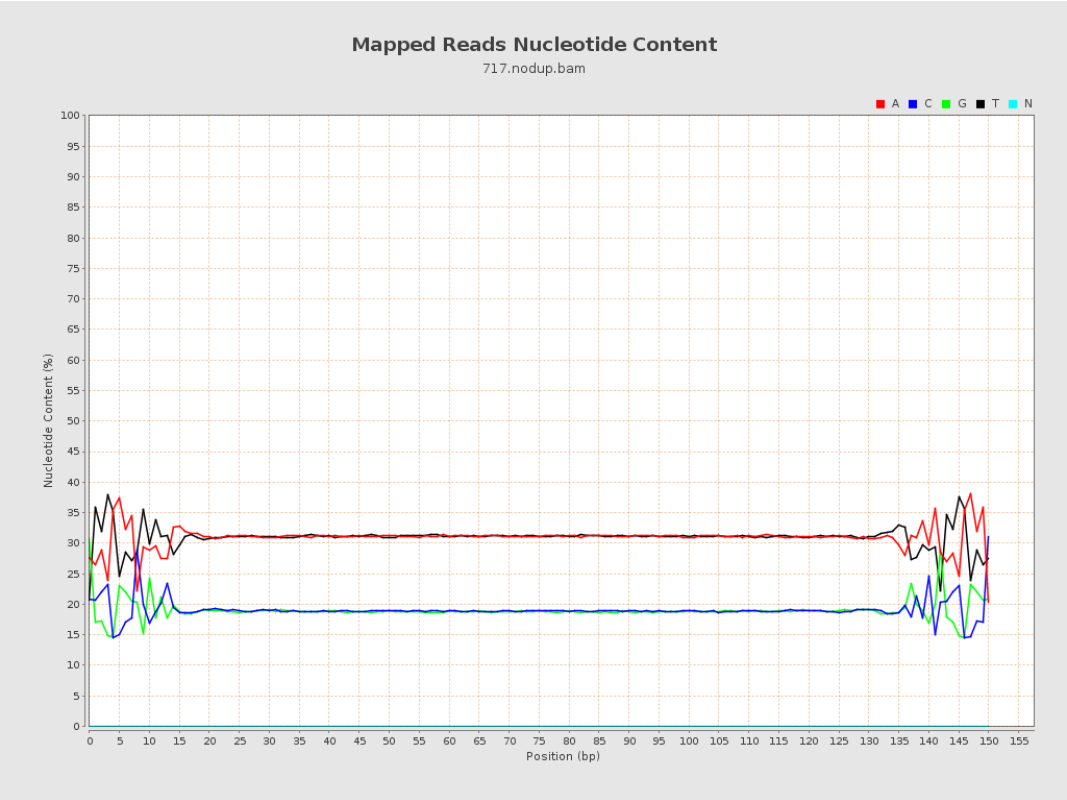
6. Results : Genome Fraction Coverage



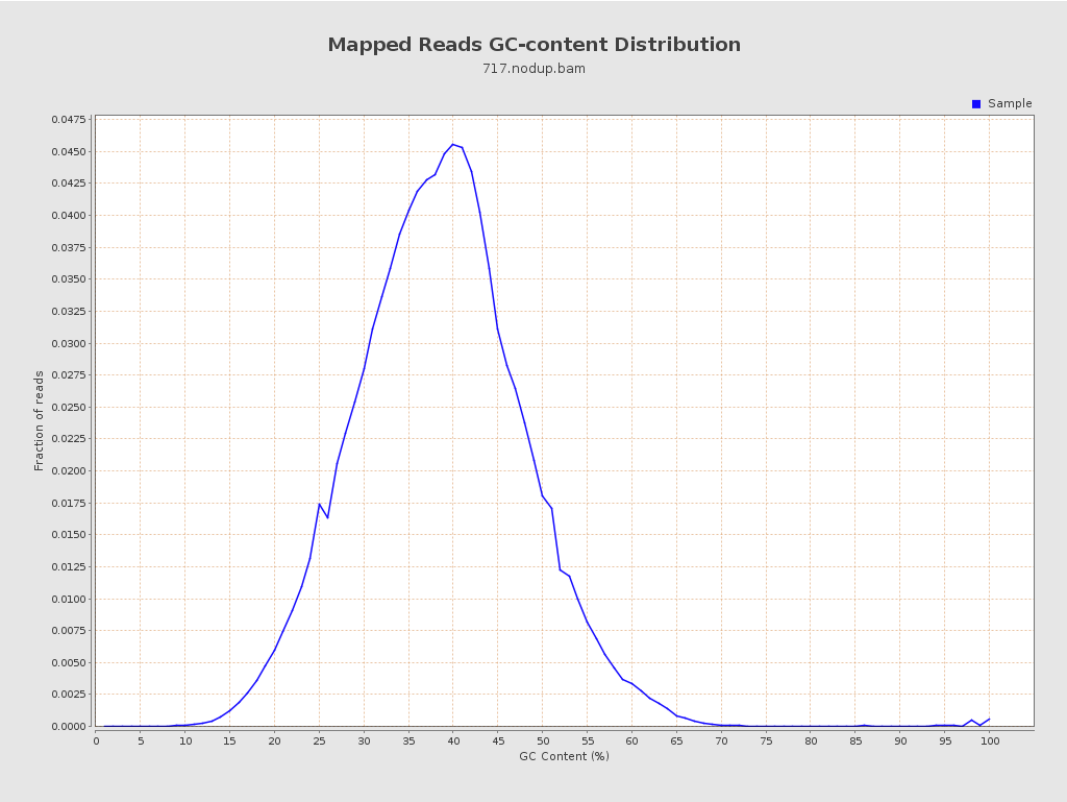
7. Results : Duplication Rate Histogram



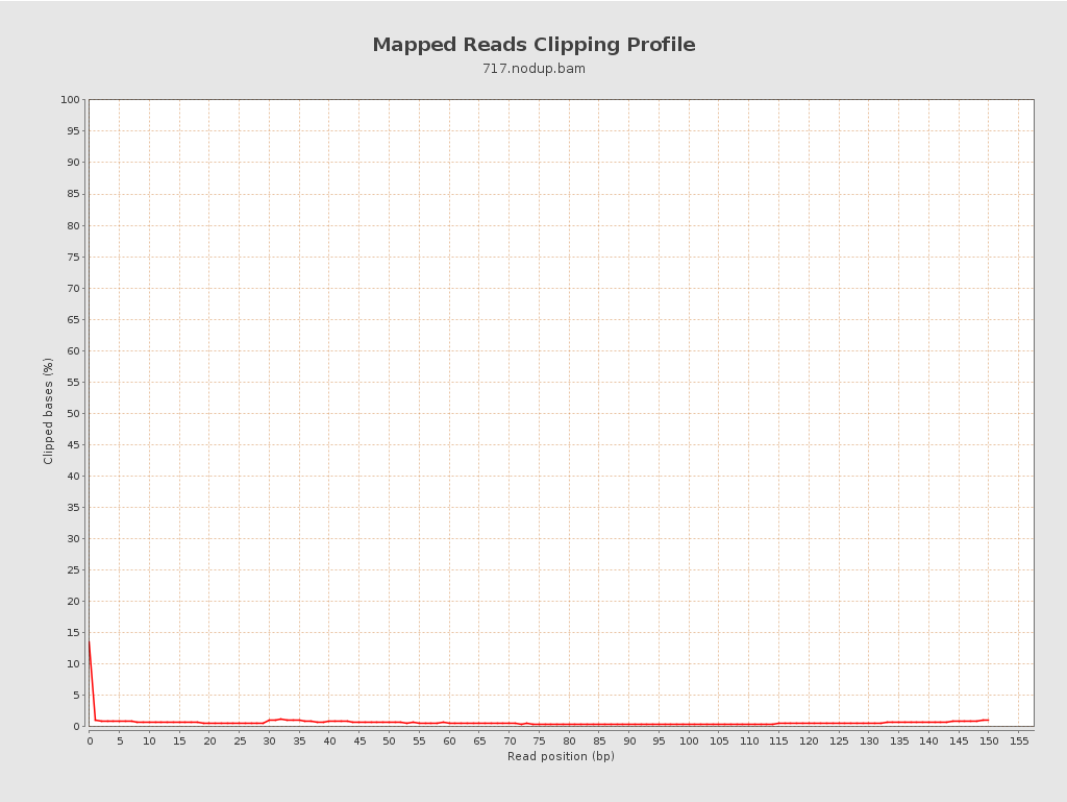
8. Results : Mapped Reads Nucleotide Content



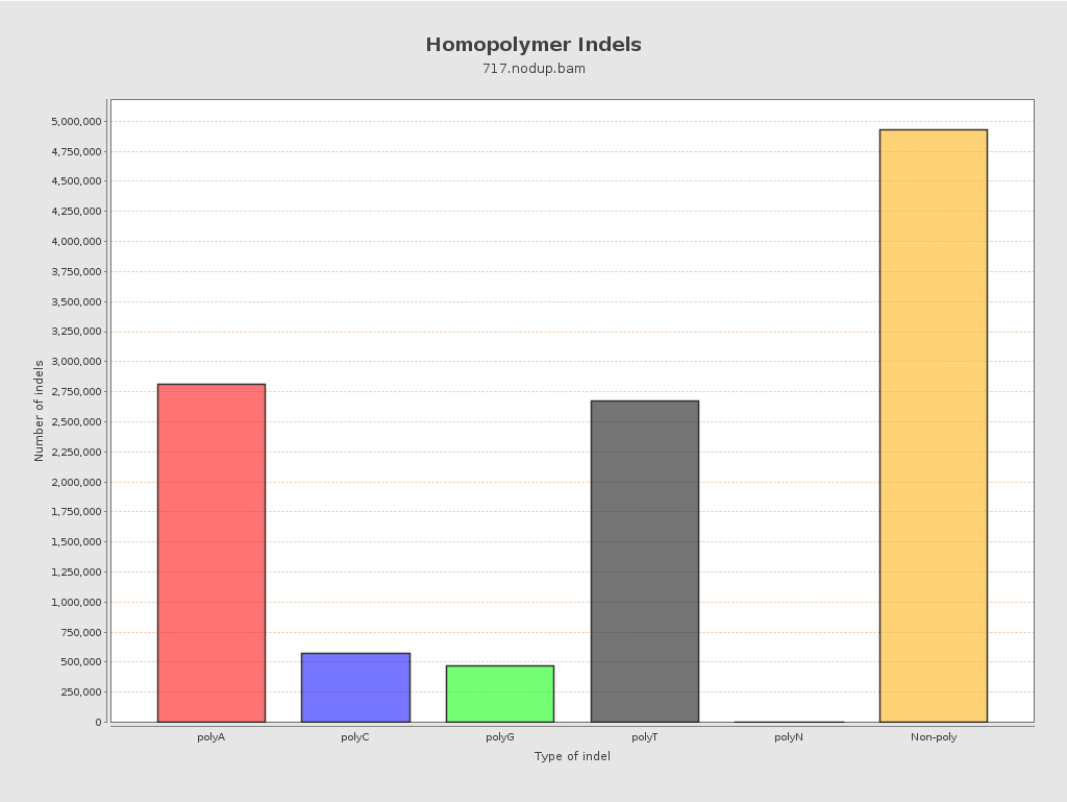
9. Results : Mapped Reads GC-content Distribution



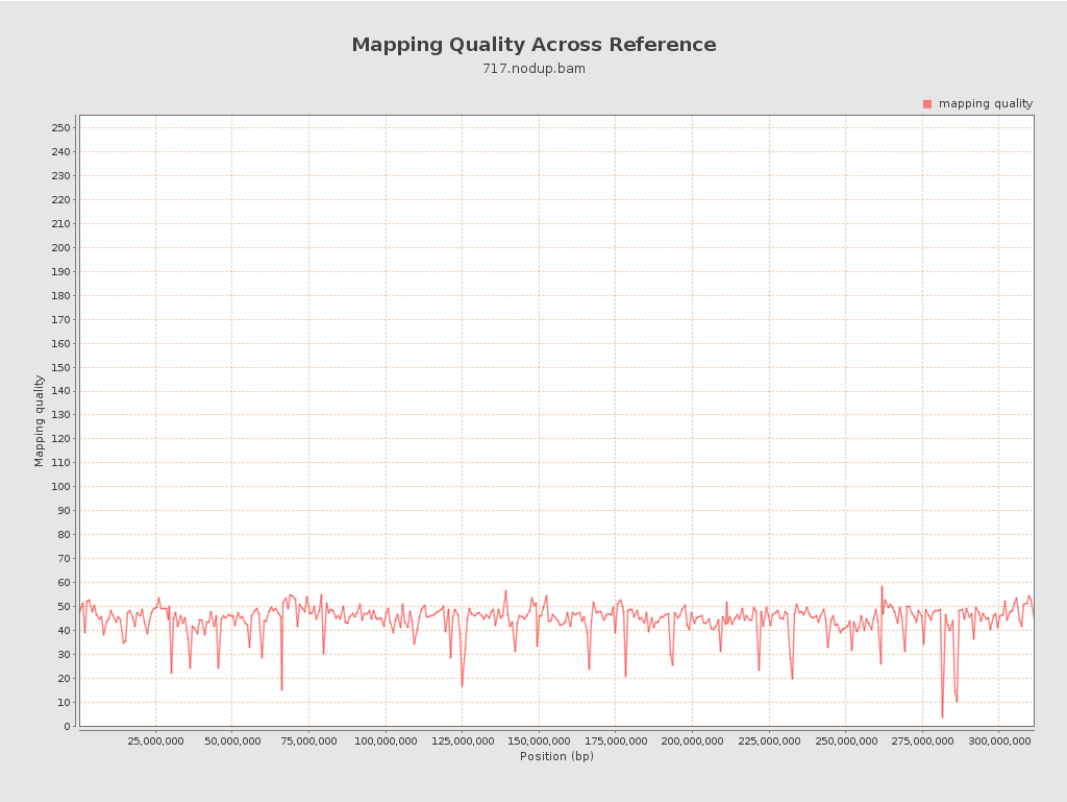
10. Results : Mapped Reads Clipping Profile



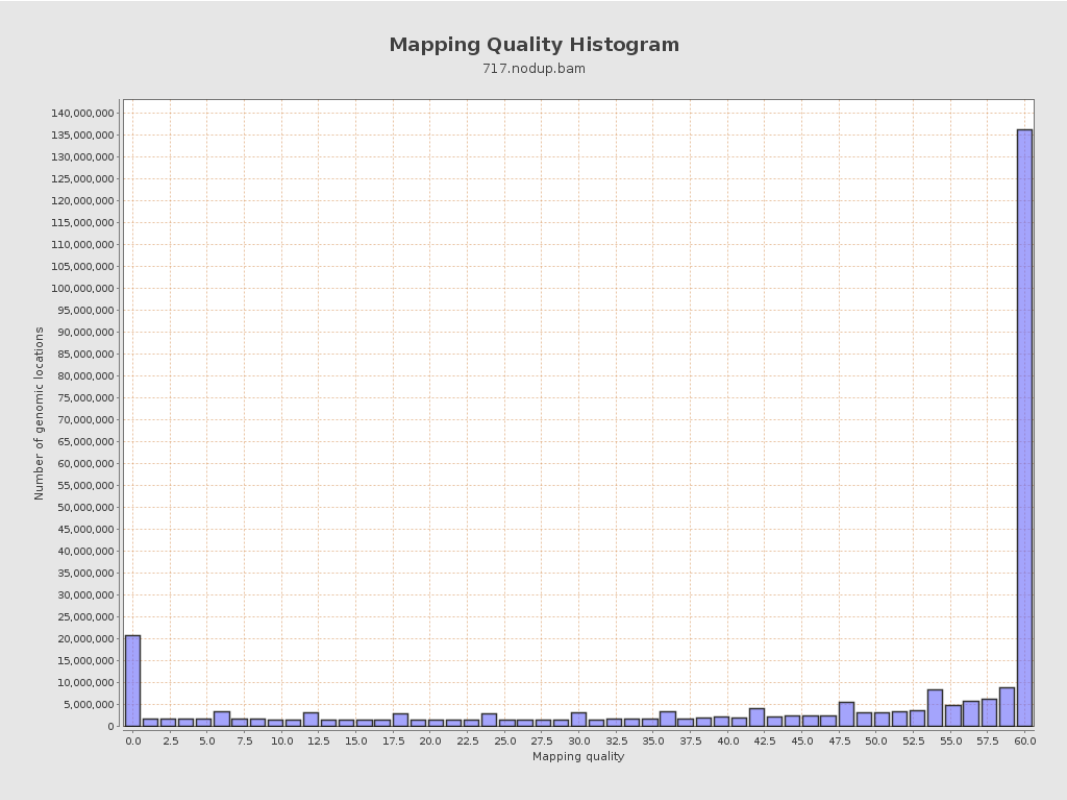
11. Results : Homopolymer Indels



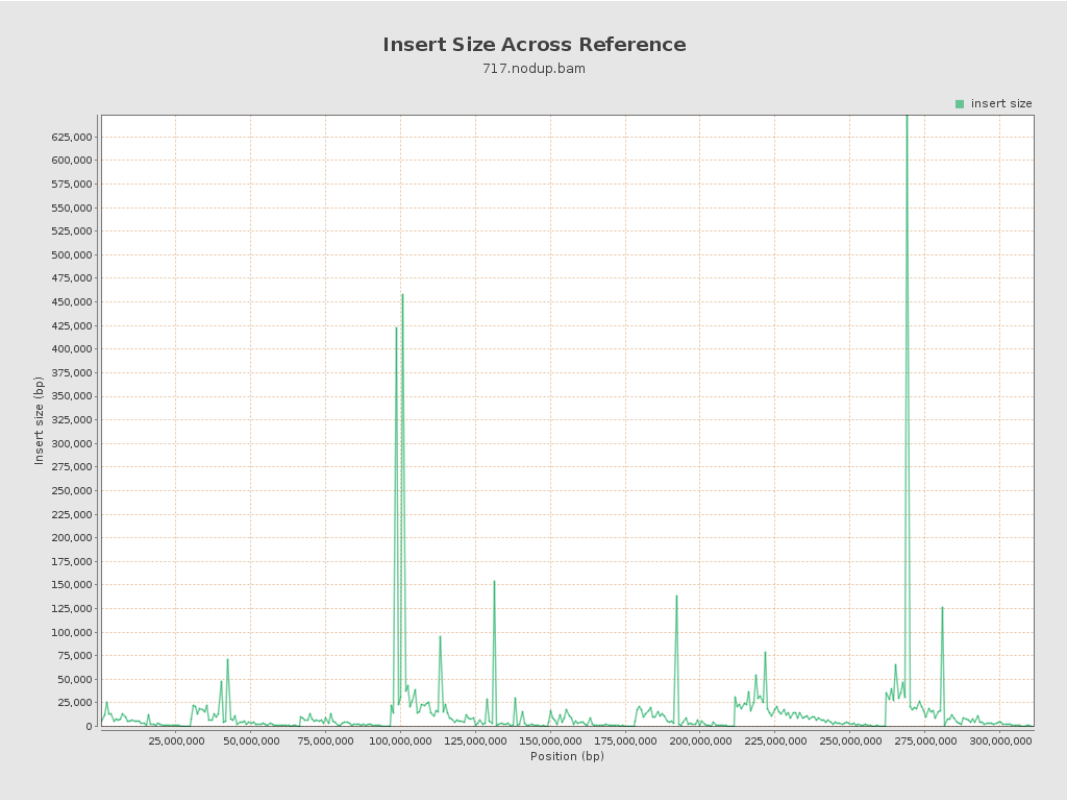
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram