Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/716.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/716.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_294/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_294_S375_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_294/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_294_S375_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:27:51 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	61,320,049
Mapped reads	57,857,920 / 94.35%
Unmapped reads	3,462,129 / 5.65%
Mapped paired reads	57,857,920 / 94.35%
Mapped reads, first in pair	28,983,793 / 47.27%
Mapped reads, second in pair	28,874,127 / 47.09%
Mapped reads, both in pair	56,817,435 / 92.66%
Mapped reads, singletons	1,040,485 / 1.7%
Read min/max/mean length	30 / 151 / 148.14
Duplicated reads (flagged)	7,370,034 / 12.02%
Clipped reads	12,661,950 / 20.65%

2.2. ACGT Content

Number/percentage of A's	2,490,535,830 / 30.99%
Number/percentage of C's	1,529,789,488 / 19.04%
Number/percentage of T's	2,488,932,237 / 30.97%
Number/percentage of G's	1,526,895,162 / 19%
Number/percentage of N's	29,954 / 0%
GC Percentage	38.04%

2.3. Coverage

Mean	25.8514
Standard Deviation	185.938

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Insert size

Mean	211,608.59
Standard Deviation	2,175,264.55
P25/Median/P75	313 / 411 / 533

2.6. Mismatches and indels

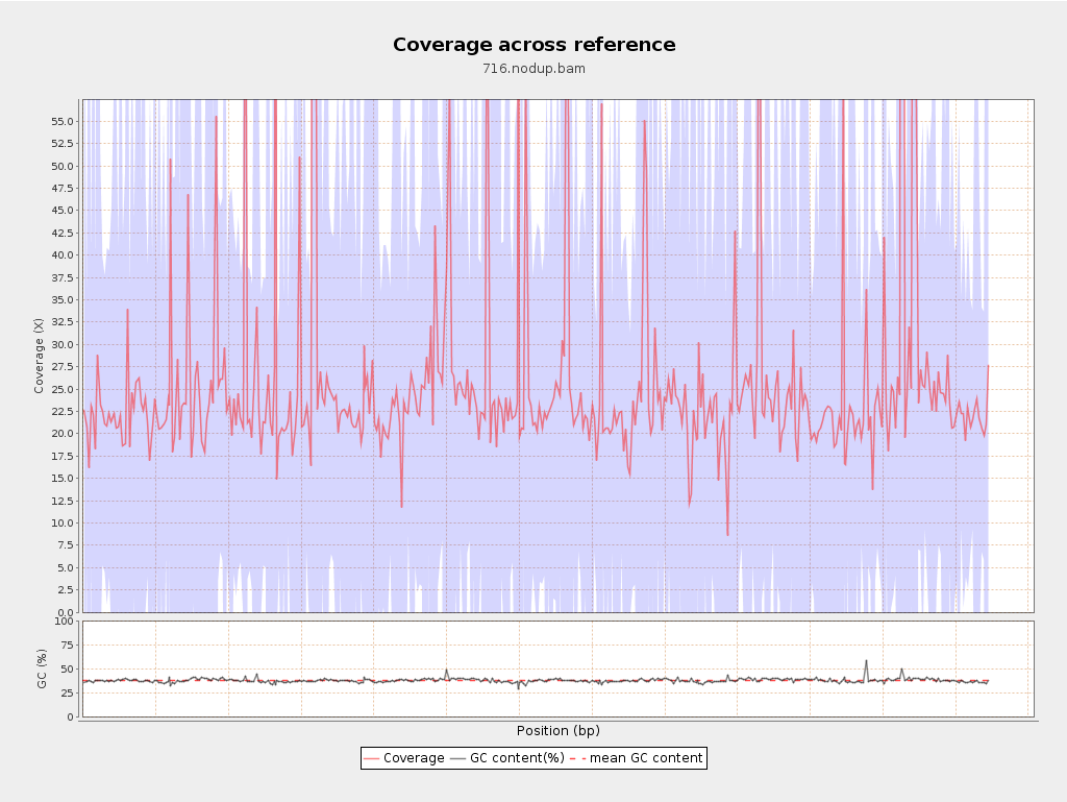
General error rate	2.19%
Mismatches	161,255,334
Insertions	5,259,978
Mapped reads with at least one insertion	8.19%
Deletions	5,368,601
Mapped reads with at least one deletion	8.25%
Homopolymer indels	57.07%

2.7. Chromosome stats

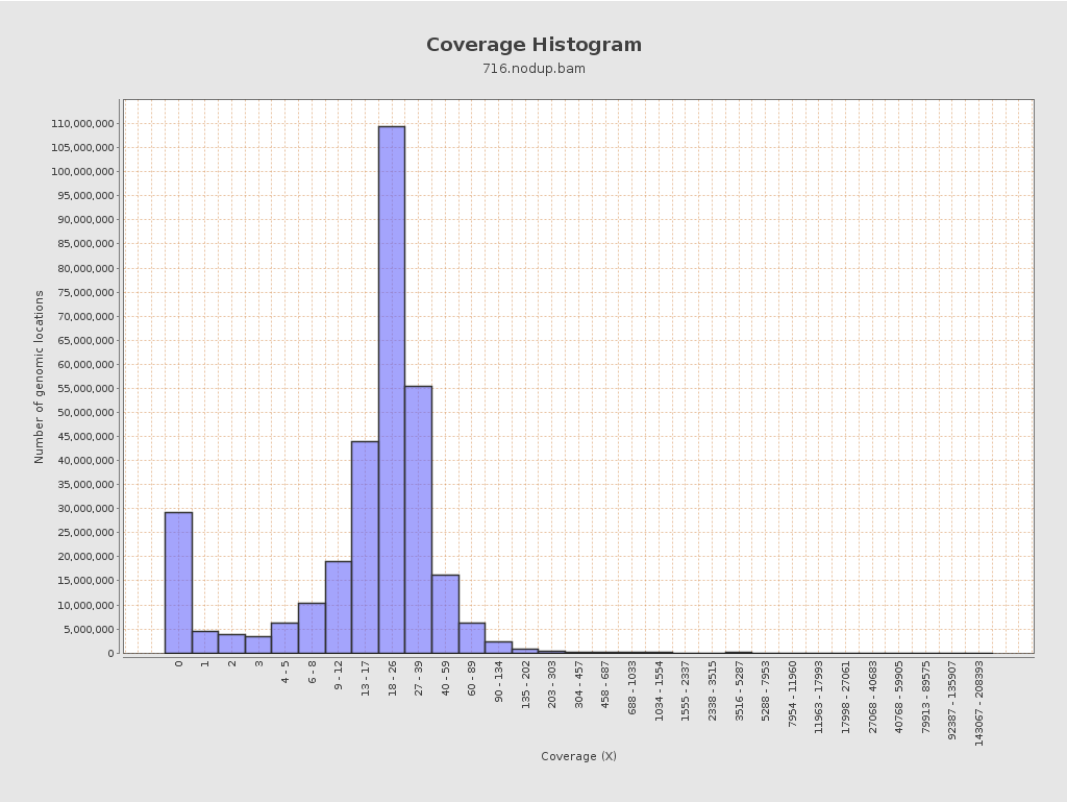
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	658704854	22.1605	46.8677

LT669789.1	36598175	965319973	26.3762	194.6088
LT669790.1	30422129	844929401	27.7735	188.5111
LT669791.1	52758100	1334241473	25.2898	145.2396
LT669792.1	28376109	730123188	25.7302	210.869
LT669793.1	33388210	795210911	23.8171	103.2893
LT669794.1	50579949	1230562328	24.3291	161.0599
LT669795.1	49795044	1497278361	30.0688	290.3304

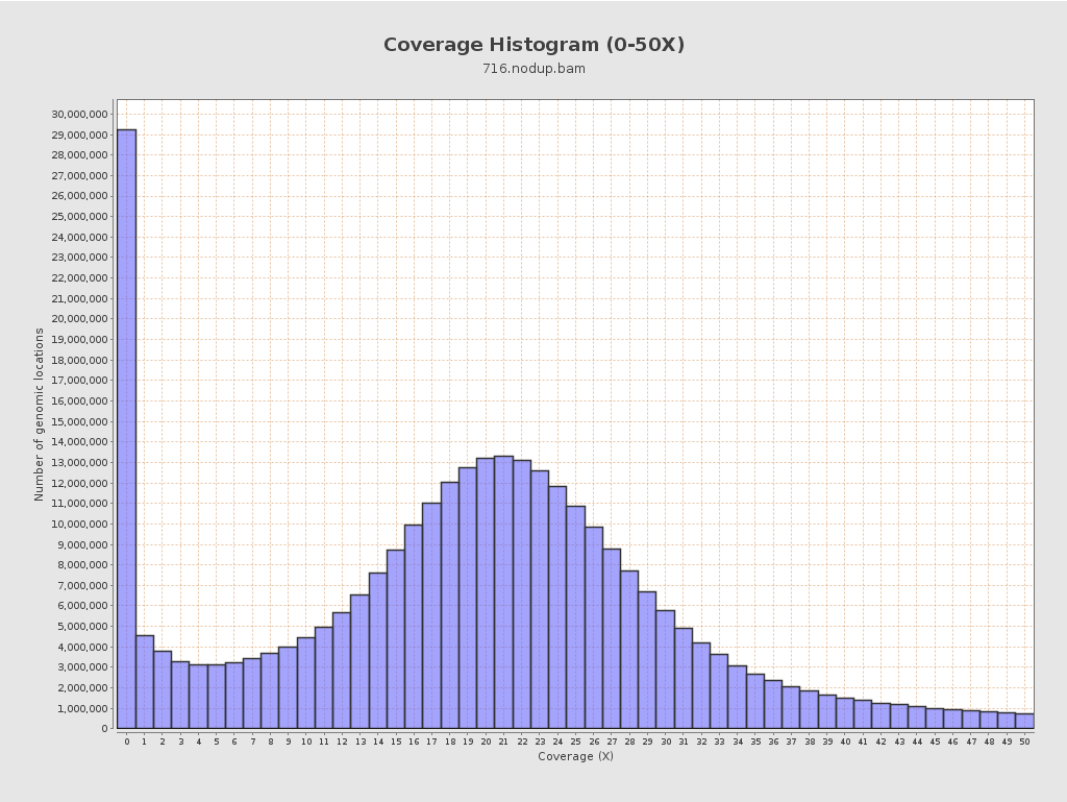
3. Results : Coverage across reference



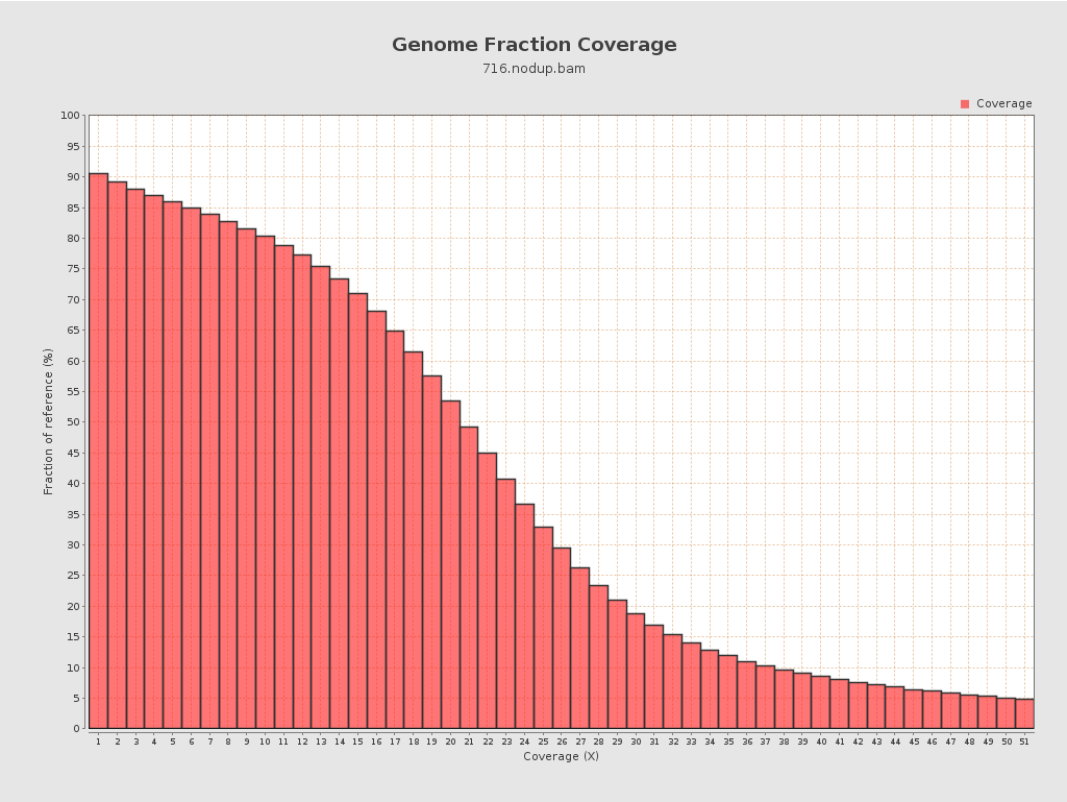
4. Results : Coverage Histogram



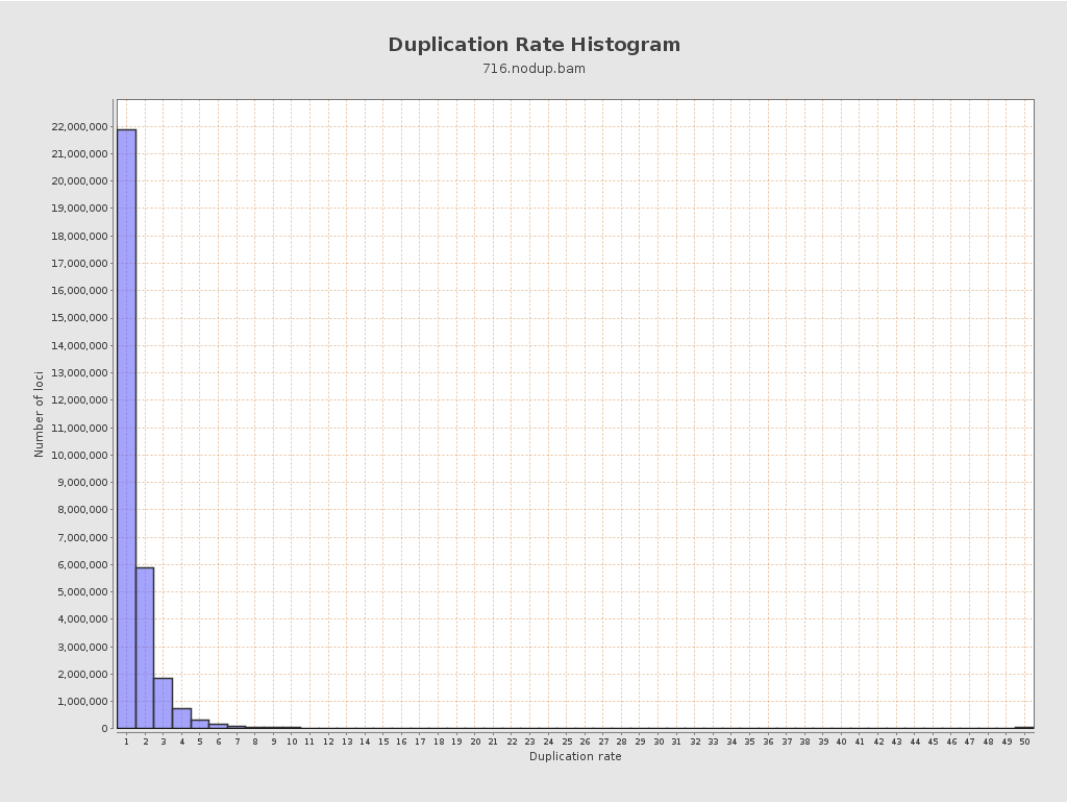
5. Results : Coverage Histogram (0-50X)



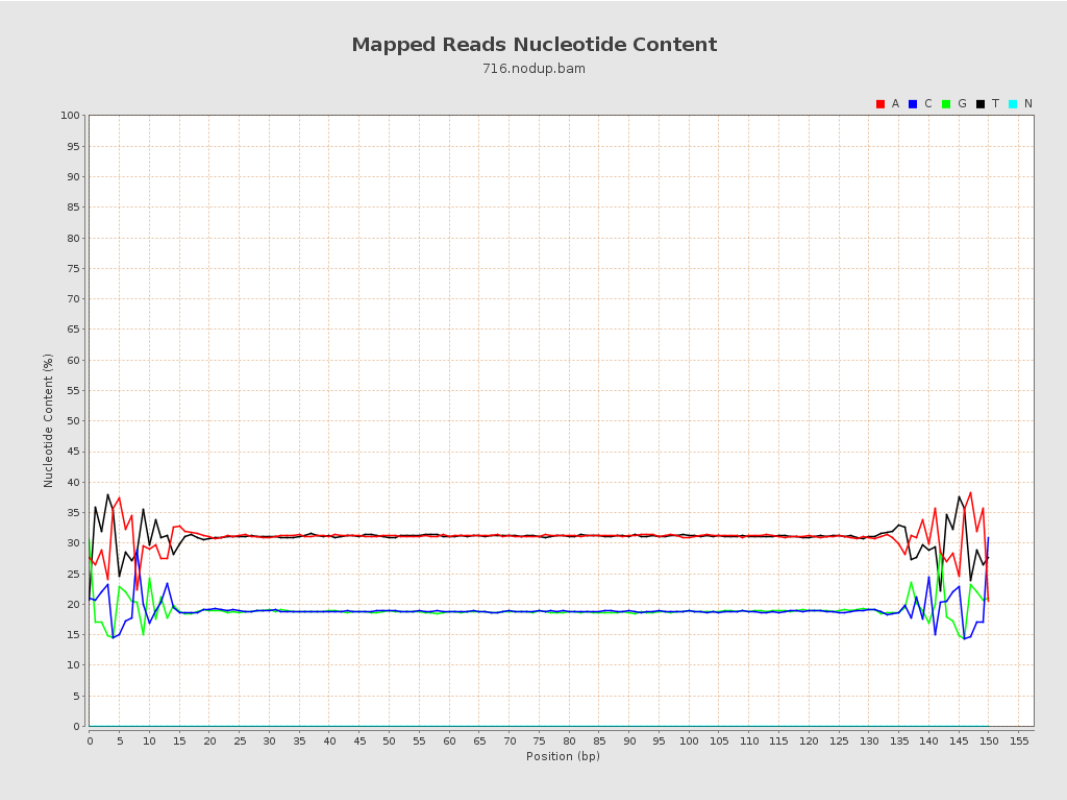
6. Results : Genome Fraction Coverage



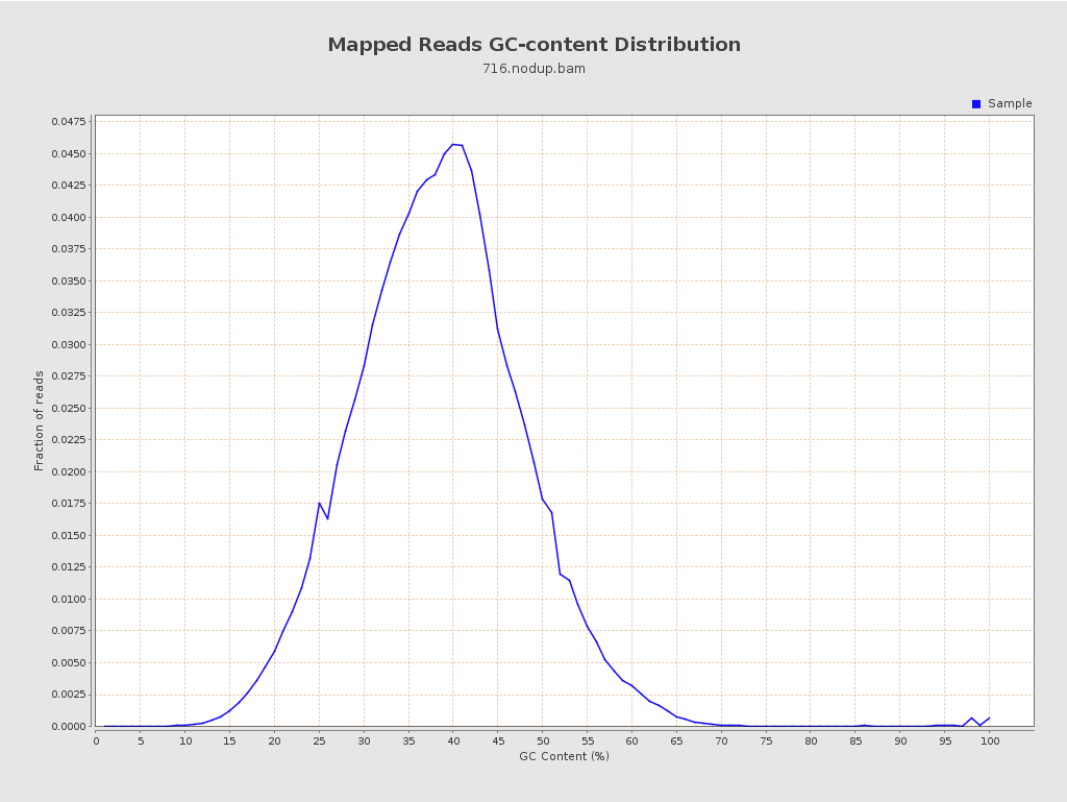
7. Results : Duplication Rate Histogram



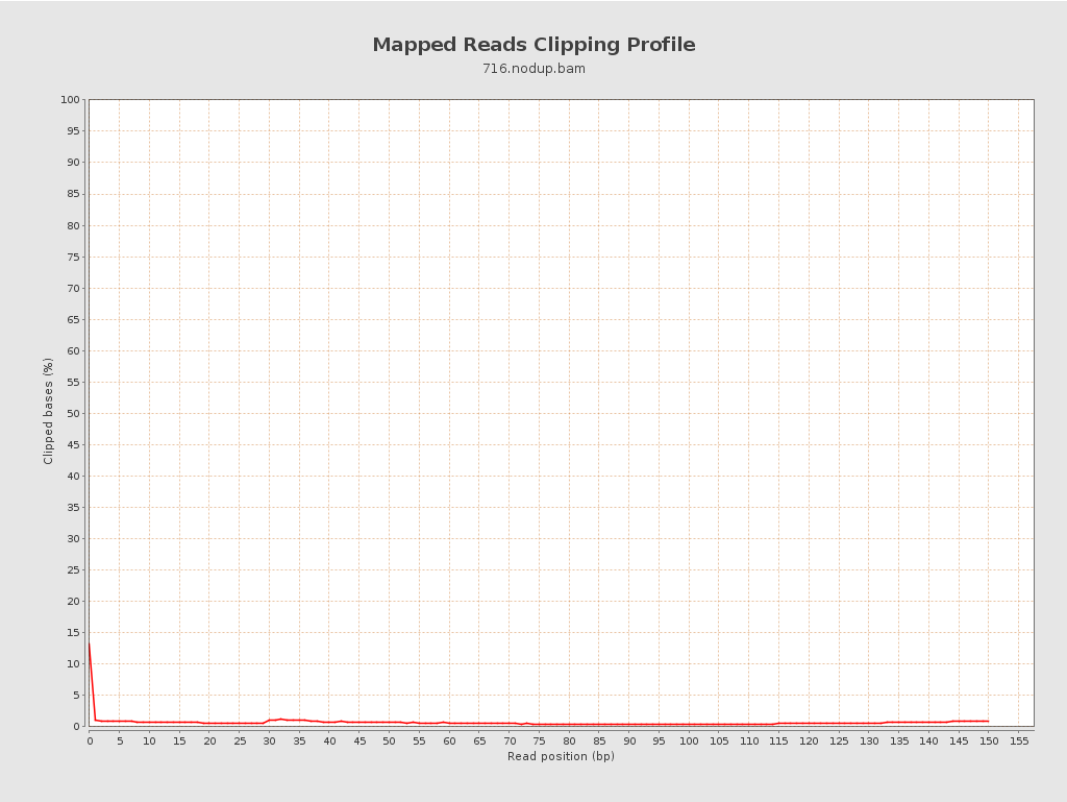
8. Results : Mapped Reads Nucleotide Content



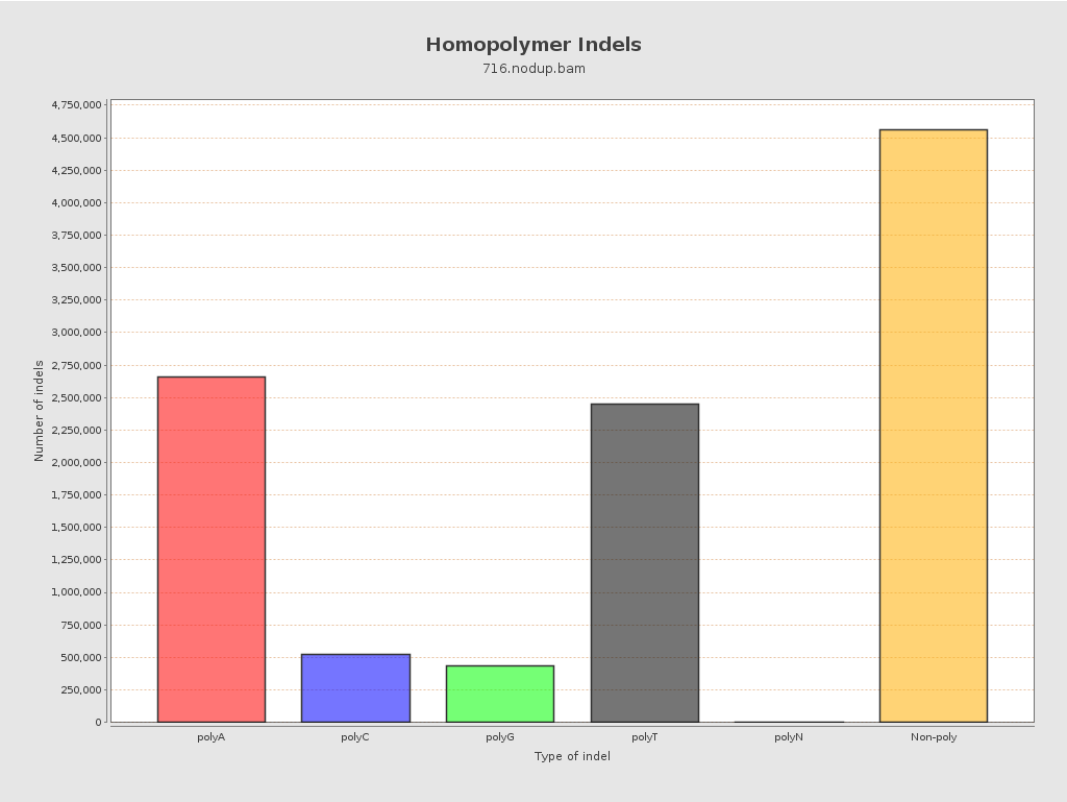
9. Results : Mapped Reads GC-content Distribution



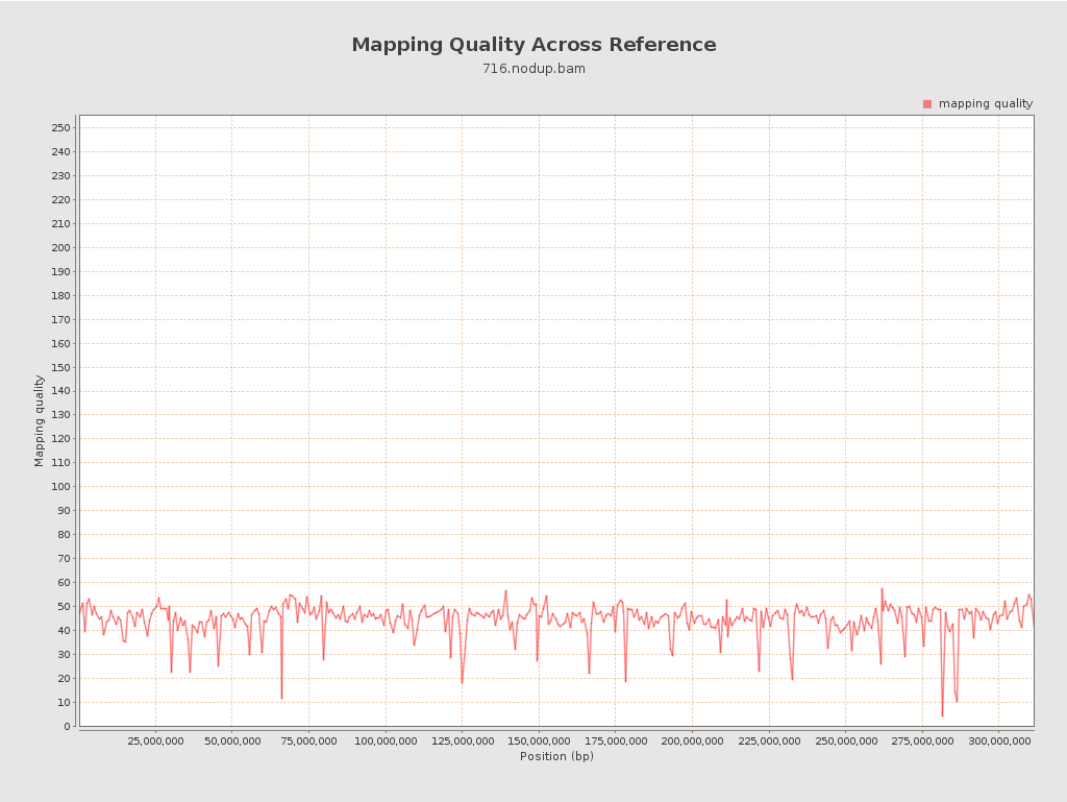
10. Results : Mapped Reads Clipping Profile



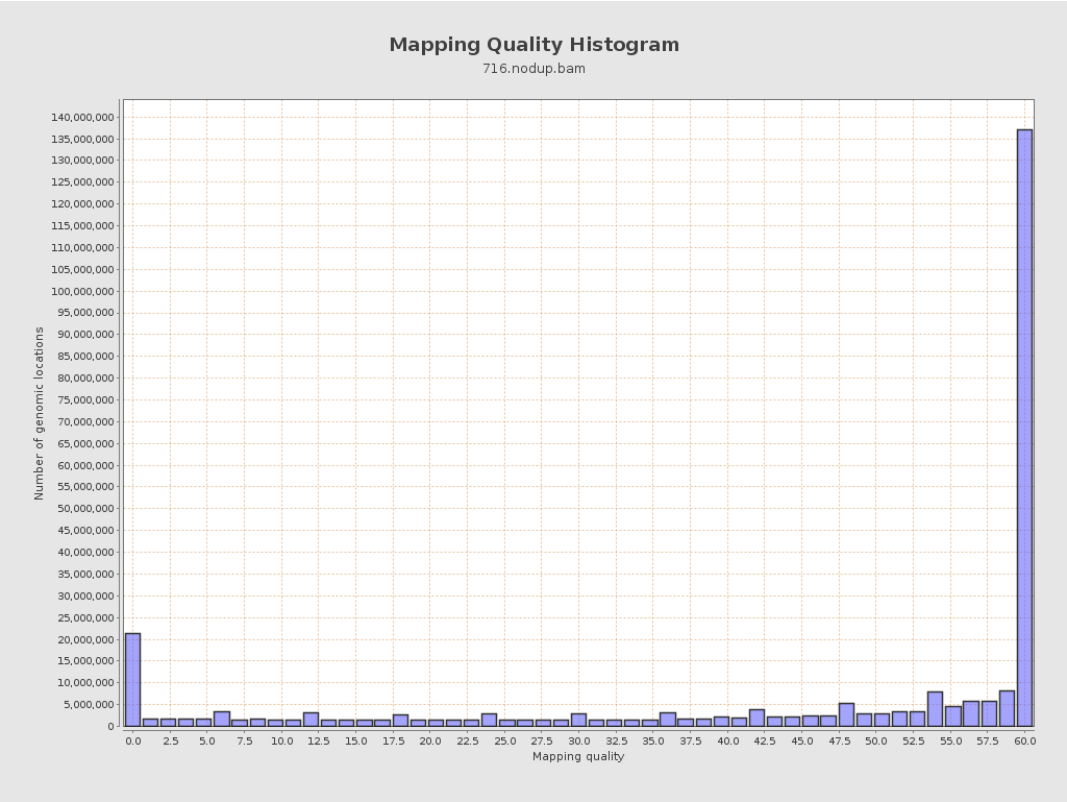
11. Results : Homopolymer Indels



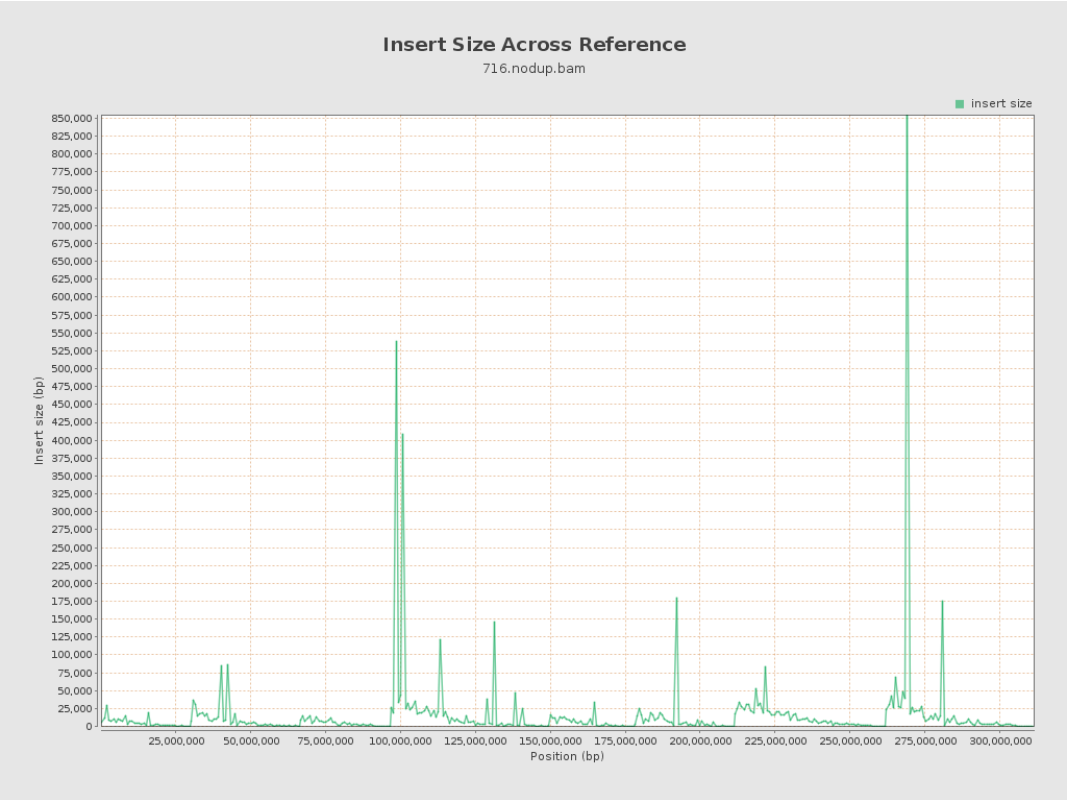
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram