Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/415.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/415.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_172/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_172_S262_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_172/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_172_S262_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

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

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	60,723,171
Mapped reads	55,210,543 / 90.92%
Unmapped reads	5,512,628 / 9.08%
Mapped paired reads	55,210,543 / 90.92%
Mapped reads, first in pair	27,664,030 / 45.56%
Mapped reads, second in pair	27,546,513 / 45.36%
Mapped reads, both in pair	53,682,371 / 88.41%
Mapped reads, singletons	1,528,172 / 2.52%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	9,067,785 / 14.93%
Clipped reads	12,867,599 / 21.19%

2.2. ACGT Content

Number/percentage of A's	2,354,757,653 / 30.92%
Number/percentage of C's	1,452,205,872 / 19.07%
Number/percentage of T's	2,354,214,004 / 30.92%
Number/percentage of G's	1,453,358,157 / 19.09%
Number/percentage of N's	31,459 / 0%
GC Percentage	38.16%

2.3. Coverage

Mean	24.4965
Standard Deviation	196.5648

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Insert size

Mean	263,931.24
Standard Deviation	2,453,481.12
P25/Median/P75	378 / 492 / 639

2.6. Mismatches and indels

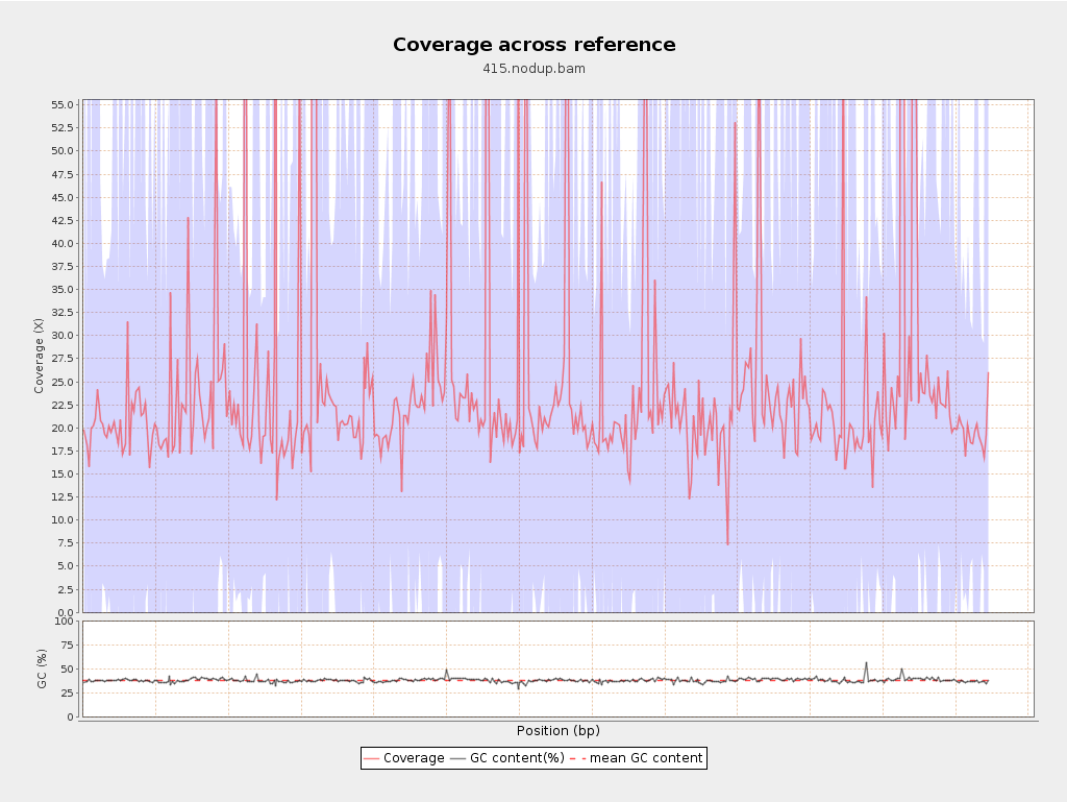
General error rate	2.41%
Mismatches	168,889,274
Insertions	5,261,346
Mapped reads with at least one insertion	8.53%
Deletions	5,260,020
Mapped reads with at least one deletion	8.47%
Homopolymer indels	56.97%

2.7. Chromosome stats

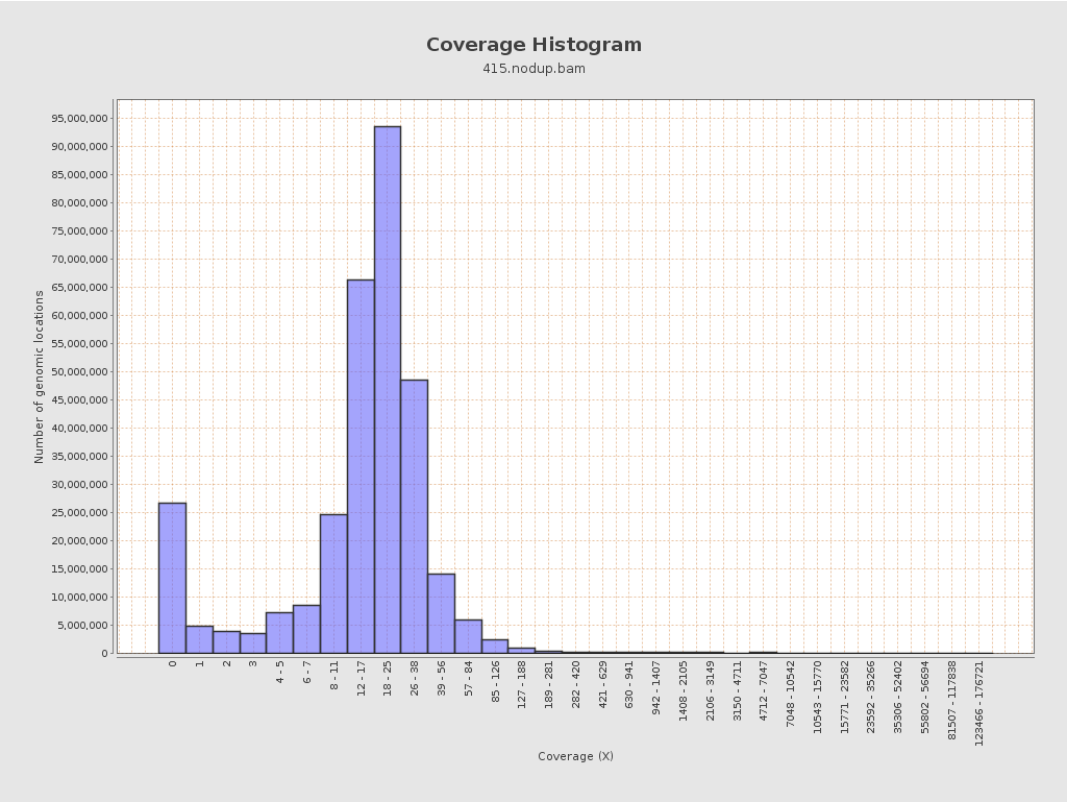
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	598617070	20.1389	67.1997

LT669789.1	36598175	934971967	25.547	214.8814
LT669790.1	30422129	832671301	27.3706	236.7859
LT669791.1	52758100	1280513688	24.2714	189.0496
LT669792.1	28376109	699056312	24.6354	223.7105
LT669793.1	33388210	765779078	22.9356	139.8099
LT669794.1	50579949	1187947915	23.4865	173.2962
LT669795.1	49795044	1334576983	26.8014	246.7892

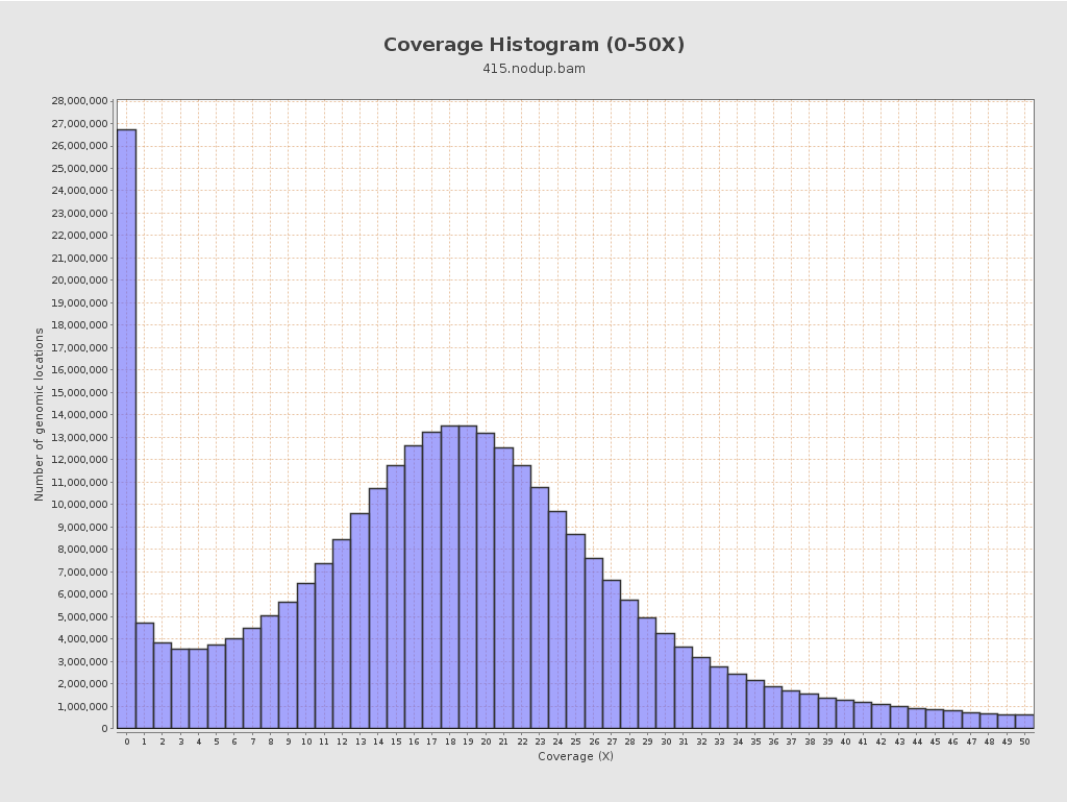
3. Results : Coverage across reference



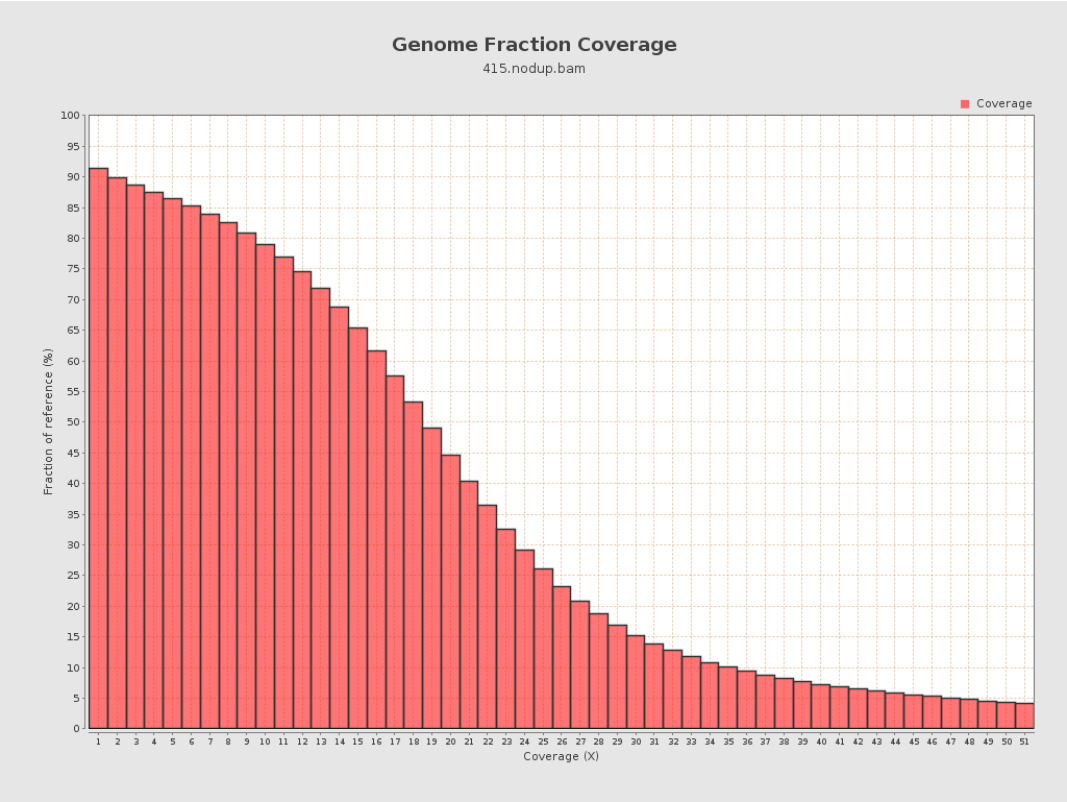
4. Results : Coverage Histogram



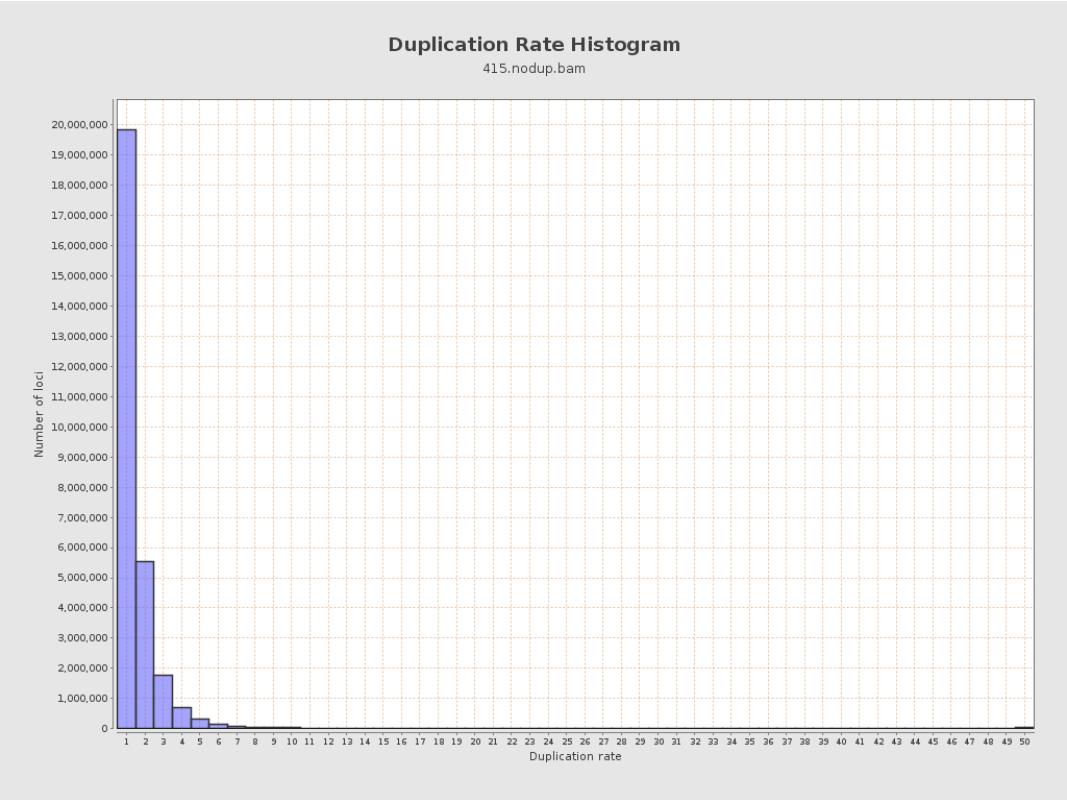
5. Results : Coverage Histogram (0-50X)



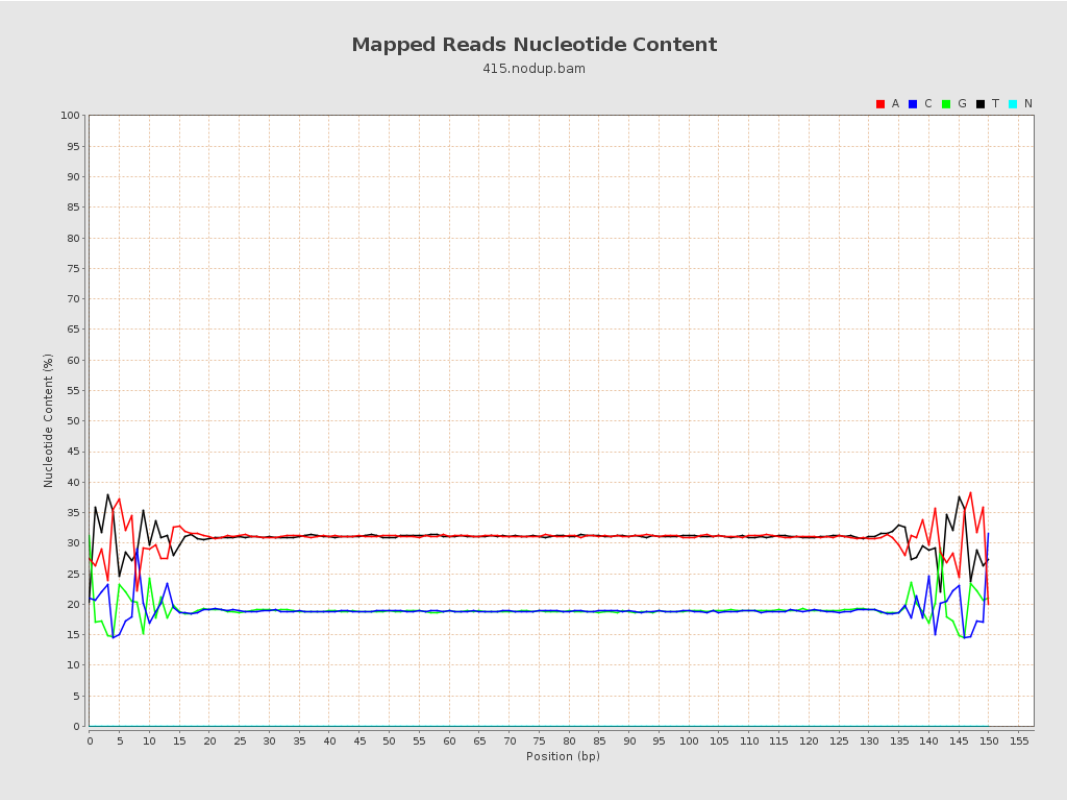
6. Results : Genome Fraction Coverage



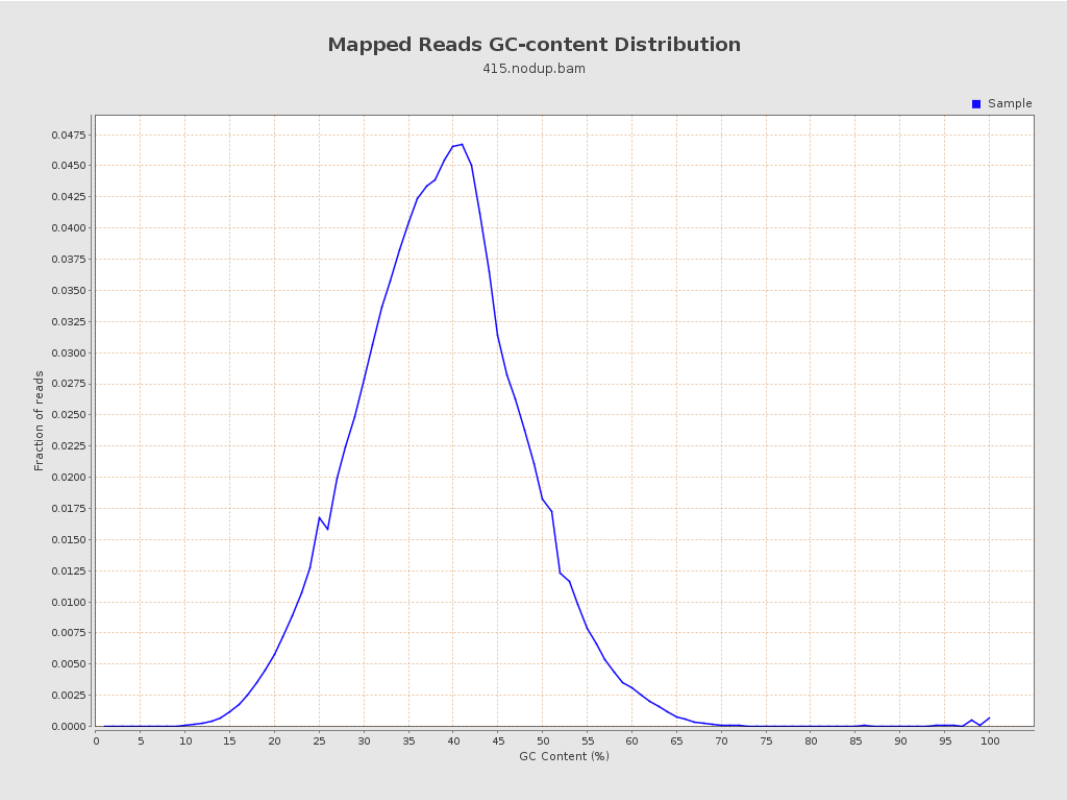
7. Results : Duplication Rate Histogram



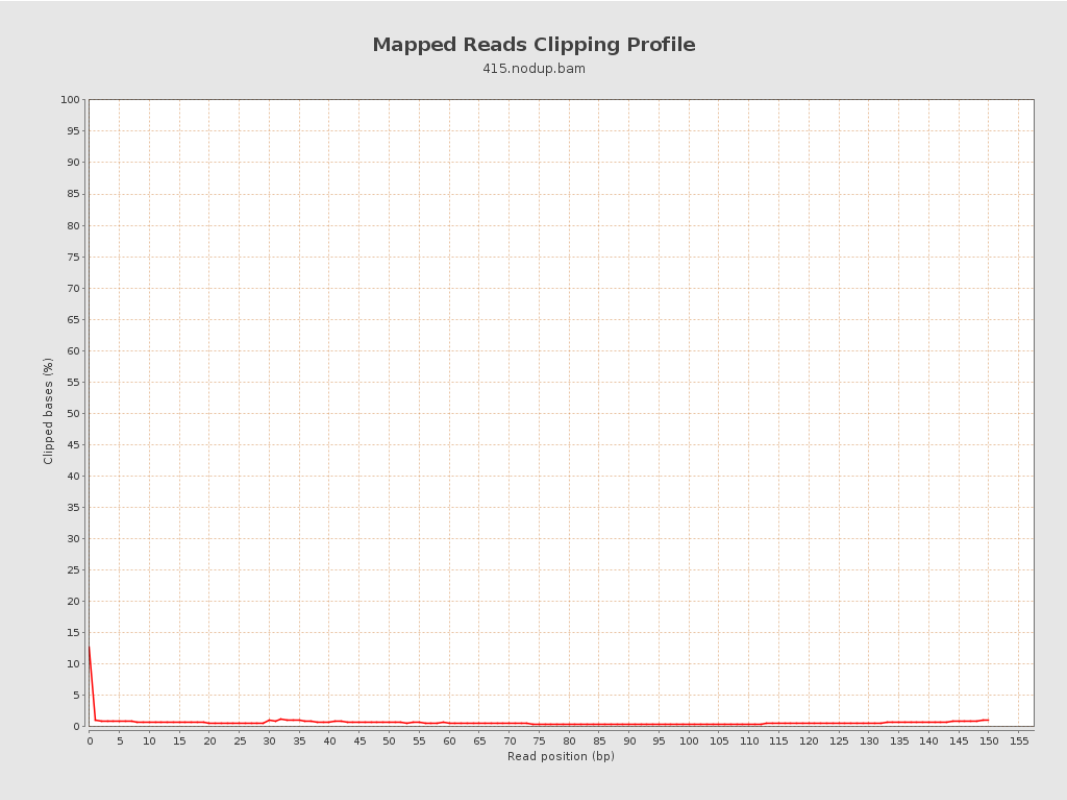
8. Results : Mapped Reads Nucleotide Content



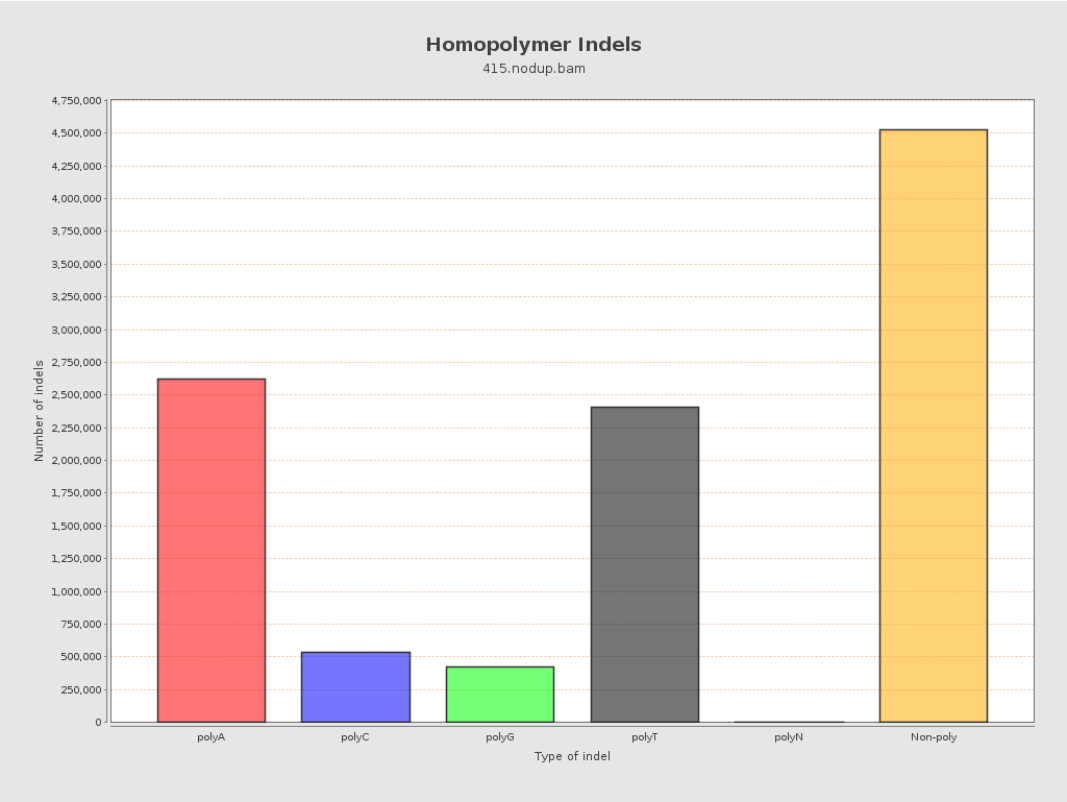
9. Results : Mapped Reads GC-content Distribution



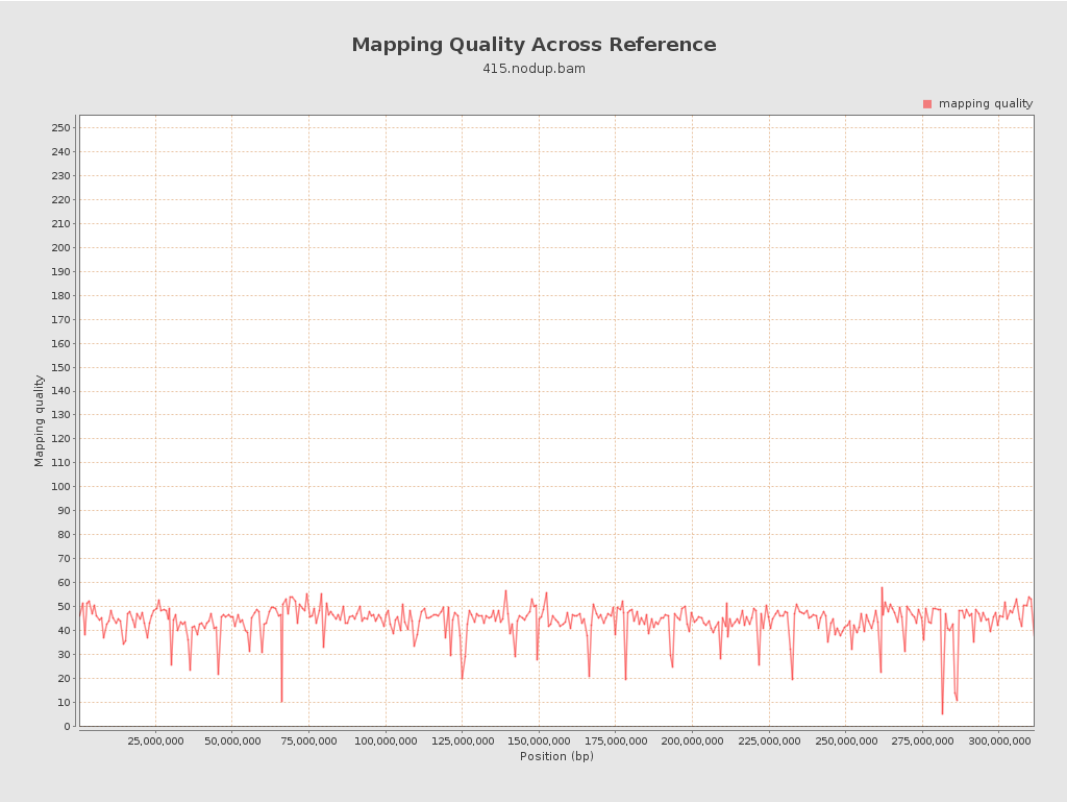
10. Results : Mapped Reads Clipping Profile



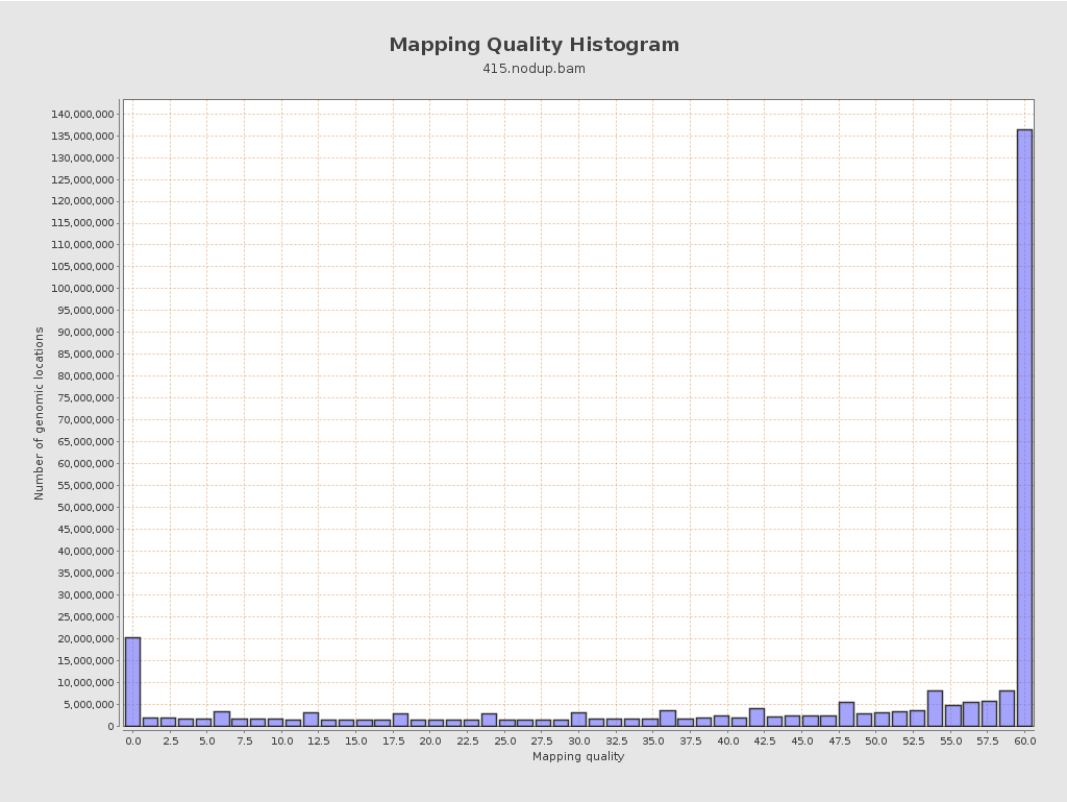
11. Results : Homopolymer Indels



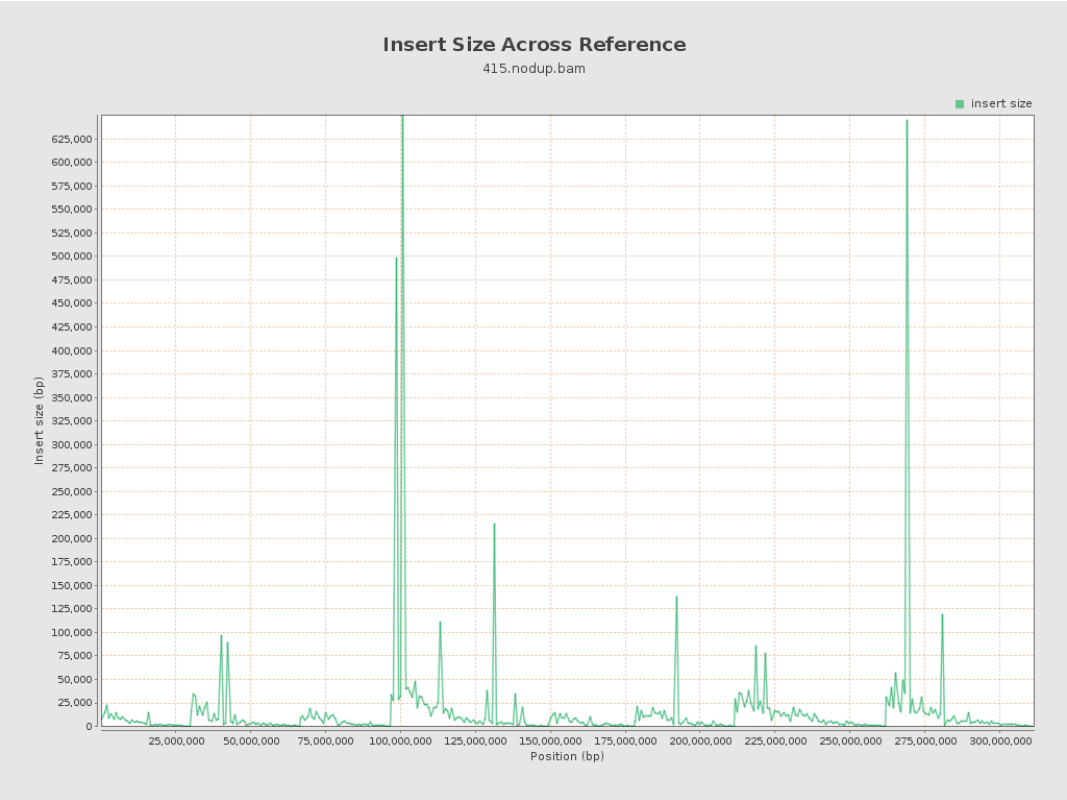
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram