

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:41

1. Input data & parameters

1.1. QualiMap command line

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

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/400.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_161/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_161_S251_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_161/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_161_S251_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:33:40 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	70,545,483
Mapped reads	66,336,247 / 94.03%
Unmapped reads	4,209,236 / 5.97%
Mapped paired reads	66,336,247 / 94.03%
Mapped reads, first in pair	33,233,709 / 47.11%
Mapped reads, second in pair	33,102,538 / 46.92%
Mapped reads, both in pair	64,957,370 / 92.08%
Mapped reads, singletons	1,378,877 / 1.95%
Read min/max/mean length	30 / 151 / 148.13
Duplicated reads (flagged)	10,686,279 / 15.15%
Clipped reads	14,564,542 / 20.65%

2.2. ACGT Content

Number/percentage of A's	2,848,868,042 / 30.93%
Number/percentage of C's	1,759,010,648 / 19.1%
Number/percentage of T's	2,848,950,239 / 30.93%
Number/percentage of G's	1,754,661,812 / 19.05%
Number/percentage of N's	39,095 / 0%
GC Percentage	38.14%

2.3. Coverage

Mean	29.6337
Standard Deviation	231.8884

2.4. Mapping Quality

Mean Mapping Quality	44.49
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2.5. Insert size

Mean	228,408.93
Standard Deviation	2,267,407.93
P25/Median/P75	334 / 438 / 575

2.6. Mismatches and indels

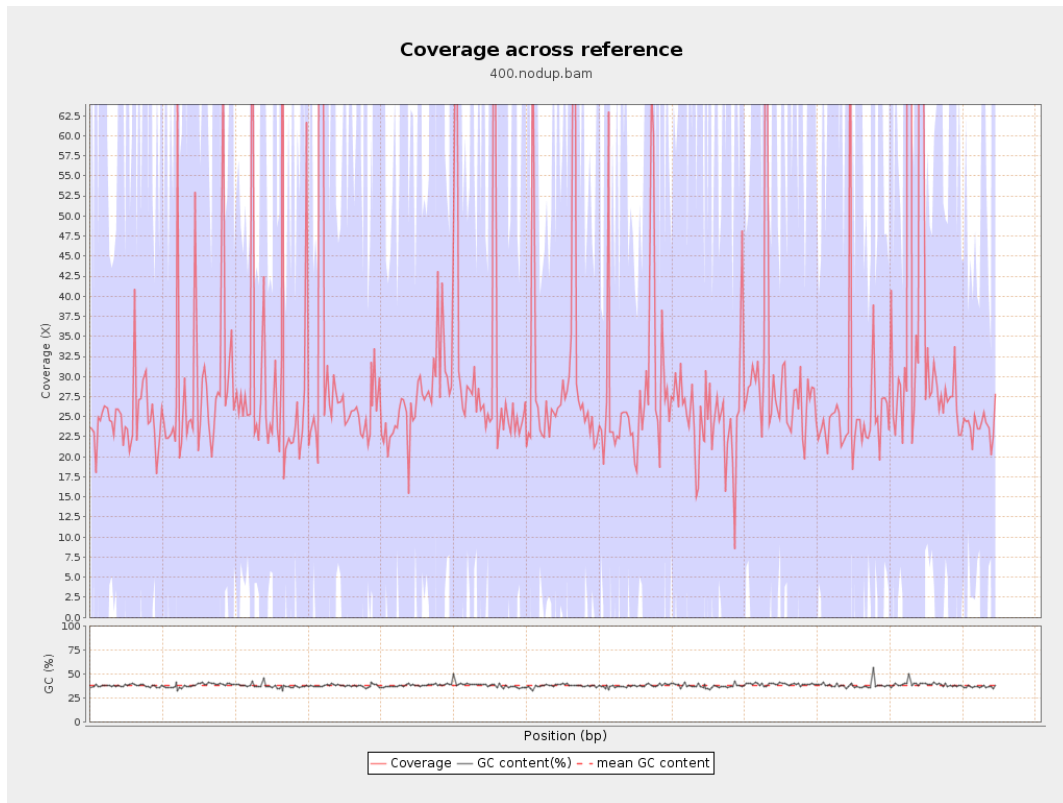
General error rate	2.24%
Mismatches	189,649,584
Insertions	6,095,641
Mapped reads with at least one insertion	8.27%
Deletions	6,285,739
Mapped reads with at least one deletion	8.42%
Homopolymer indels	56.78%

2.7. Chromosome stats

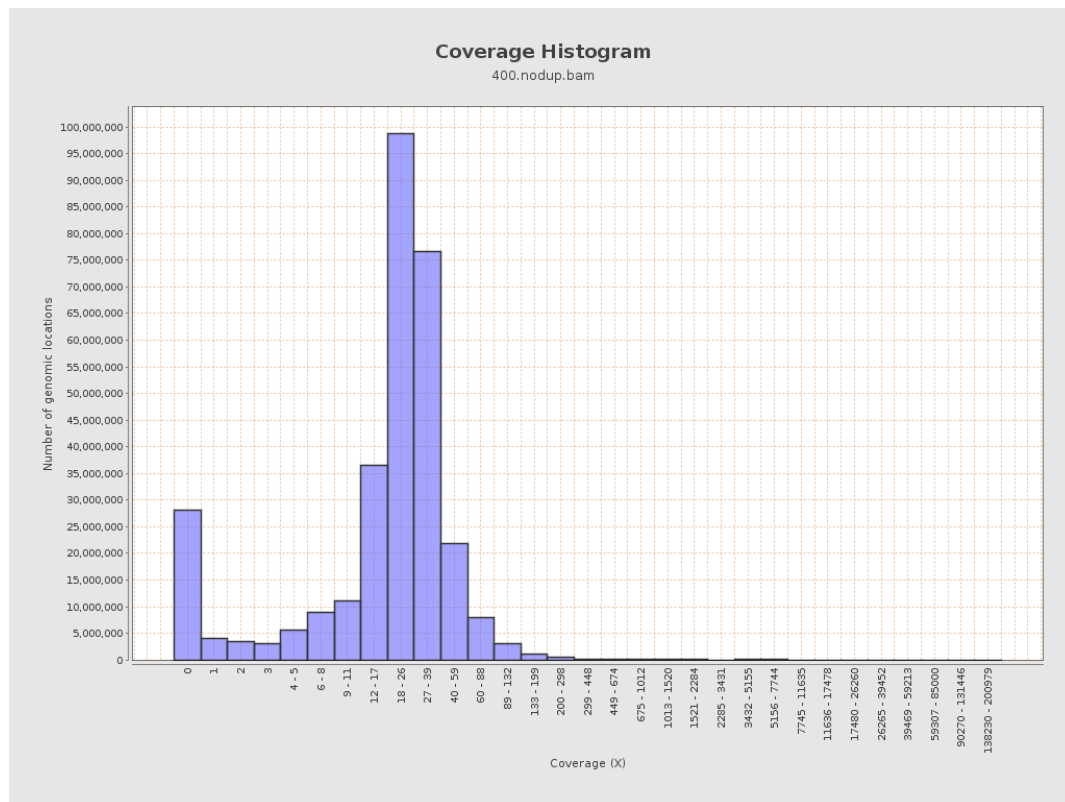
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	729584081	24.545	67.5003

LT669789.1	36598175	1108720703	30.2944	243.7243
LT669790.1	30422129	961264354	31.5975	233.6599
LT669791.1	52758100	1527079778	28.9449	189.3457
LT669792.1	28376109	819107195	28.8661	236.3936
LT669793.1	33388210	910909082	27.2824	120.3369
LT669794.1	50579949	1416931005	28.0137	210.3022
LT669795.1	49795044	1761516704	35.3753	363.6989

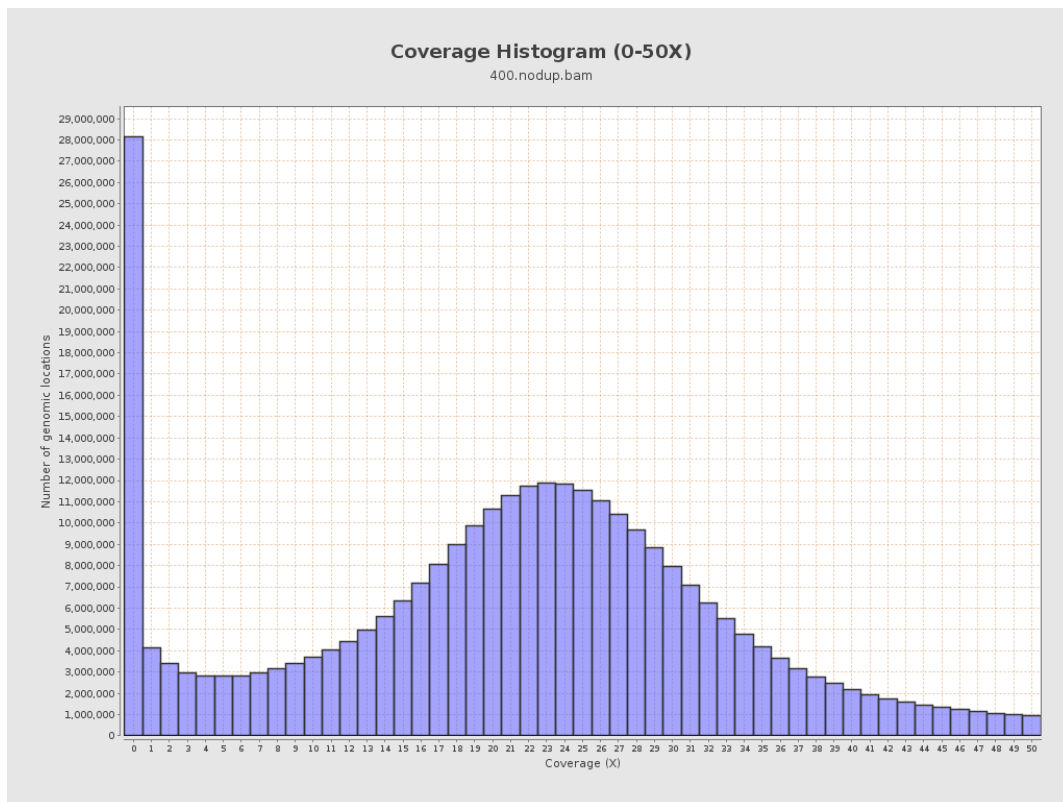
3. Results : Coverage across reference



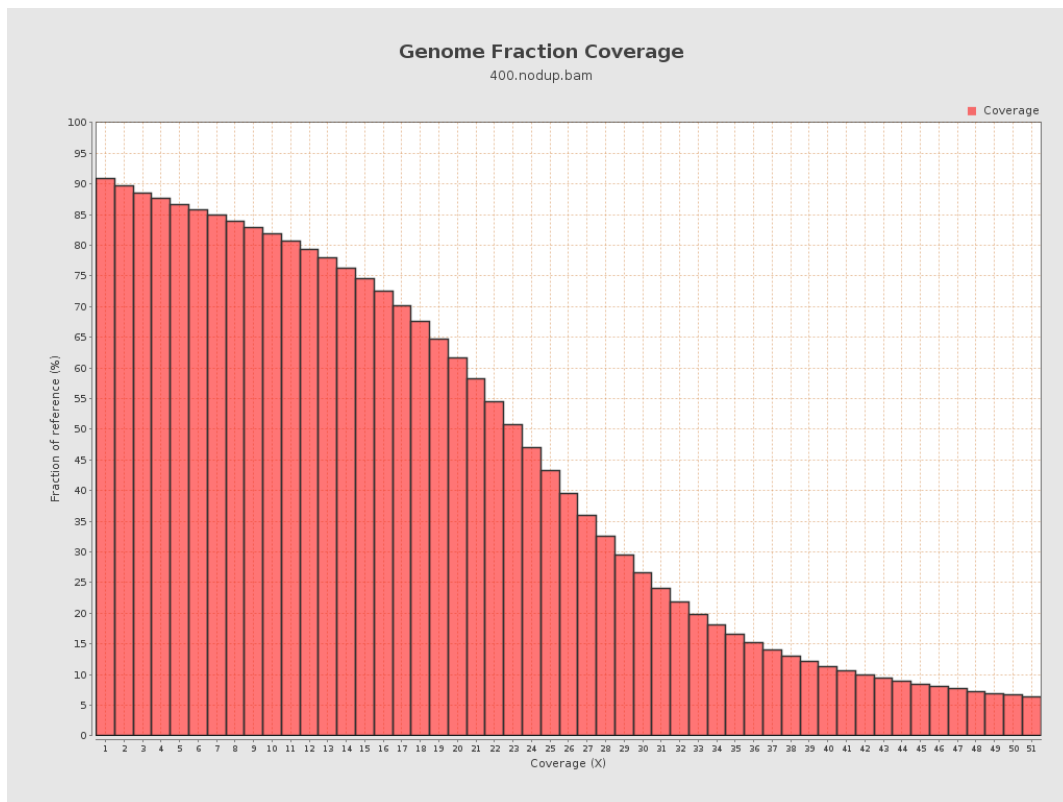
4. Results : Coverage Histogram



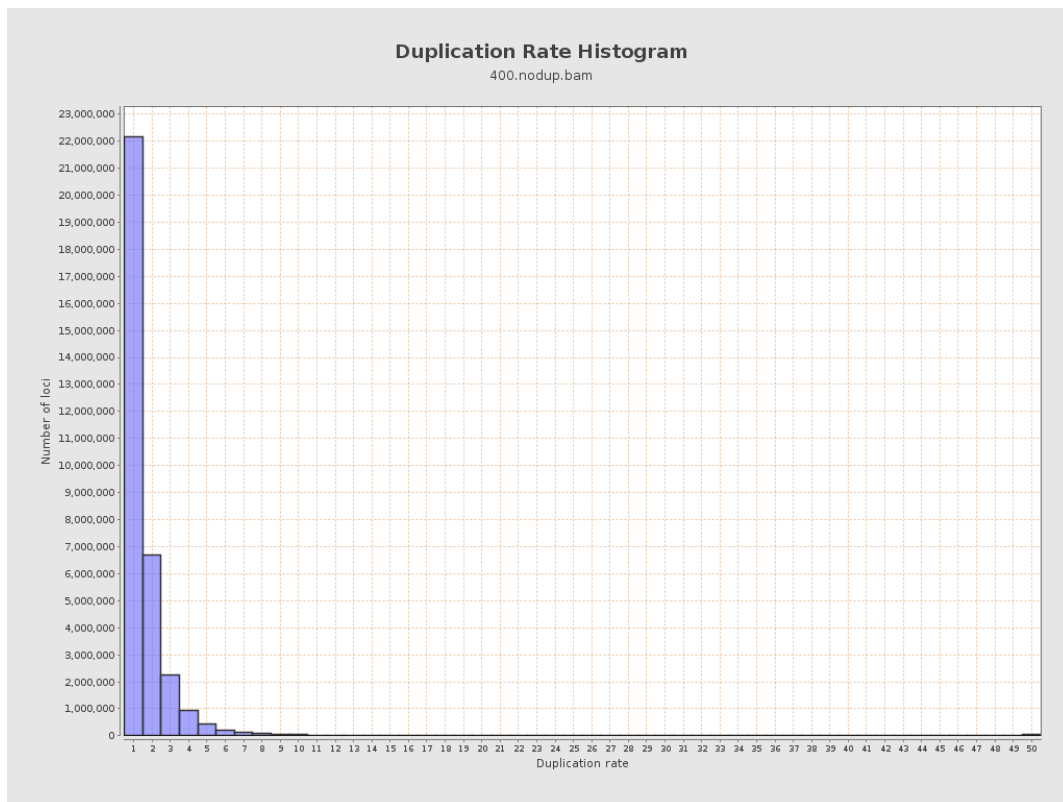
5. Results : Coverage Histogram (0-50X)



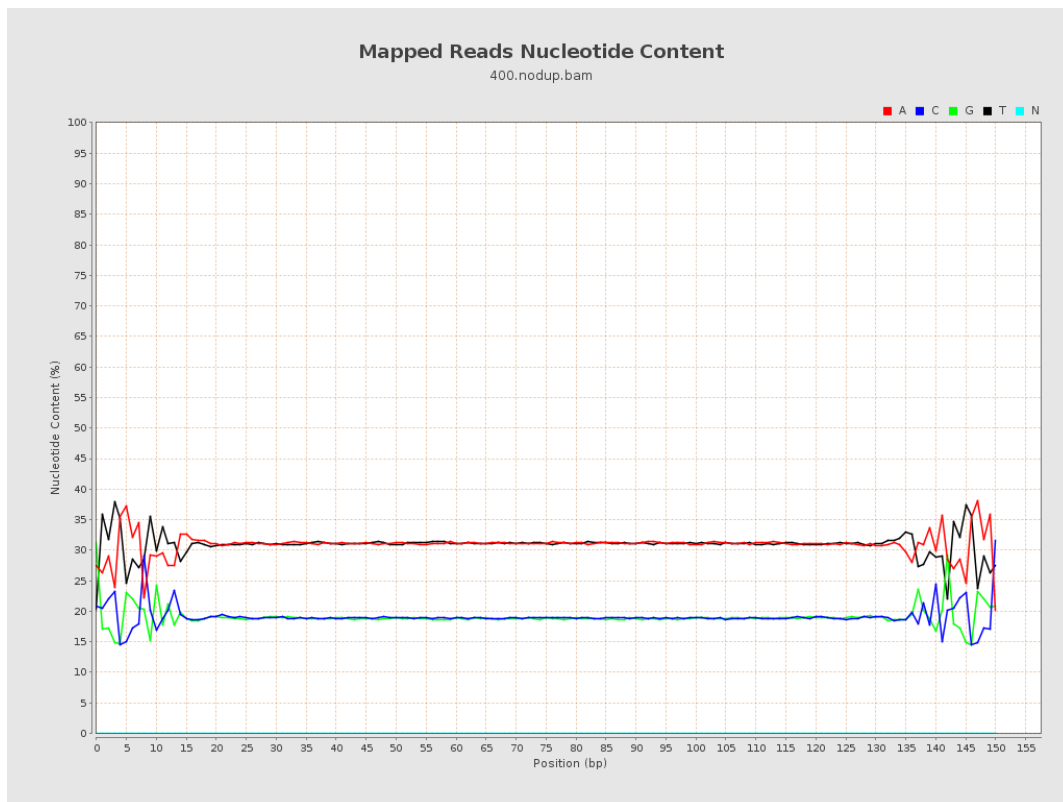
6. Results : Genome Fraction Coverage



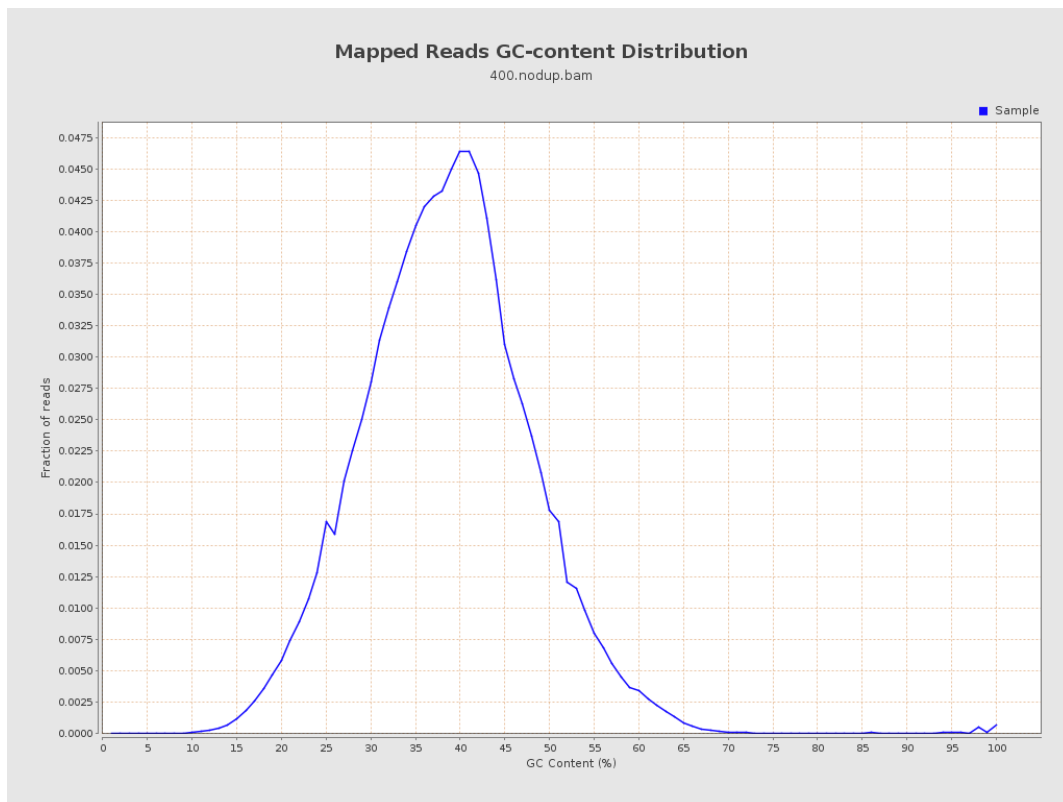
7. Results : Duplication Rate Histogram



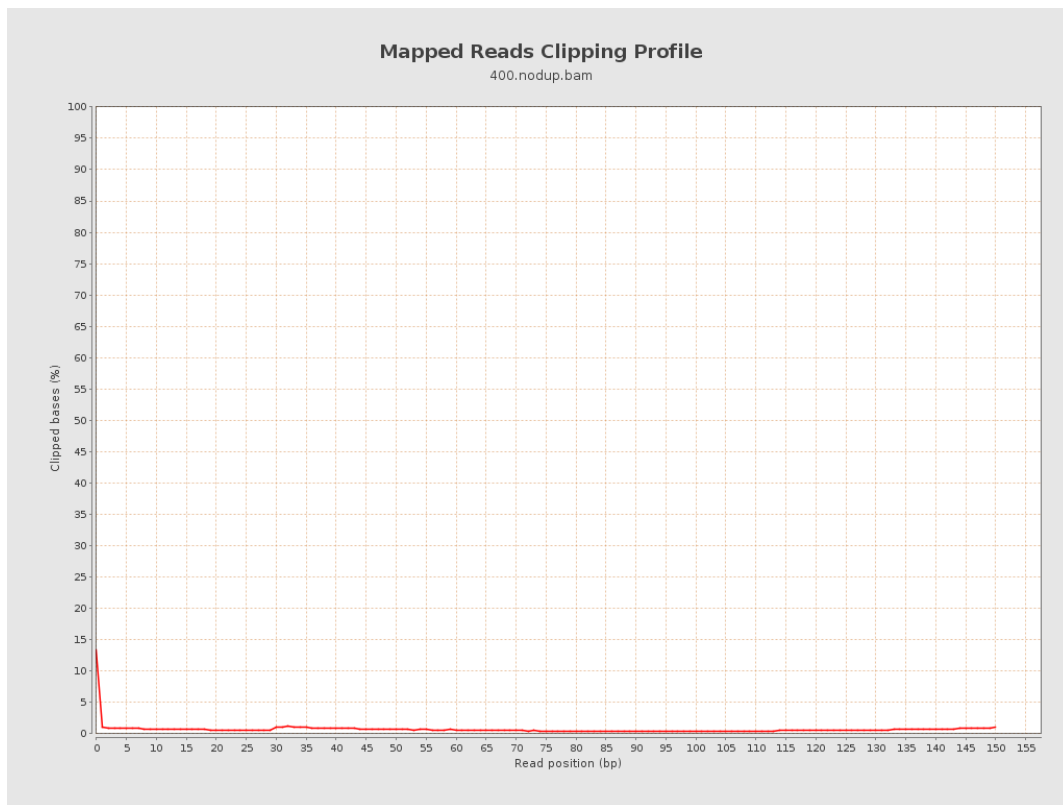
8. Results : Mapped Reads Nucleotide Content



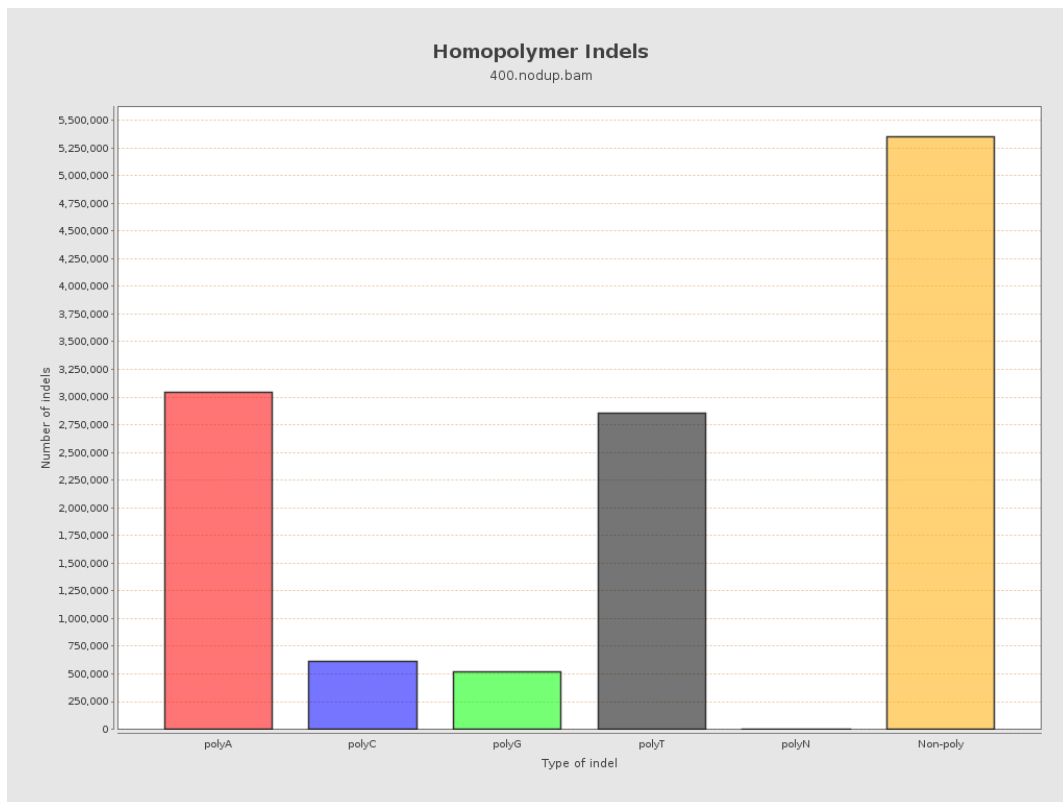
9. Results : Mapped Reads GC-content Distribution



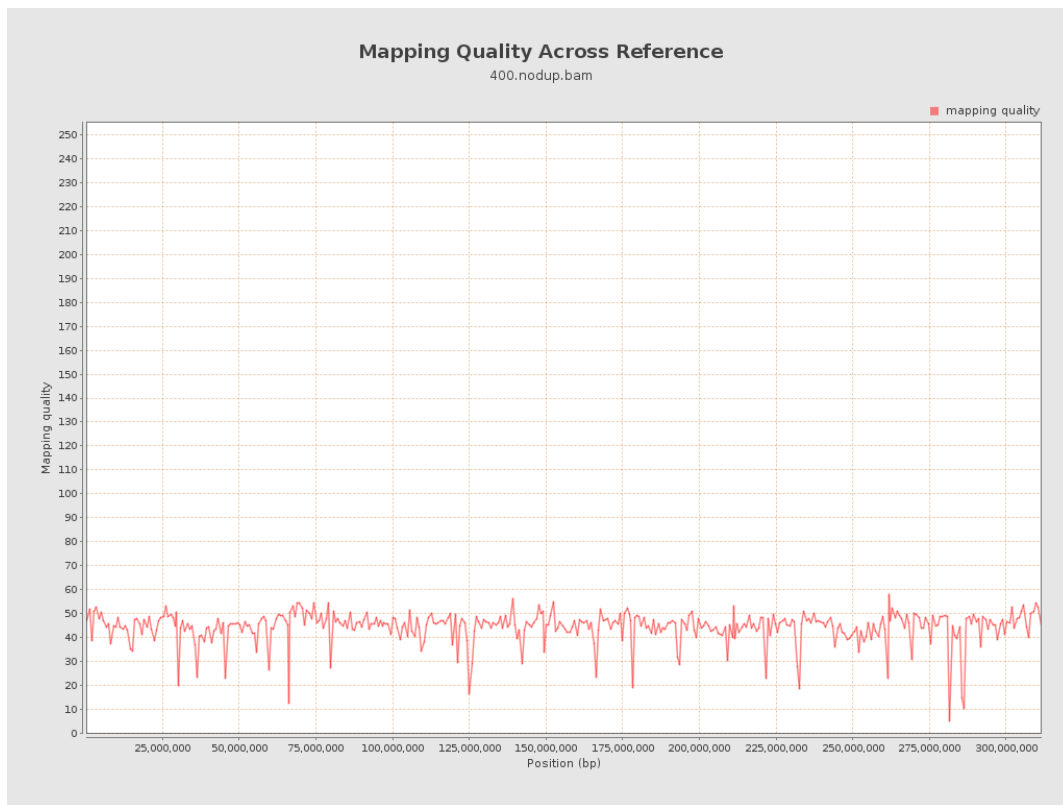
10. Results : Mapped Reads Clipping Profile



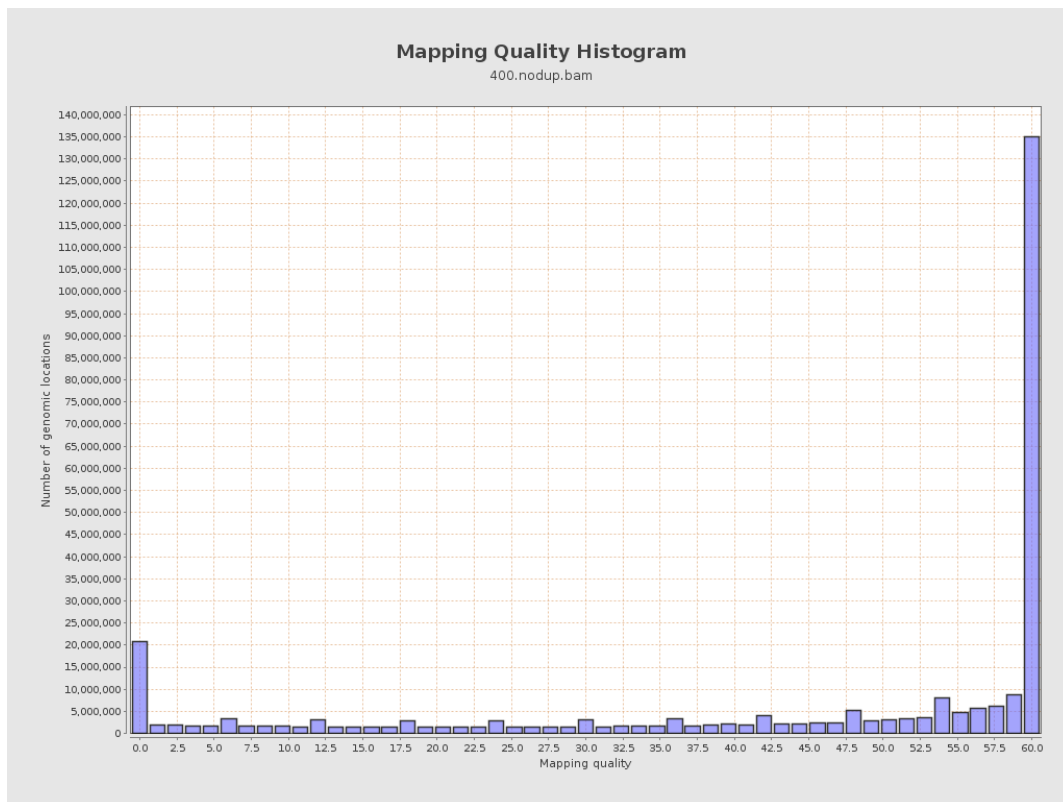
11. Results : Homopolymer Indels



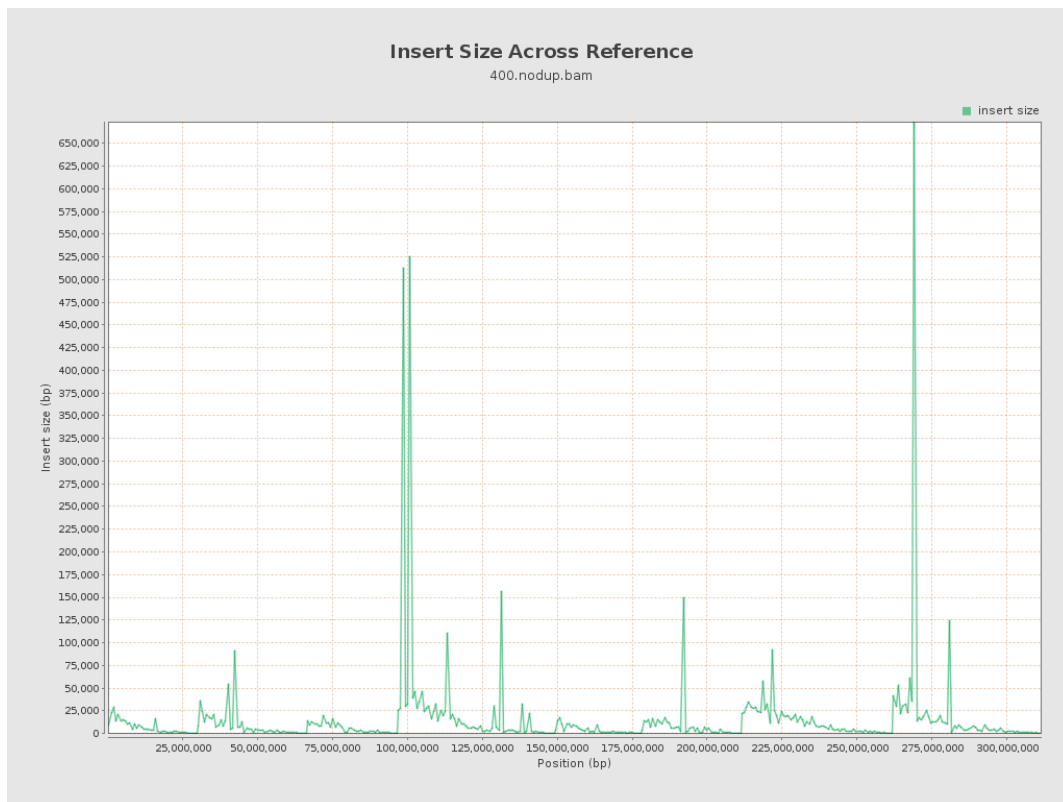
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

