

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/866
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 866 .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\t SM:\$sample /proj/uppstore2018210/Aalpina/data/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_467/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_467_S442_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_467/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_467_S442_L004 _R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:32 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	65,572,386
Mapped reads	60,724,393 / 92.61%
Unmapped reads	4,847,993 / 7.39%
Mapped paired reads	60,724,393 / 92.61%
Mapped reads, first in pair	30,429,751 / 46.41%
Mapped reads, second in pair	30,294,642 / 46.2%
Mapped reads, both in pair	59,418,105 / 90.61%
Mapped reads, singletons	1,306,288 / 1.99%
Read min/max/mean length	30 / 151 / 148.23
Duplicated reads (flagged)	9,993,373 / 15.24%
Clipped reads	12,914,946 / 19.7%

2.2. ACGT Content

Number/percentage of A's	2,614,204,455 / 30.89%
Number/percentage of C's	1,618,507,754 / 19.12%
Number/percentage of T's	2,616,802,540 / 30.92%
Number/percentage of G's	1,614,552,290 / 19.08%
Number/percentage of N's	29,512 / 0%
GC Percentage	38.2%

2.3. Coverage

Mean	27.2289
Standard Deviation	204.7307

2.4. Mapping Quality

Mean Mapping Quality	44.2
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2.5. Insert size

Mean	245,575.35
Standard Deviation	2,358,580.46
P25/Median/P75	378 / 487 / 627

2.6. Mismatches and indels

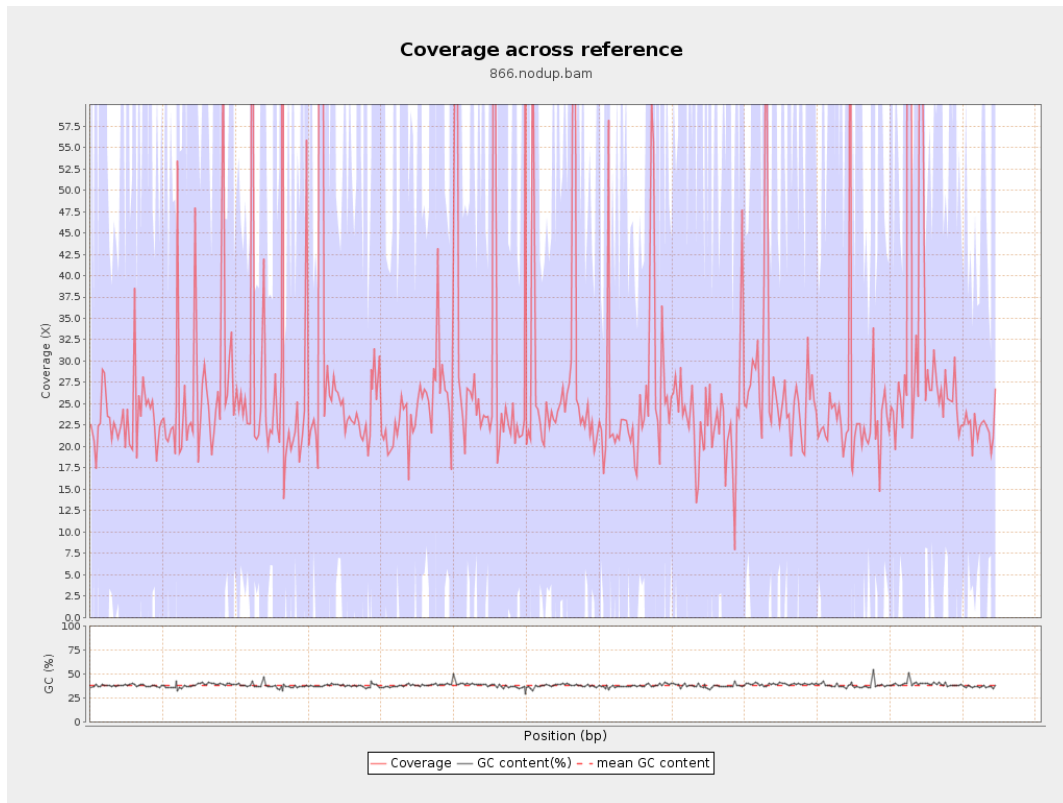
General error rate	2.28%
Mismatches	177,242,573
Insertions	5,670,789
Mapped reads with at least one insertion	8.4%
Deletions	5,783,821
Mapped reads with at least one deletion	8.45%
Homopolymer indels	56.37%

2.7. Chromosome stats

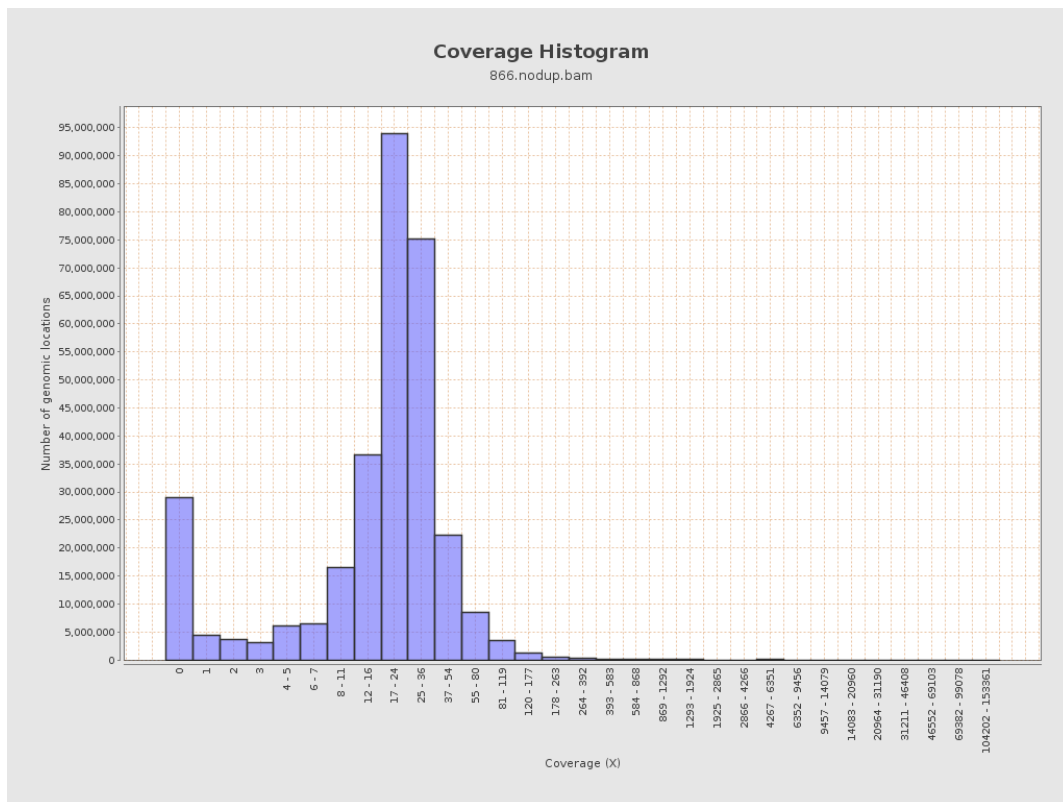
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	686883939	23.1085	78.9197

LT669789.1	36598175	1034810707	28.2749	243.3761
LT669790.1	30422129	878127461	28.8648	200.4967
LT669791.1	52758100	1401220805	26.5593	204.7396
LT669792.1	28376109	764765610	26.951	231.7884
LT669793.1	33388210	839437201	25.1417	108.5945
LT669794.1	50579949	1325220663	26.2005	205.9313
LT669795.1	49795044	1555196654	31.232	253.9017

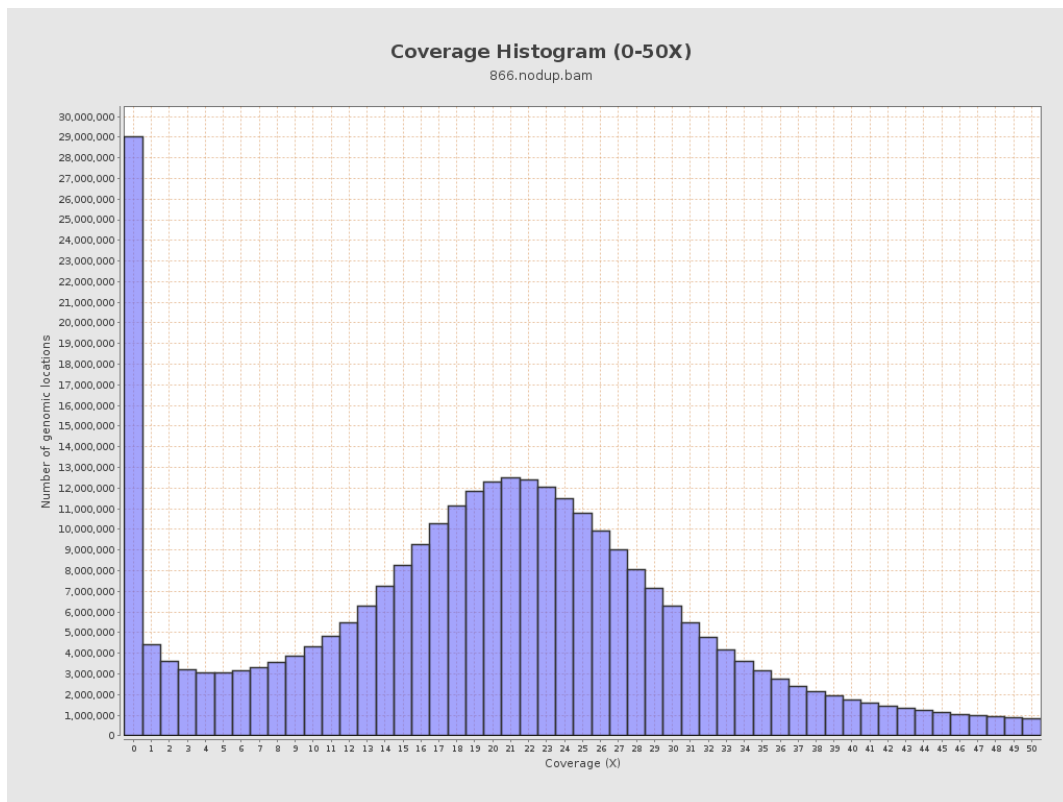
3. Results : Coverage across reference



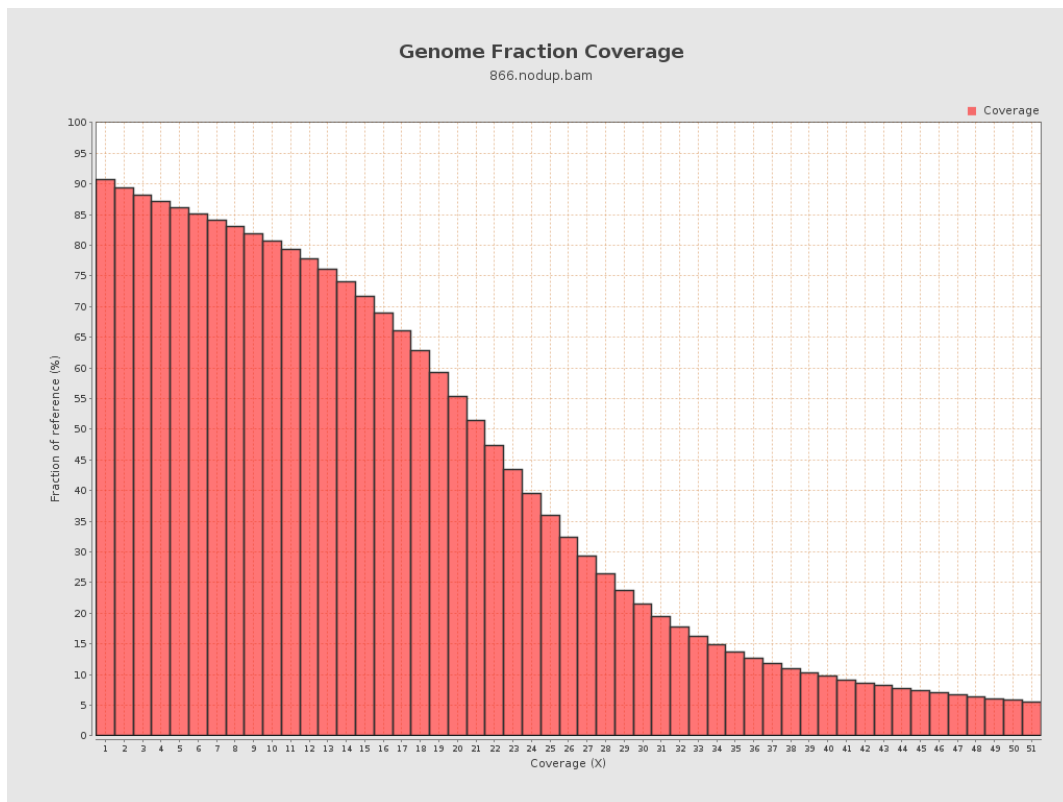
4. Results : Coverage Histogram



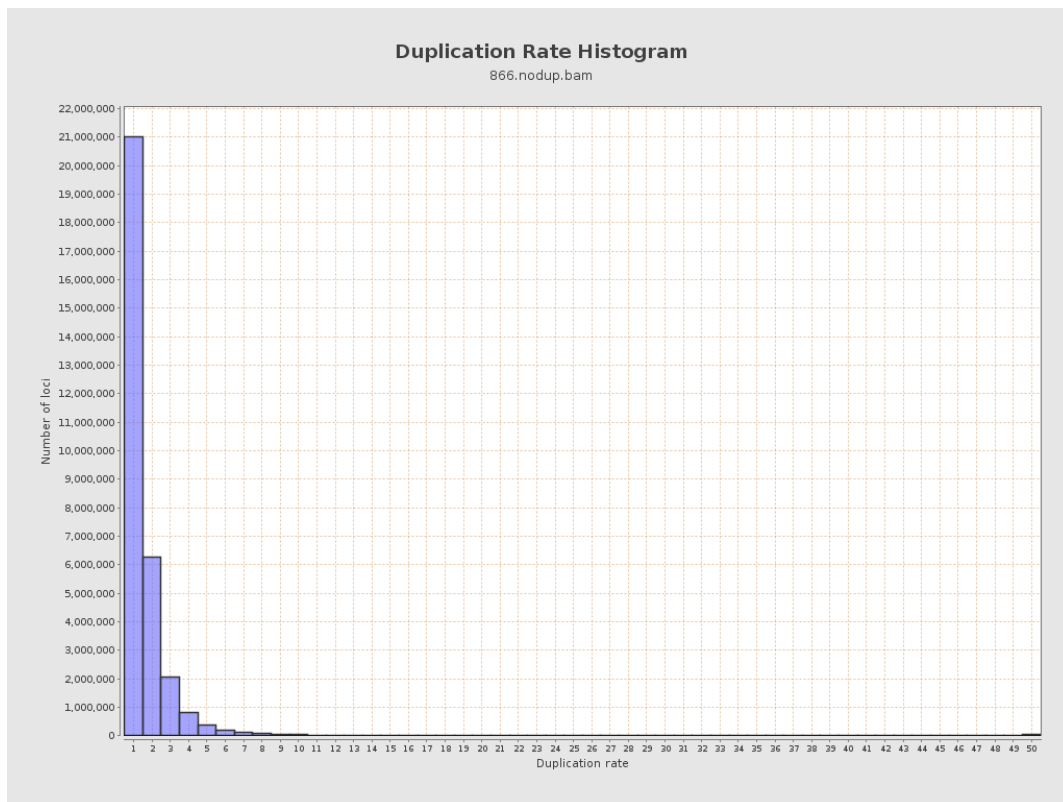
5. Results : Coverage Histogram (0-50X)



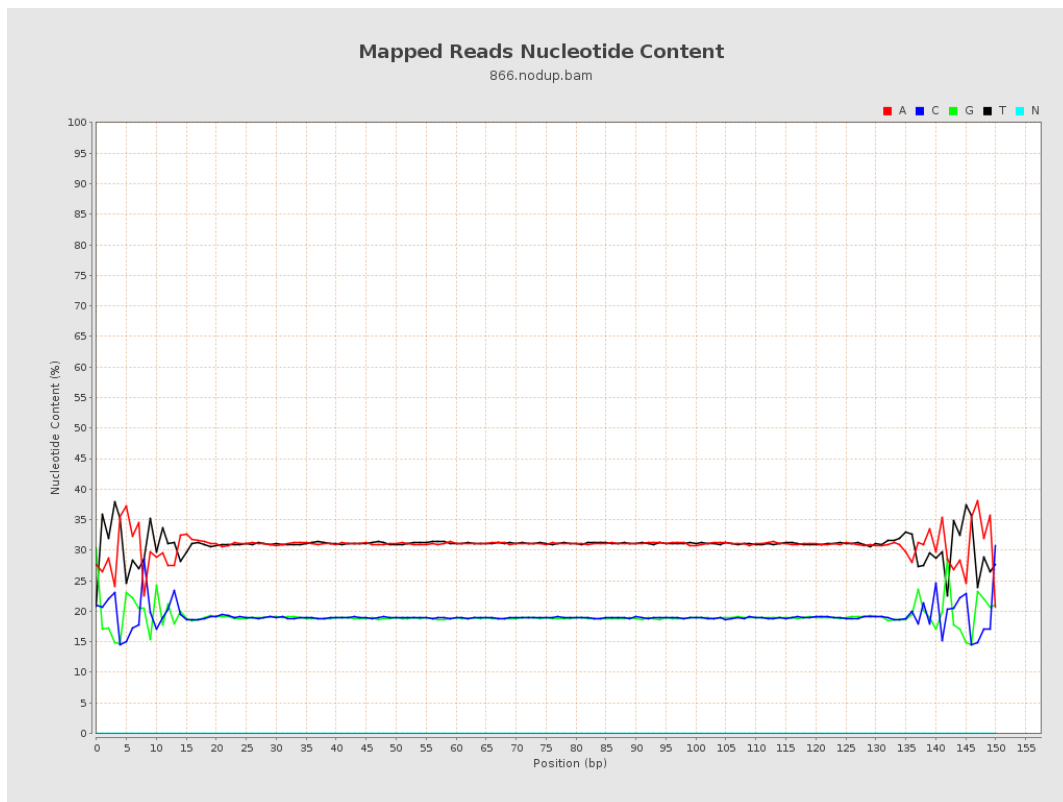
6. Results : Genome Fraction Coverage



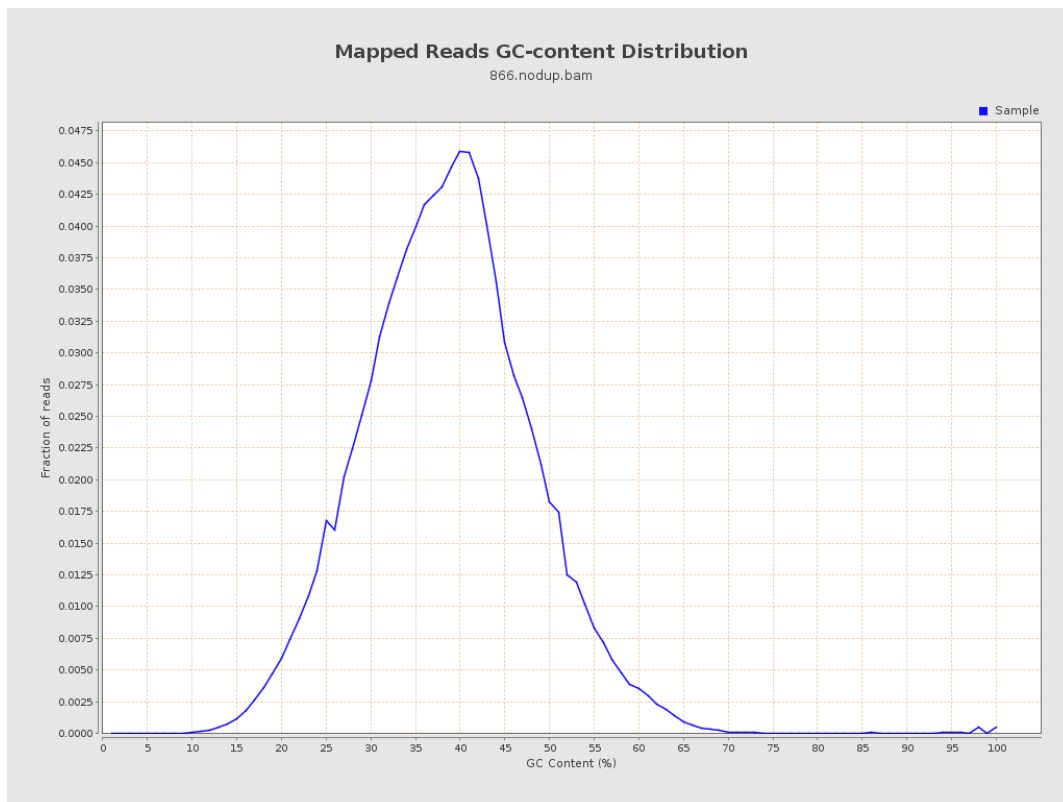
7. Results : Duplication Rate Histogram



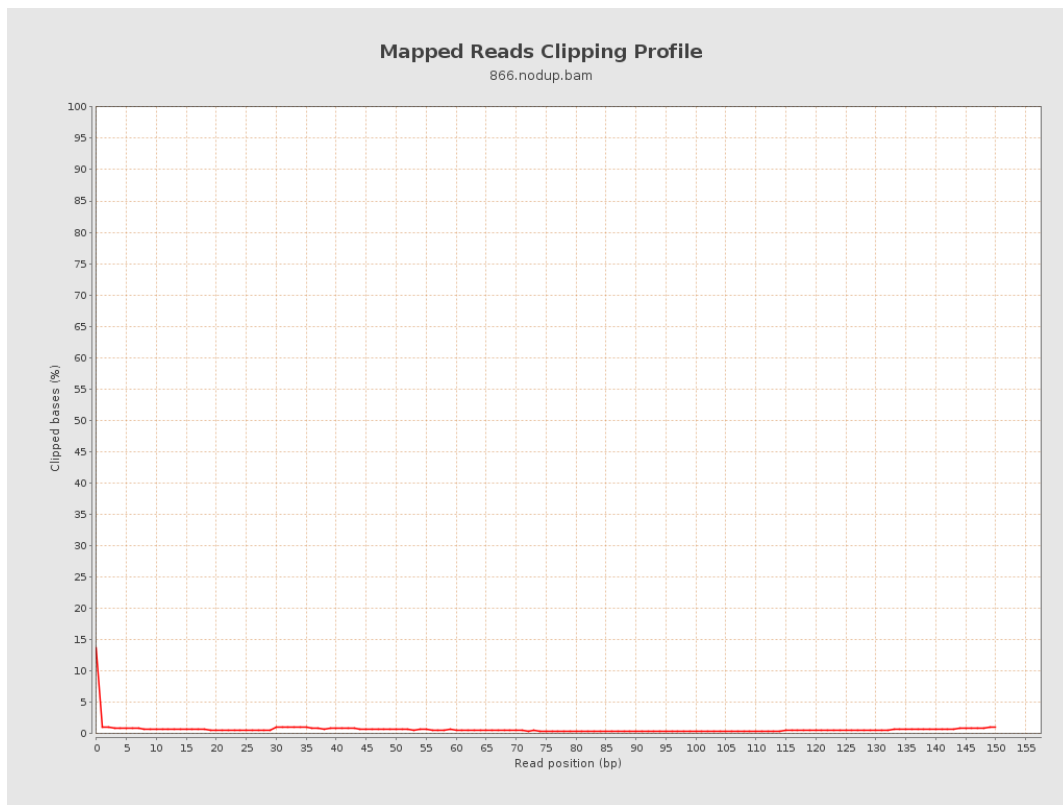
8. Results : Mapped Reads Nucleotide Content



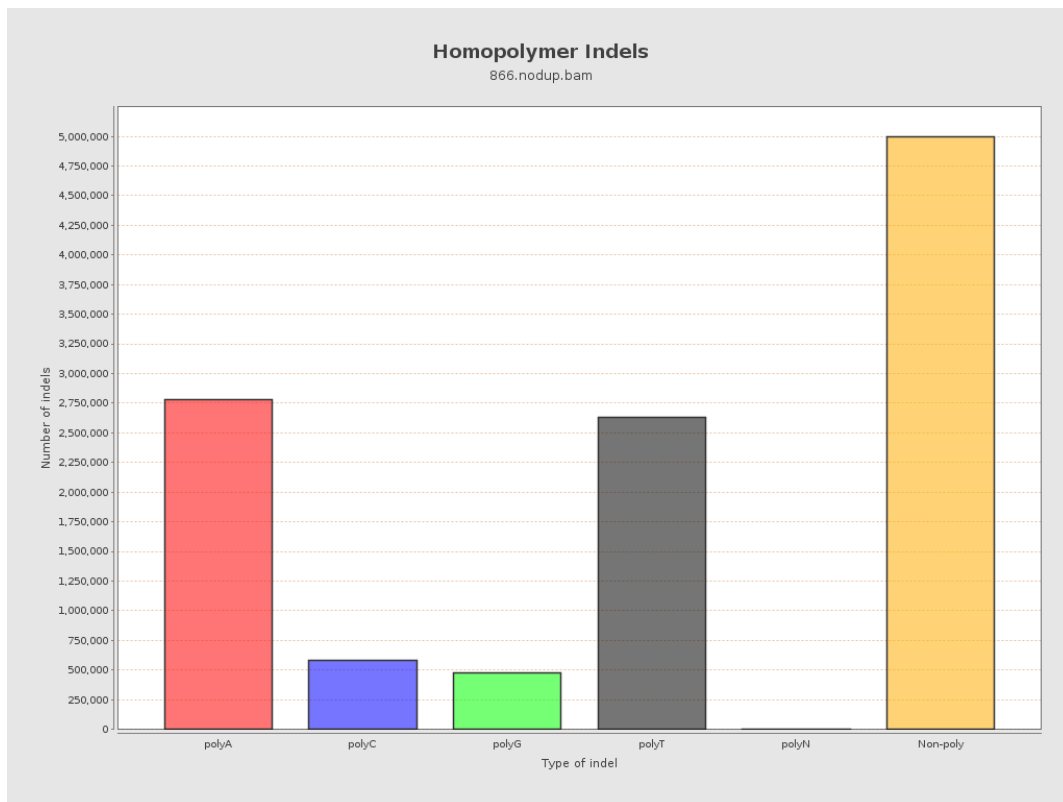
9. Results : Mapped Reads GC-content Distribution



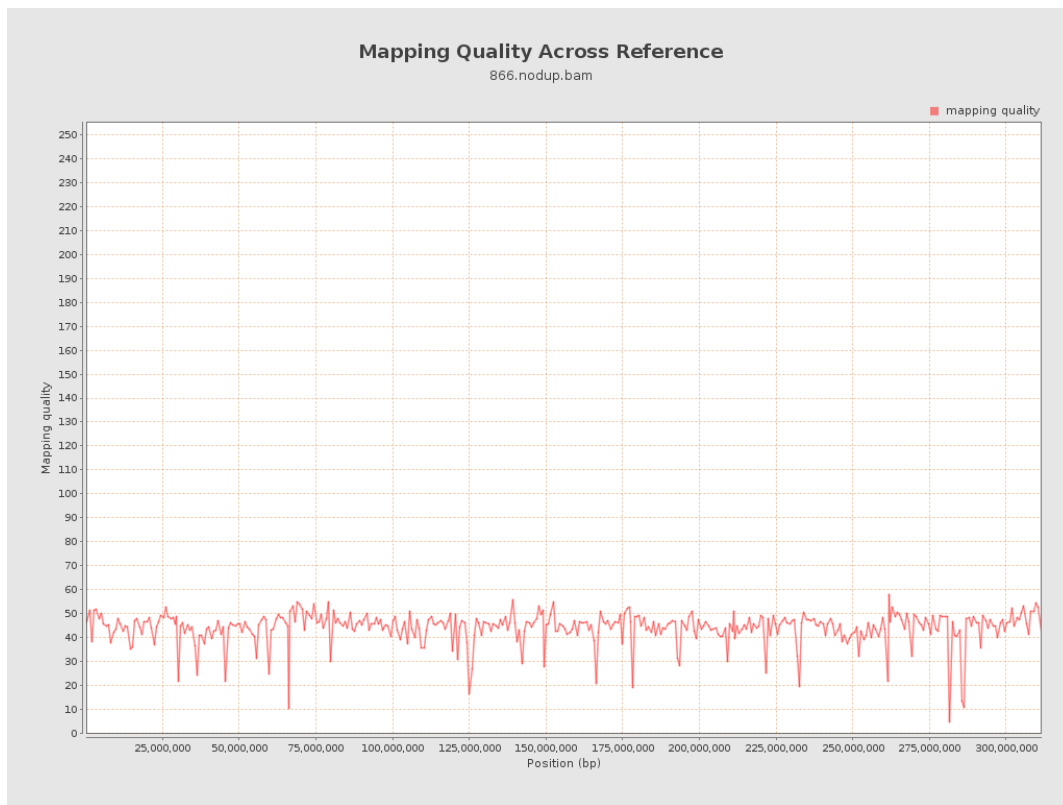
10. Results : Mapped Reads Clipping Profile



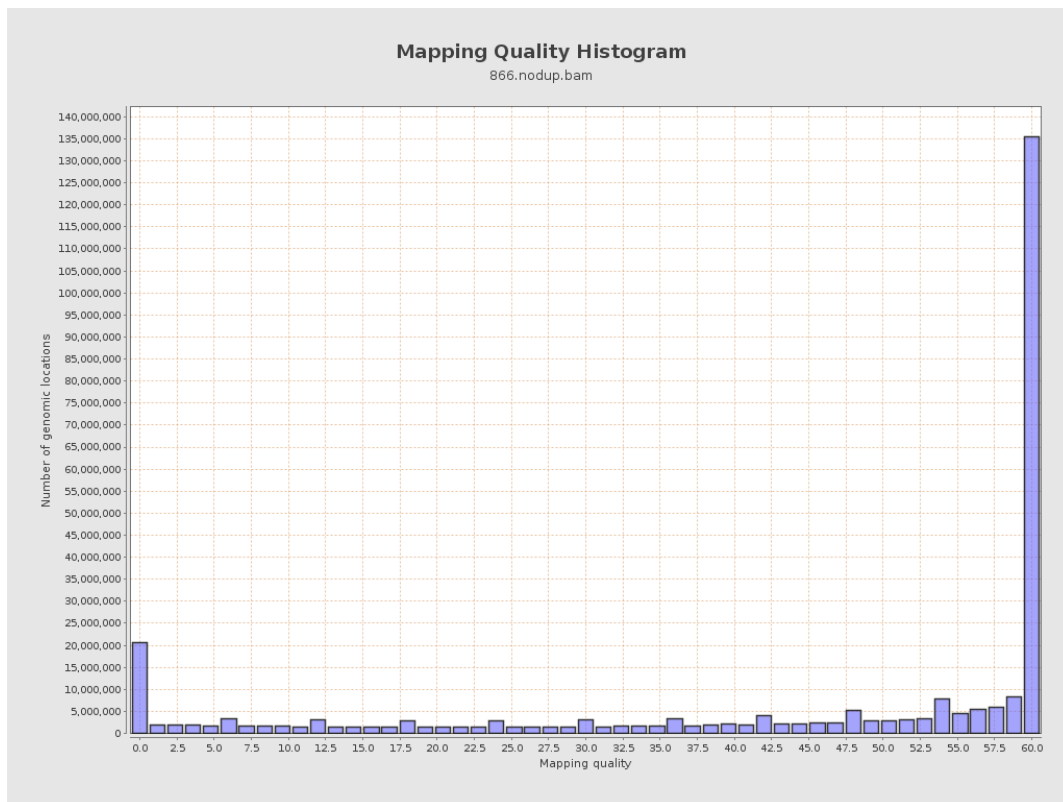
11. Results : Homopolymer Indels



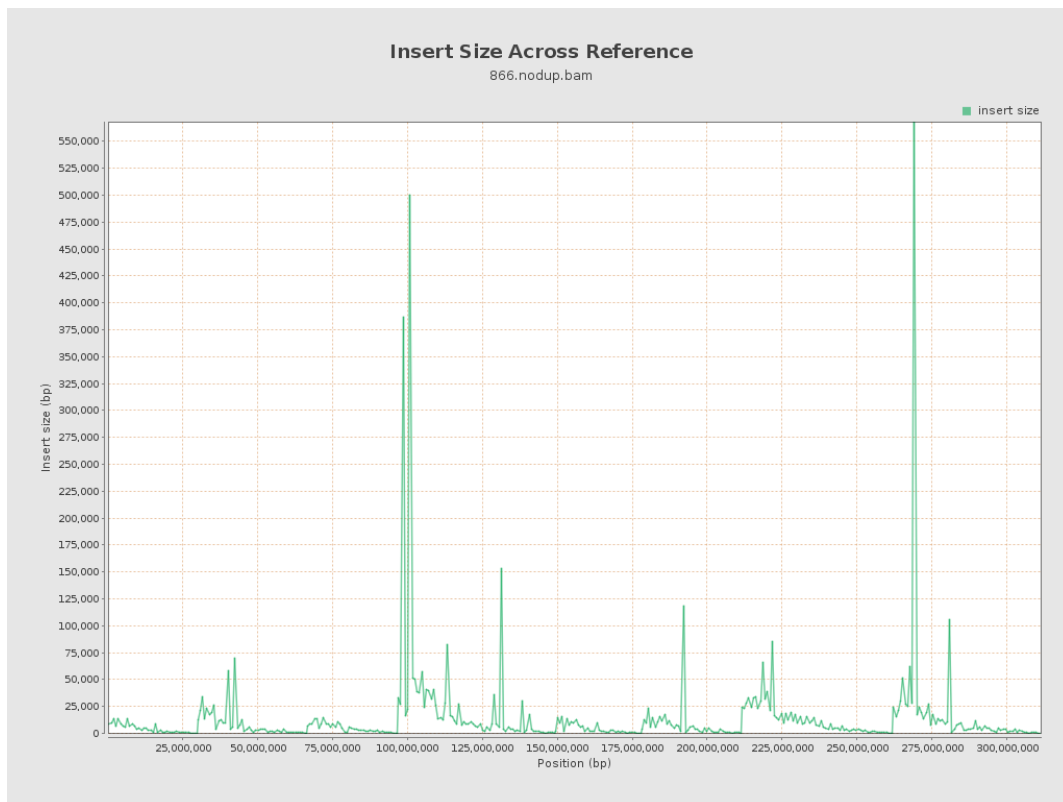
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

