

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:37:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/805
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/805 .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/awdata/P26207/P26207_231/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_231_S312_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_231/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_231_S312_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:37:29 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	80,361,815
Mapped reads	75,972,250 / 94.54%
Unmapped reads	4,389,565 / 5.46%
Mapped paired reads	75,972,250 / 94.54%
Mapped reads, first in pair	38,023,703 / 47.32%
Mapped reads, second in pair	37,948,547 / 47.22%
Mapped reads, both in pair	74,551,673 / 92.77%
Mapped reads, singletons	1,420,577 / 1.77%
Read min/max/mean length	30 / 151 / 148.26
Duplicated reads (flagged)	11,283,301 / 14.04%
Clipped reads	16,429,130 / 20.44%

2.2. ACGT Content

Number/percentage of A's	3,267,025,272 / 30.91%
Number/percentage of C's	2,021,377,894 / 19.12%
Number/percentage of T's	3,268,679,329 / 30.92%
Number/percentage of G's	2,013,491,964 / 19.05%
Number/percentage of N's	37,922 / 0%
GC Percentage	38.17%

2.3. Coverage

Mean	34.0025
Standard Deviation	278.5556

2.4. Mapping Quality

Mean Mapping Quality	44.82
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2.5. Insert size

Mean	204,235.89
Standard Deviation	2,137,923.9
P25/Median/P75	307 / 402 / 524

2.6. Mismatches and indels

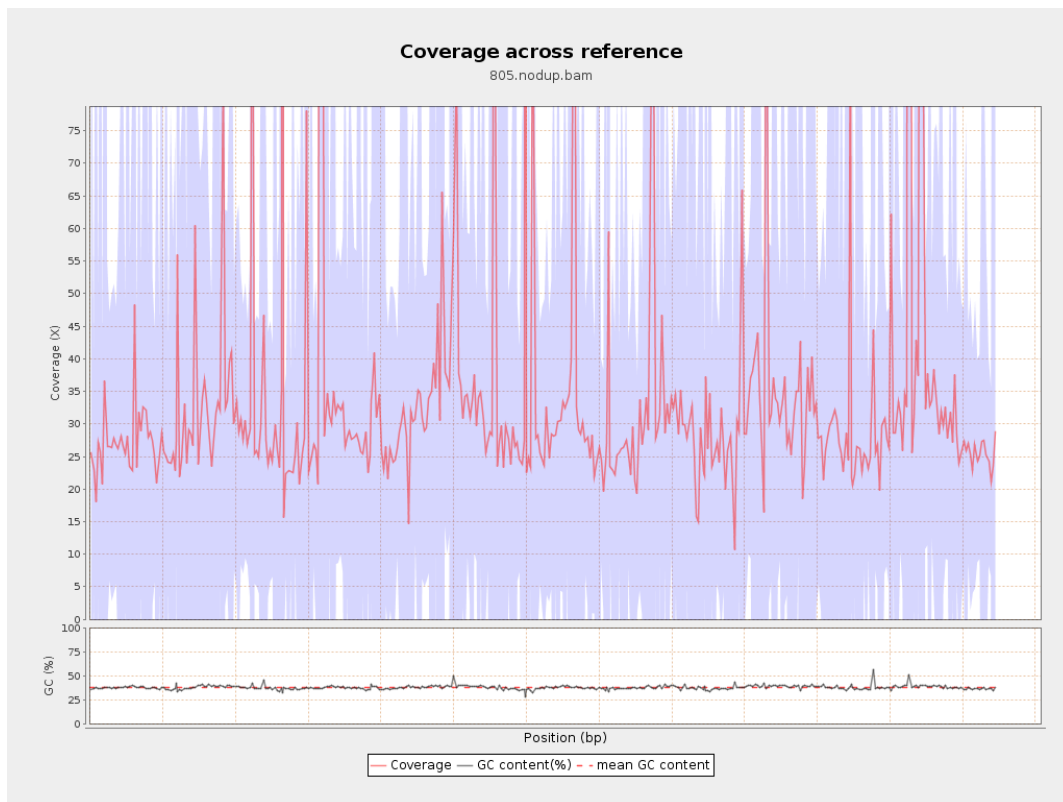
General error rate	2.24%
Mismatches	217,270,934
Insertions	6,920,318
Mapped reads with at least one insertion	8.2%
Deletions	6,971,430
Mapped reads with at least one deletion	8.19%
Homopolymer indels	57.13%

2.7. Chromosome stats

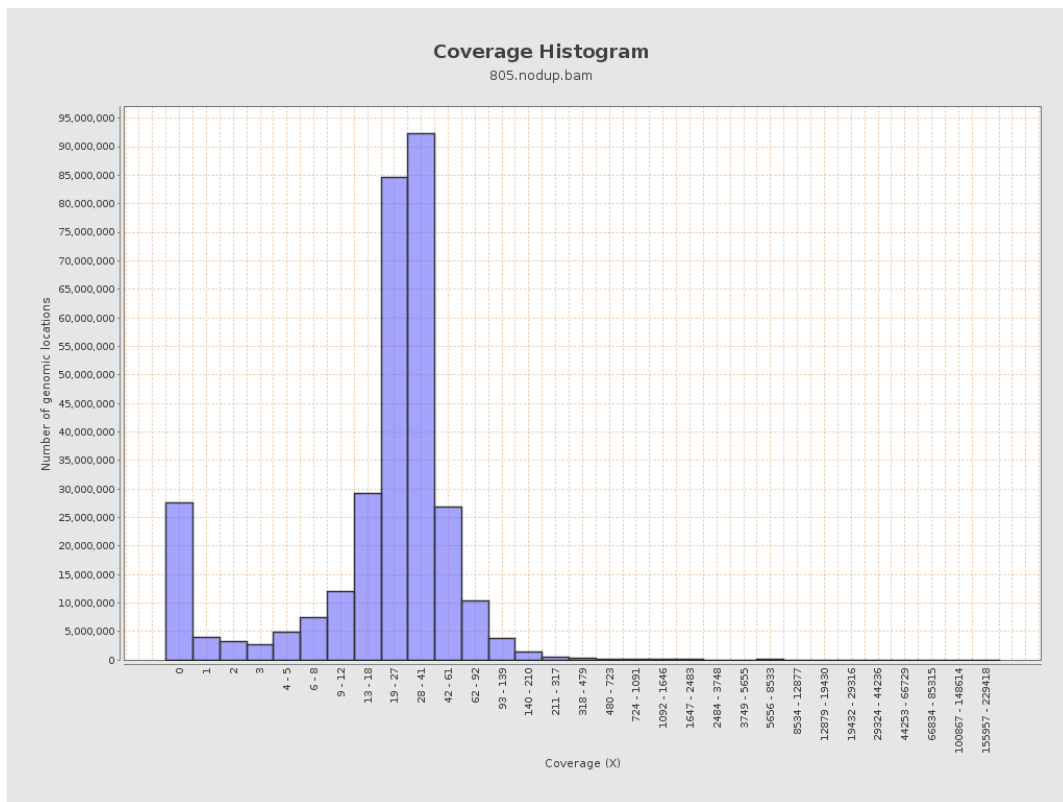
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	798130830	26.8511	72.8464

LT669789.1	36598175	1265727904	34.5845	290.0455
LT669790.1	30422129	1102500945	36.2401	298.2148
LT669791.1	52758100	1785654452	33.8461	226.8259
LT669792.1	28376109	945477977	33.3195	308.4514
LT669793.1	33388210	1048105559	31.3915	199.0658
LT669794.1	50579949	1643735290	32.4978	241.5812
LT669795.1	49795044	2007276962	40.3108	414.275

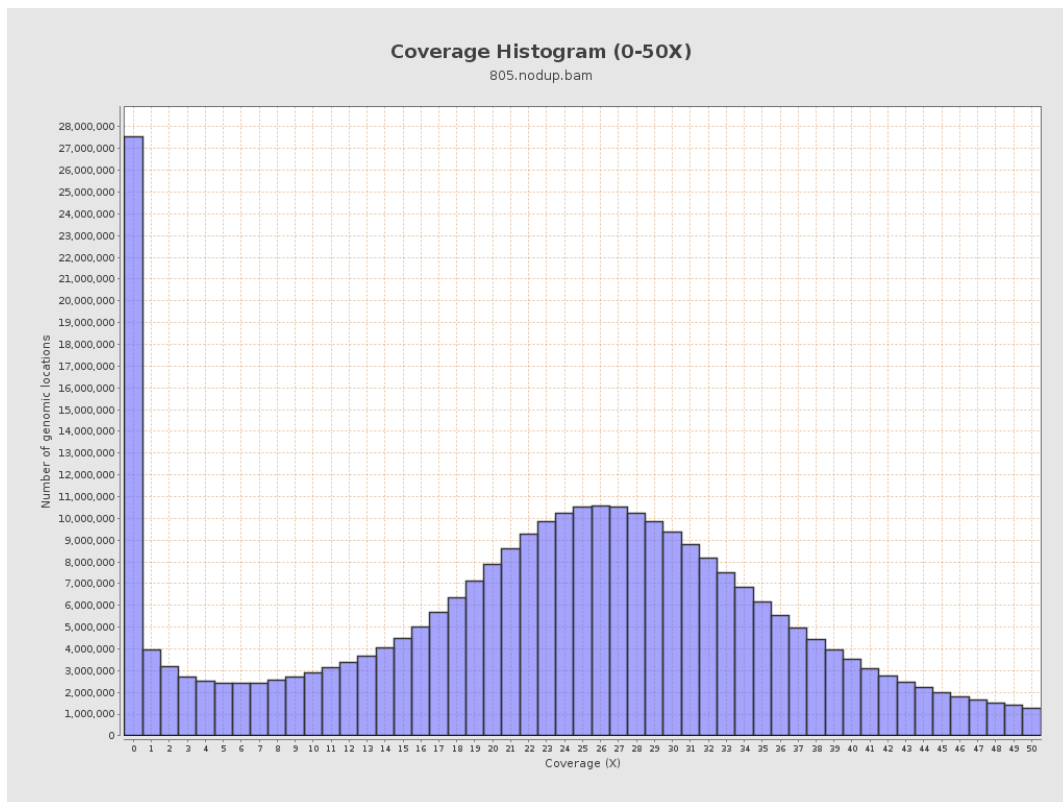
3. Results : Coverage across reference



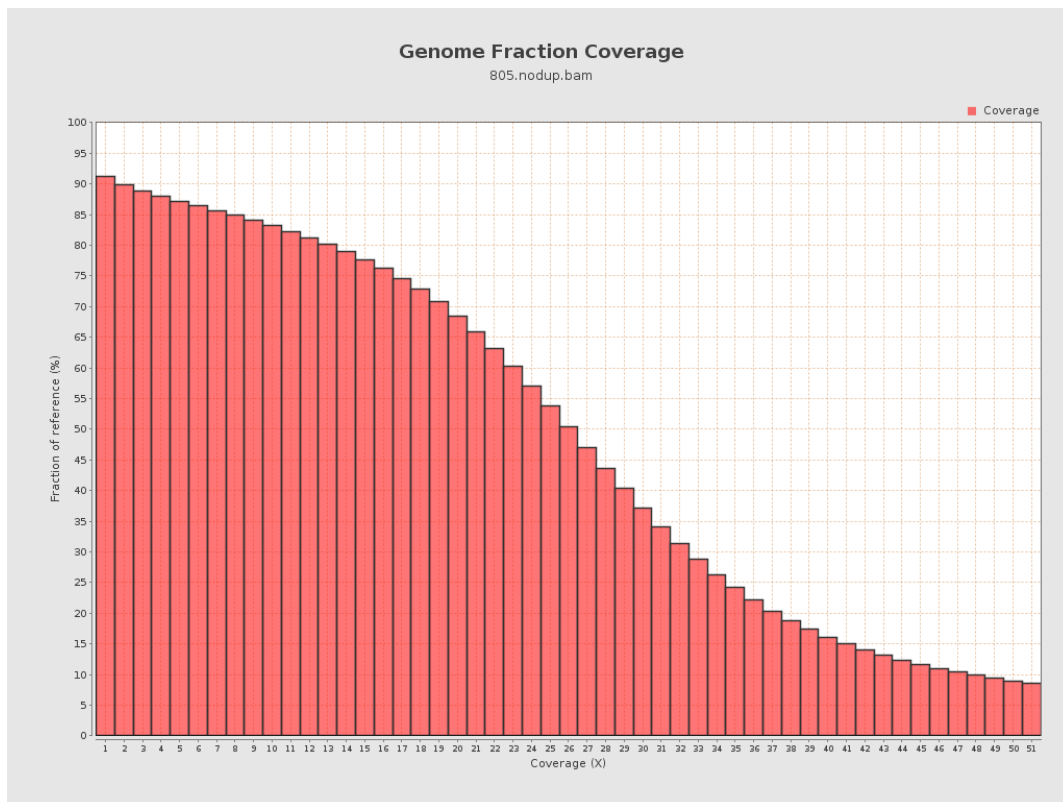
4. Results : Coverage Histogram



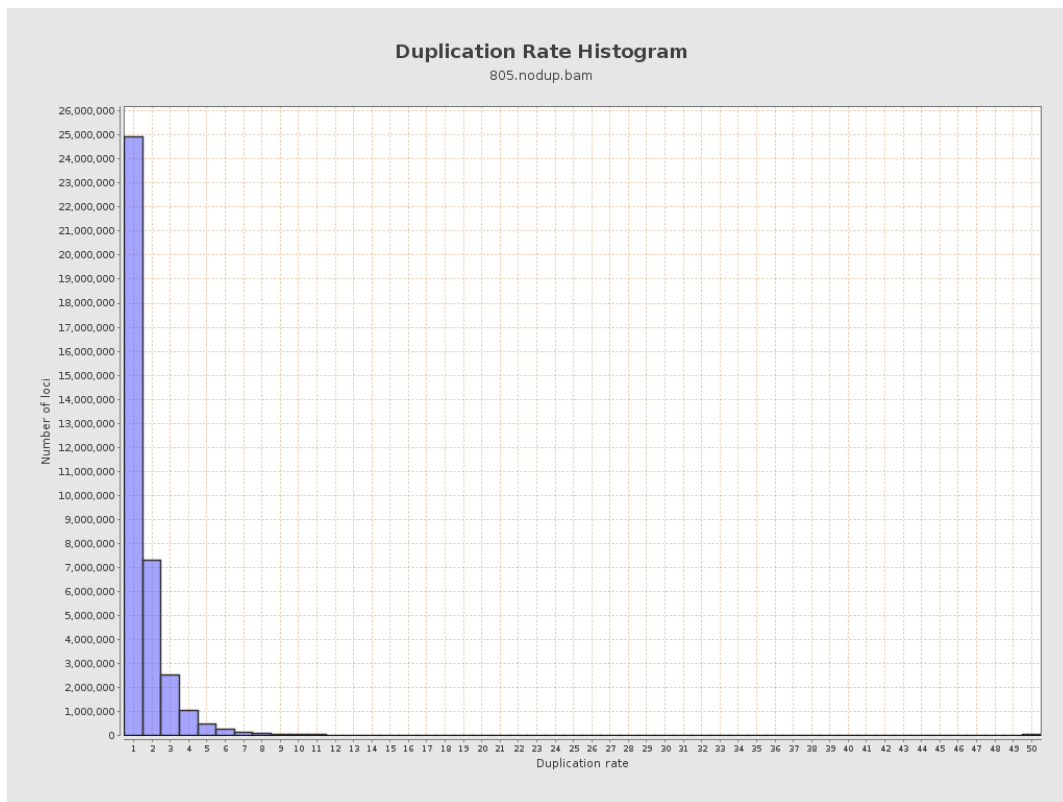
5. Results : Coverage Histogram (0-50X)



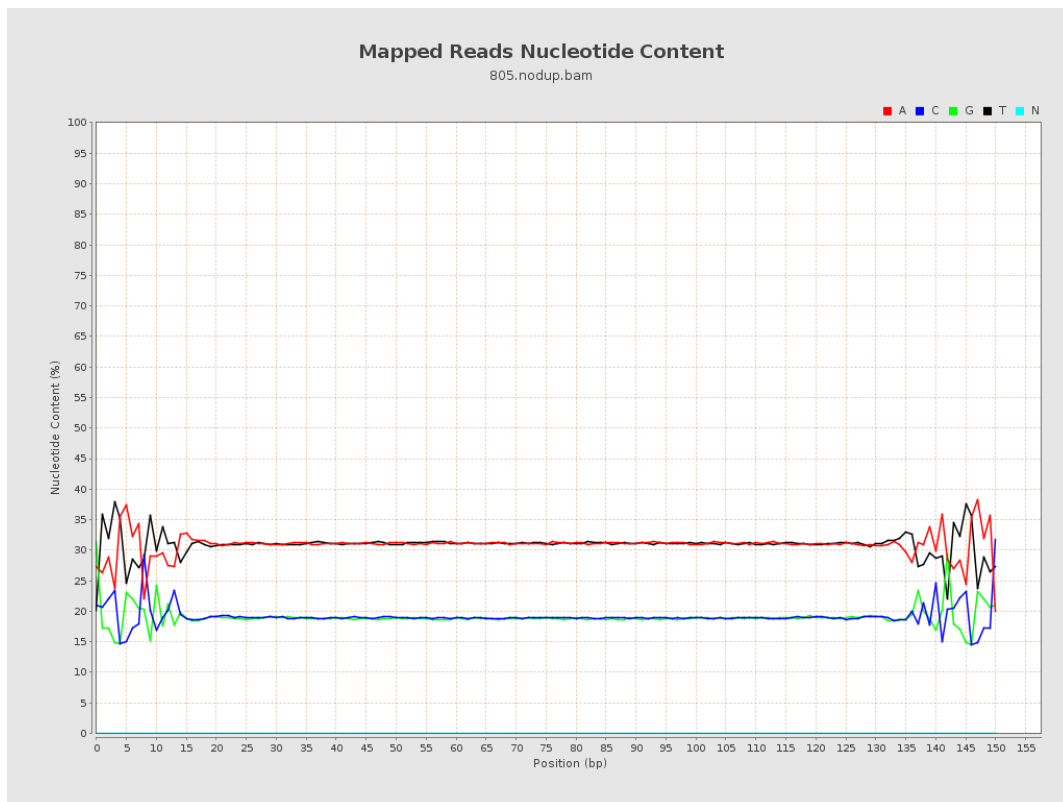
6. Results : Genome Fraction Coverage



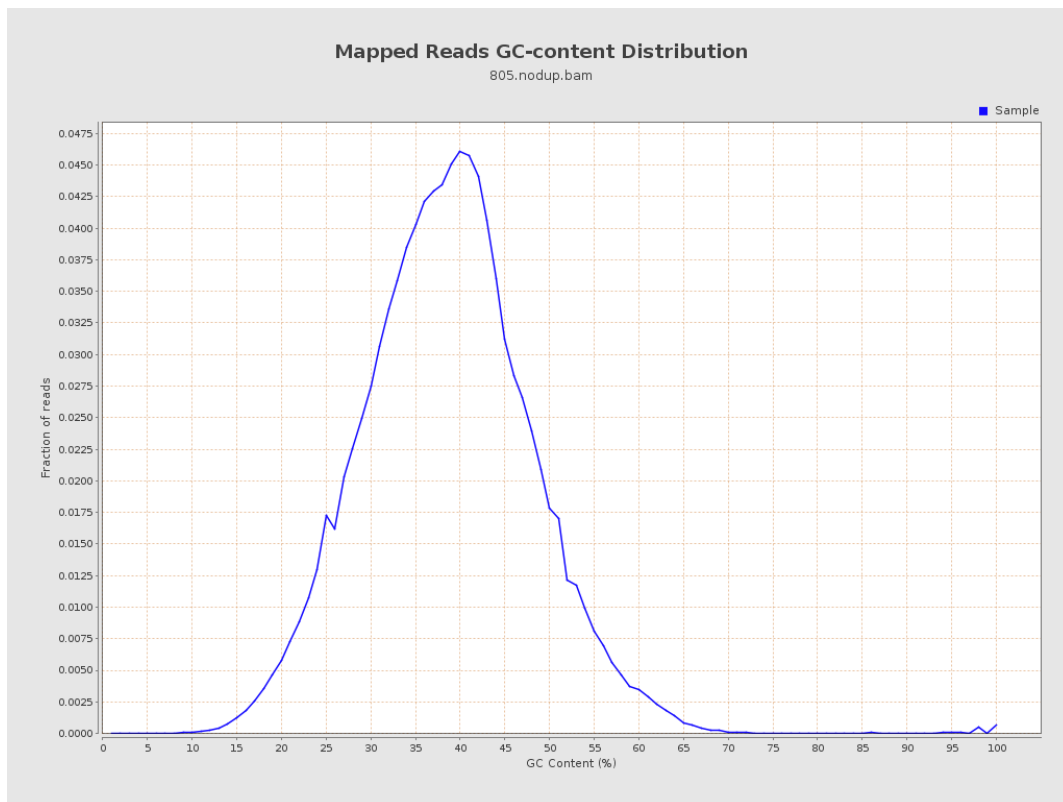
7. Results : Duplication Rate Histogram



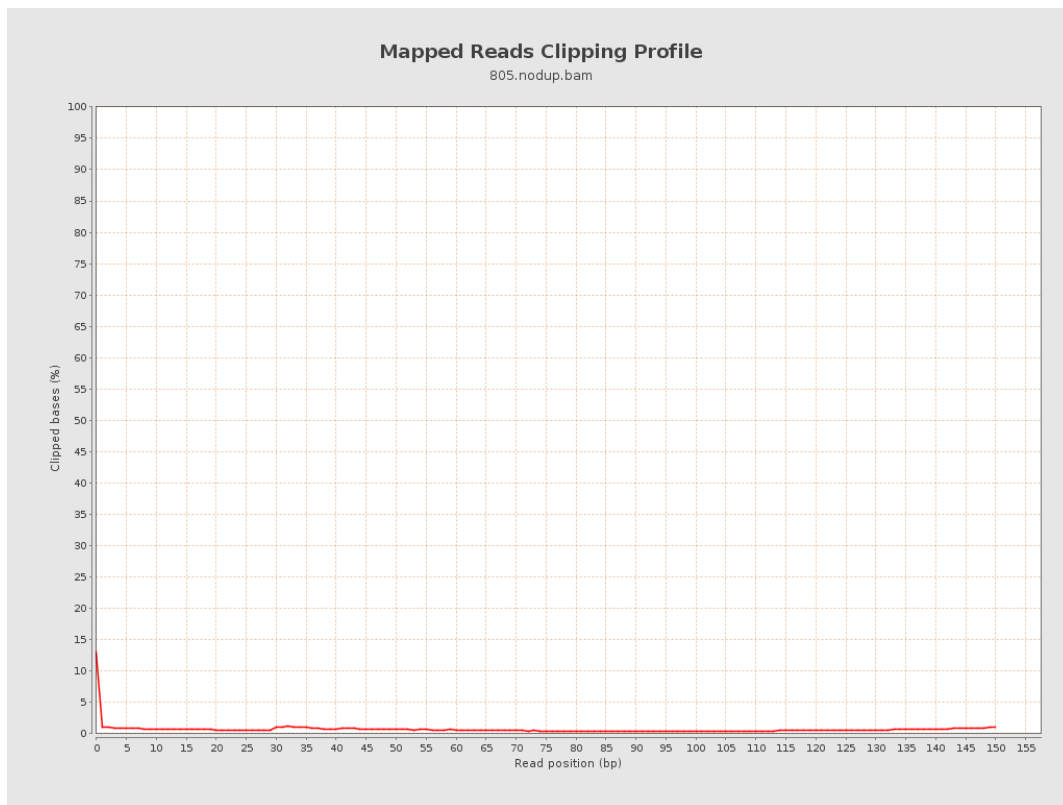
8. Results : Mapped Reads Nucleotide Content



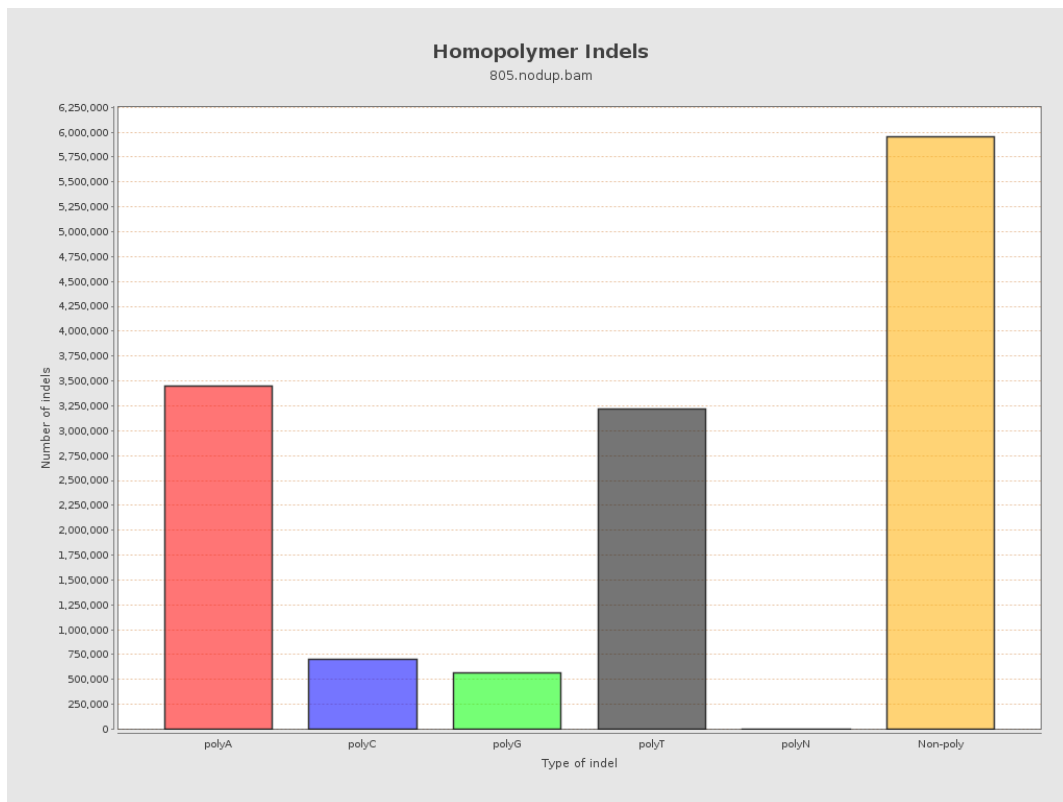
9. Results : Mapped Reads GC-content Distribution



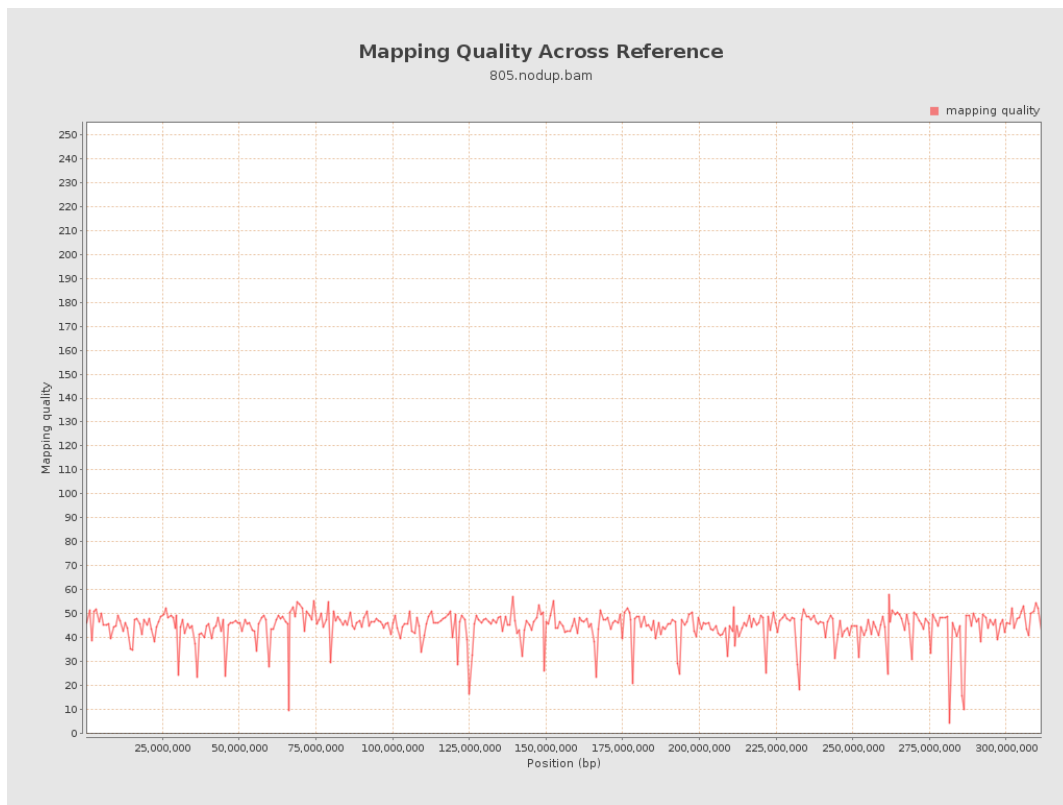
10. Results : Mapped Reads Clipping Profile



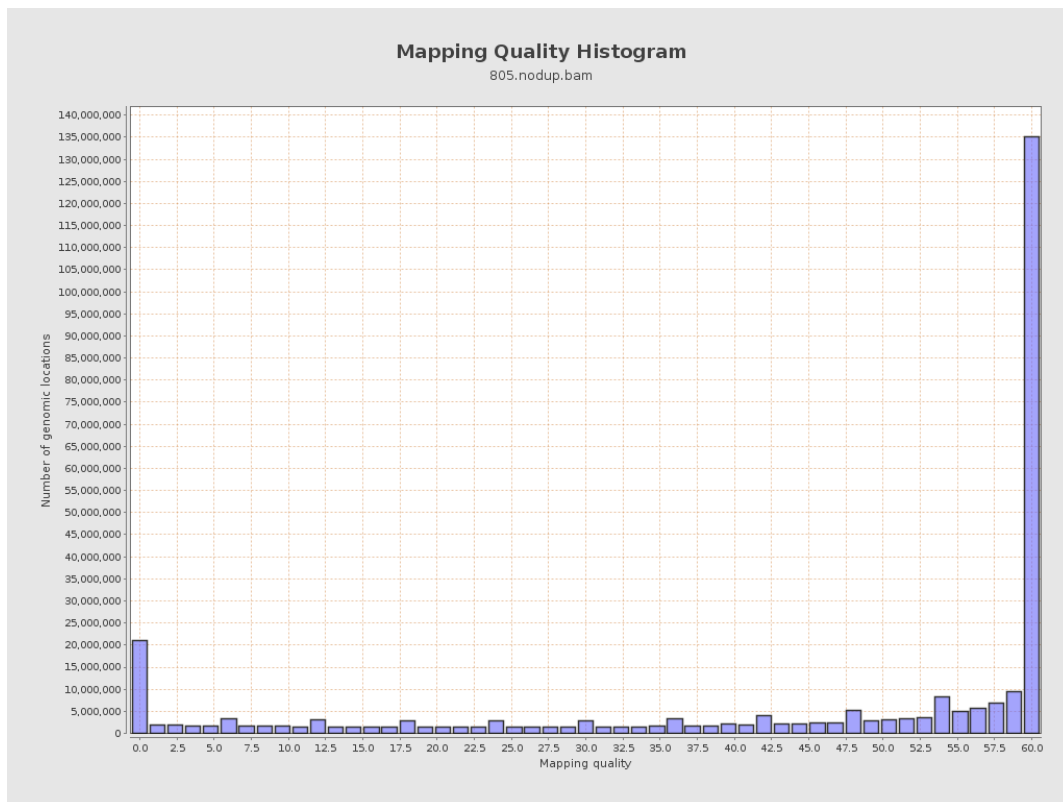
11. Results : Homopolymer Indels



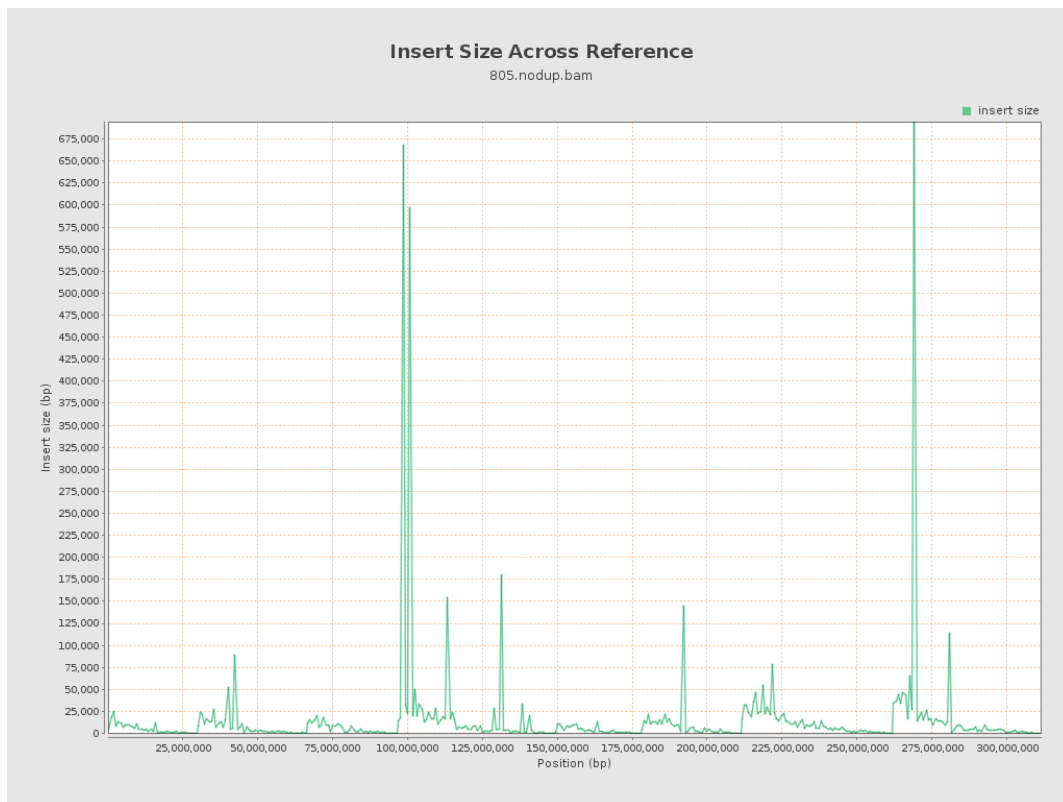
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

