

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/862
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/862 .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_466/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_466_S441_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_466/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_466_S441_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:27:01 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	52,759,397
Mapped reads	49,192,826 / 93.24%
Unmapped reads	3,566,571 / 6.76%
Mapped paired reads	49,192,826 / 93.24%
Mapped reads, first in pair	24,633,142 / 46.69%
Mapped reads, second in pair	24,559,684 / 46.55%
Mapped reads, both in pair	48,026,726 / 91.03%
Mapped reads, singletons	1,166,100 / 2.21%
Read min/max/mean length	30 / 151 / 148.29
Duplicated reads (flagged)	7,281,614 / 13.8%
Clipped reads	10,560,116 / 20.02%

2.2. ACGT Content

Number/percentage of A's	2,114,149,369 / 30.88%
Number/percentage of C's	1,309,267,642 / 19.12%
Number/percentage of T's	2,117,739,489 / 30.93%
Number/percentage of G's	1,305,140,315 / 19.06%
Number/percentage of N's	22,603 / 0%
GC Percentage	38.19%

2.3. Coverage

Mean	22.0242
Standard Deviation	170.0306

2.4. Mapping Quality

Mean Mapping Quality	44.63
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2.5. Insert size

Mean	244,027.12
Standard Deviation	2,373,505.09
P25/Median/P75	360 / 468 / 607

2.6. Mismatches and indels

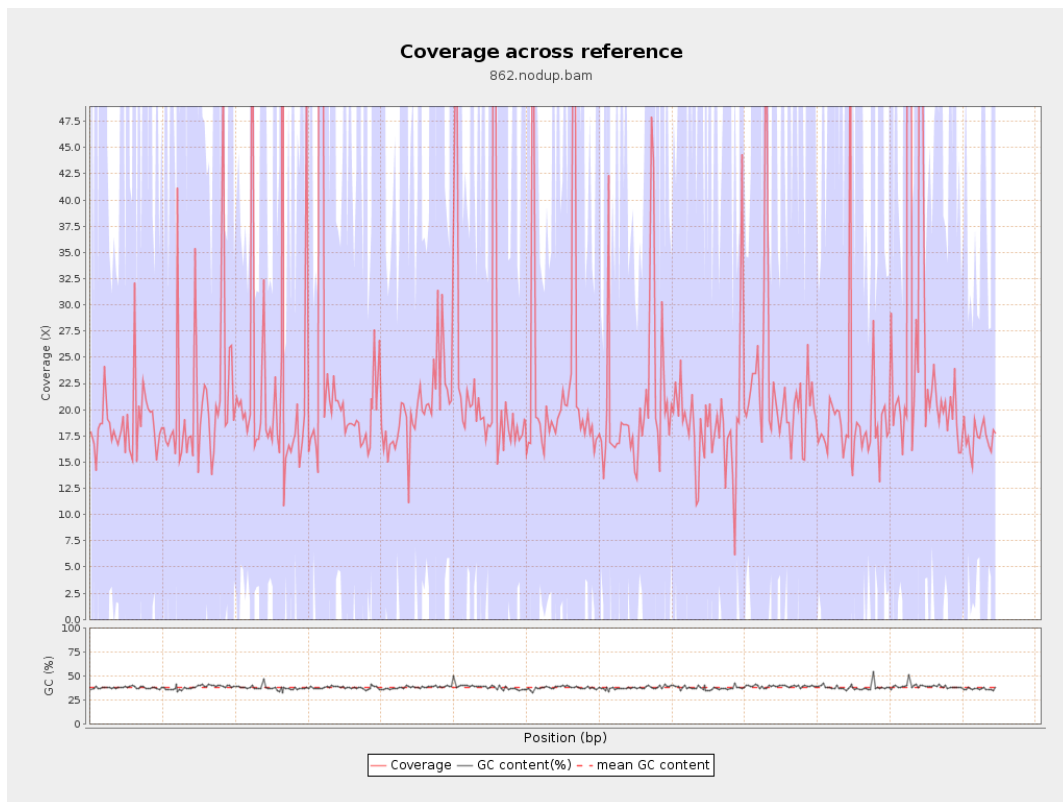
General error rate	2.3%
Mismatches	144,602,260
Insertions	4,617,895
Mapped reads with at least one insertion	8.42%
Deletions	4,610,006
Mapped reads with at least one deletion	8.33%
Homopolymer indels	56.75%

2.7. Chromosome stats

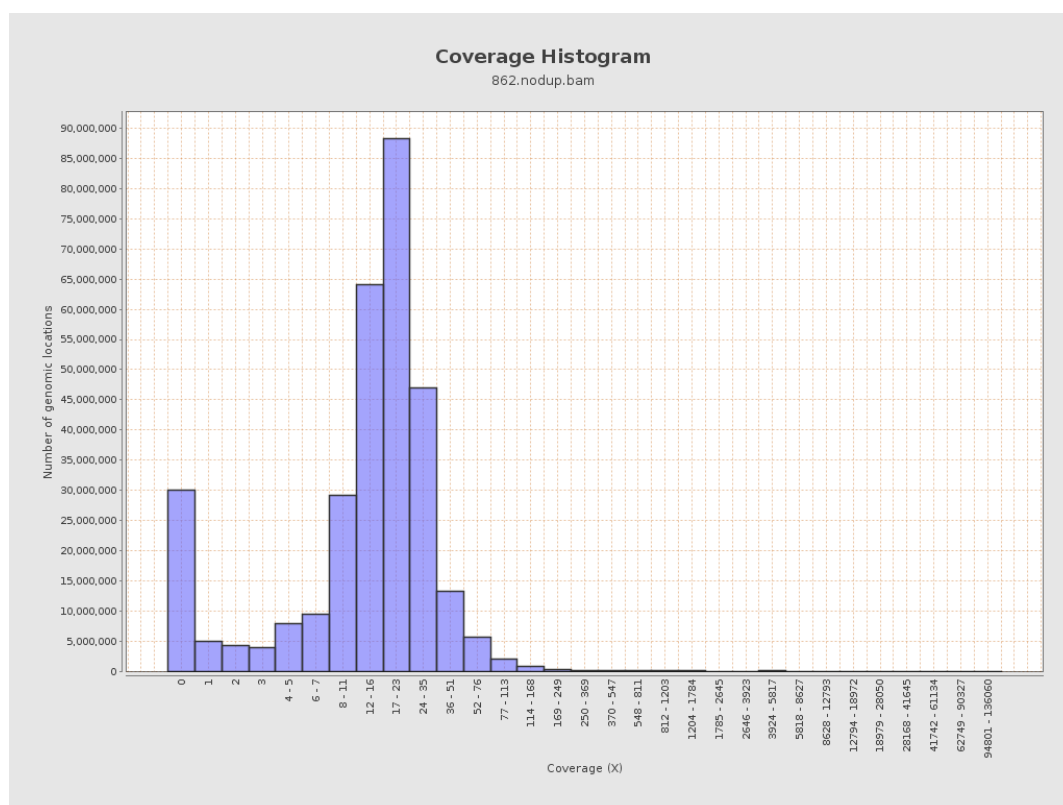
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	548220612	18.4435	57.4497

LT669789.1	36598175	808555617	22.0928	188.1602
LT669790.1	30422129	738735584	24.2828	197.8378
LT669791.1	52758100	1145854022	21.719	161.7181
LT669792.1	28376109	615754835	21.6998	192.7554
LT669793.1	33388210	668586653	20.0246	89.8021
LT669794.1	50579949	1061074456	20.9782	149.3497
LT669795.1	49795044	1276870917	25.6425	228.1626

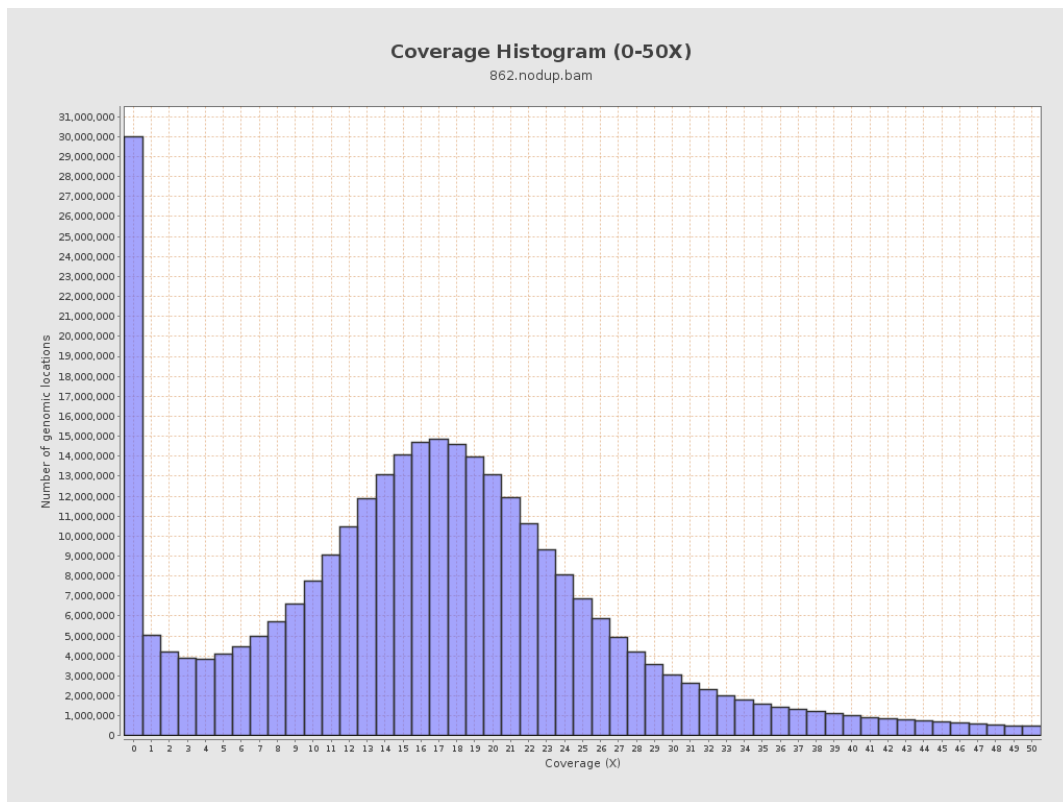
3. Results : Coverage across reference



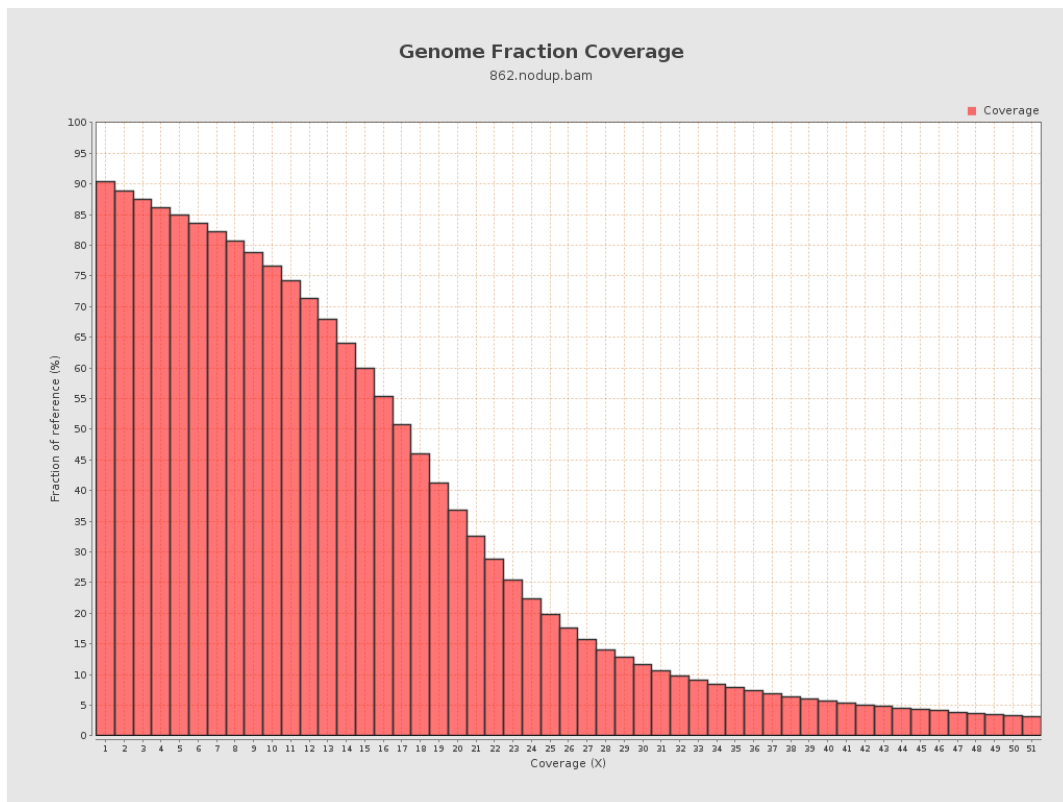
4. Results : Coverage Histogram



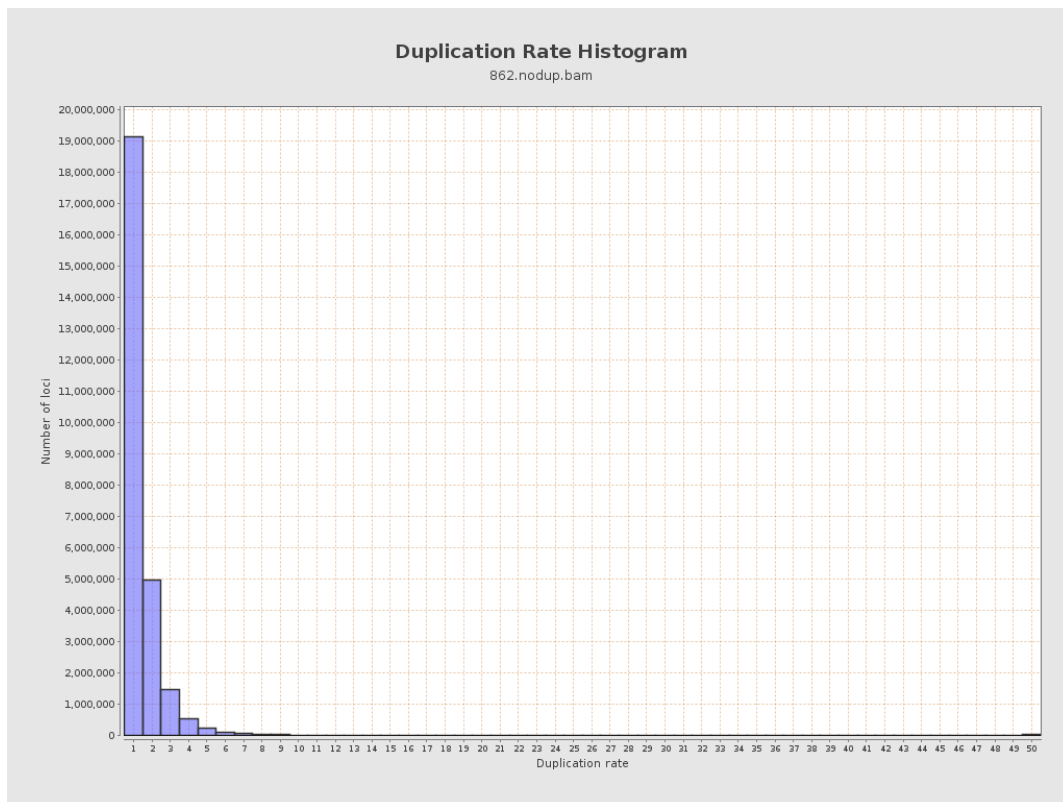
5. Results : Coverage Histogram (0-50X)



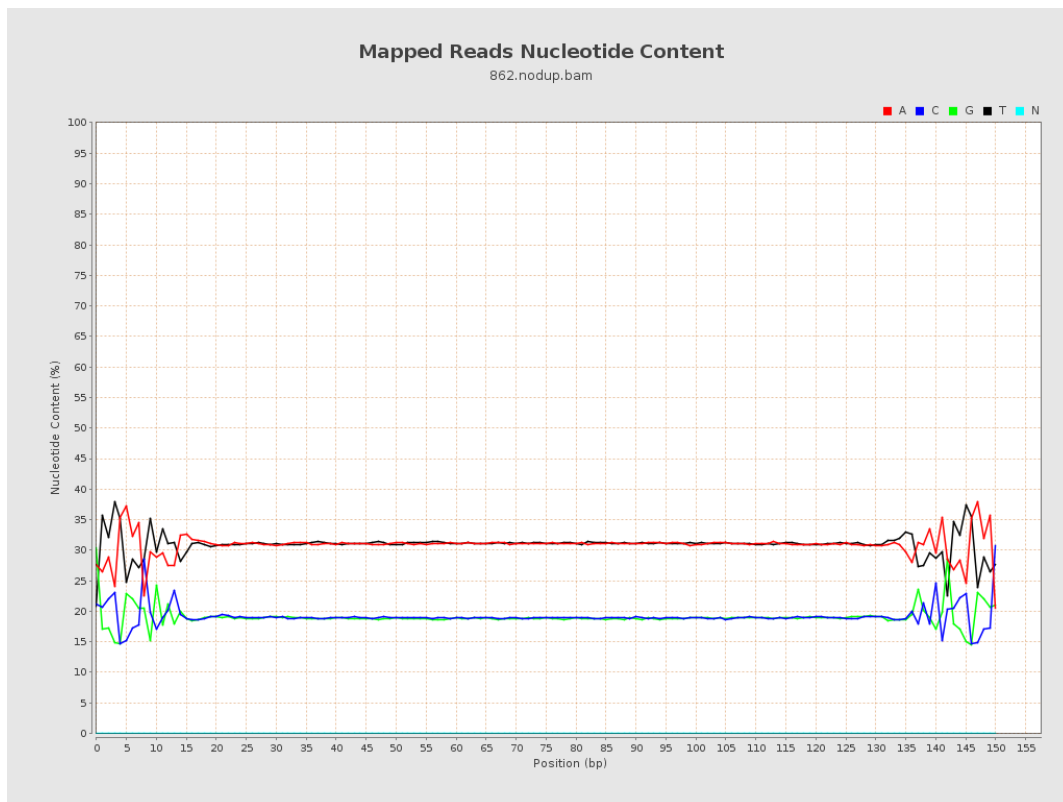
6. Results : Genome Fraction Coverage



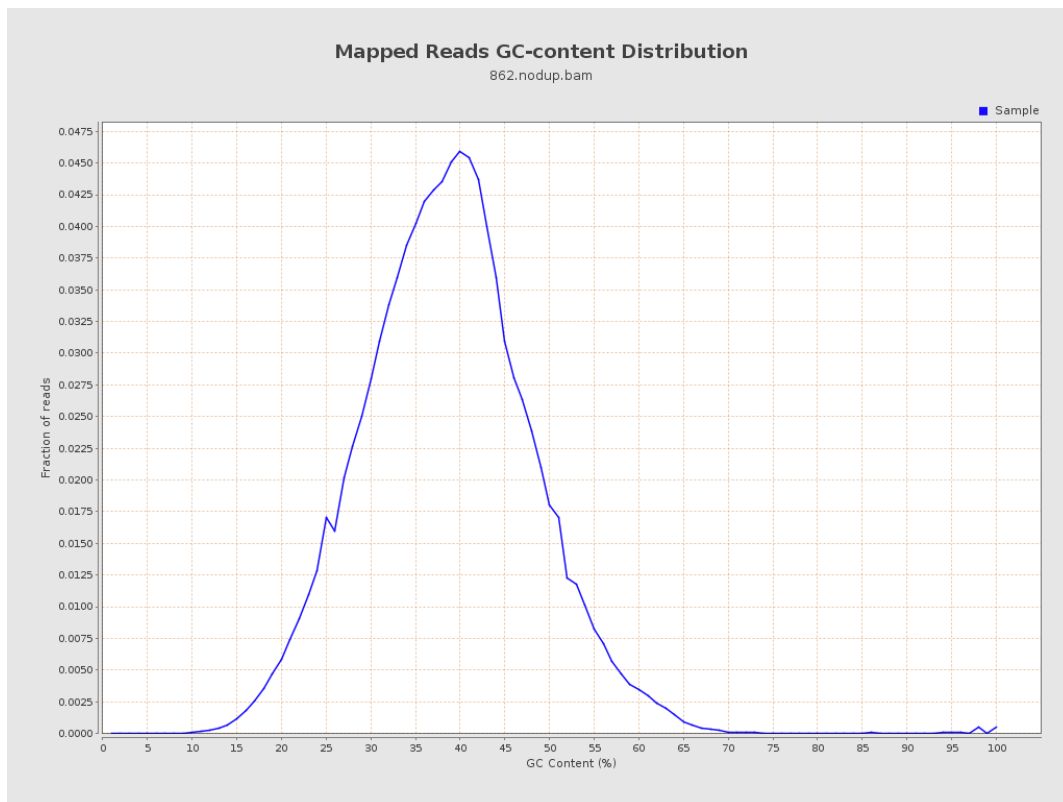
7. Results : Duplication Rate Histogram



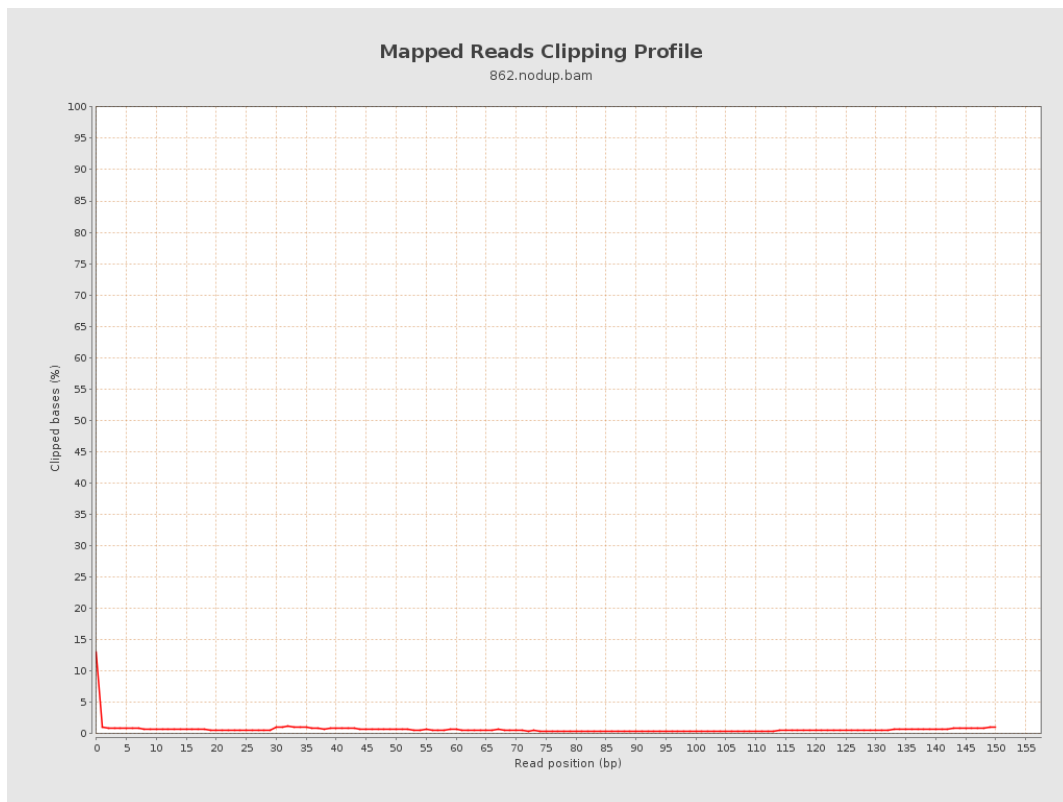
8. Results : Mapped Reads Nucleotide Content



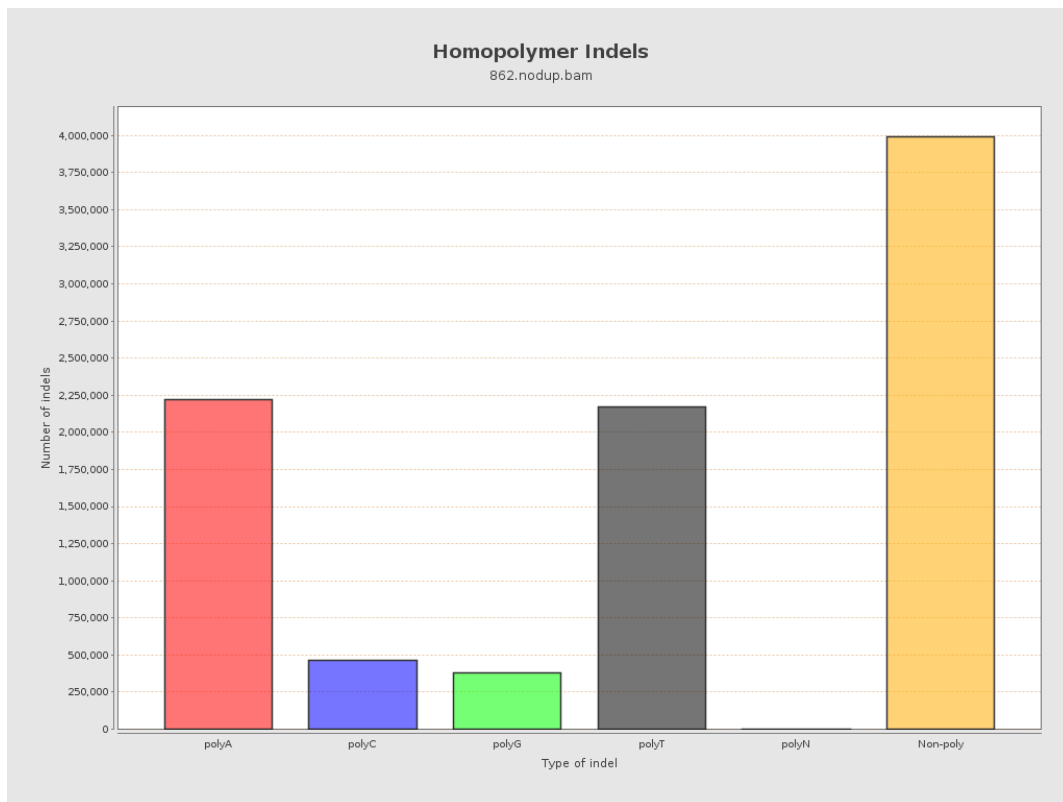
9. Results : Mapped Reads GC-content Distribution



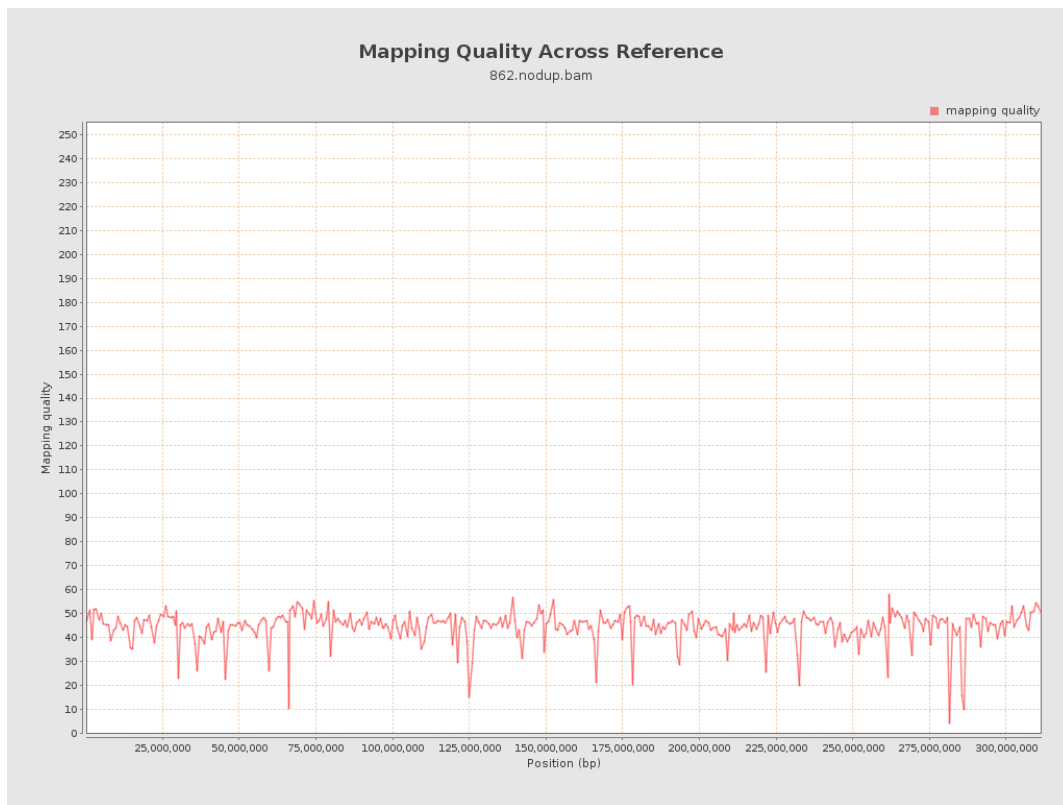
10. Results : Mapped Reads Clipping Profile



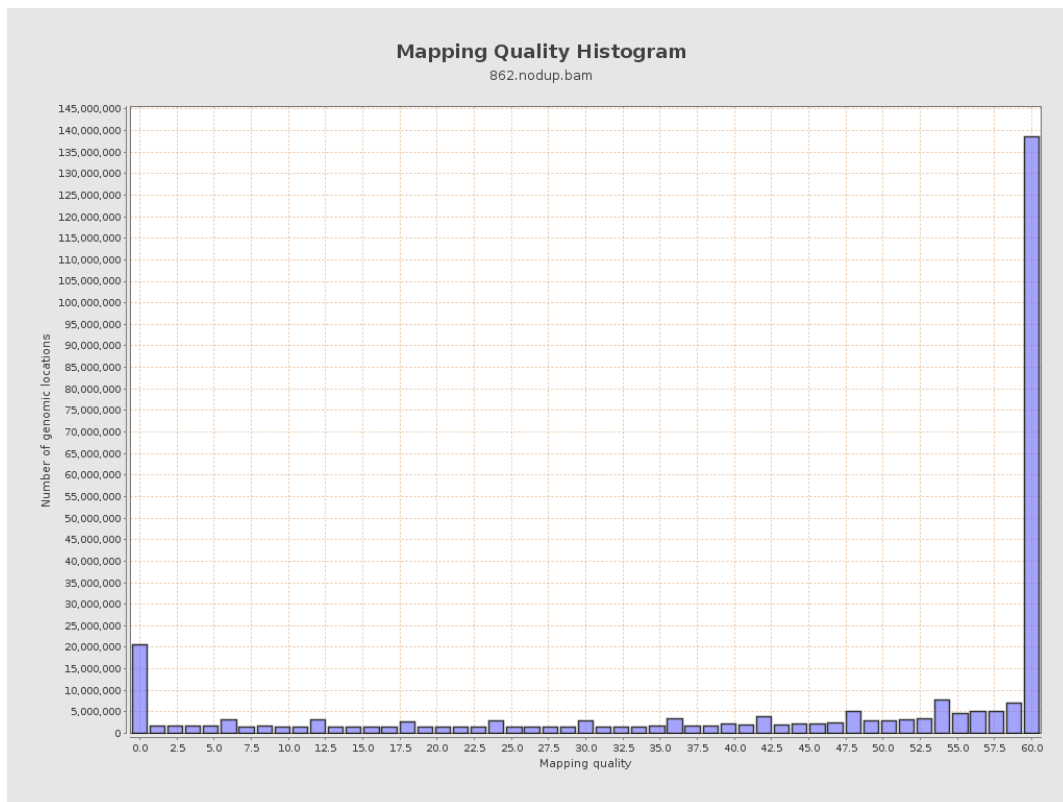
11. Results : Homopolymer Indels



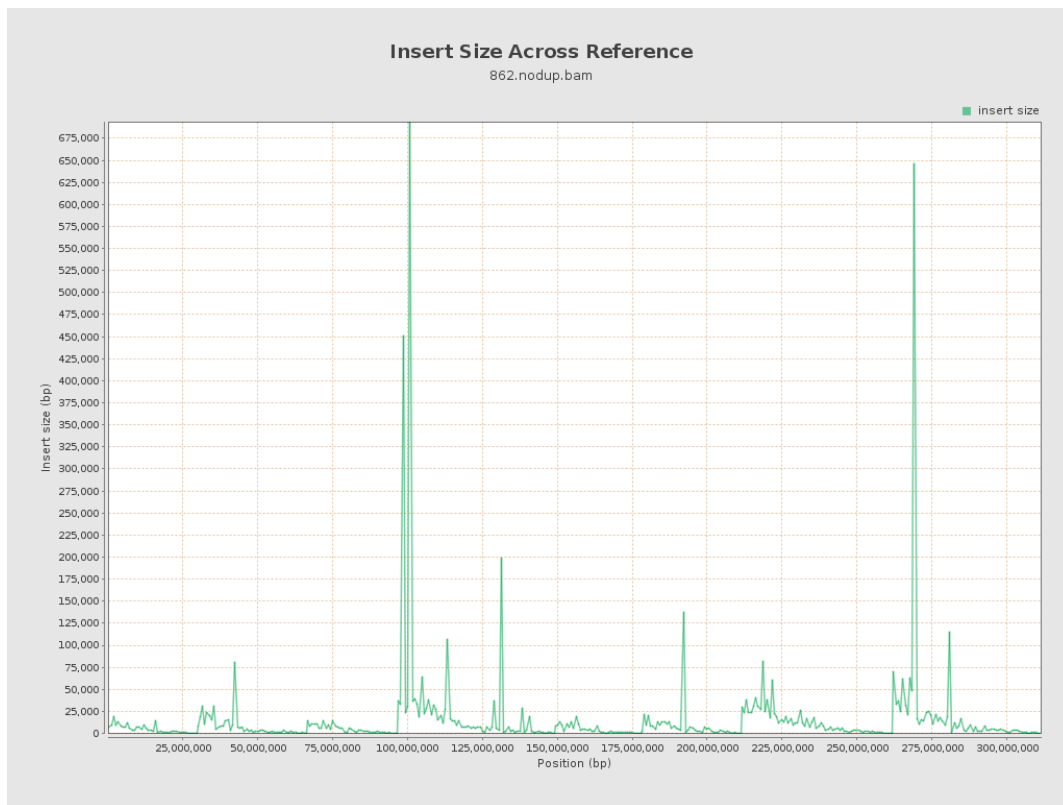
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

