

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 11:07:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618652.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR618652 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618652.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 11:07:38 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618652.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	54,769,551
Mapped reads	53,102,546 / 96.96%
Unmapped reads	1,667,005 / 3.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	120,905 / 0.22%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	23,983,634 / 43.79%
Duplication rate	33.72%
Clipped reads	4,518,419 / 8.25%

2.2. ACGT Content

Number/percentage of A's	1,355,119,443 / 26.04%
Number/percentage of C's	1,239,558,514 / 23.82%
Number/percentage of T's	1,388,389,872 / 26.68%
Number/percentage of G's	1,219,562,540 / 23.44%
Number/percentage of N's	904,717 / 0.02%
GC Percentage	47.26%

2.3. Coverage

Mean	1.6823

Standard Deviation	34.7484
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2.4. Mapping Quality

Mean Mapping Quality	49.92
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2.5. Mismatches and indels

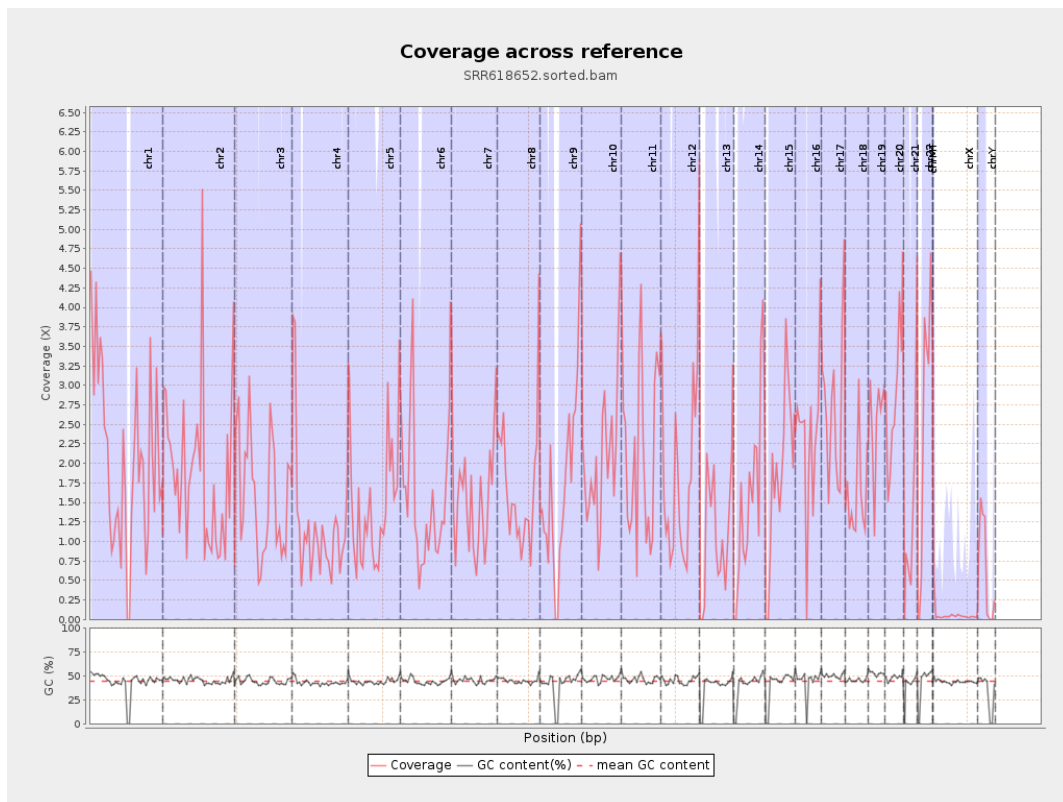
General error rate	0.89%
Mismatches	44,504,462
Insertions	859,003
Mapped reads with at least one insertion	1.59%
Deletions	2,289,005
Mapped reads with at least one deletion	4.22%
Homopolymer indels	51.2%

2.6. Chromosome stats

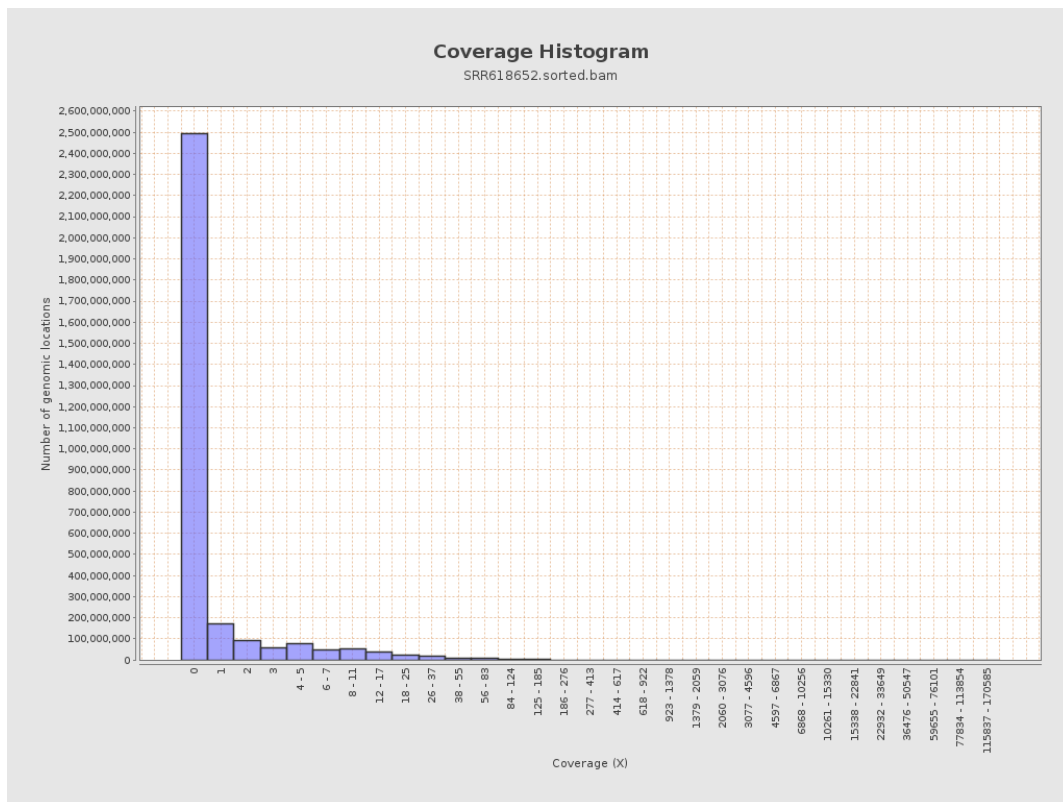
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	506092625	2.0305	20.9294
chr2	243199373	455714998	1.8738	106.3441
chr3	198022430	311300910	1.572	14.8036
chr4	191154276	227080309	1.1879	15.0404
chr5	180915260	272866407	1.5083	12.8763
chr6	171115067	264707099	1.547	14.6697
chr7	159138663	252885603	1.5891	19.7446

chr8	146364022	243945613	1.6667	16.8501
chr9	141213431	246664464	1.7467	23.3374
chr10	135534747	279153558	2.0596	22.6087
chr11	135006516	290451766	2.1514	26.1696
chr12	133851895	246411084	1.8409	21.4779
chr13	115169878	127503552	1.1071	13.9934
chr14	107349540	169512806	1.5791	17.7732
chr15	102531392	190537365	1.8583	20.0446
chr16	90354753	211115648	2.3365	31.4818
chr17	81195210	216358718	2.6647	22.7587
chr18	78077248	122006655	1.5626	14.9803
chr19	59128983	148543258	2.5122	17.142
chr20	63025520	179324359	2.8453	20.9806
chr21	48129895	68227619	1.4176	14.6978
chr22	51304566	129669938	2.5275	15.5104
chrMT	16571	35489	2.1416	7.9941
chrX	155270560	8512728	0.0548	1.8492
chrY	59373566	39282350	0.6616	8.9908

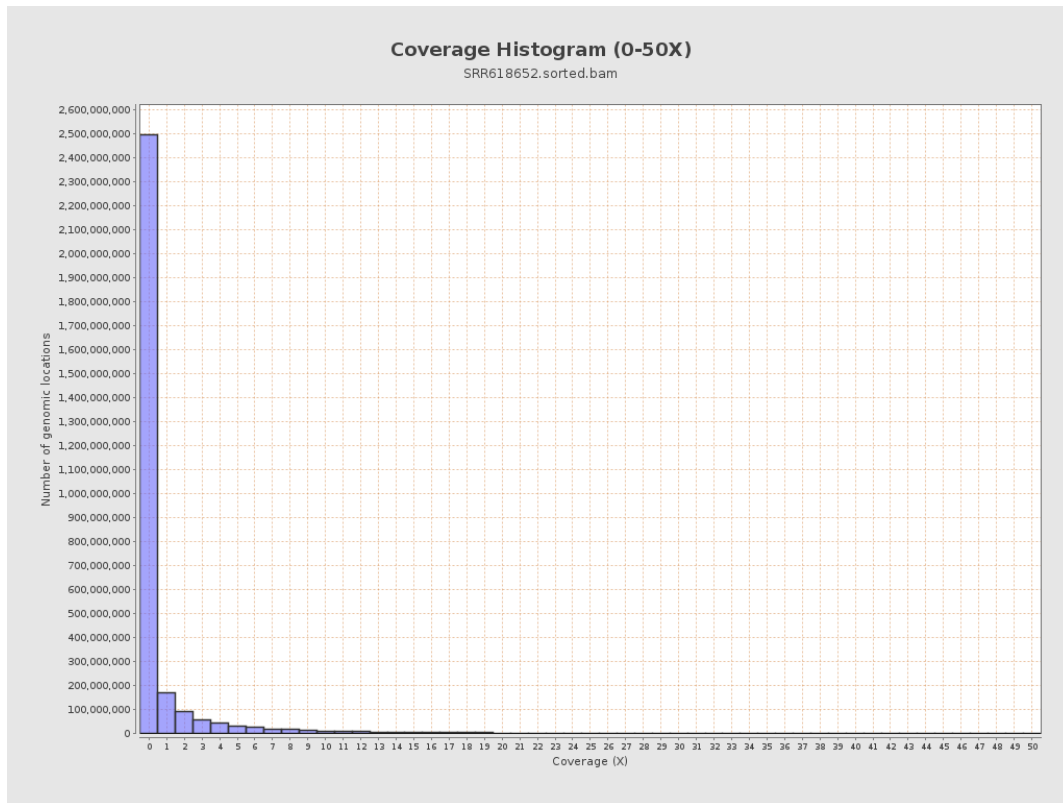
3. Results : Coverage across reference



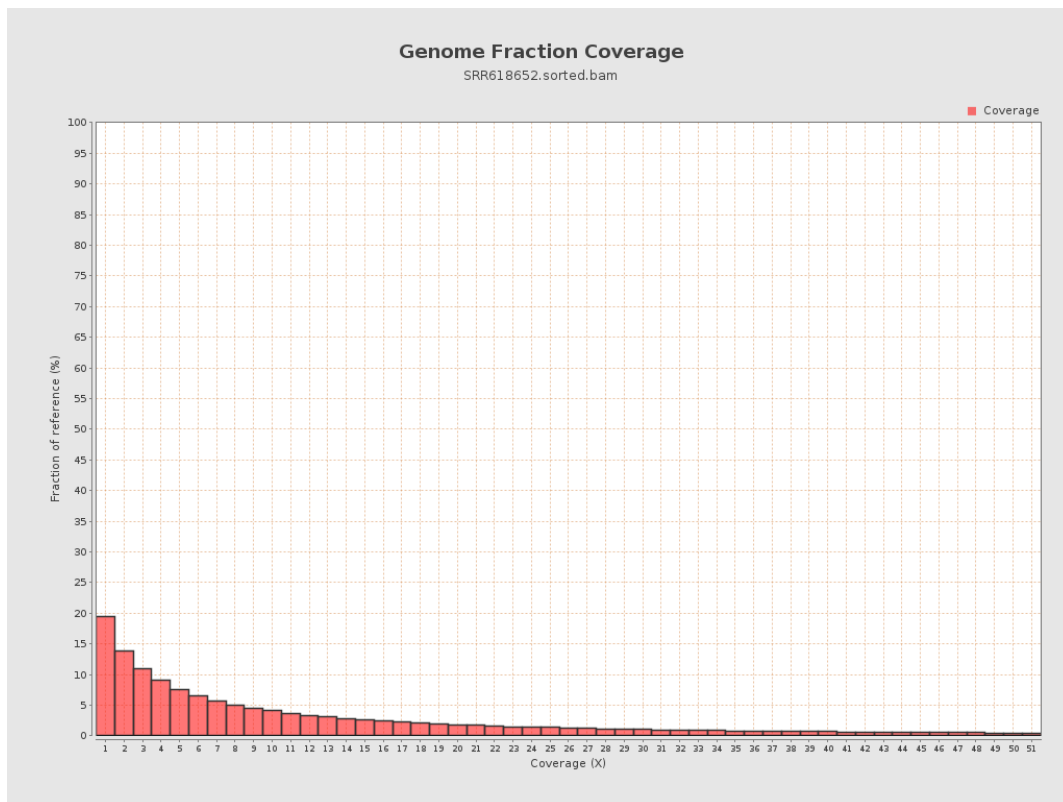
4. Results : Coverage Histogram



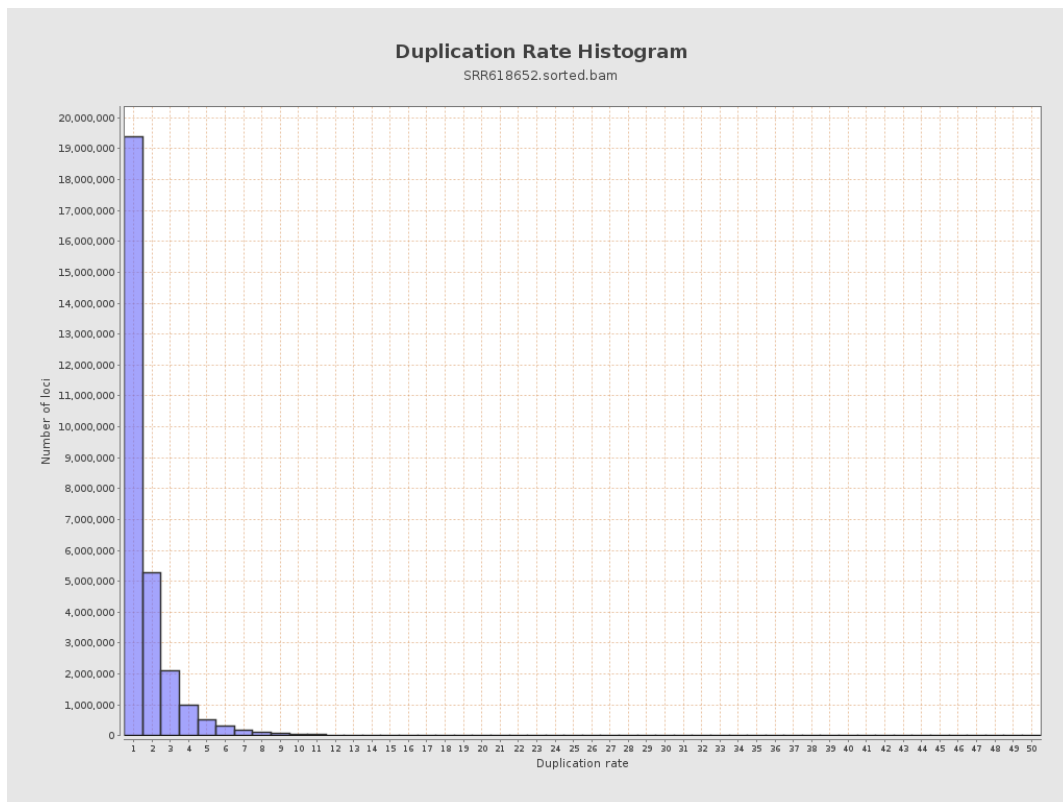
5. Results : Coverage Histogram (0-50X)



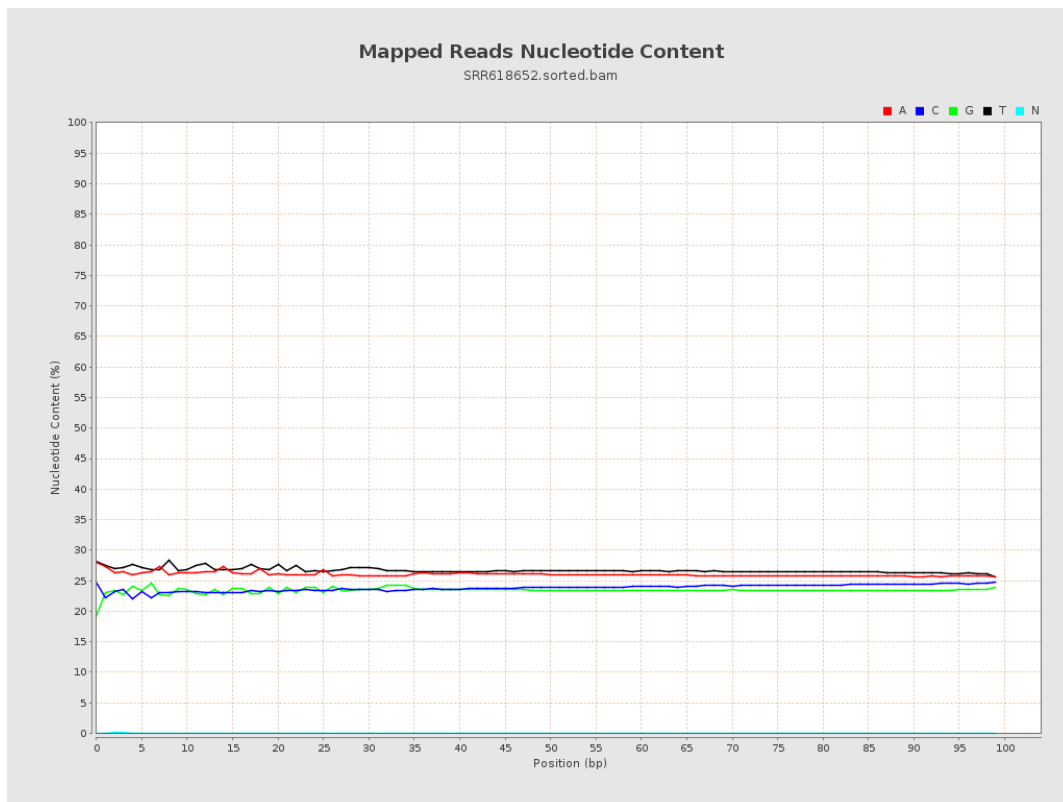
6. Results : Genome Fraction Coverage



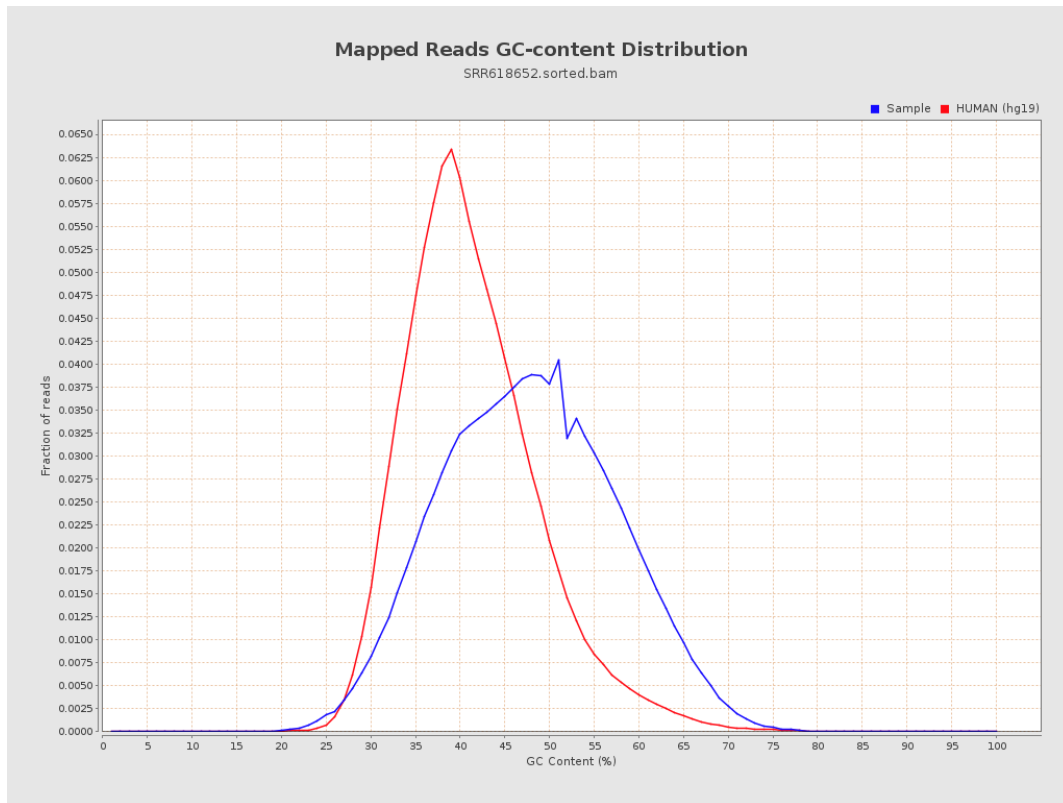
7. Results : Duplication Rate Histogram



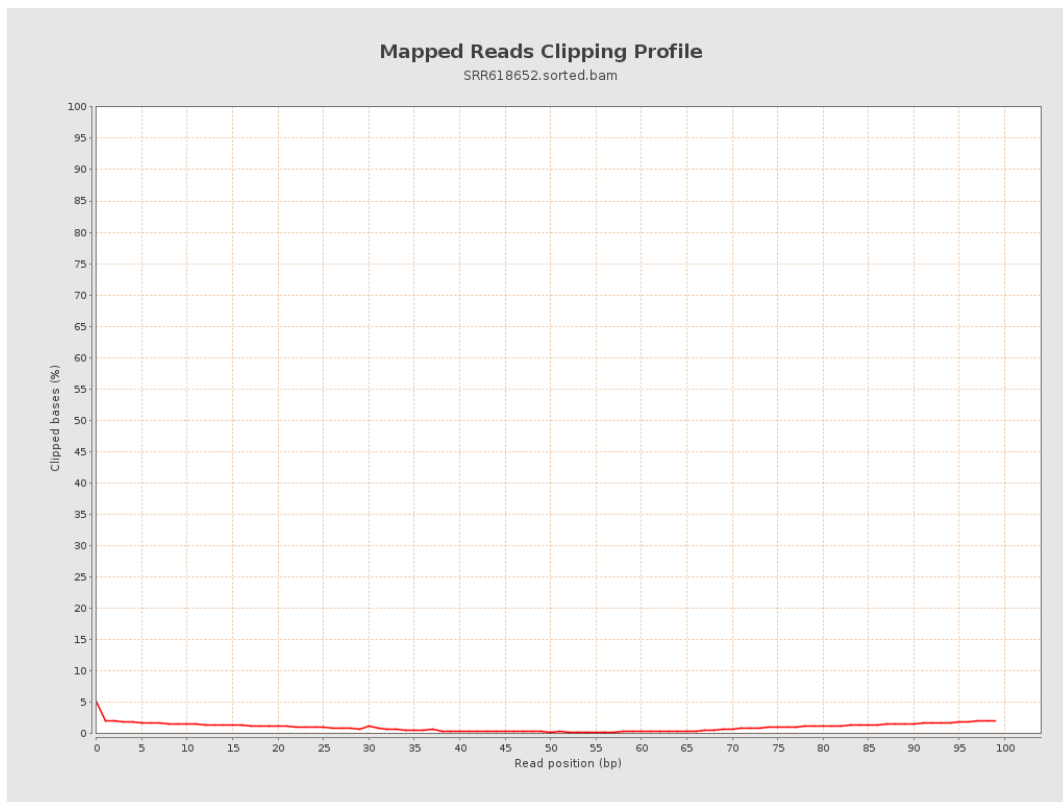
8. Results : Mapped Reads Nucleotide Content



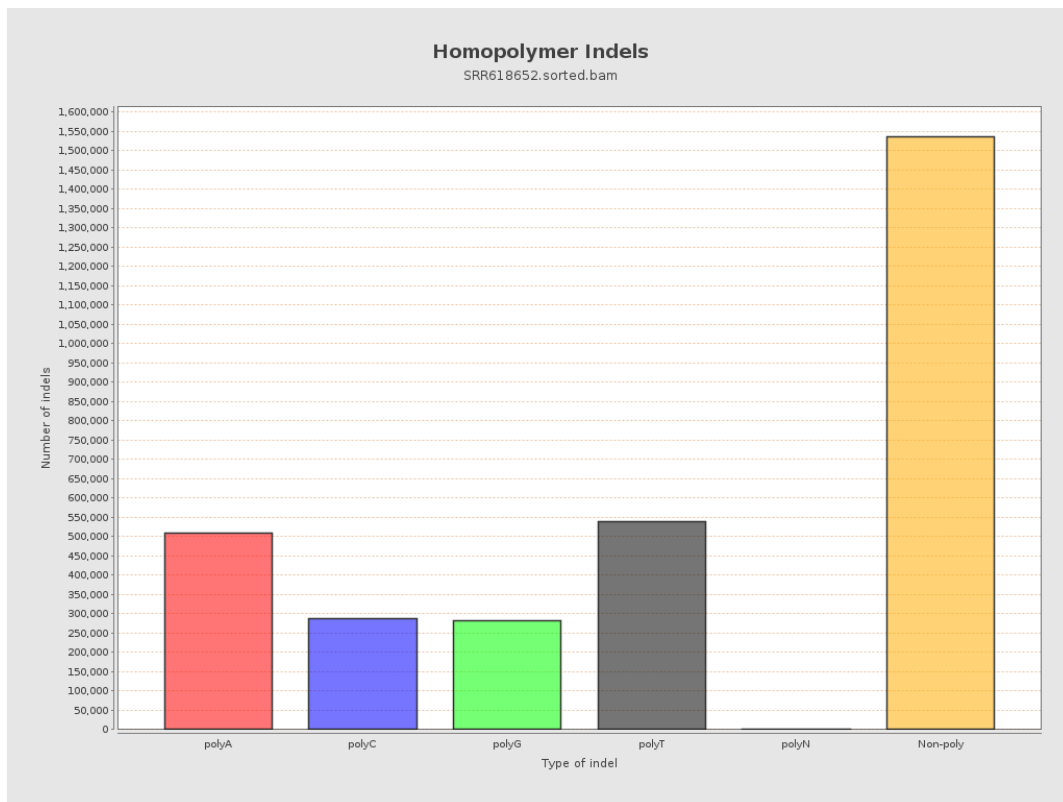
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

