Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 07:23:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618647.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_SRR618647 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618647.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 07:23:01 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618647.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	77,260,458
Mapped reads	73,152,467 / 94.68%
Unmapped reads	4,107,991 / 5.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	119,178 / 0.15%
Read min/max/mean length	30 / 100 / 100.06
Duplicated reads (estimated)	47,618,464 / 61.63%
Duplication rate	41.49%
Clipped reads	8,735,347 / 11.31%

2.2. ACGT Content

Number/percentage of A's	1,878,773,031 / 26.41%
Number/percentage of C's	1,657,835,309 / 23.3%
Number/percentage of T's	2,123,671,348 / 29.85%
Number/percentage of G's	1,453,031,116 / 20.43%
Number/percentage of N's	344,892 / 0%
GC Percentage	43.73%

2.3. Coverage

Mean	2.2995

Standard Deviation	55.7753

2.4. Mapping Quality

Mean Mapping Quality	50.02

2.5. Mismatches and indels

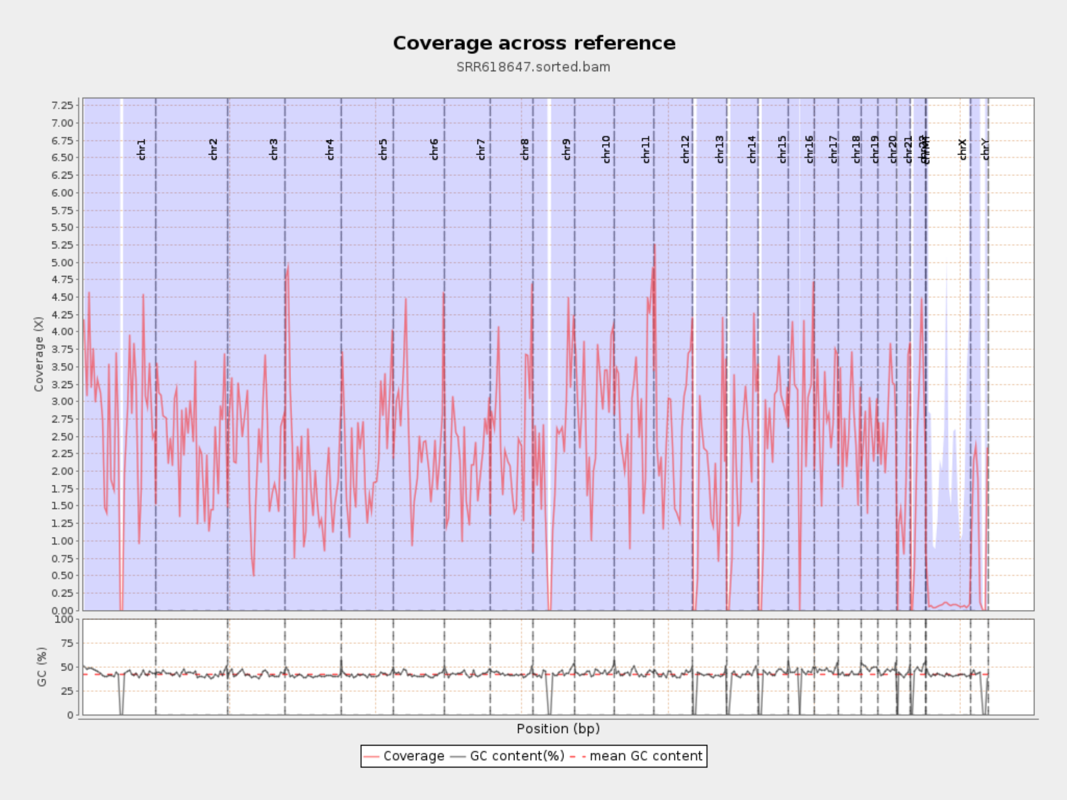
General error rate	0.86%
Mismatches	59,119,924
Insertions	1,208,093
Mapped reads with at least one insertion	1.62%
Deletions	3,248,166
Mapped reads with at least one deletion	4.34%
Homopolymer indels	52.48%

2.6. Chromosome stats

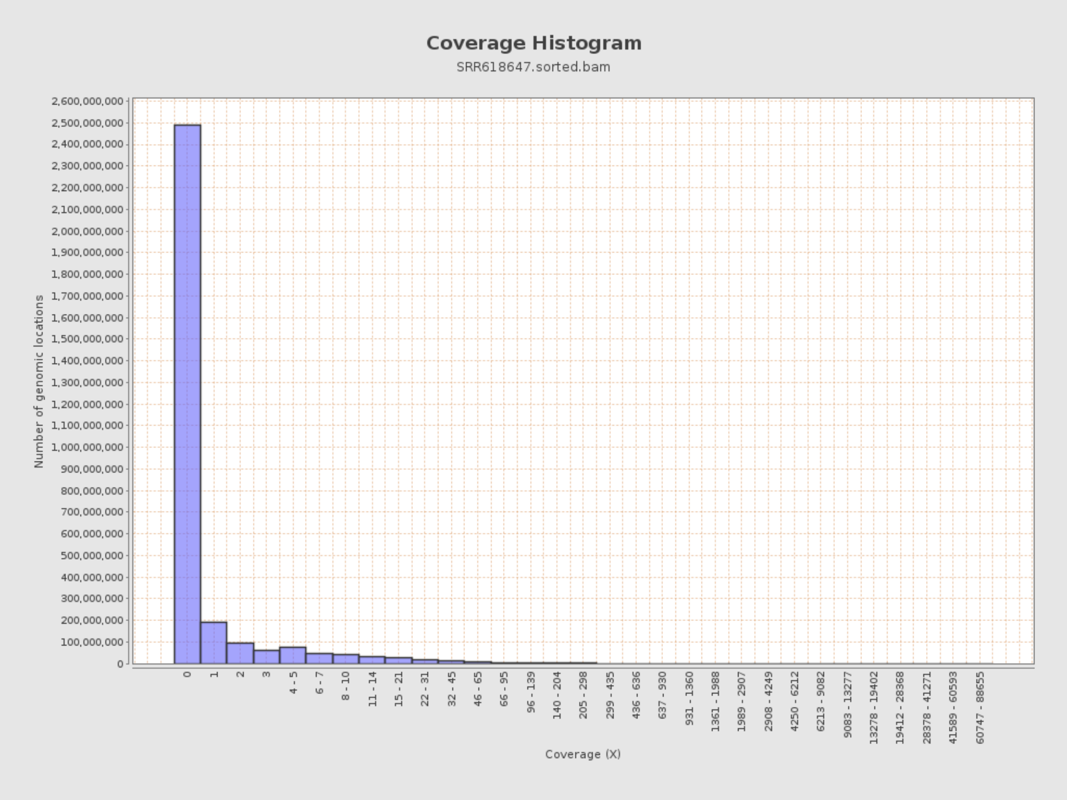
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	683014190	2.7403	63.6707
chr2	243199373	595016380	2.4466	55.8786
chr3	198022430	449939891	2.2722	48.0491
chr4	191154276	382399225	2.0005	46.6776
chr5	180915260	423127582	2.3388	51.1335
chr6	171115067	415870088	2.4304	54.9662
chr7	159138663	340439091	2.1393	51.89

chr8	146364022	374971480	2.5619	58.9237
chr9	141213431	316560083	2.2417	46.0743
chr10	135534747	392246044	2.8941	62.6566
chr11	135006516	392926342	2.9104	63.4353
chr12	133851895	351706675	2.6276	70.589
chr13	115169878	208396598	1.8095	93.97
chr14	107349540	229143232	2.1346	45.06
chr15	102531392	241427356	2.3547	59.6184
chr16	90354753	273048665	3.022	55.7334
chr17	81195210	231035371	2.8454	64.9398
chr18	78077248	201264398	2.5778	63.0905
chr19	59128983	145989055	2.469	37.9041
chr20	63025520	176608153	2.8022	36.0479
chr21	48129895	88386275	1.8364	36.7662
chr22	51304566	115590074	2.253	52.6614
chrMT	16571	13943	0.8414	3.134
chrX	155270560	14735948	0.0949	6.81
chrY	59373566	74660772	1.2575	41.5054

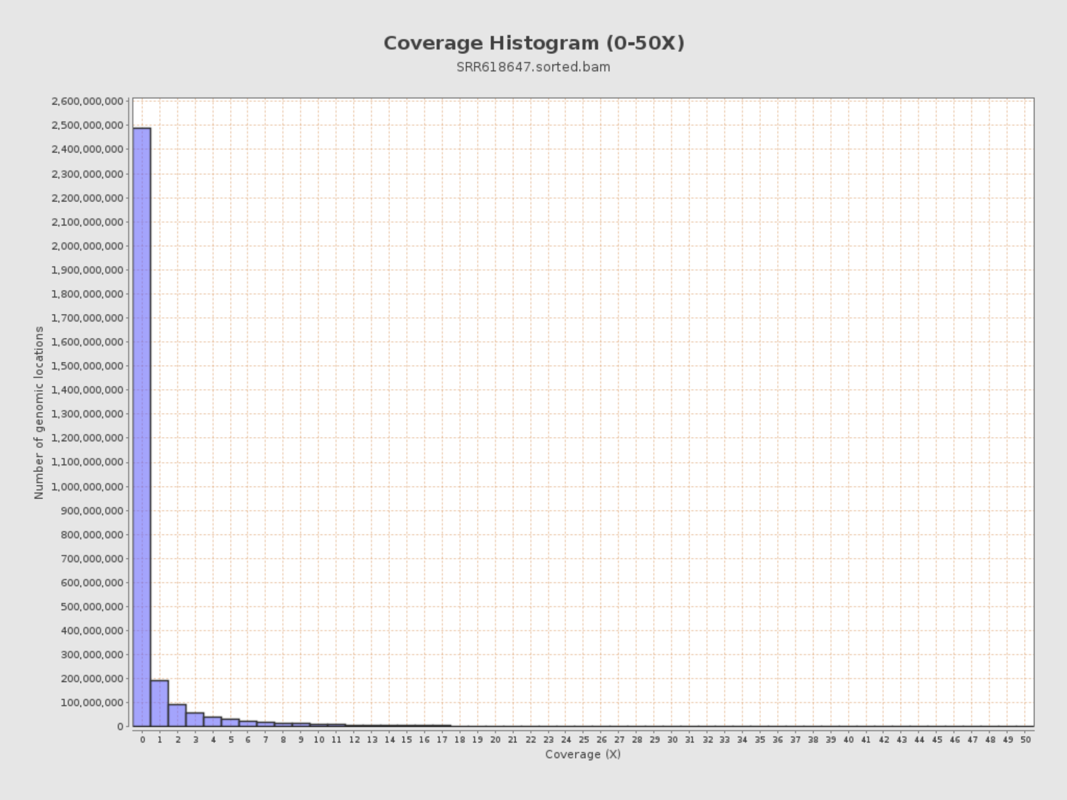
3. Results : Coverage across reference



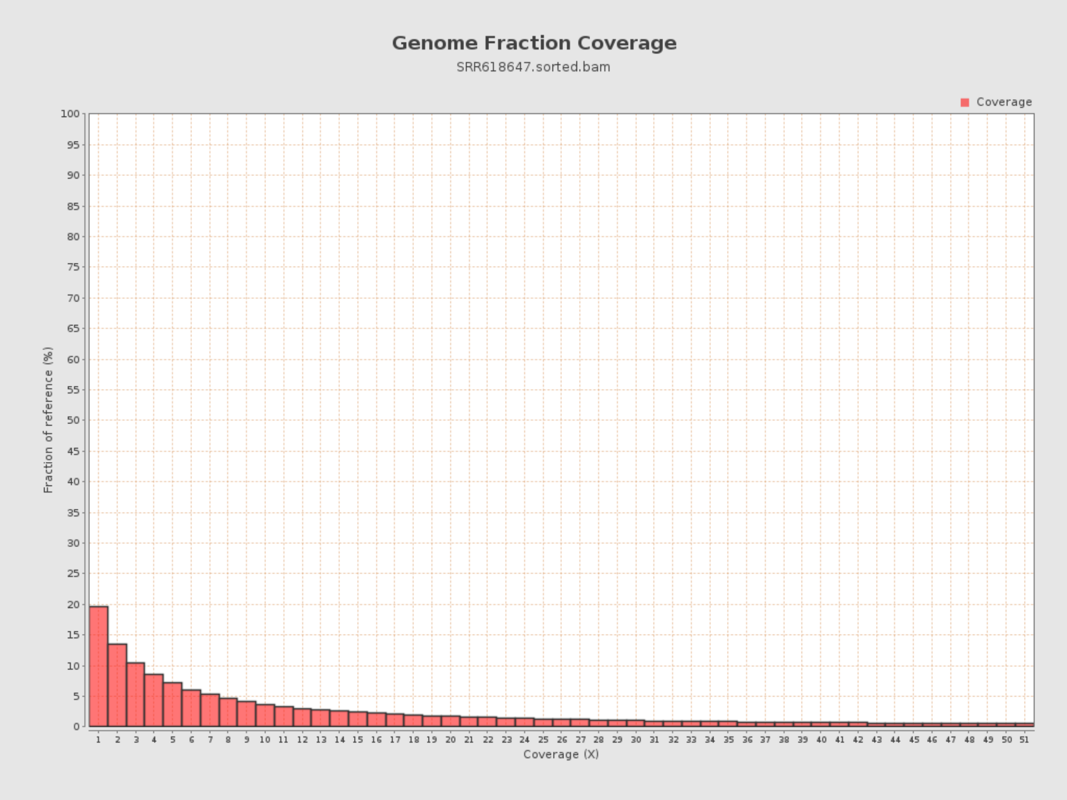
4. Results : Coverage Histogram



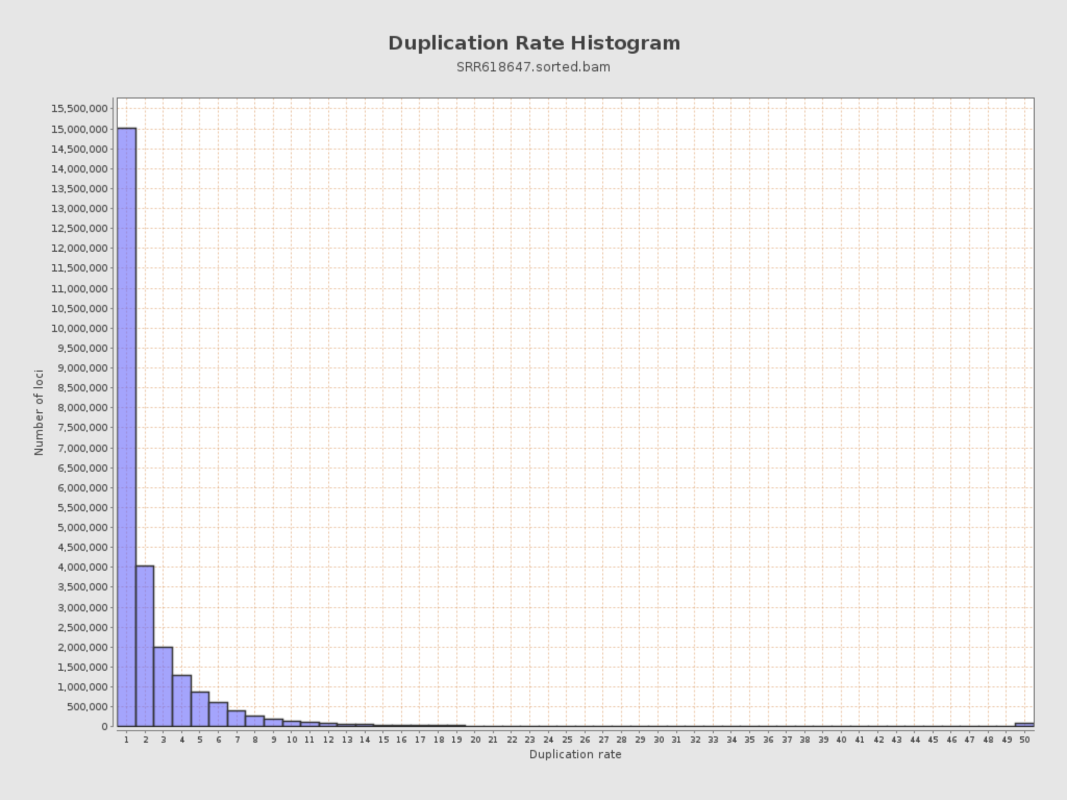
5. Results : Coverage Histogram (0-50X)



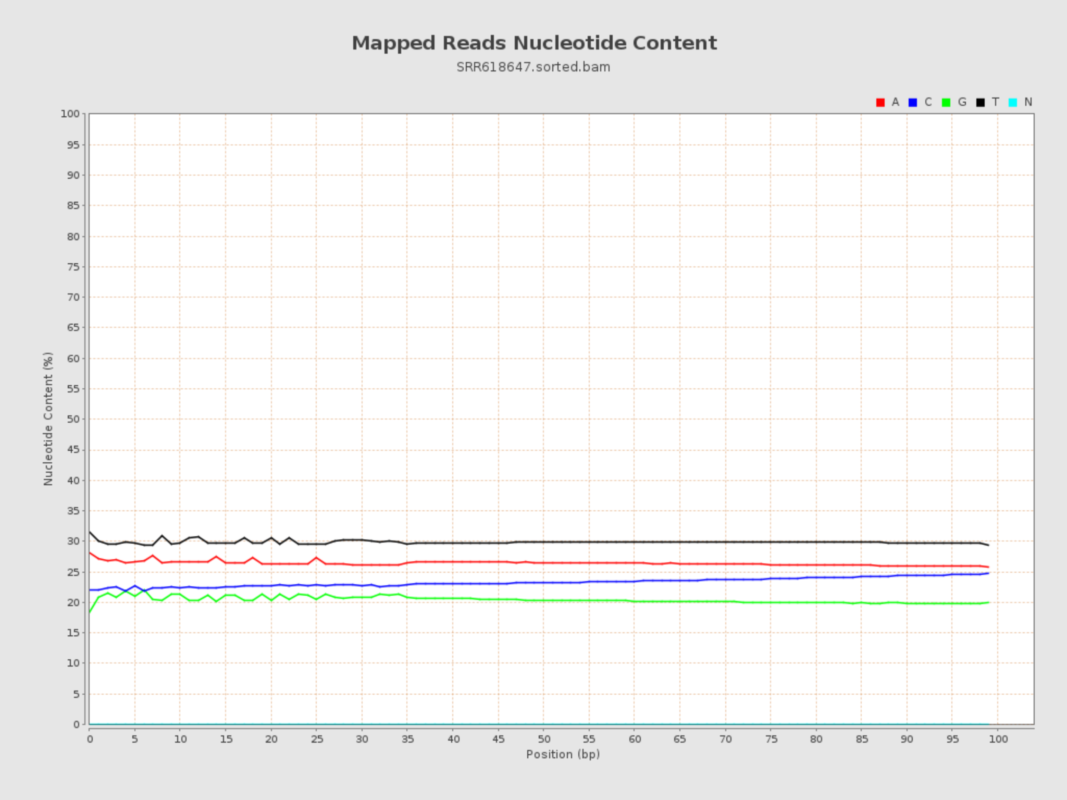
6. Results : Genome Fraction Coverage



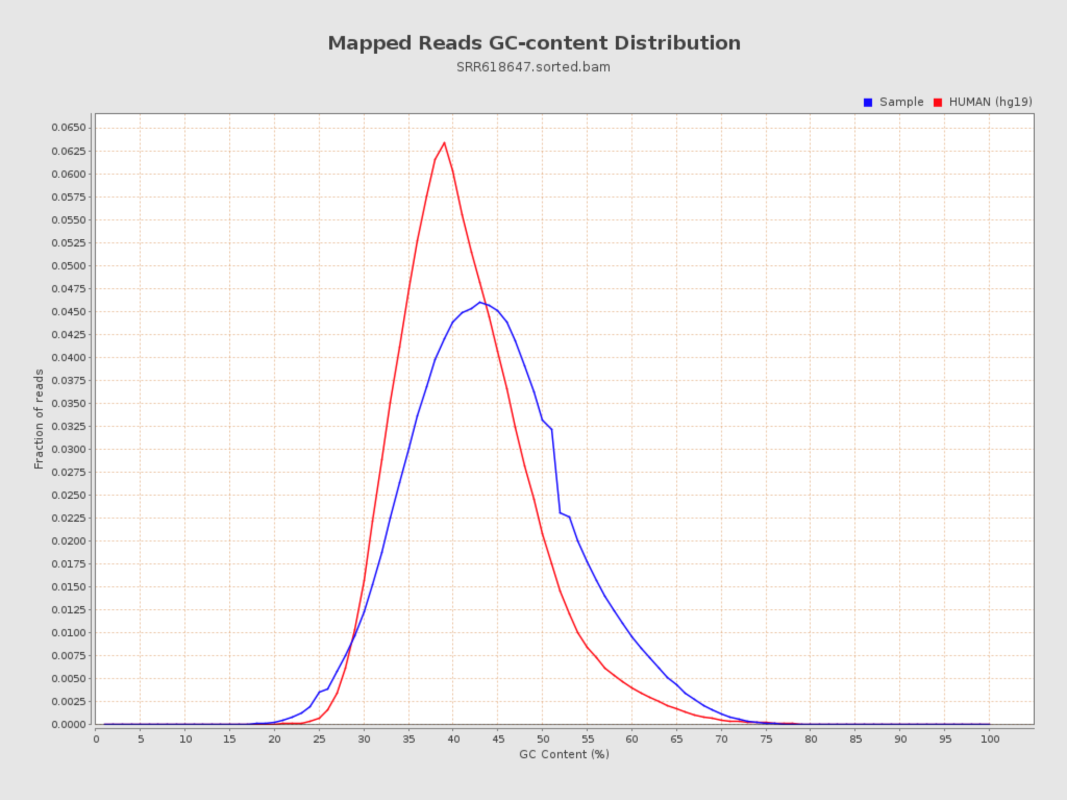
7. Results : Duplication Rate Histogram



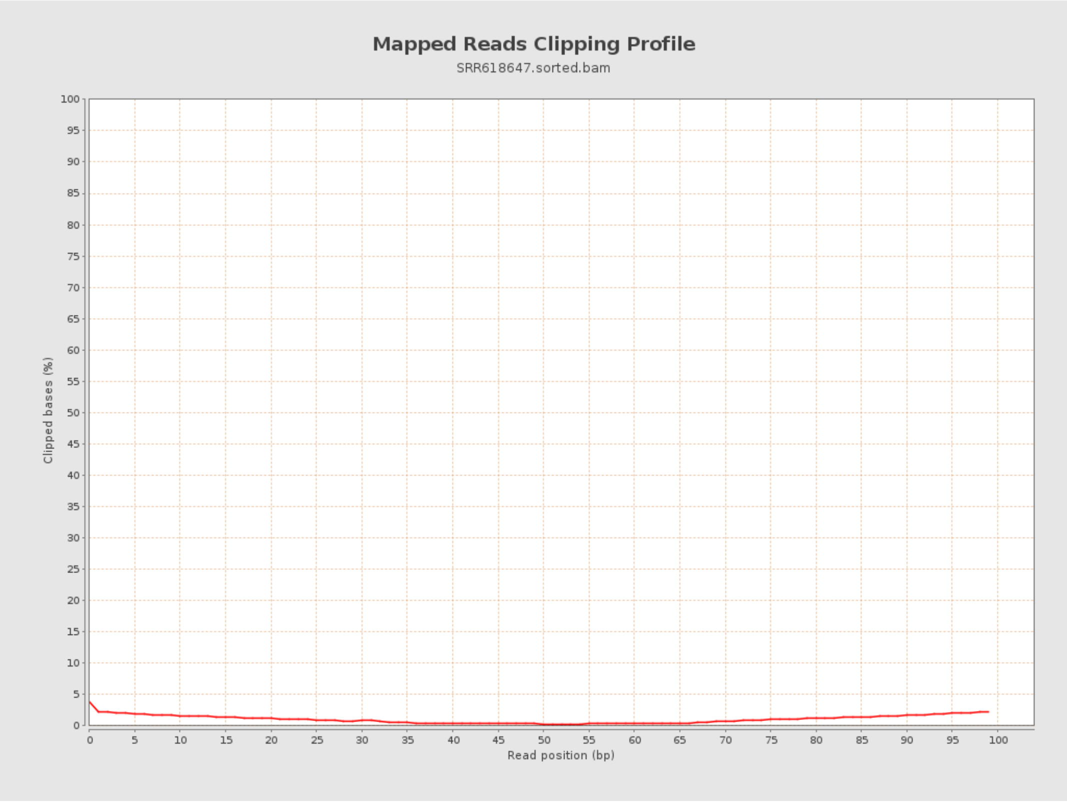
8. Results : Mapped Reads Nucleotide Content



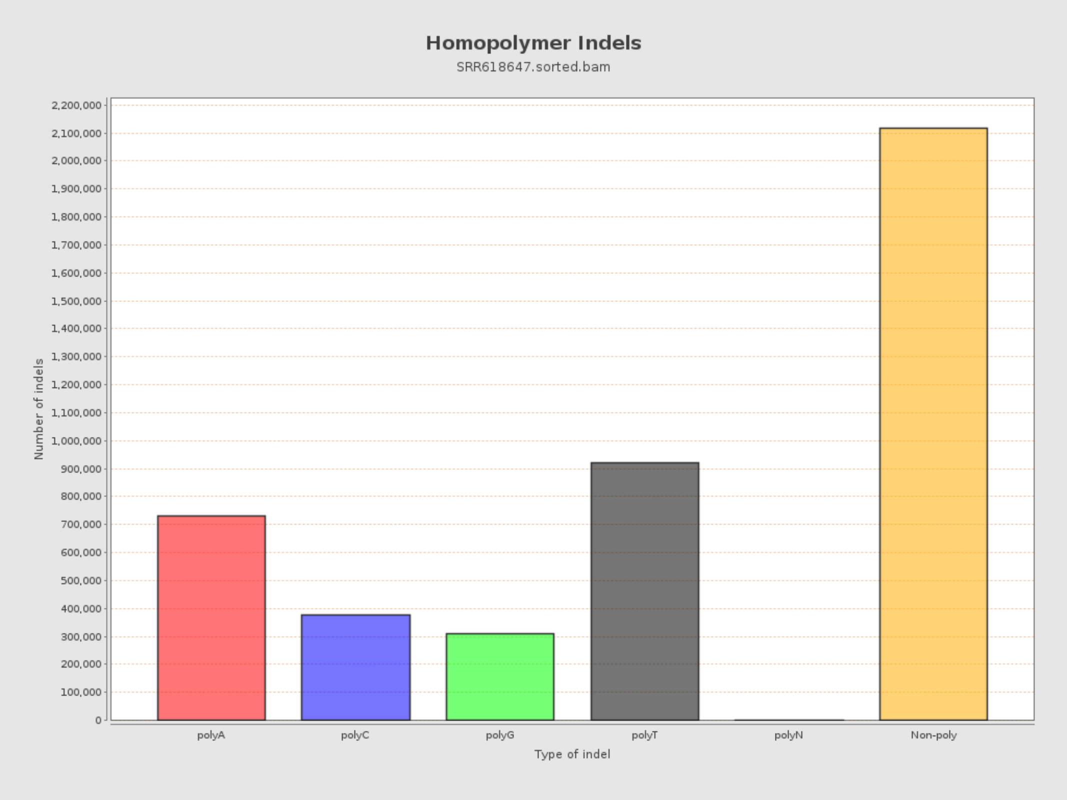
9. Results : Mapped Reads GC-content Distribution



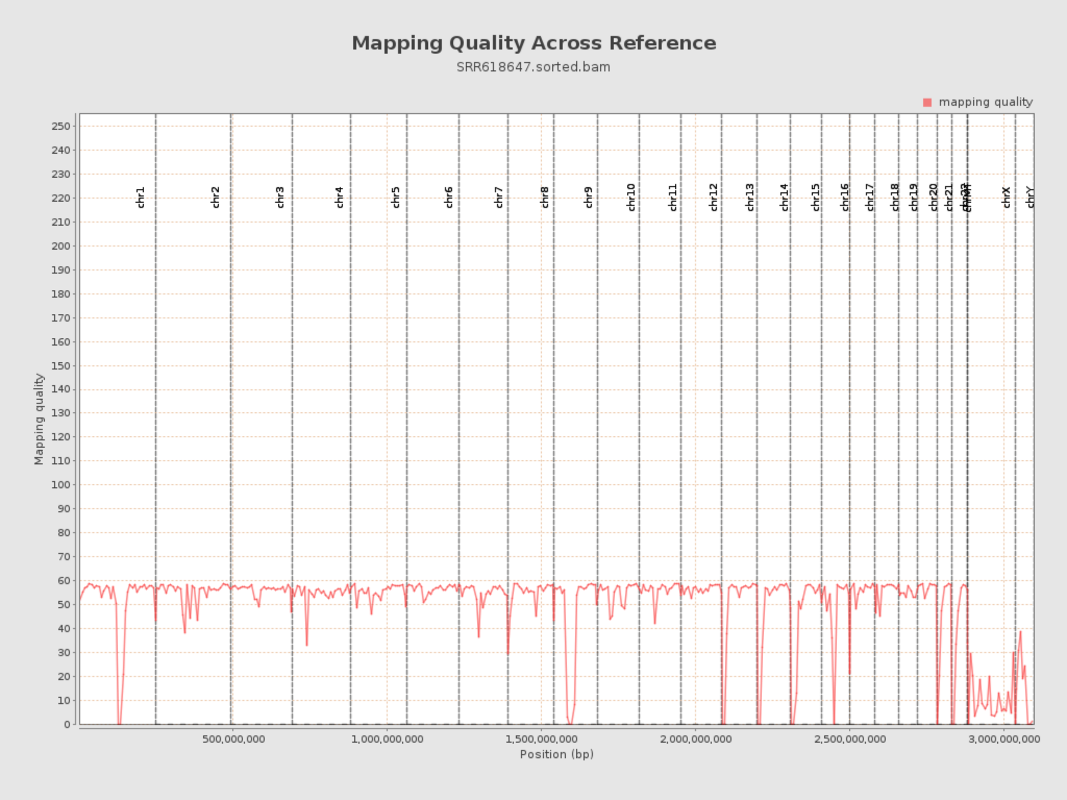
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram