Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:47:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234128.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_SRR6234128 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234128.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:47:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234128.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,979,702
Mapped reads	5,610,258 / 93.82%
Unmapped reads	369,444 / 6.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	56,241 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	932,289 / 15.59%
Duplication rate	7.25%
Clipped reads	2,071,820 / 34.65%

2.2. ACGT Content

Number/percentage of A's	98,385,362 / 25.61%
Number/percentage of C's	67,932,443 / 17.68%
Number/percentage of T's	106,309,383 / 27.67%
Number/percentage of G's	111,476,086 / 29.02%
Number/percentage of N's	82,710 / 0.02%
GC Percentage	46.7%

2.3. Coverage

Mean	0.1241

Standard Deviation	69.9064

2.4. Mapping Quality

Mean Mapping Quality	46.23

2.5. Mismatches and indels

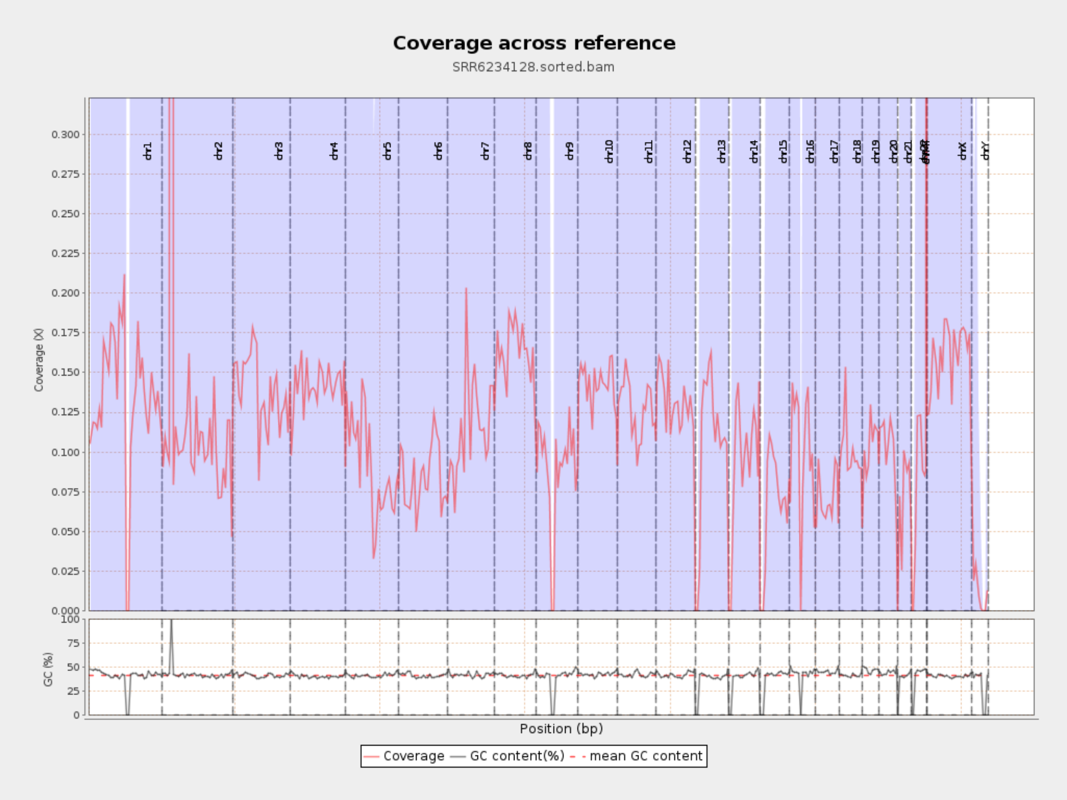
General error rate	0.61%
Mismatches	2,317,251
Insertions	23,106
Mapped reads with at least one insertion	0.41%
Deletions	83,762
Mapped reads with at least one deletion	1.48%
Homopolymer indels	46.7%

2.6. Chromosome stats

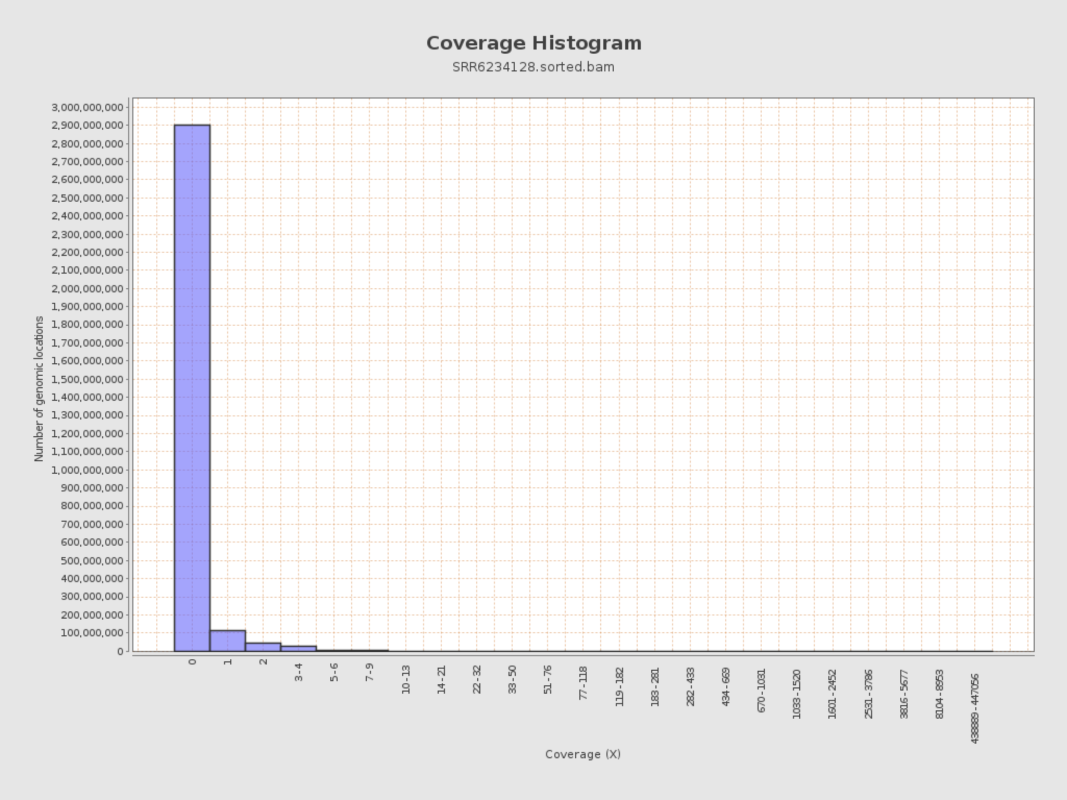
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33763019	0.1355	1.3776
chr2	243199373	59782035	0.2458	249.3946
chr3	198022430	27412062	0.1384	0.6025
chr4	191154276	27129476	0.1419	0.6155
chr5	180915260	16343373	0.0903	0.4817
chr6	171115067	14336016	0.0838	0.5129
chr7	159138663	18483932	0.1161	1.3815

chr8	146364022	23939252	0.1636	1.0832
chr9	141213431	12474547	0.0883	0.6624
chr10	135534747	19489197	0.1438	0.7831
chr11	135006516	17094309	0.1266	0.8882
chr12	133851895	17458798	0.1304	0.5925
chr13	115169878	12030693	0.1045	0.5189
chr14	107349540	9858081	0.0918	0.6471
chr15	102531392	6854507	0.0669	0.4156
chr16	90354753	9054597	0.1002	0.543
chr17	81195210	5704591	0.0703	0.504
chr18	78077248	7911333	0.1013	1.2696
chr19	59128983	6087072	0.1029	0.9805
chr20	63025520	6493983	0.103	0.545
chr21	48129895	3198126	0.0664	0.4415
chr22	51304566	3740364	0.0729	0.4395
chrMT	16571	23733	1.4322	1.9827
chrX	155270560	24827128	0.1599	0.7018
chrY	59373566	832365	0.014	0.1951

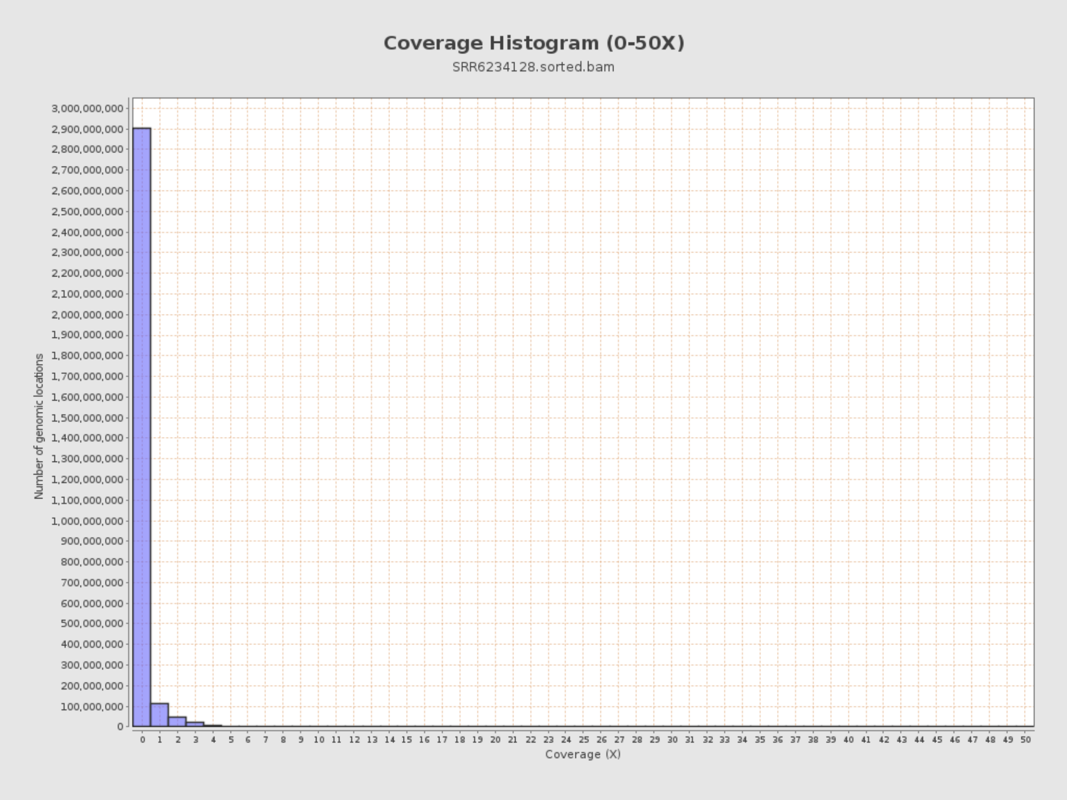
3. Results : Coverage across reference



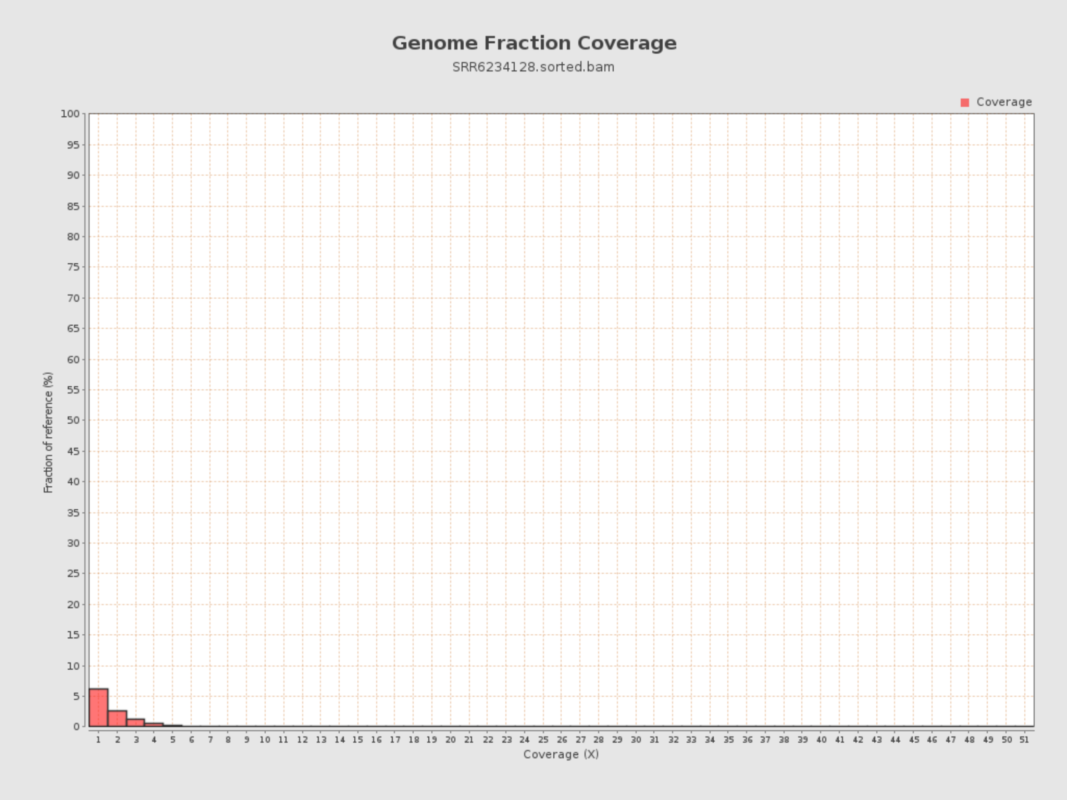
4. Results : Coverage Histogram



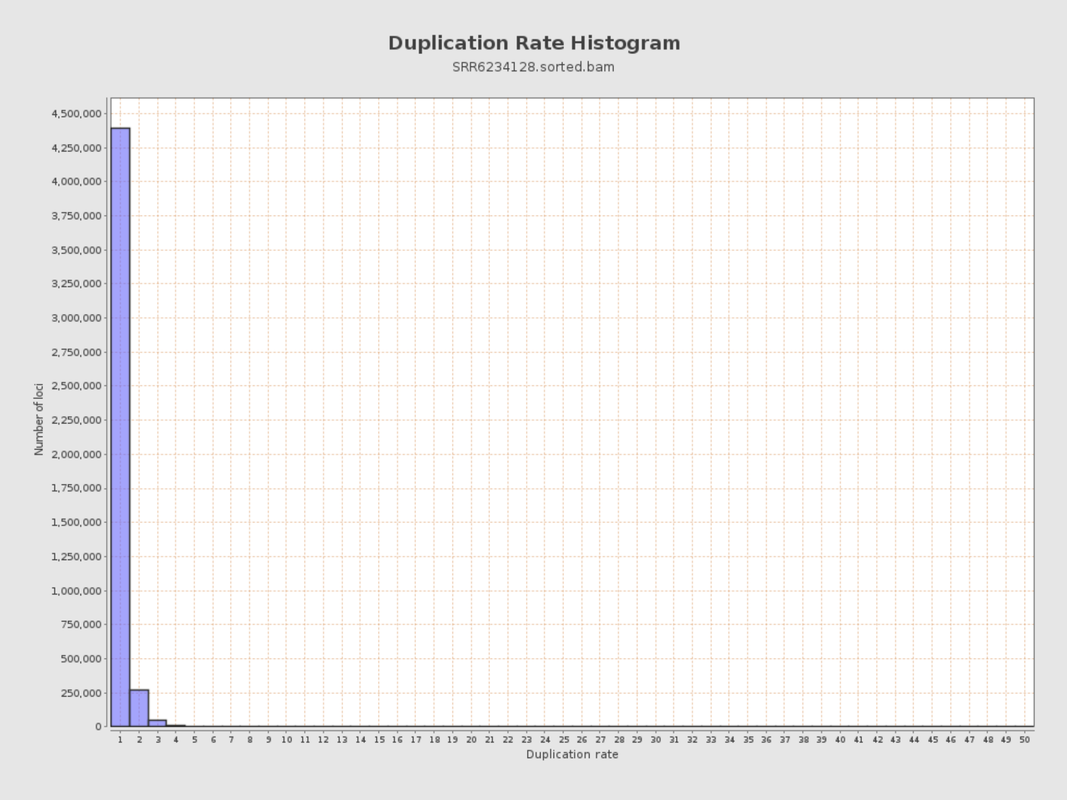
5. Results : Coverage Histogram (0-50X)



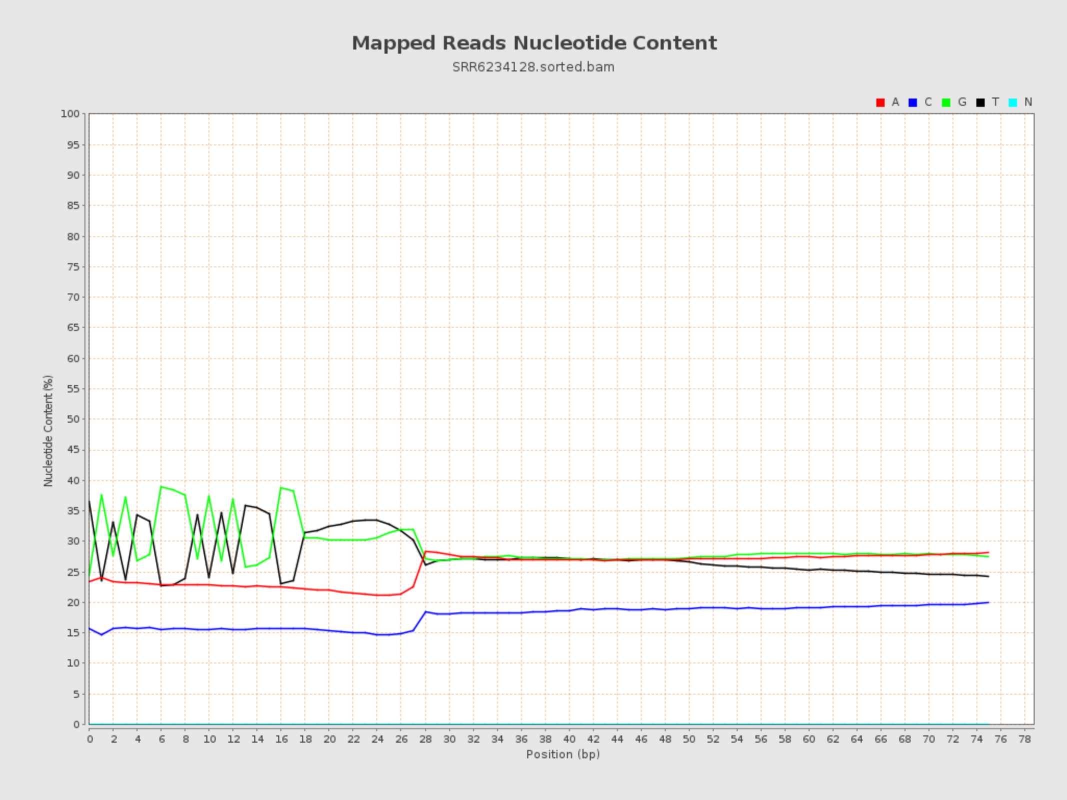
6. Results : Genome Fraction Coverage



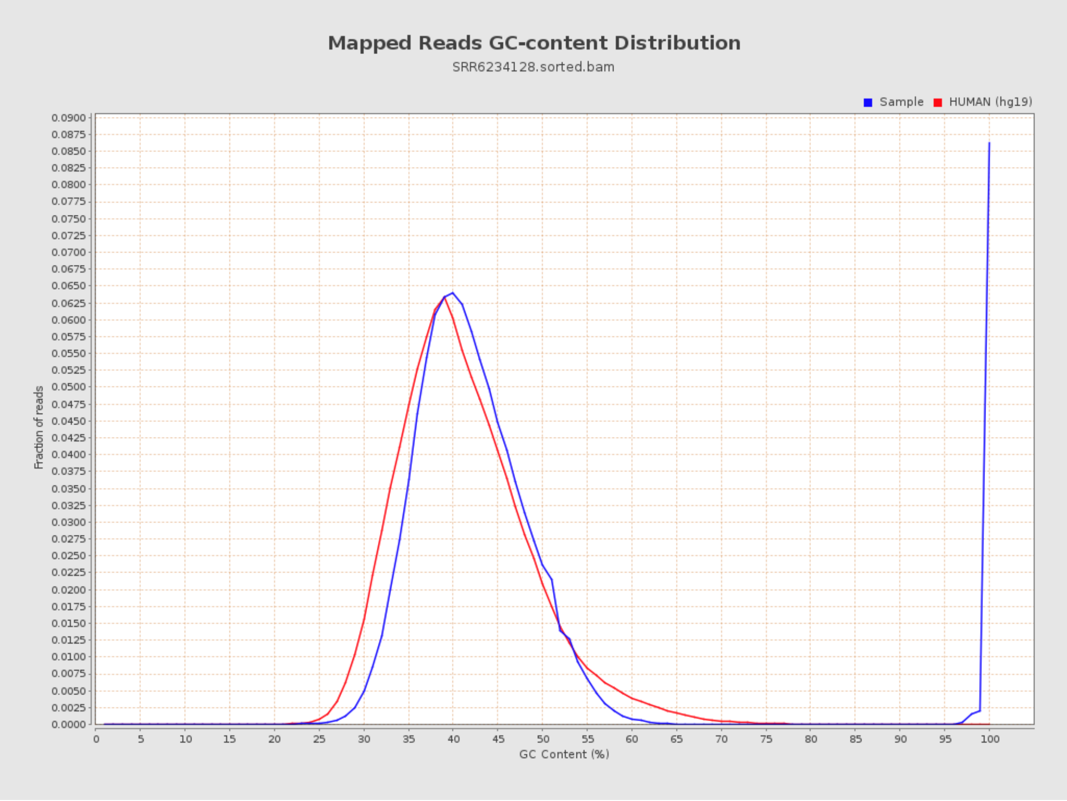
7. Results : Duplication Rate Histogram



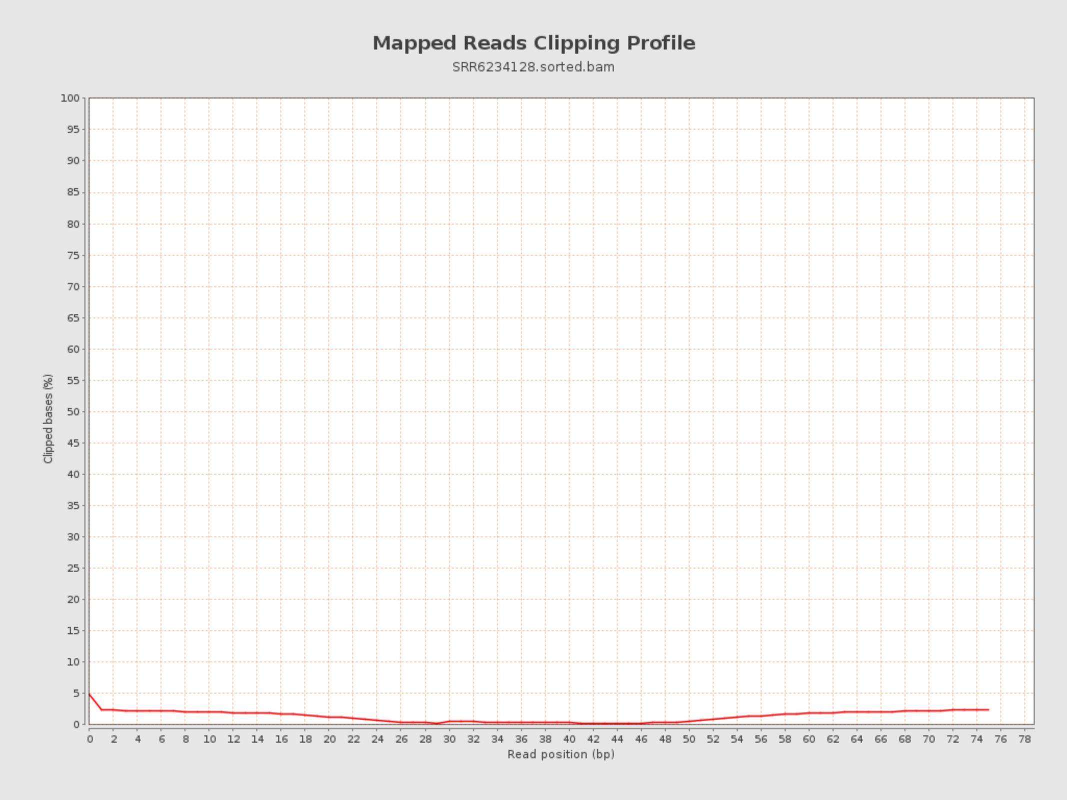
8. Results : Mapped Reads Nucleotide Content



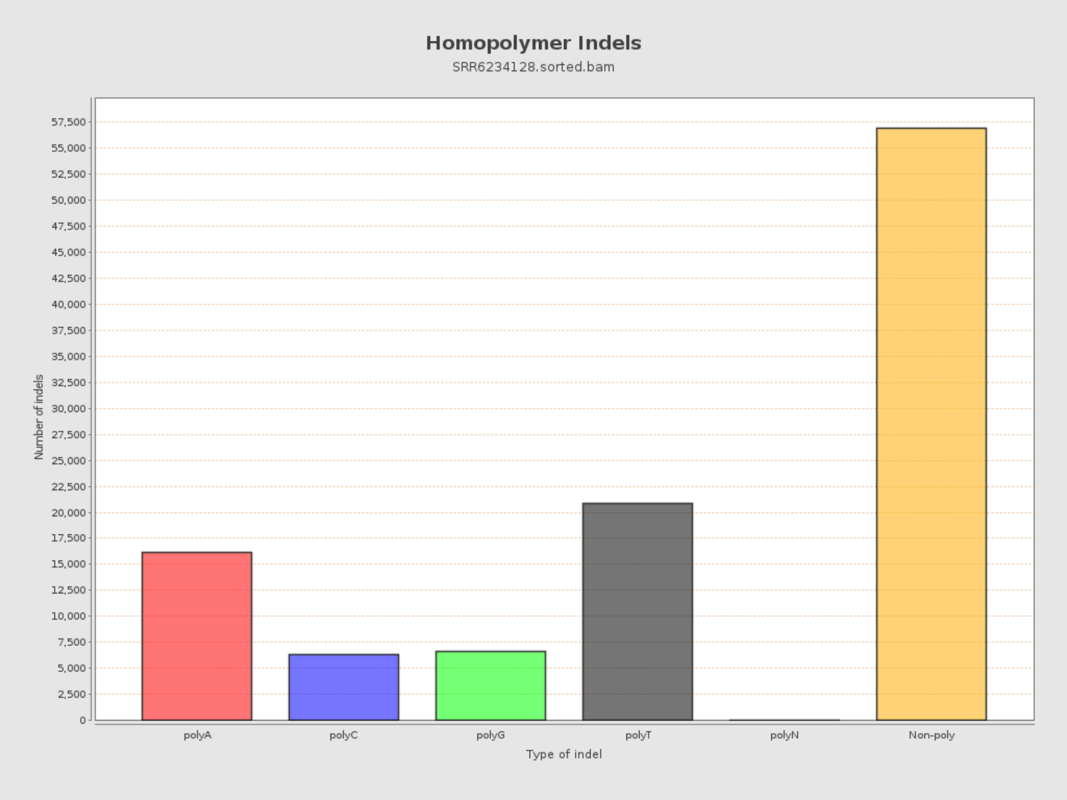
9. Results : Mapped Reads GC-content Distribution



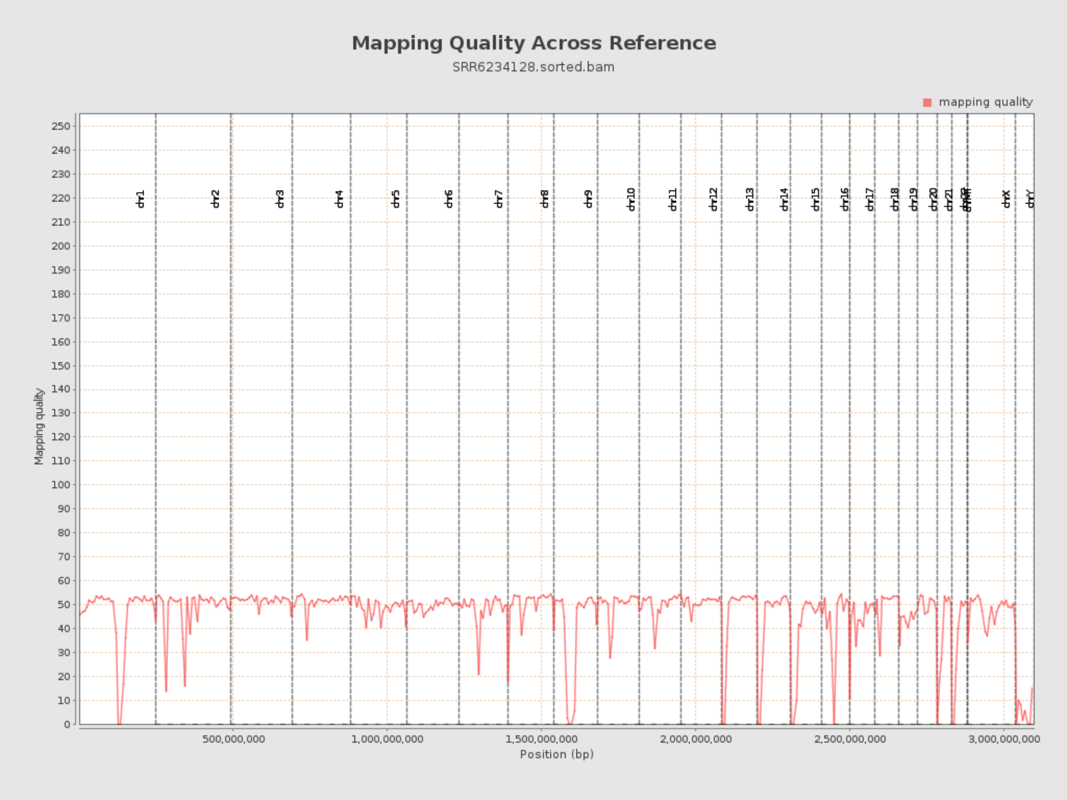
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram