Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2024/09/16 14:53:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234087.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_SRR6234087 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234087.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:53:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234087.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	913,801
Mapped reads	523,483 / 57.29%
Unmapped reads	390,318 / 42.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,128 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	26,037 / 2.85%
Duplication rate	4.31%
Clipped reads	359,399 / 39.33%

2.2. ACGT Content

Number/percentage of A's	8,358,265 / 26.56%
Number/percentage of C's	5,059,715 / 16.08%
Number/percentage of T's	10,500,157 / 33.37%
Number/percentage of G's	7,543,067 / 23.97%
Number/percentage of N's	4,703 / 0.01%
GC Percentage	40.05%

2.3. Coverage

Mean	0.0102

Standard Deviation	0.1337

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

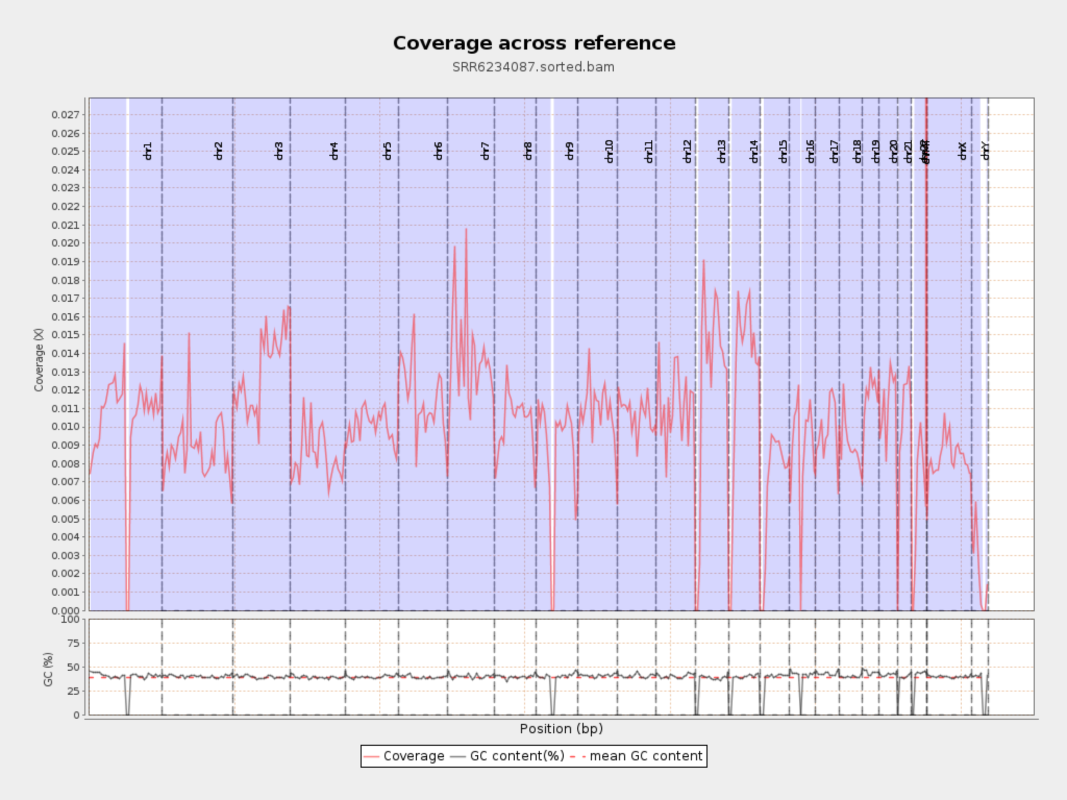
General error rate	0.96%
Mismatches	298,254
Insertions	2,537
Mapped reads with at least one insertion	0.48%
Deletions	12,519
Mapped reads with at least one deletion	2.36%
Homopolymer indels	47.46%

2.6. Chromosome stats

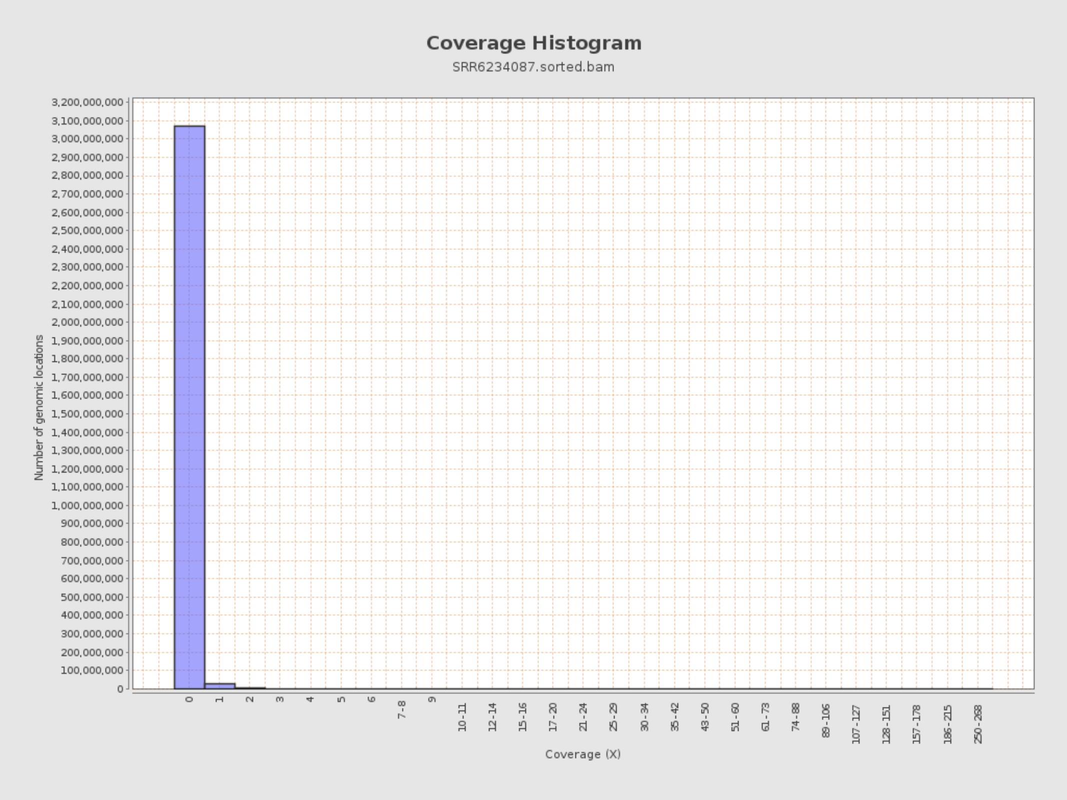
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2585338	0.0104	0.1521
chr2	243199373	2142833	0.0088	0.1301
chr3	198022430	2598509	0.0131	0.1286
chr4	191154276	1598756	0.0084	0.1049
chr5	180915260	1814973	0.01	0.1128
chr6	171115067	1988484	0.0116	0.1298
chr7	159138663	2205653	0.0139	0.1993

chr8	146364022	1491002	0.0102	0.1904
chr9	141213431	1222110	0.0087	0.1172
chr10	135534747	1482043	0.0109	0.127
chr11	135006516	1431505	0.0106	0.1381
chr12	133851895	1489367	0.0111	0.1182
chr13	115169878	1424858	0.0124	0.1271
chr14	107349540	1347856	0.0126	0.129
chr15	102531392	697745	0.0068	0.0928
chr16	90354753	804070	0.0089	0.1087
chr17	81195210	787626	0.0097	0.1145
chr18	78077248	712019	0.0091	0.1801
chr19	59128983	695074	0.0118	0.1326
chr20	63025520	698335	0.0111	0.1241
chr21	48129895	487563	0.0101	0.1132
chr22	51304566	295743	0.0058	0.0837
chrMT	16571	79822	4.817	3.828
chrX	155270560	1288117	0.0083	0.1044
chrY	59373566	118207	0.002	0.0524

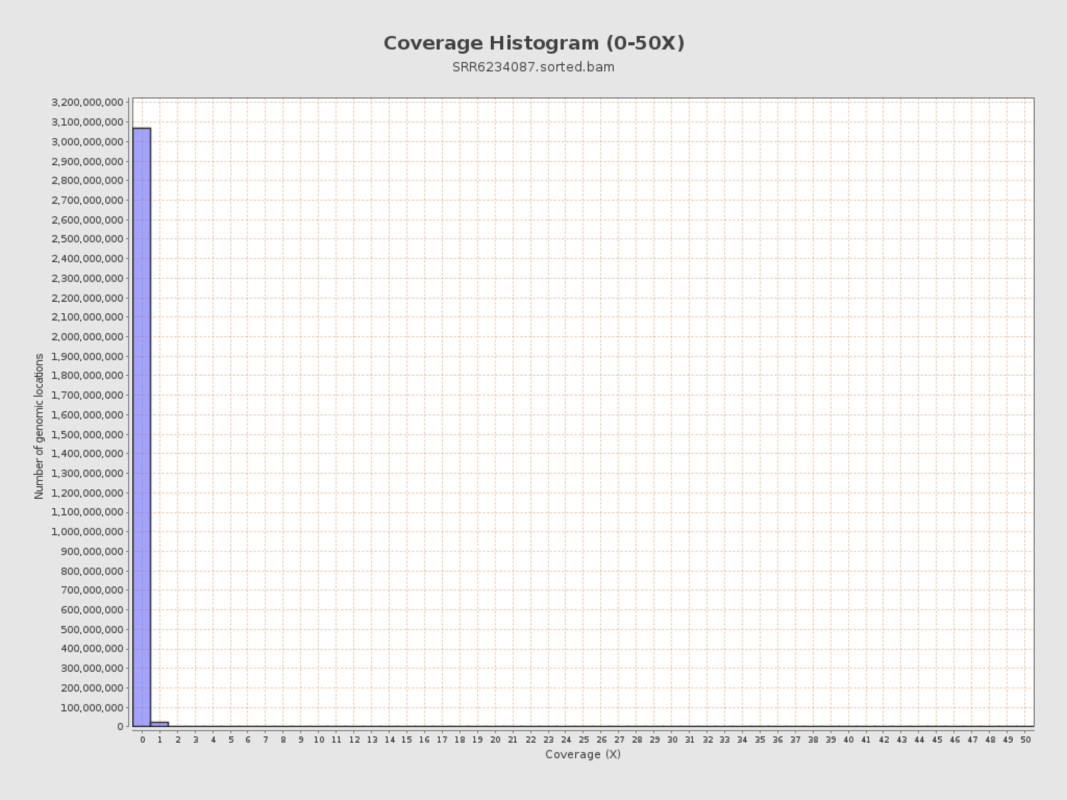
3. Results : Coverage across reference



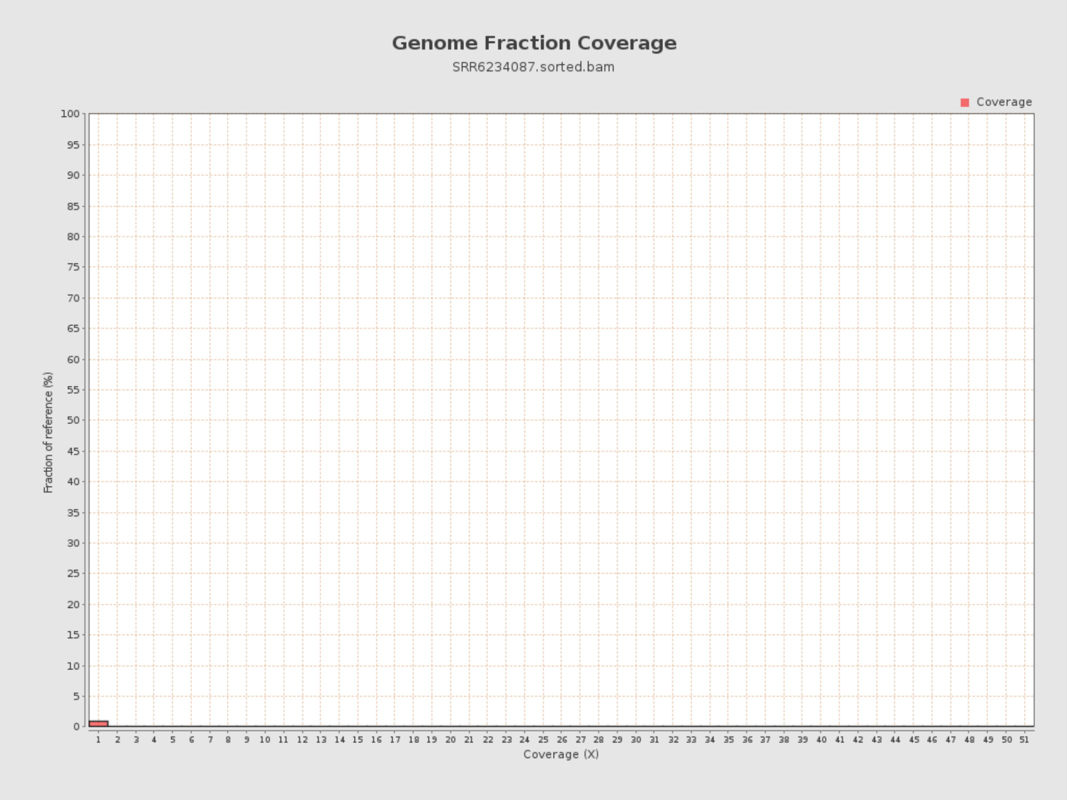
4. Results : Coverage Histogram



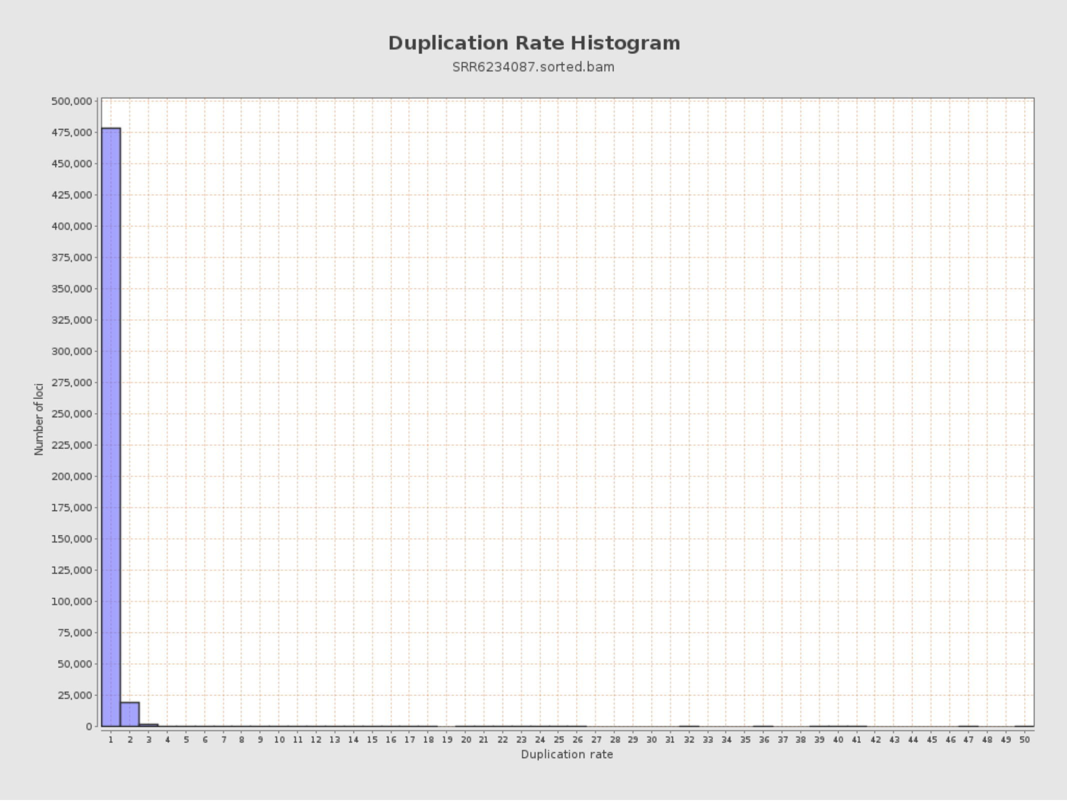
5. Results : Coverage Histogram (0-50X)



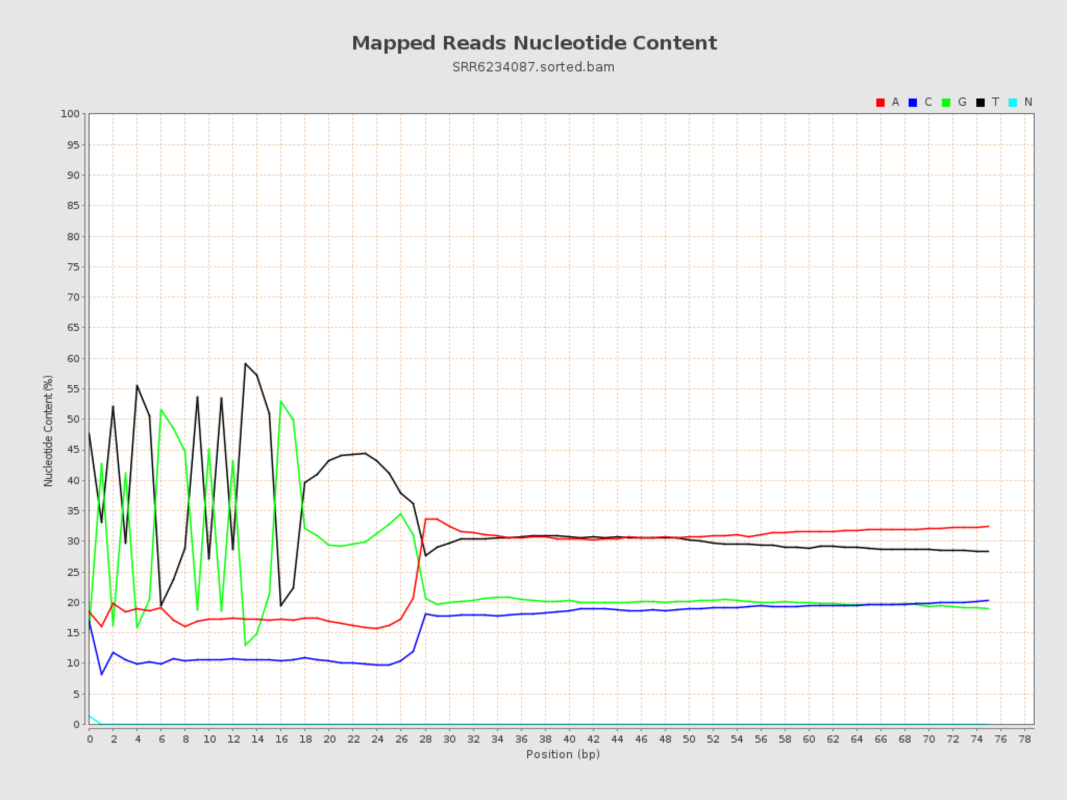
6. Results : Genome Fraction Coverage



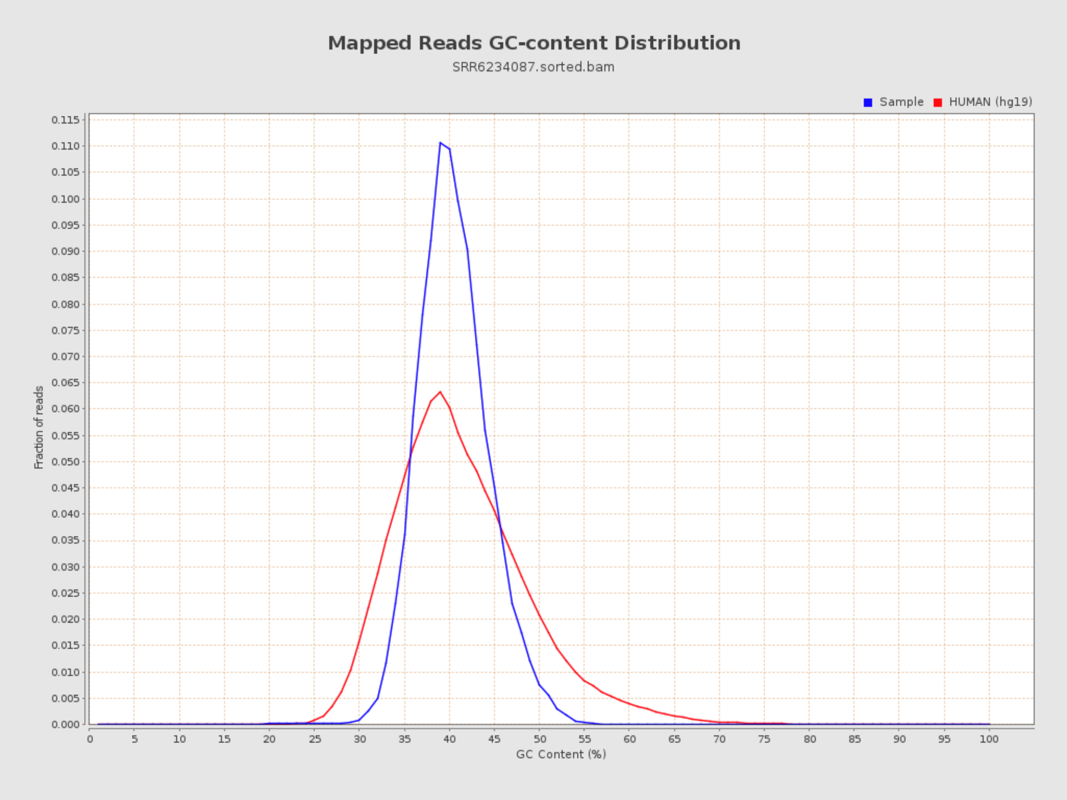
7. Results : Duplication Rate Histogram



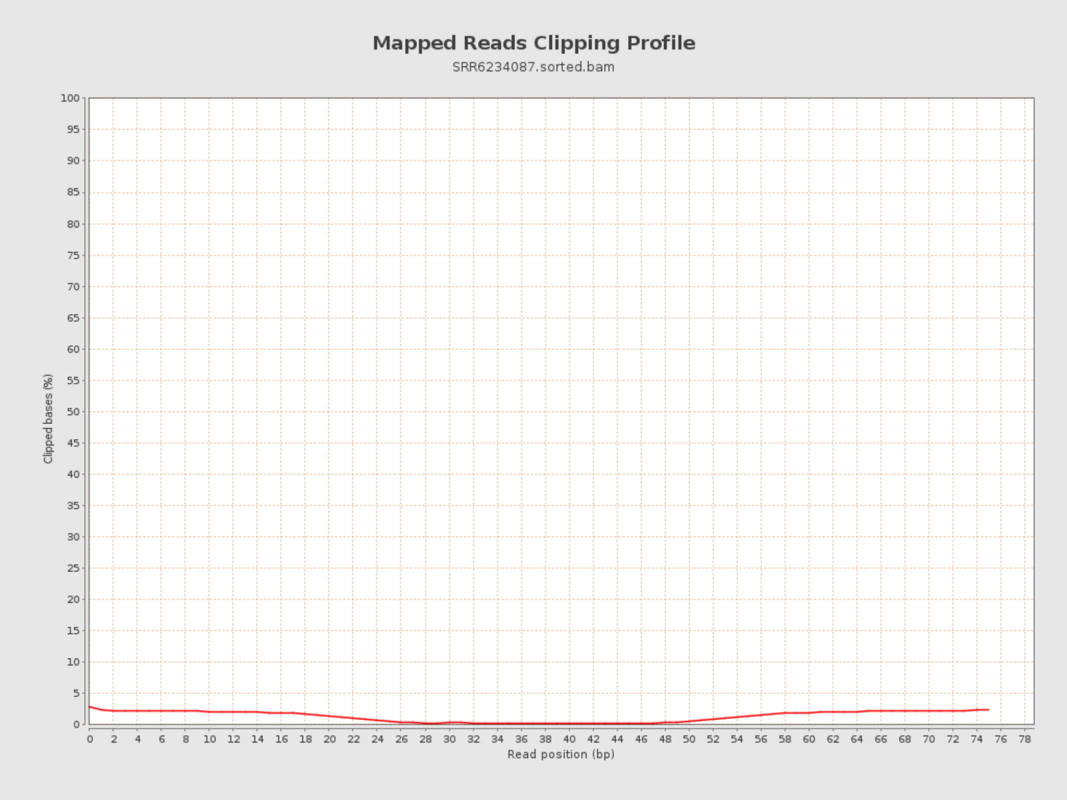
8. Results : Mapped Reads Nucleotide Content



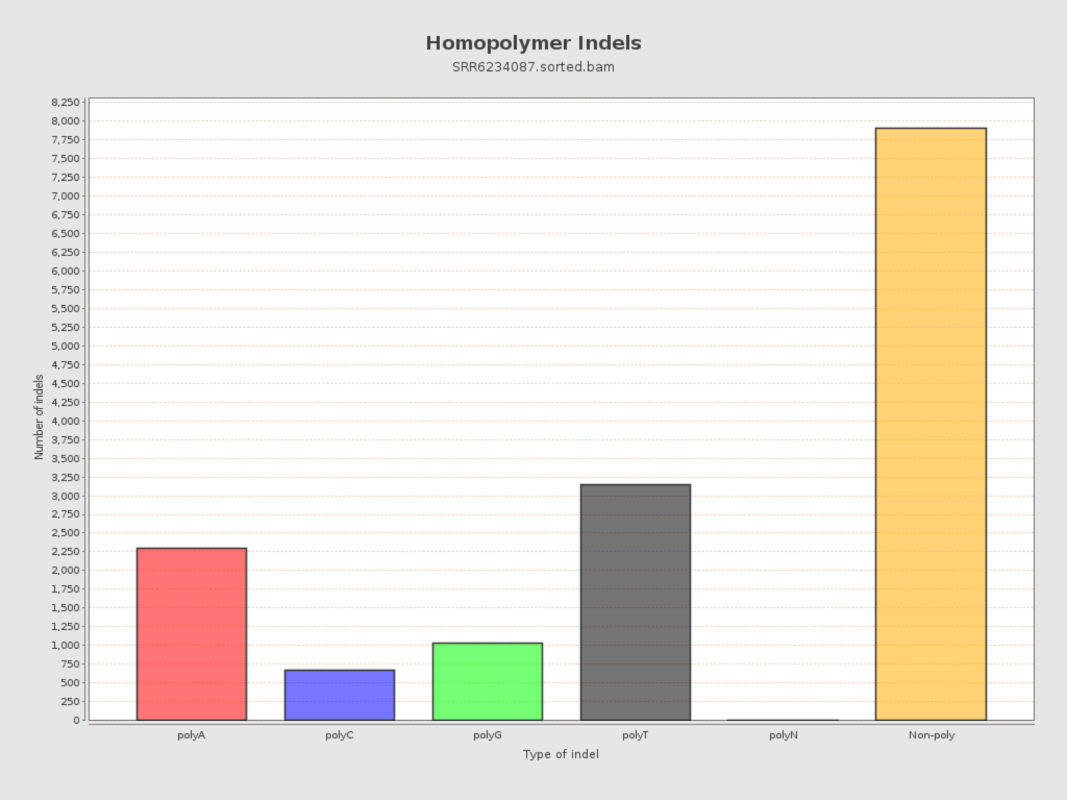
9. Results : Mapped Reads GC-content Distribution



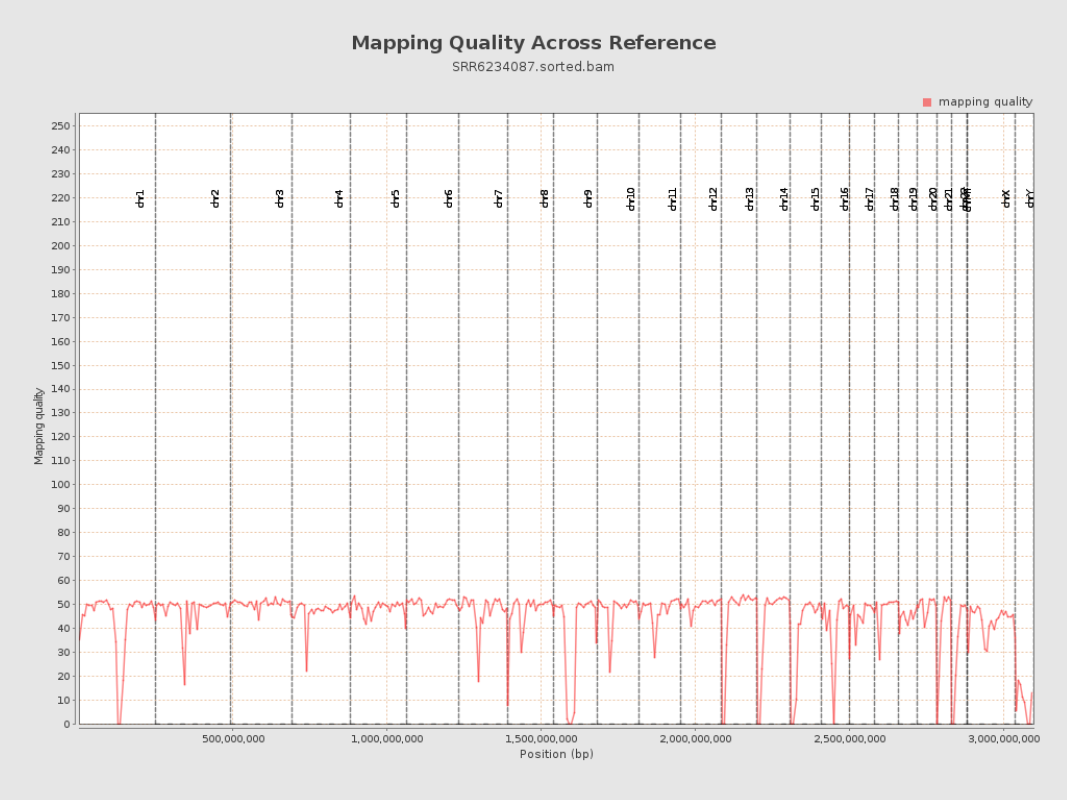
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram