Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:39:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234080.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_SRR6234080 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234080.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:39:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234080.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,076,613
Mapped reads	669,893 / 62.22%
Unmapped reads	406,720 / 37.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,450 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	25,412 / 2.36%
Duplication rate	2.88%
Clipped reads	343,909 / 31.94%

2.2. ACGT Content

Number/percentage of A's	12,365,762 / 28.53%
Number/percentage of C's	7,239,139 / 16.7%
Number/percentage of T's	14,036,173 / 32.39%
Number/percentage of G's	9,694,064 / 22.37%
Number/percentage of N's	3,868 / 0.01%
GC Percentage	39.07%

2.3. Coverage

Mean	0.014

Standard Deviation	0.1824

2.4. Mapping Quality

Mean Mapping Quality	45.79

2.5. Mismatches and indels

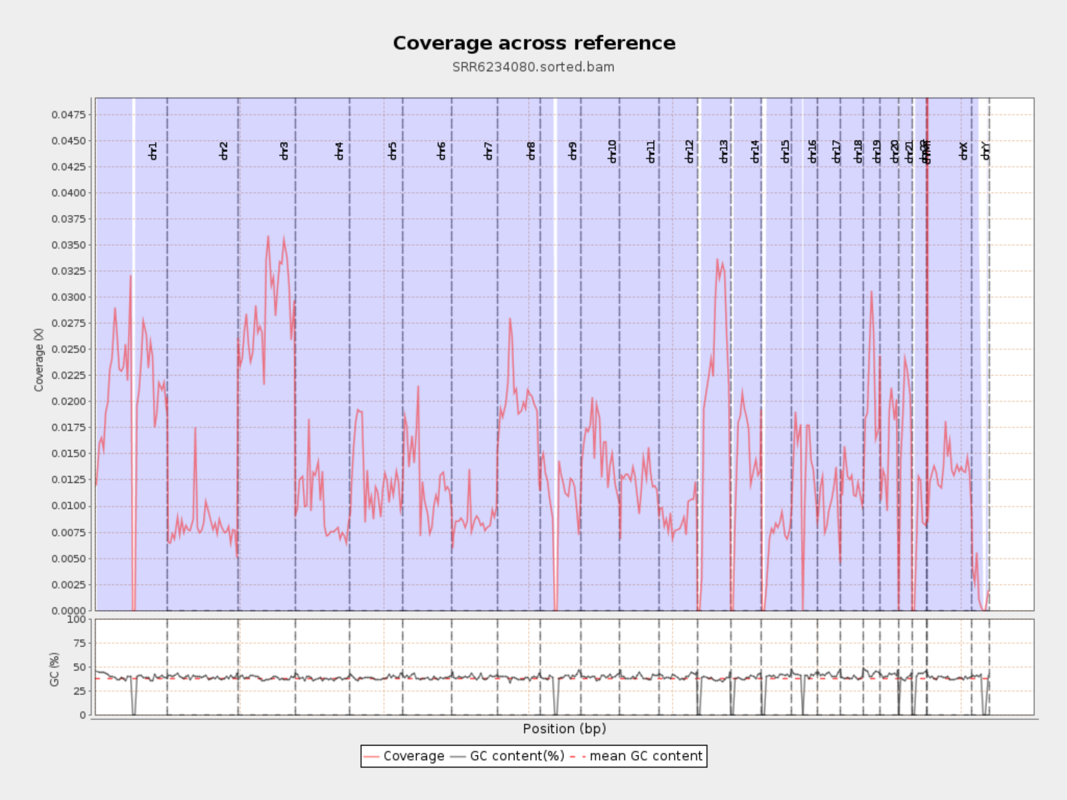
General error rate	1.03%
Mismatches	441,369
Insertions	3,956
Mapped reads with at least one insertion	0.59%
Deletions	13,578
Mapped reads with at least one deletion	2%
Homopolymer indels	45.29%

2.6. Chromosome stats

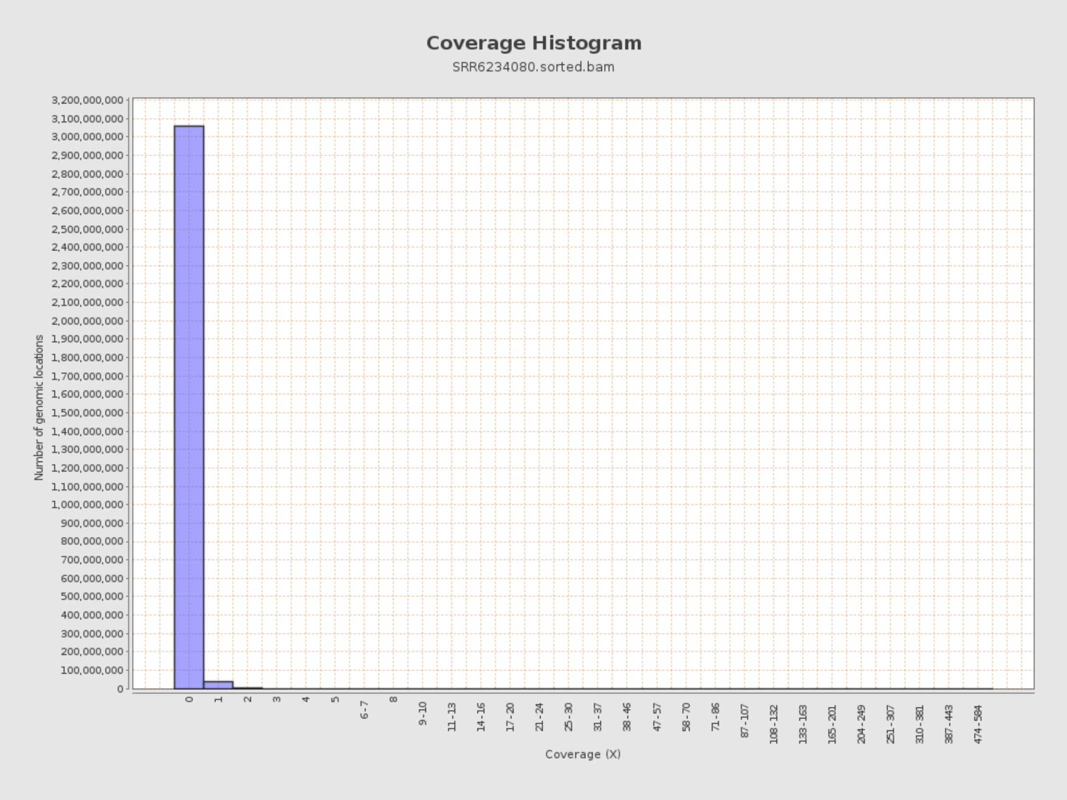
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5163635	0.0207	0.3294
chr2	243199373	1985182	0.0082	0.1634
chr3	198022430	5702748	0.0288	0.1869
chr4	191154276	1884266	0.0099	0.1105
chr5	180915260	2300923	0.0127	0.1225
chr6	171115067	2158087	0.0126	0.1321
chr7	159138663	1378407	0.0087	0.1205

chr8	146364022	2956292	0.0202	0.3865
chr9	141213431	1496601	0.0106	0.1263
chr10	135534747	2087159	0.0154	0.1505
chr11	135006516	1680584	0.0124	0.1362
chr12	133851895	1200844	0.009	0.1048
chr13	115169878	2515312	0.0218	0.161
chr14	107349540	1473161	0.0137	0.132
chr15	102531392	643159	0.0063	0.0864
chr16	90354753	1220790	0.0135	0.1418
chr17	81195210	820902	0.0101	0.1105
chr18	78077248	951789	0.0122	0.2241
chr19	59128983	1272687	0.0215	0.2145
chr20	63025520	977148	0.0155	0.145
chr21	48129895	866139	0.018	0.1471
chr22	51304566	389239	0.0076	0.0939
chrMT	16571	35403	2.1364	2.3287
chrX	155270560	2092211	0.0135	0.1312
chrY	59373566	110206	0.0019	0.0552

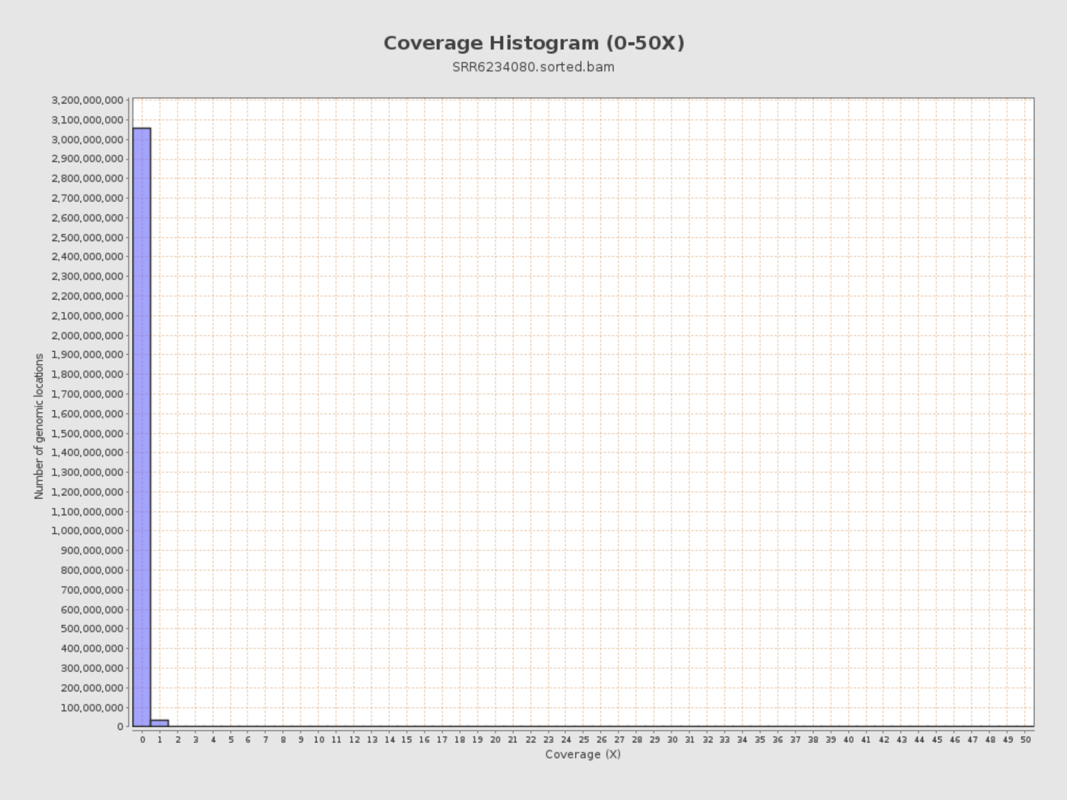
3. Results : Coverage across reference



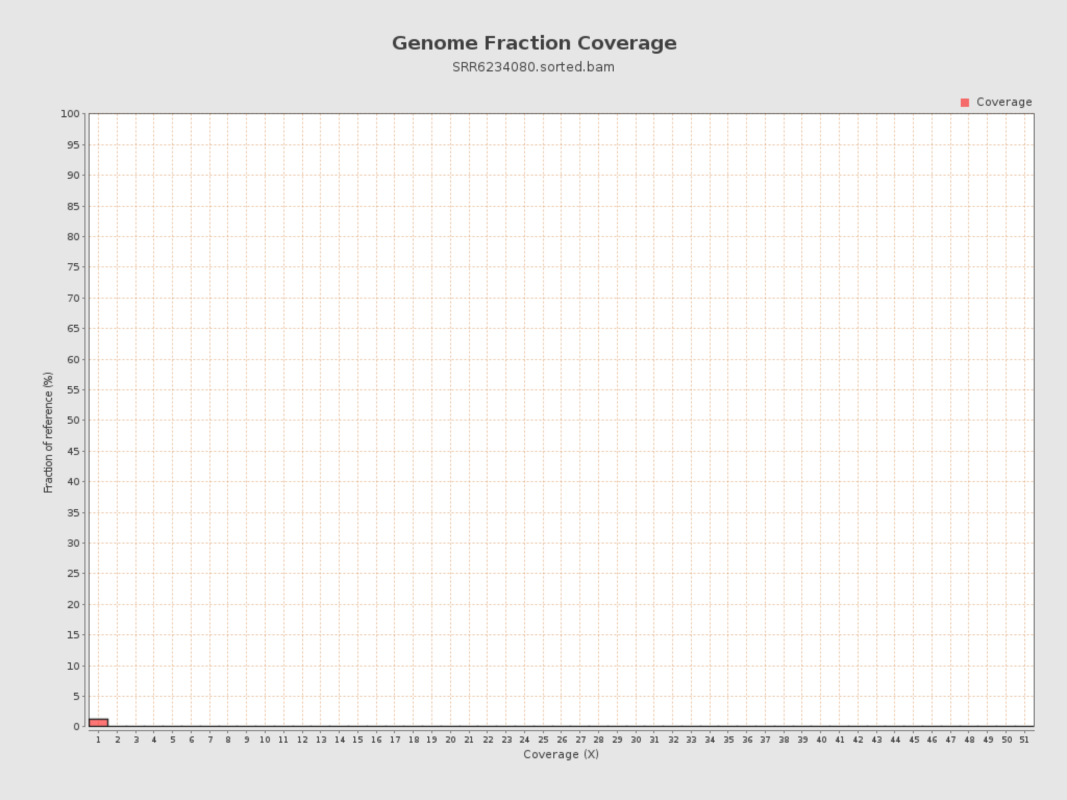
4. Results : Coverage Histogram



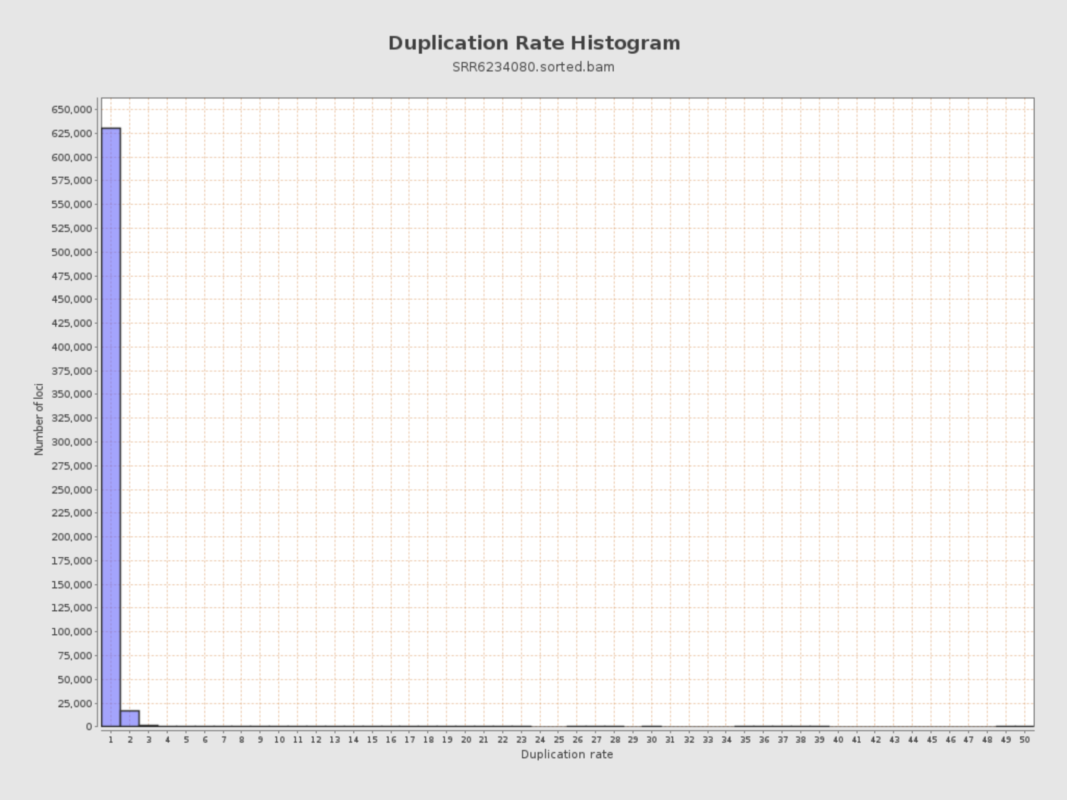
5. Results : Coverage Histogram (0-50X)



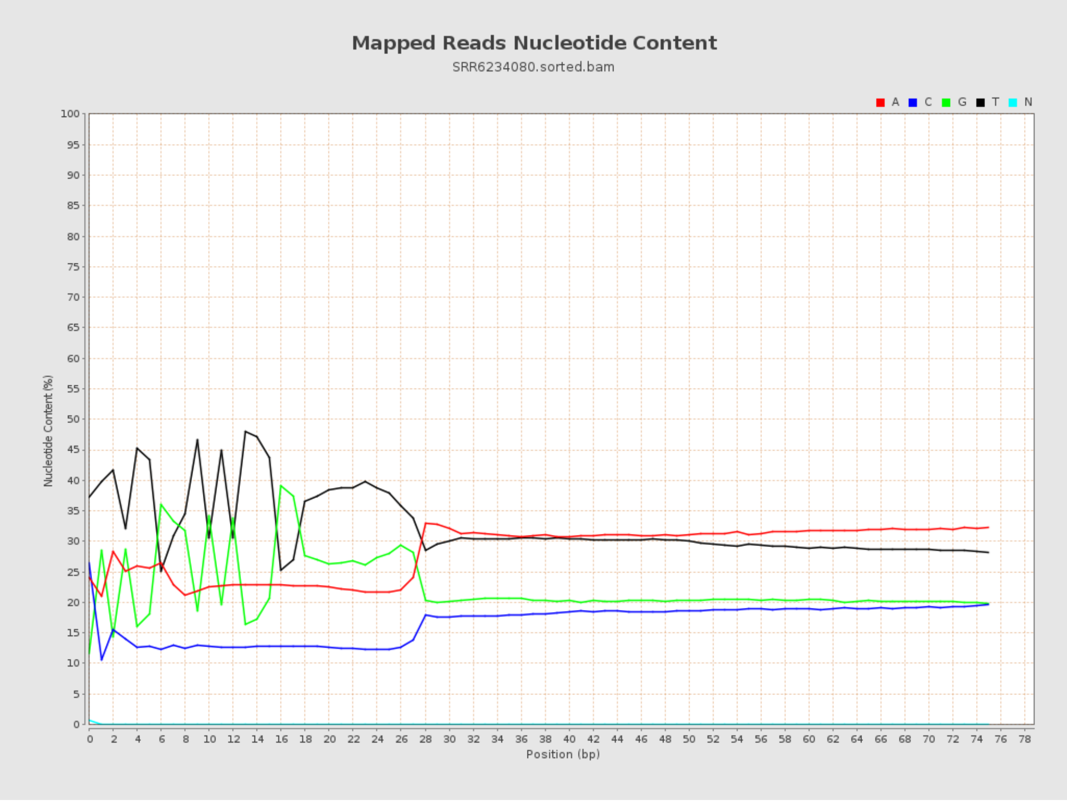
6. Results : Genome Fraction Coverage



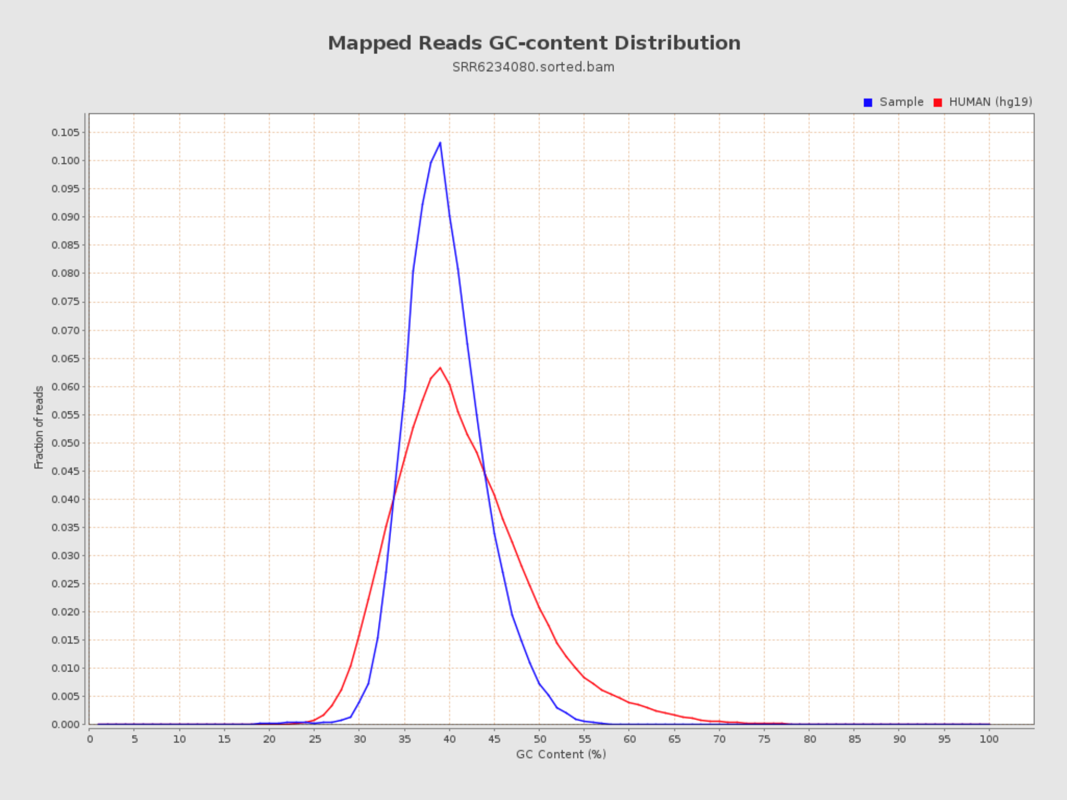
7. Results : Duplication Rate Histogram



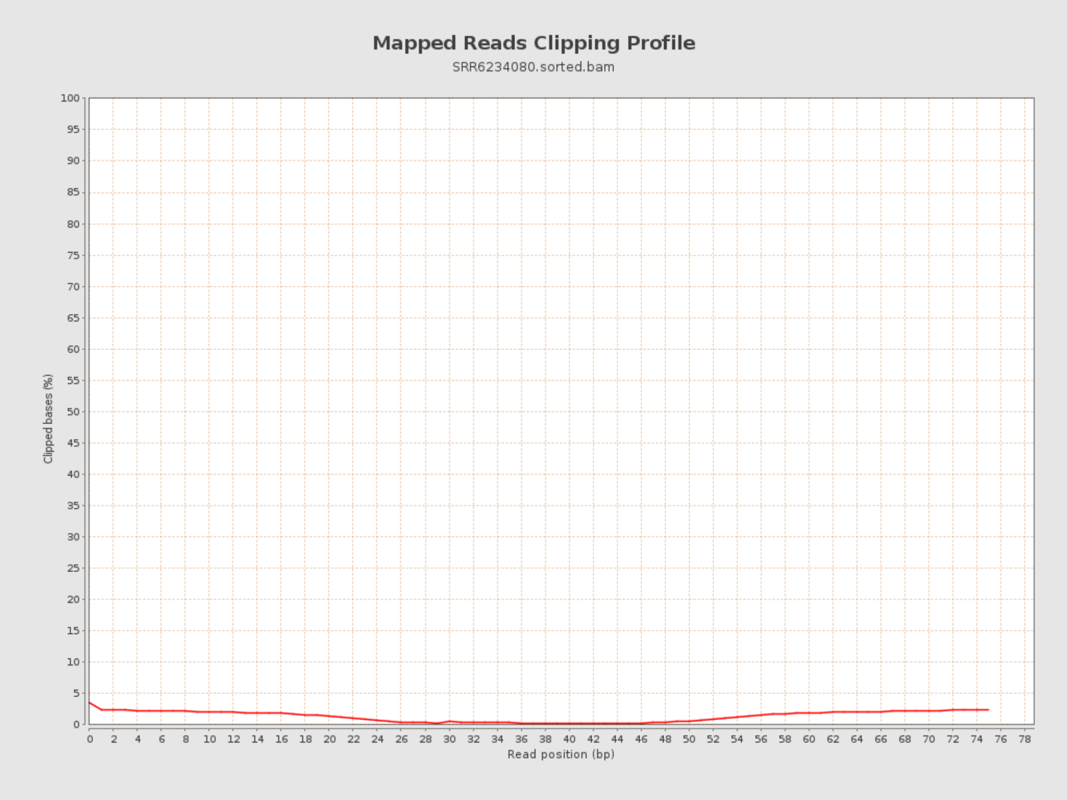
8. Results : Mapped Reads Nucleotide Content



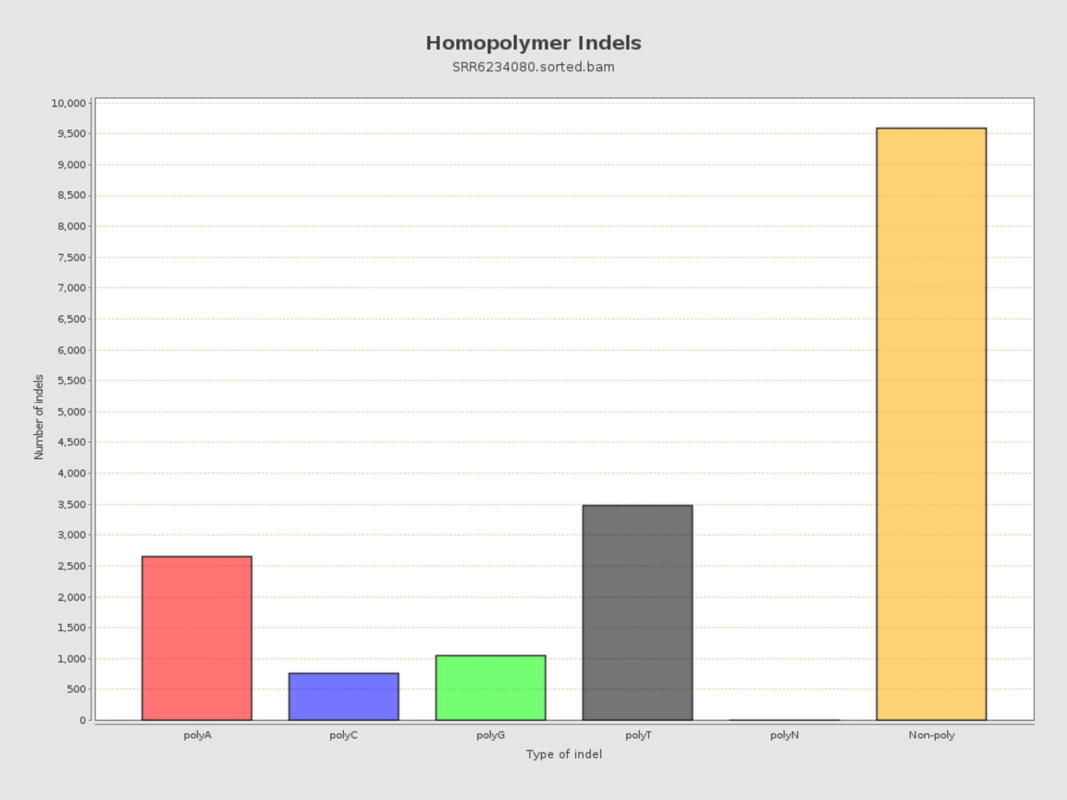
9. Results : Mapped Reads GC-content Distribution



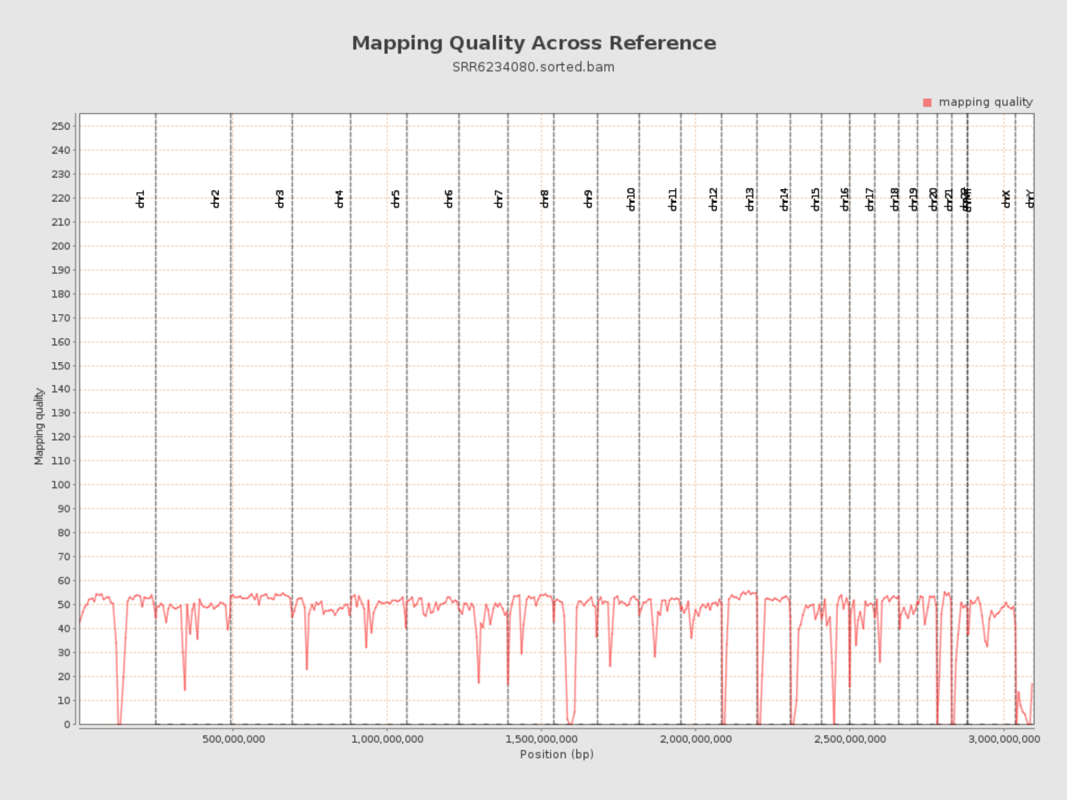
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram