Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 15:23:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234095.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_SRR6234095 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234095.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 15:23:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234095.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,716,285
Mapped reads	5,410,265 / 94.65%
Unmapped reads	306,020 / 5.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,016 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	797,345 / 13.95%
Duplication rate	12.1%
Clipped reads	2,756,441 / 48.22%

2.2. ACGT Content

Number/percentage of A's	89,742,788 / 25.59%
Number/percentage of C's	64,663,498 / 18.44%
Number/percentage of T's	112,475,437 / 32.07%
Number/percentage of G's	83,774,659 / 23.89%
Number/percentage of N's	34,448 / 0.01%
GC Percentage	42.33%

2.3. Coverage

Mean	0.1133

Standard Deviation	1.103

2.4. Mapping Quality

Mean Mapping Quality	42.75

2.5. Mismatches and indels

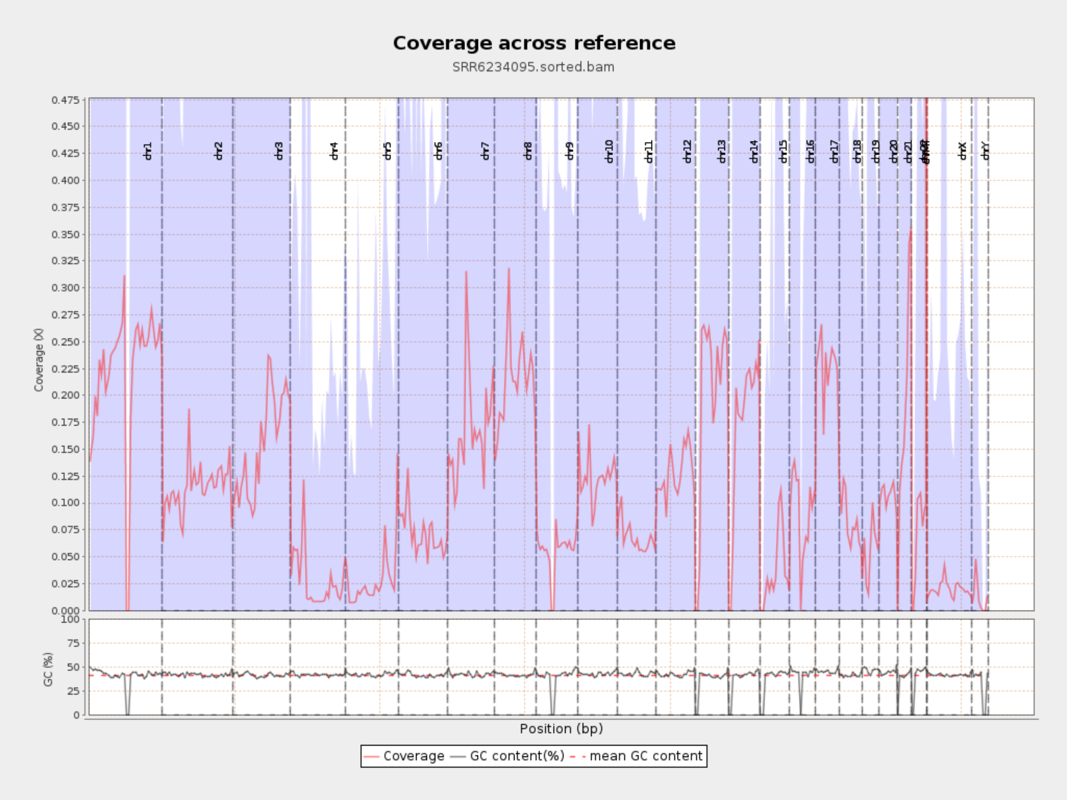
General error rate	0.55%
Mismatches	1,877,036
Insertions	23,036
Mapped reads with at least one insertion	0.42%
Deletions	80,326
Mapped reads with at least one deletion	1.47%
Homopolymer indels	44.16%

2.6. Chromosome stats

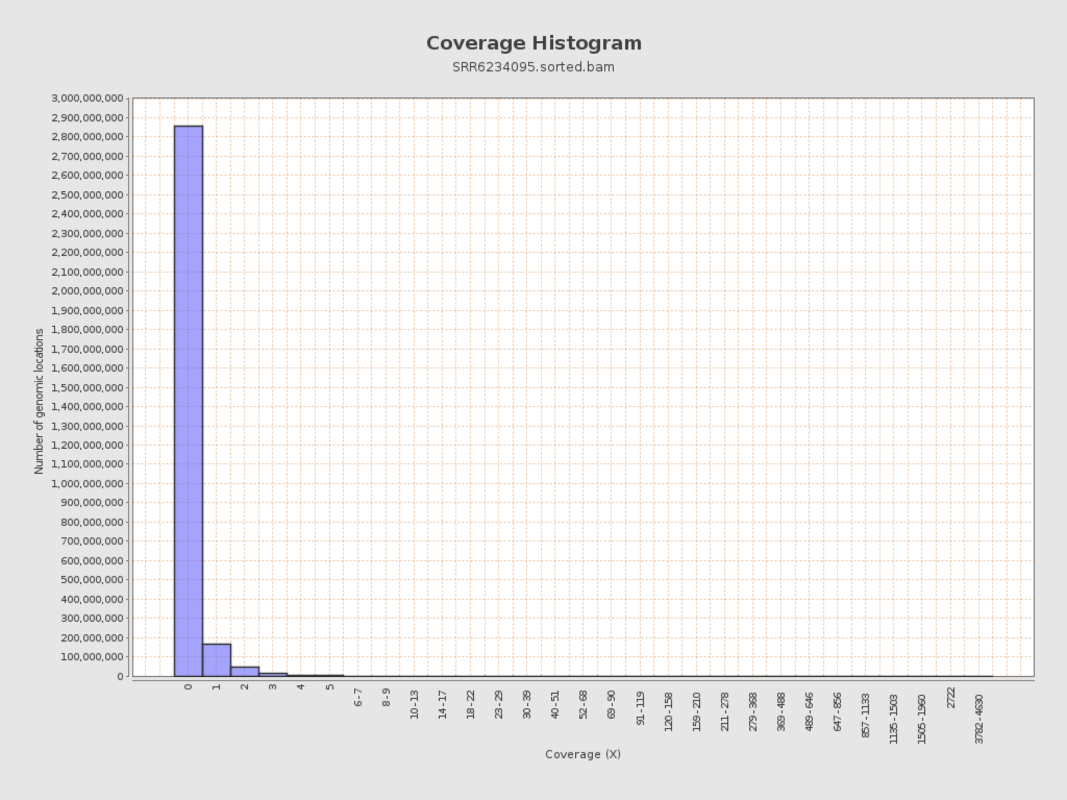
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	55341633	0.222	1.7227
chr2	243199373	27899692	0.1147	2.1143
chr3	198022430	30710226	0.1551	0.534
chr4	191154276	5240187	0.0274	0.3728
chr5	180915260	4898042	0.0271	0.2502
chr6	171115067	12243148	0.0715	0.5998
chr7	159138663	27041327	0.1699	2.0732

chr8	146364022	31312453	0.2139	1.3681
chr9	141213431	7691041	0.0545	0.5298
chr10	135534747	16778998	0.1238	0.8955
chr11	135006516	9137613	0.0677	0.5917
chr12	133851895	17267878	0.129	0.4927
chr13	115169878	22906097	0.1989	0.6622
chr14	107349540	18213312	0.1697	0.6121
chr15	102531392	3857129	0.0376	0.3273
chr16	90354753	8345009	0.0924	0.5358
chr17	81195210	18322929	0.2257	0.7798
chr18	78077248	6589132	0.0844	1.761
chr19	59128983	3302307	0.0558	1.0607
chr20	63025520	6771574	0.1074	0.5588
chr21	48129895	9173638	0.1906	0.6449
chr22	51304566	3422703	0.0667	0.3417
chrMT	16571	531572	32.0785	19.1065
chrX	155270560	3114145	0.0201	0.3796
chrY	59373566	719684	0.0121	0.3201

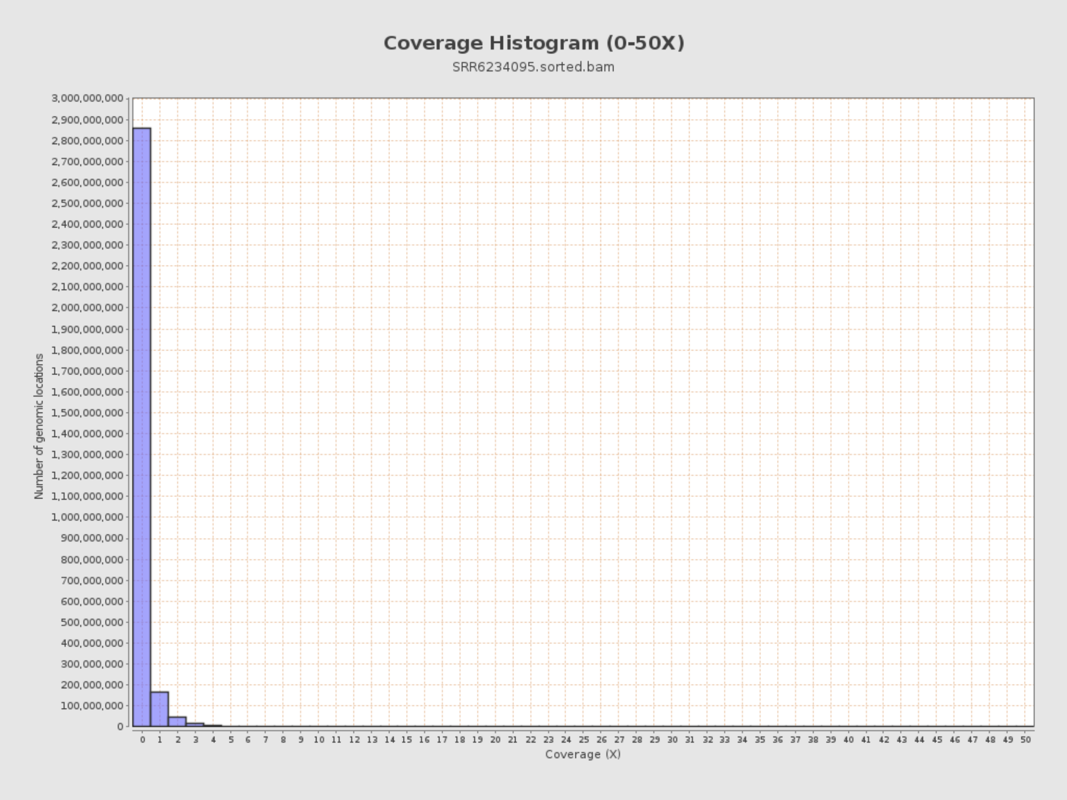
3. Results : Coverage across reference



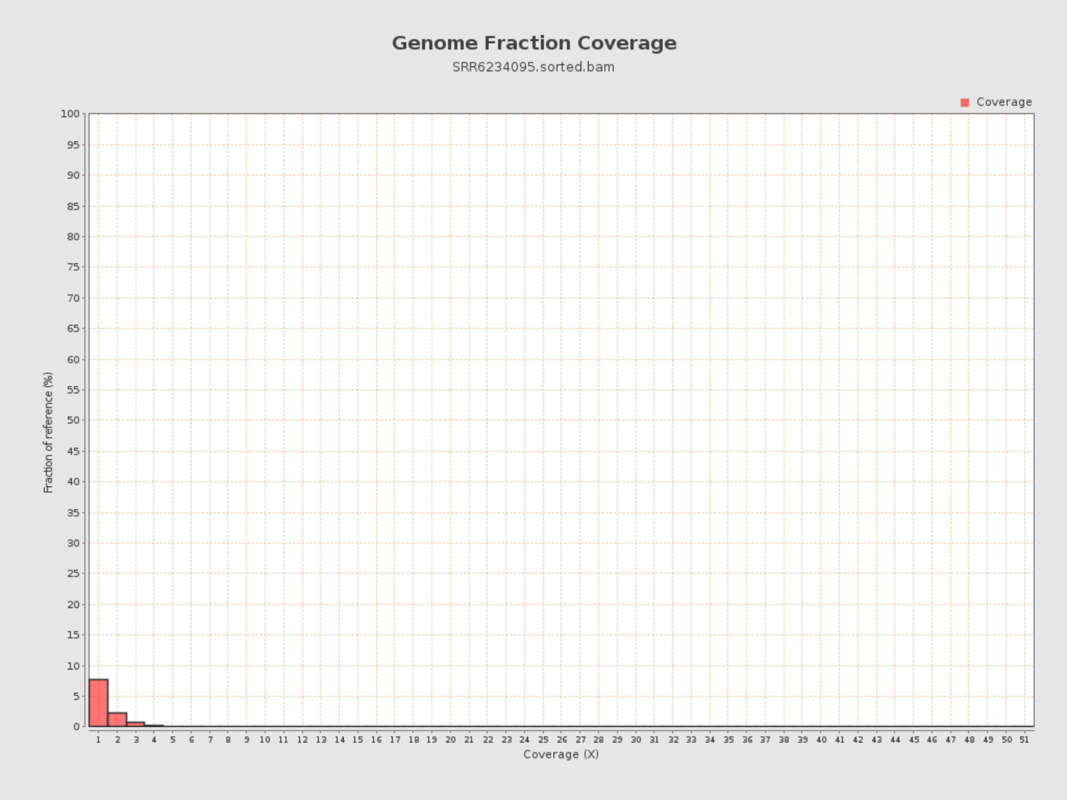
4. Results : Coverage Histogram



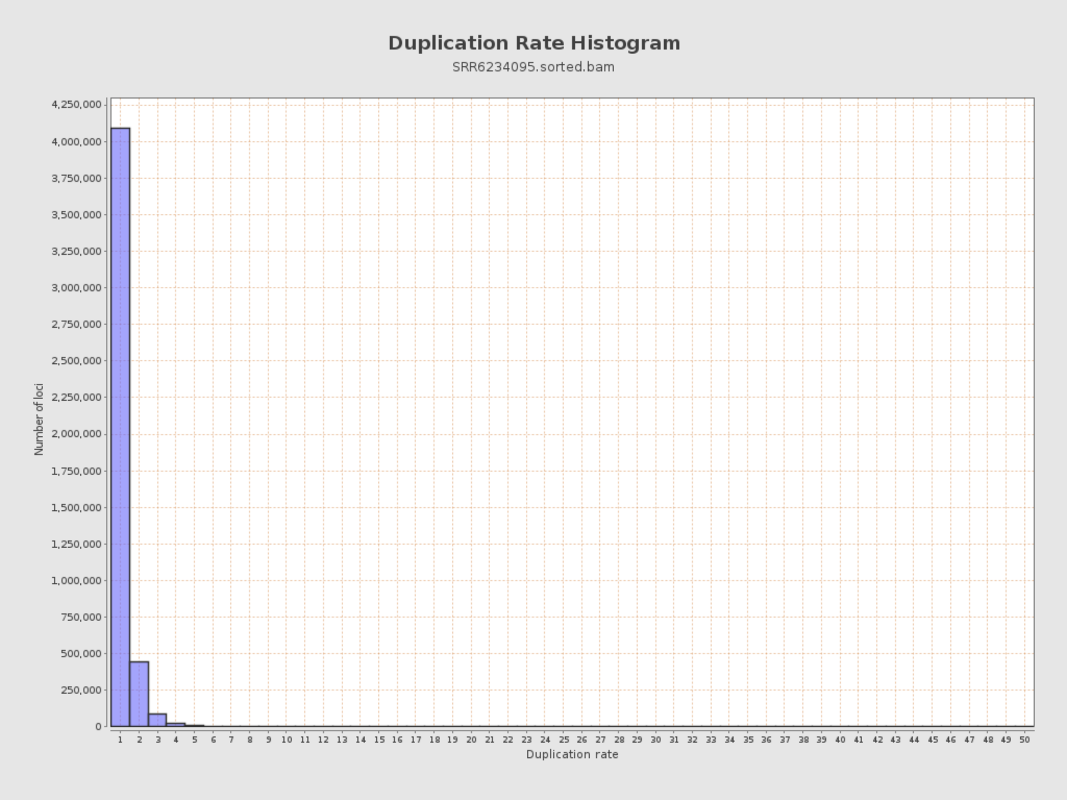
5. Results : Coverage Histogram (0-50X)



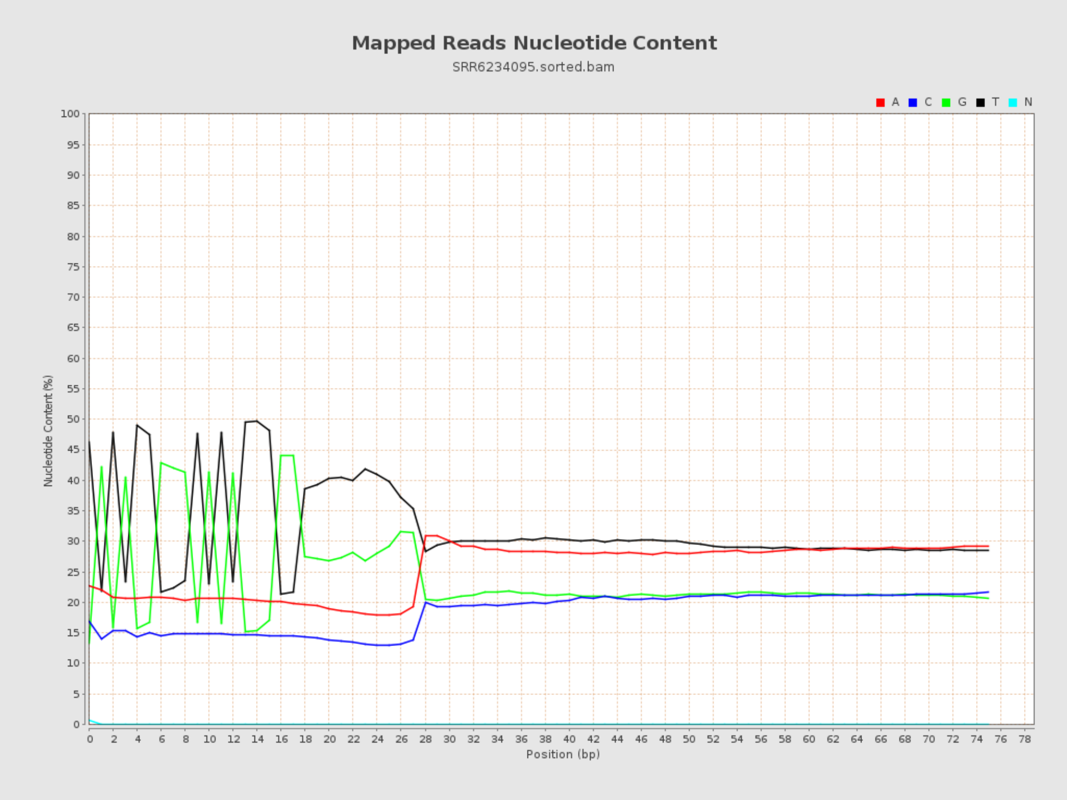
6. Results : Genome Fraction Coverage



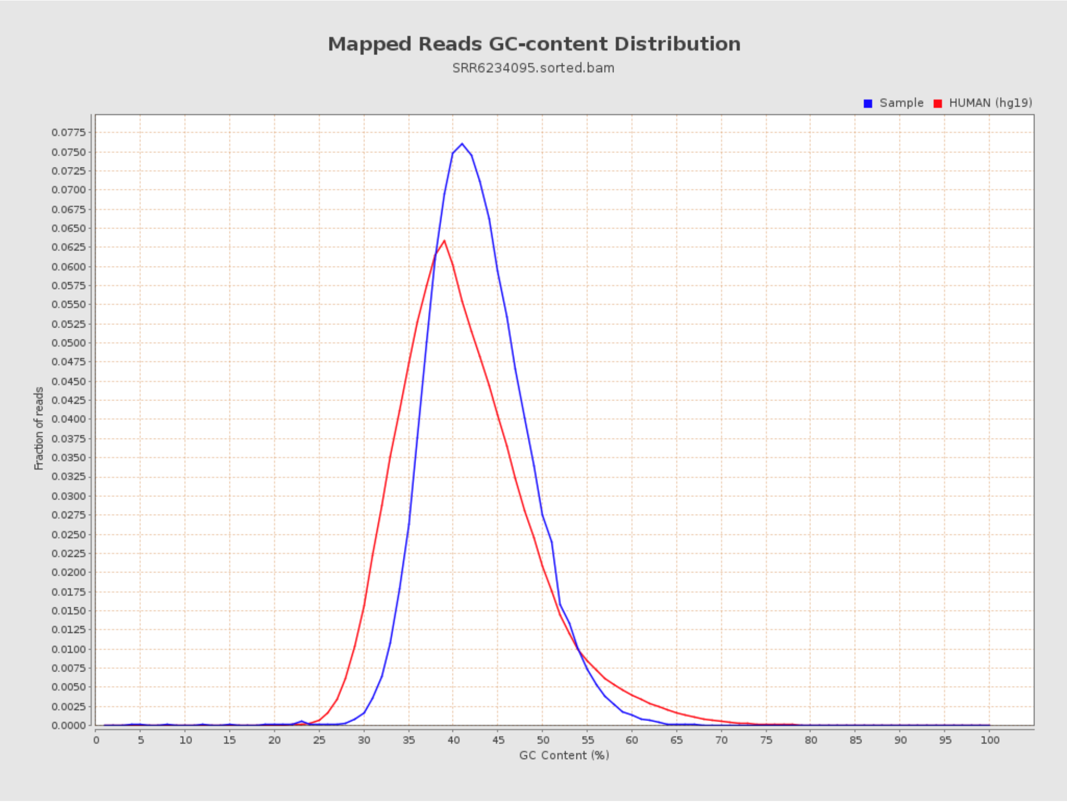
7. Results : Duplication Rate Histogram



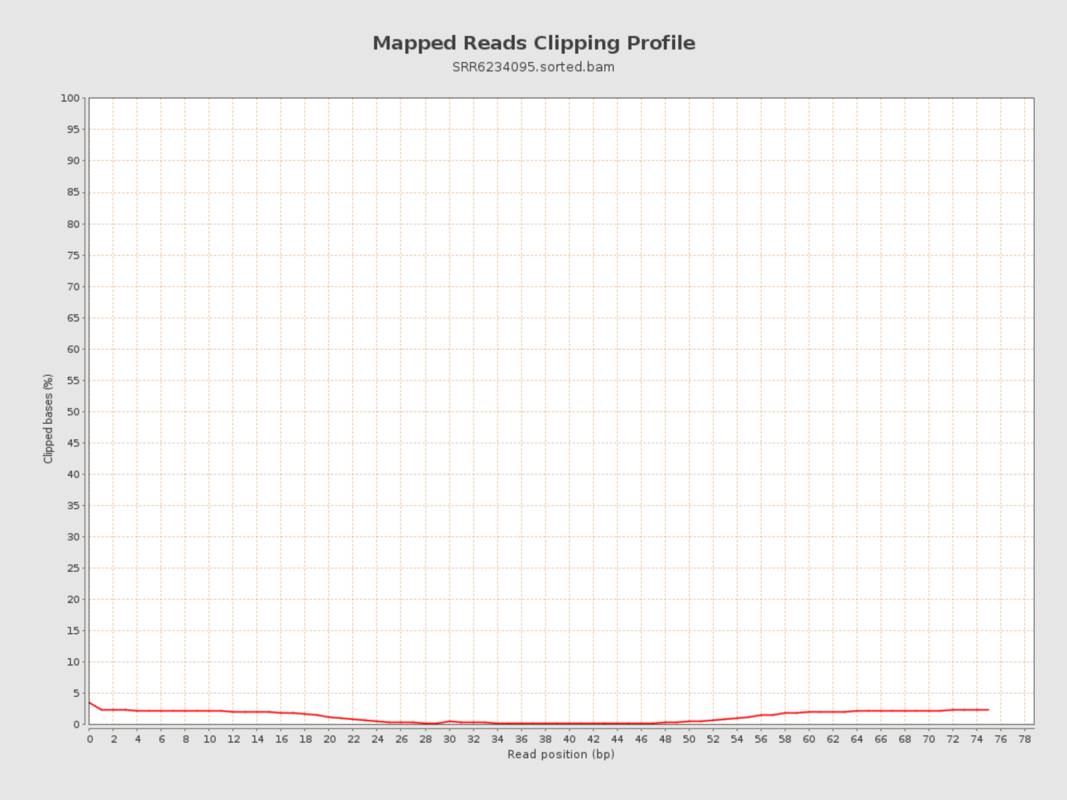
8. Results : Mapped Reads Nucleotide Content



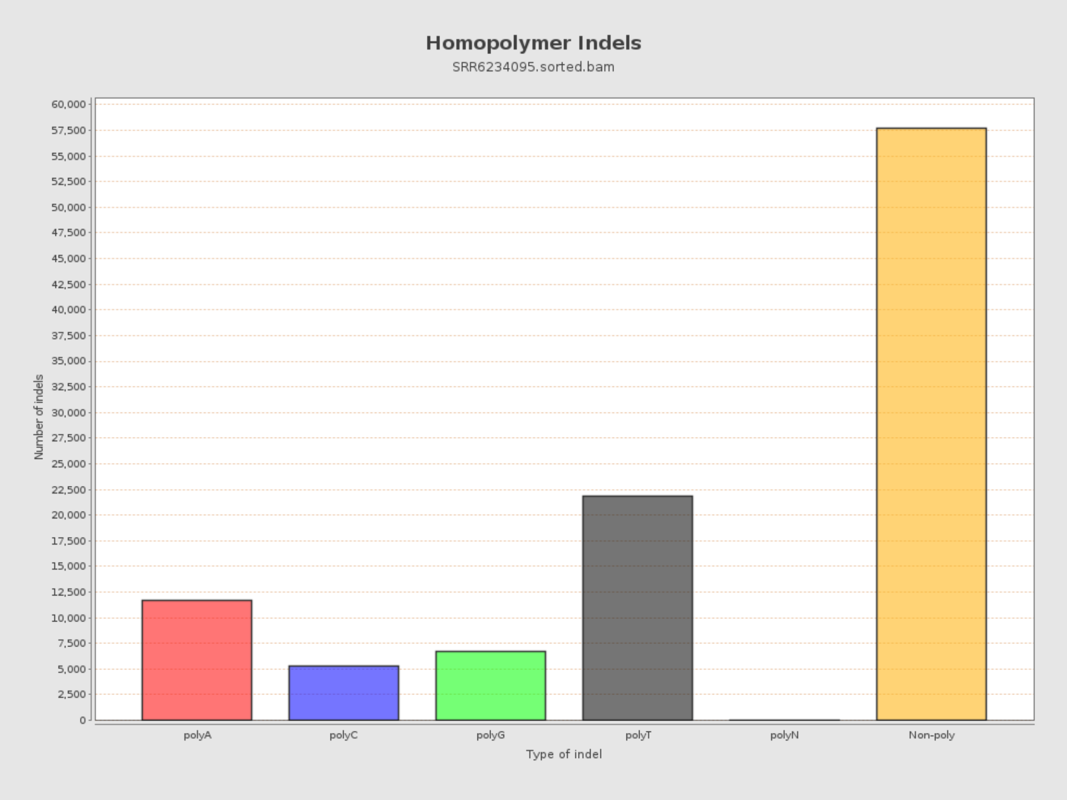
9. Results : Mapped Reads GC-content Distribution



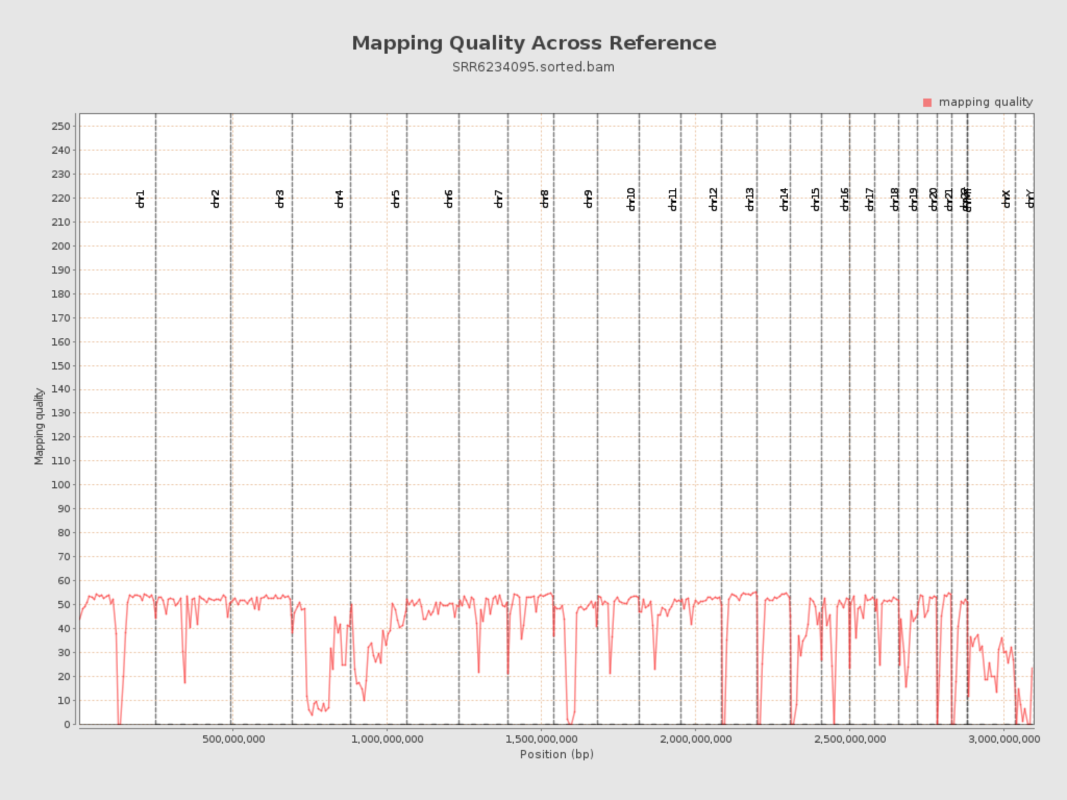
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram