Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 13:57:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234071.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_SRR6234071 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234071.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 13:57:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234071.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,605,264
Mapped reads	4,339,247 / 94.22%
Unmapped reads	266,017 / 5.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,167 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	477,114 / 10.36%
Duplication rate	9.11%
Clipped reads	2,308,818 / 50.13%

2.2. ACGT Content

Number/percentage of A's	72,052,964 / 25.82%
Number/percentage of C's	50,237,354 / 18%
Number/percentage of T's	90,972,125 / 32.6%
Number/percentage of G's	65,775,419 / 23.57%
Number/percentage of N's	26,416 / 0.01%
GC Percentage	41.57%

2.3. Coverage

Mean	0.0902

Standard Deviation	1.0071

2.4. Mapping Quality

Mean Mapping Quality	45.38

2.5. Mismatches and indels

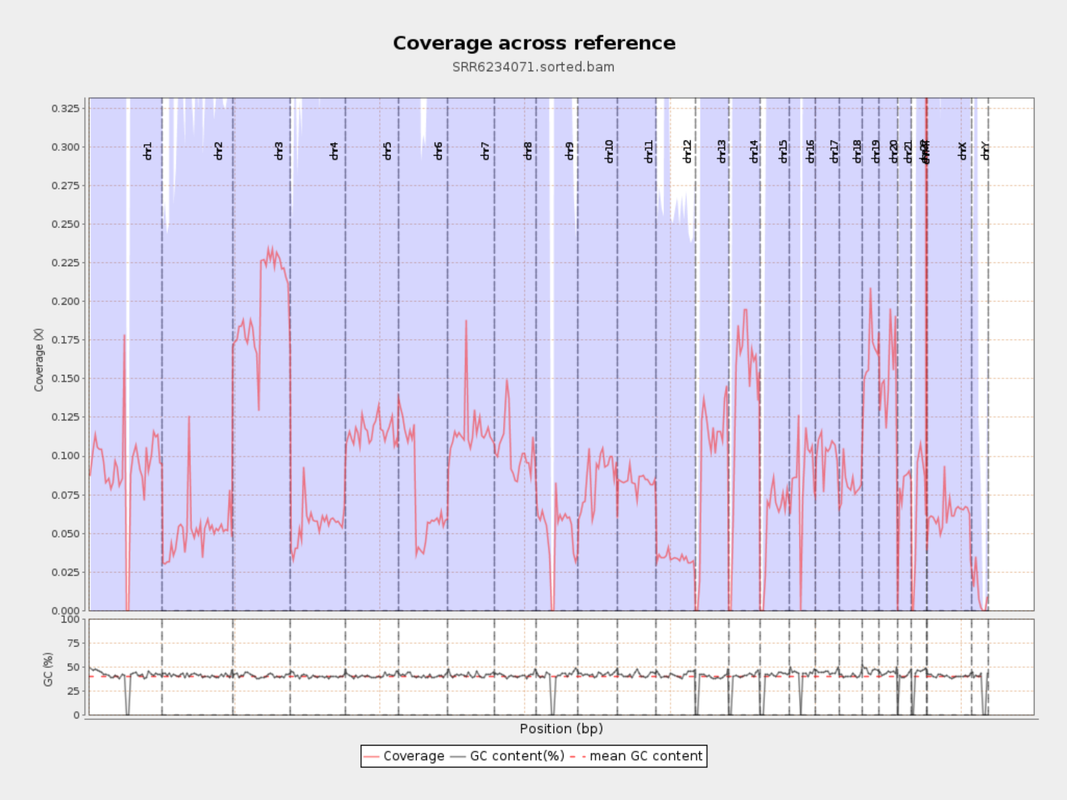
General error rate	0.56%
Mismatches	1,530,376
Insertions	17,939
Mapped reads with at least one insertion	0.41%
Deletions	62,211
Mapped reads with at least one deletion	1.42%
Homopolymer indels	44.16%

2.6. Chromosome stats

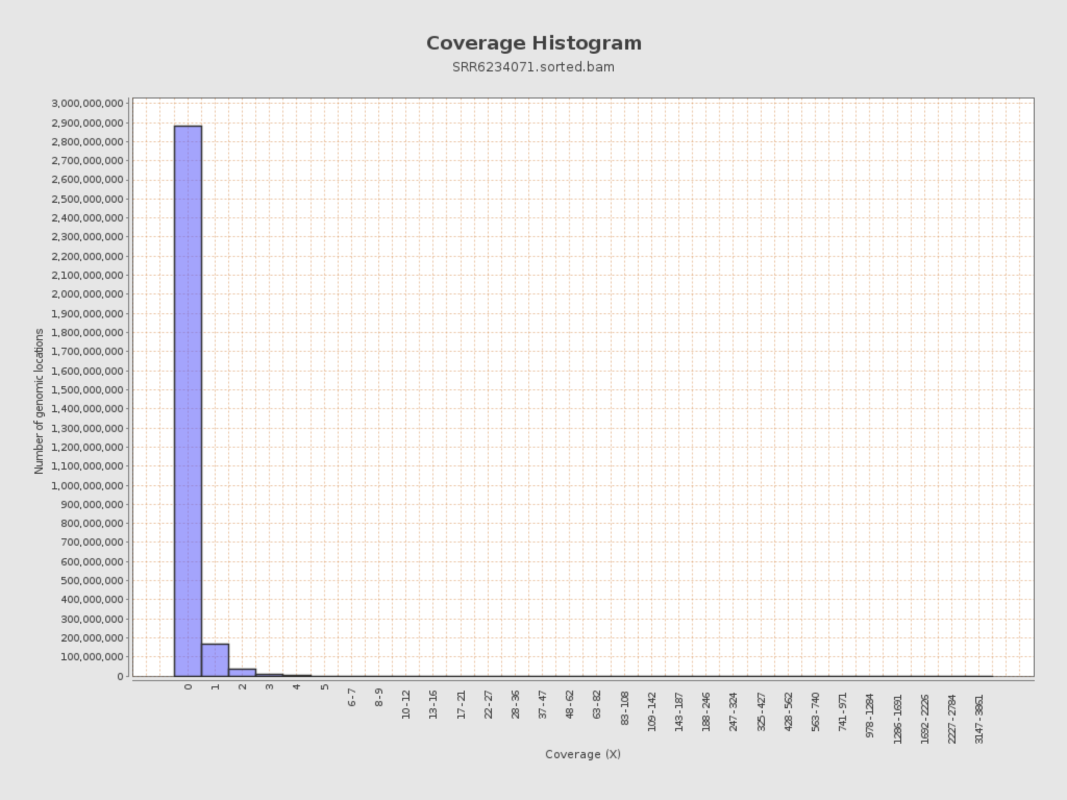
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23043474	0.0925	2.2051
chr2	243199373	12403970	0.051	1.7523
chr3	198022430	39598703	0.2	0.5651
chr4	191154276	10698817	0.056	0.3401
chr5	180915260	20879943	0.1154	0.4392
chr6	171115067	12945152	0.0757	0.562
chr7	159138663	18560572	0.1166	1.2147

chr8	146364022	15038571	0.1027	1.1803
chr9	141213431	7080507	0.0501	0.5821
chr10	135534747	11611658	0.0857	0.5992
chr11	135006516	11280716	0.0836	0.6602
chr12	133851895	4520060	0.0338	0.273
chr13	115169878	11505977	0.0999	0.4487
chr14	107349540	14872879	0.1385	0.4908
chr15	102531392	5985392	0.0584	0.3398
chr16	90354753	7807768	0.0864	0.4373
chr17	81195210	8257858	0.1017	0.4667
chr18	78077248	6336413	0.0812	1.409
chr19	59128983	9808751	0.1659	1.2219
chr20	63025520	9572509	0.1519	0.5117
chr21	48129895	3613837	0.0751	0.3702
chr22	51304566	3370787	0.0657	0.313
chrMT	16571	102224	6.1688	4.049
chrX	155270560	9637093	0.0621	0.41
chrY	59373566	637887	0.0107	0.2313

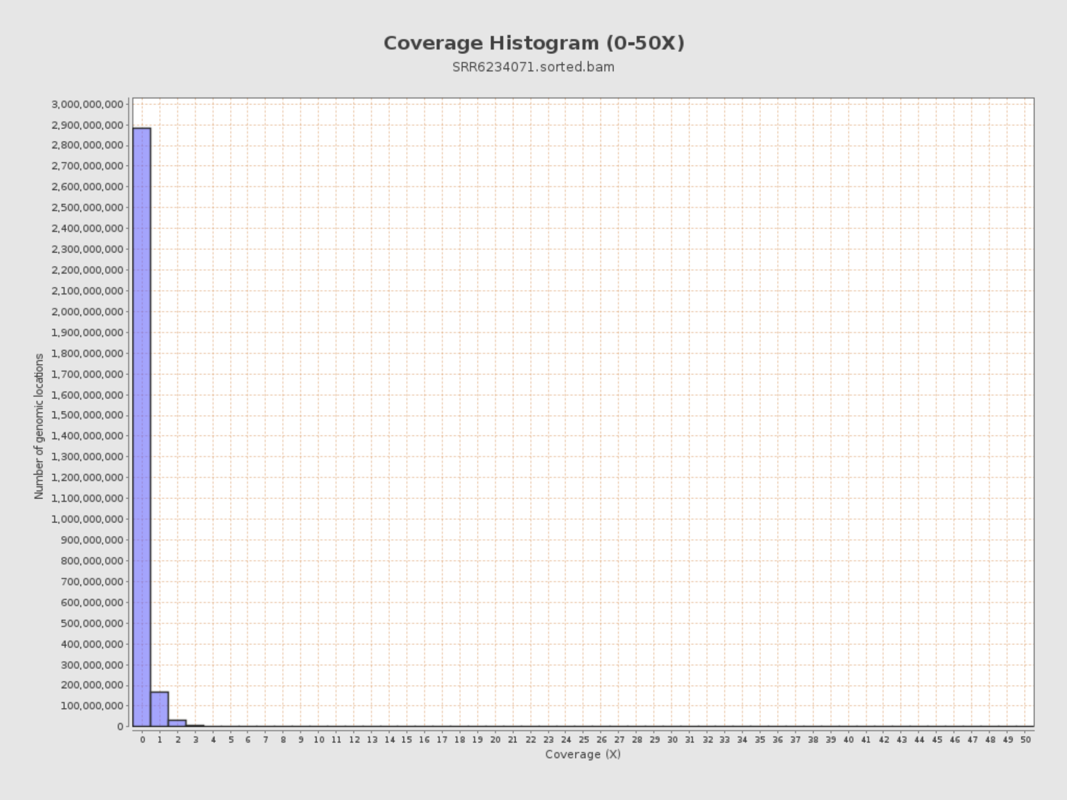
3. Results : Coverage across reference



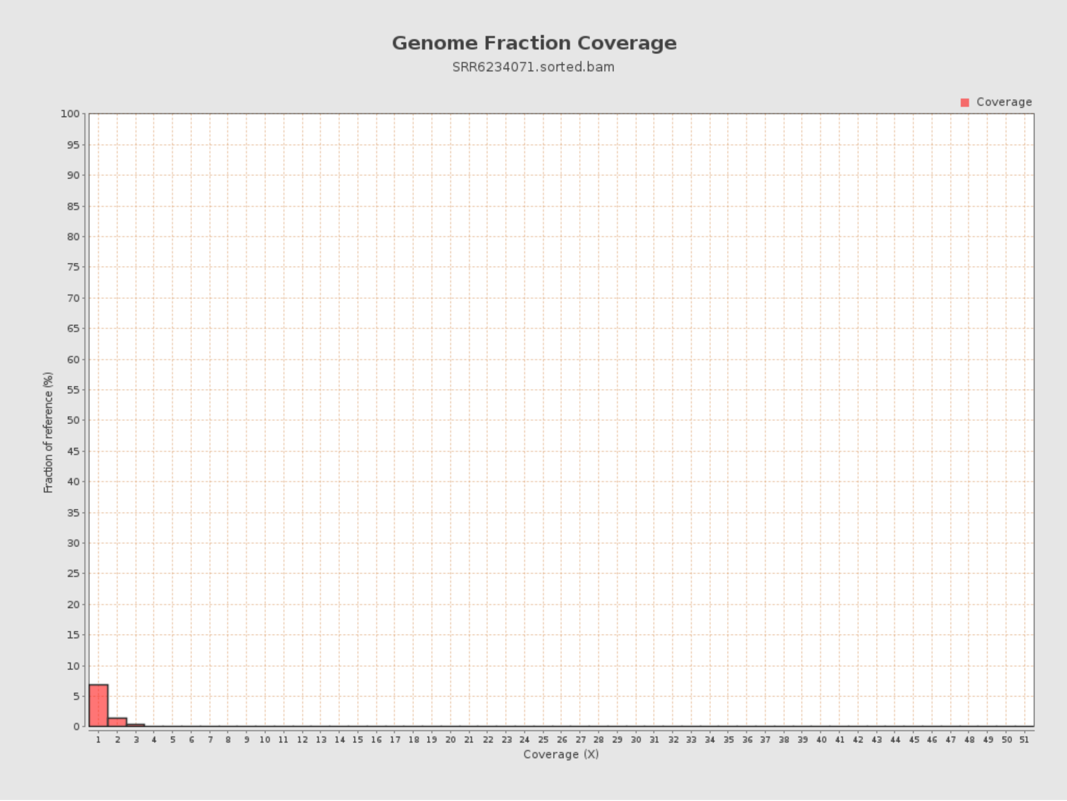
4. Results : Coverage Histogram



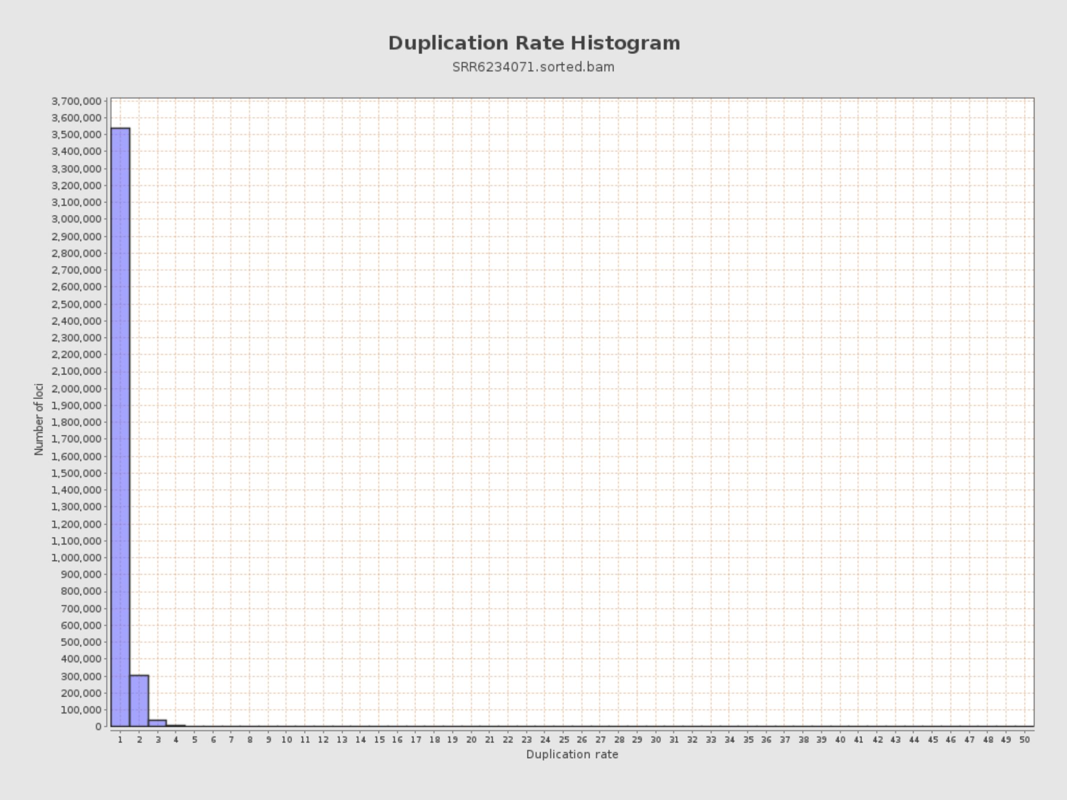
5. Results : Coverage Histogram (0-50X)



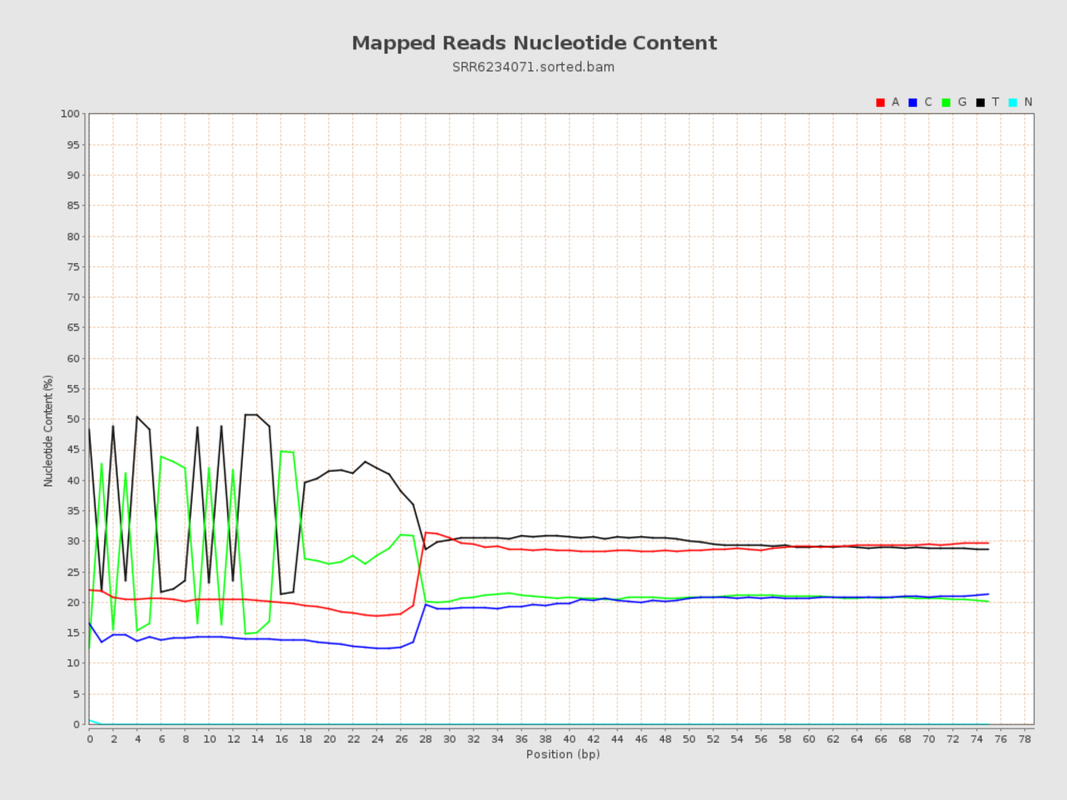
6. Results : Genome Fraction Coverage



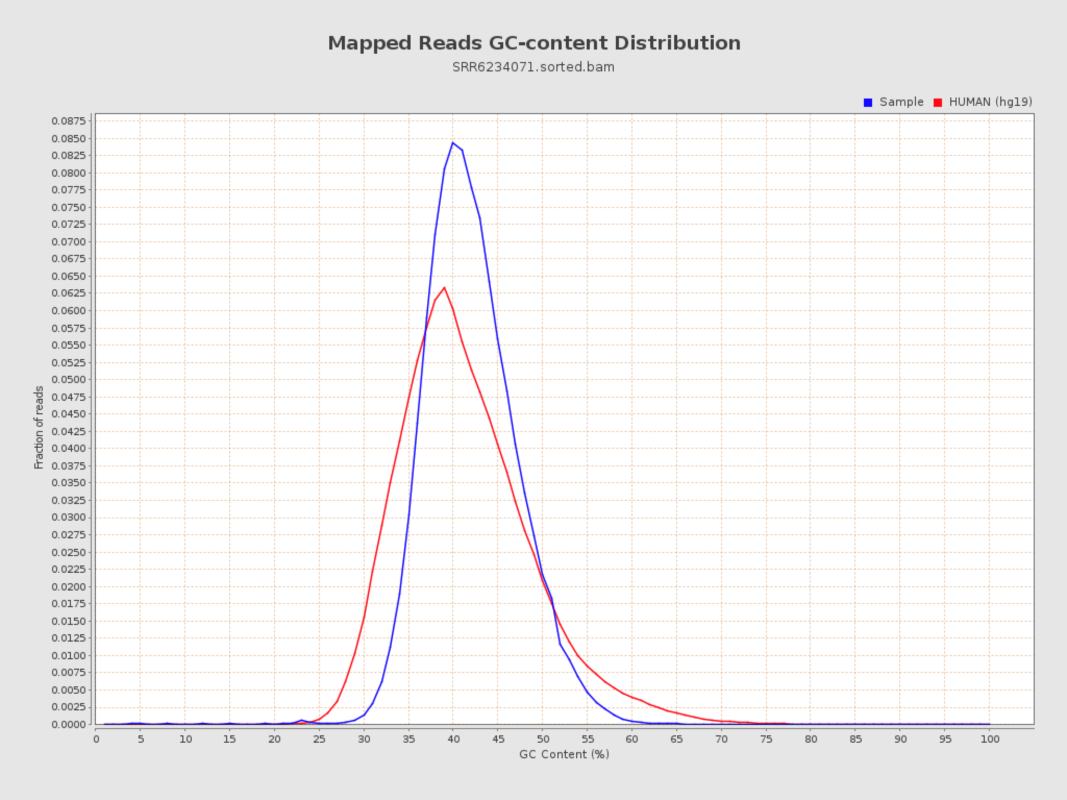
7. Results : Duplication Rate Histogram



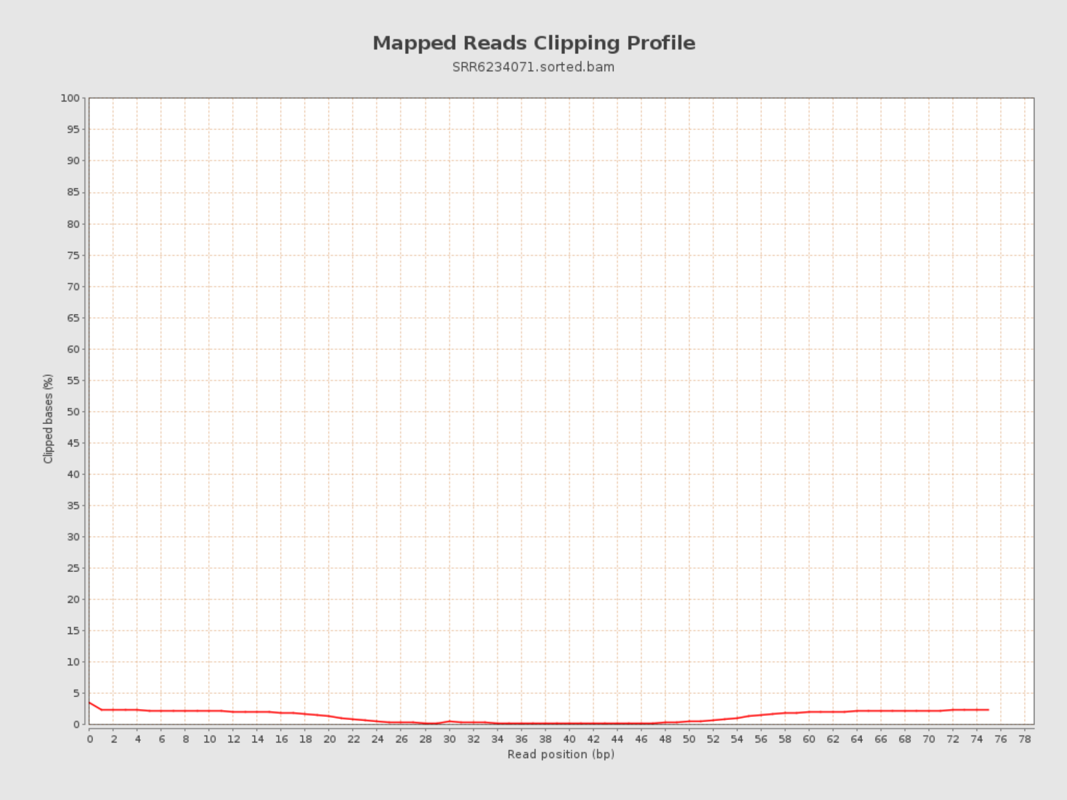
8. Results : Mapped Reads Nucleotide Content



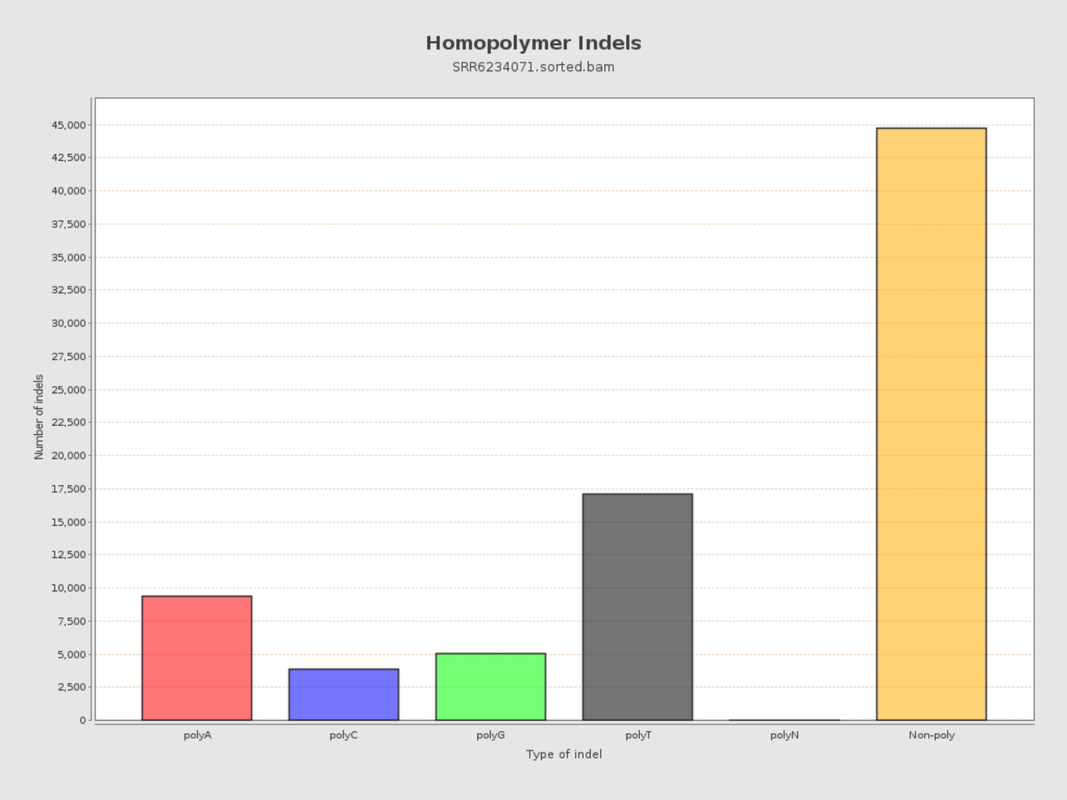
9. Results : Mapped Reads GC-content Distribution



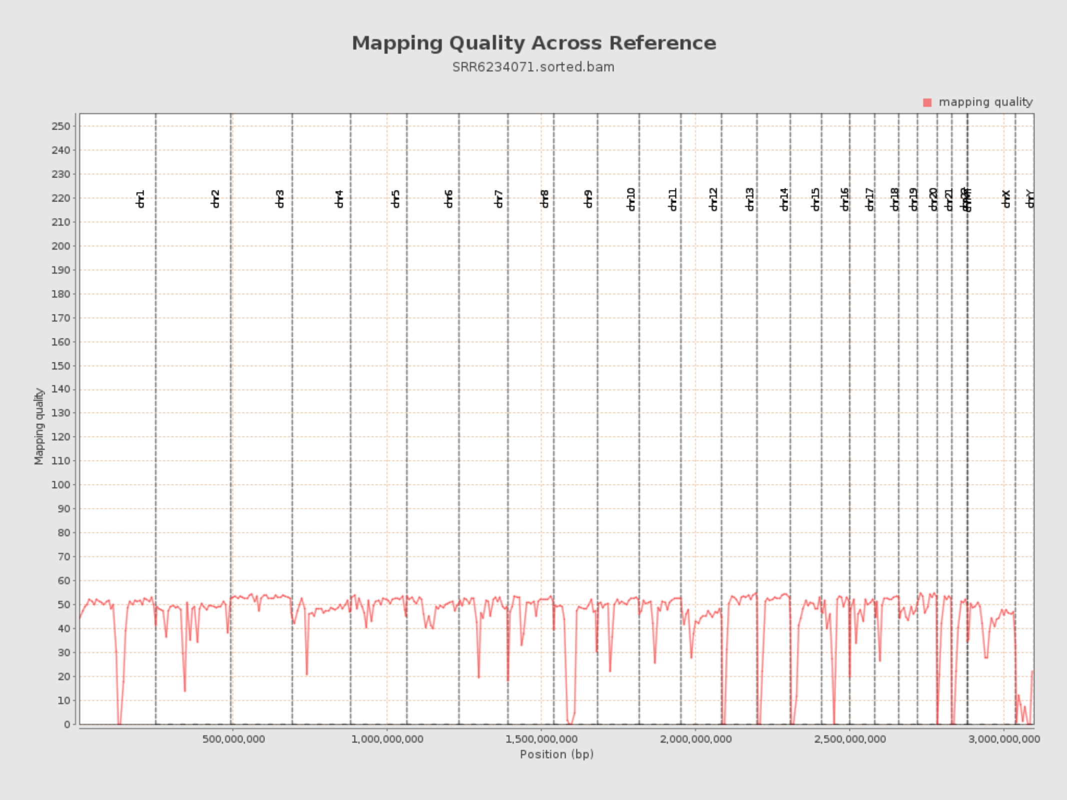
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram