Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:51:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234042.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_SRR6234042 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234042.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:51:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234042.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,814,930
Mapped reads	3,483,809 / 91.32%
Unmapped reads	331,121 / 8.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,360 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	307,772 / 8.07%
Duplication rate	6.46%
Clipped reads	1,796,701 / 47.1%

2.2. ACGT Content

Number/percentage of A's	58,032,697 / 25.69%
Number/percentage of C's	42,307,387 / 18.73%
Number/percentage of T's	71,017,888 / 31.43%
Number/percentage of G's	54,483,366 / 24.12%
Number/percentage of N's	86,445 / 0.04%
GC Percentage	42.84%

2.3. Coverage

Mean	0.073

Standard Deviation	1.1639

2.4. Mapping Quality

Mean Mapping Quality	40.36

2.5. Mismatches and indels

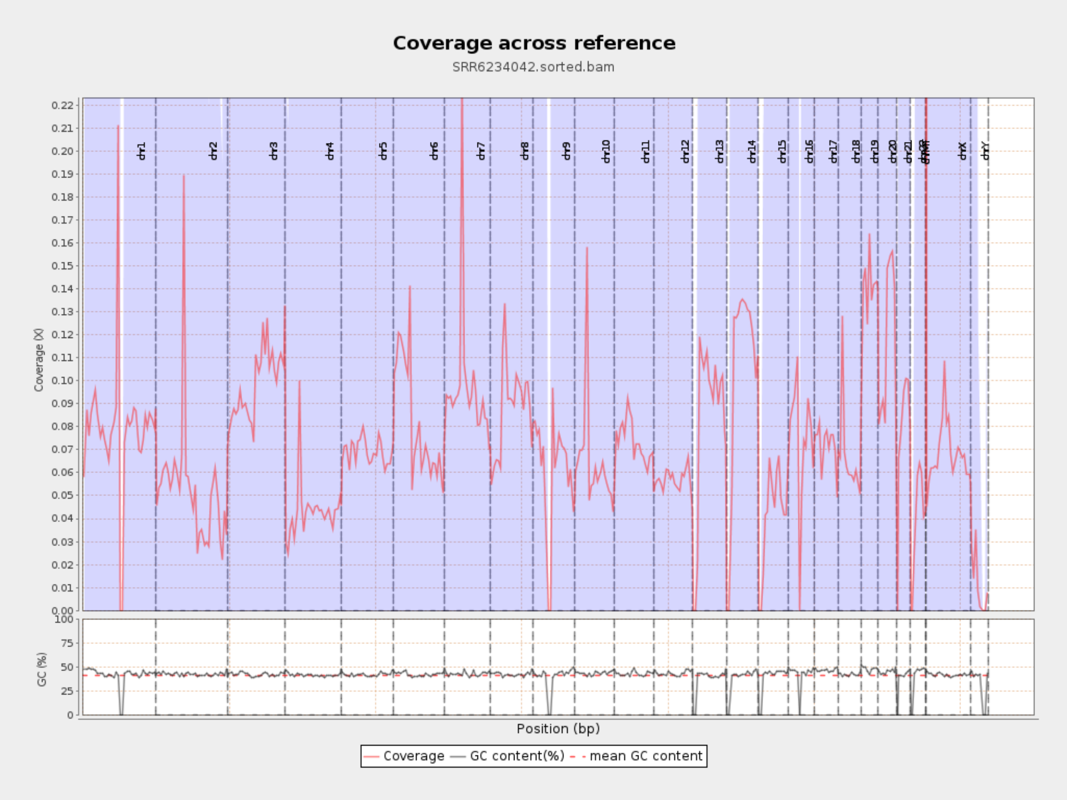
General error rate	0.73%
Mismatches	1,607,856
Insertions	17,008
Mapped reads with at least one insertion	0.48%
Deletions	57,561
Mapped reads with at least one deletion	1.63%
Homopolymer indels	43.52%

2.6. Chromosome stats

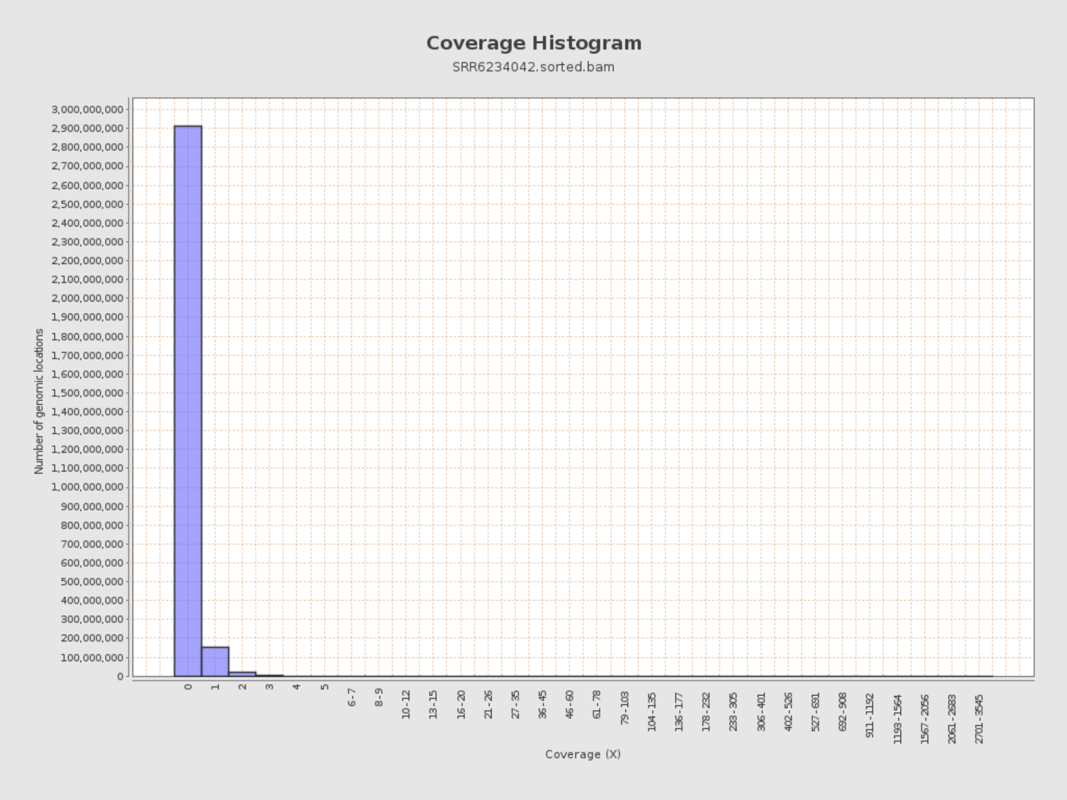
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19687287	0.079	2.9506
chr2	243199373	12815017	0.0527	1.2521
chr3	198022430	19432846	0.0981	0.3799
chr4	191154276	8284304	0.0433	0.3239
chr5	180915260	12517890	0.0692	0.3306
chr6	171115067	14050673	0.0821	0.5644
chr7	159138663	15558064	0.0978	1.9054

chr8	146364022	12872932	0.088	0.9423
chr9	141213431	8542033	0.0605	0.7699
chr10	135534747	8761381	0.0646	0.8774
chr11	135006516	9907270	0.0734	0.659
chr12	133851895	7676861	0.0574	0.3086
chr13	115169878	9683443	0.0841	0.3595
chr14	107349540	11261651	0.1049	0.4726
chr15	102531392	4214678	0.0411	0.2998
chr16	90354753	6573829	0.0728	0.4646
chr17	81195210	5903077	0.0727	0.3915
chr18	78077248	5270556	0.0675	1.7885
chr19	59128983	8296871	0.1403	1.6464
chr20	63025520	7445573	0.1181	0.4885
chr21	48129895	3808916	0.0791	0.3755
chr22	51304566	2022128	0.0394	0.2328
chrMT	16571	136742	8.2519	5.3698
chrX	155270560	10647149	0.0686	0.4499
chrY	59373566	660239	0.0111	0.2281

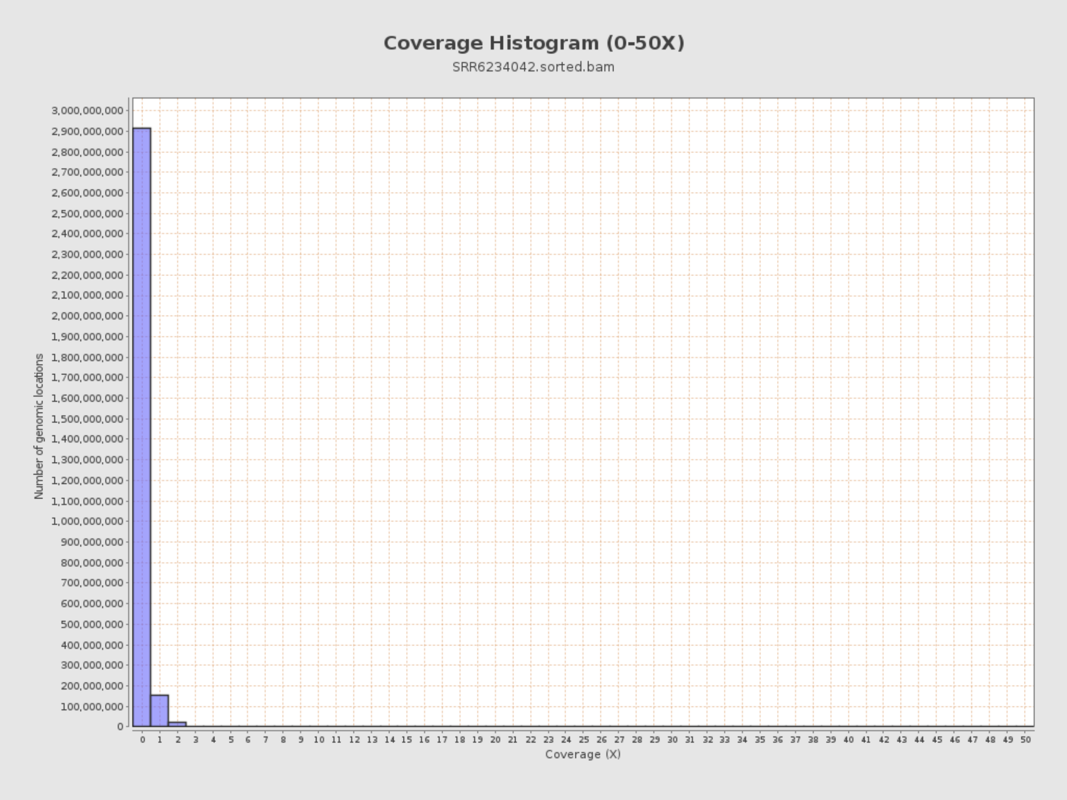
3. Results : Coverage across reference



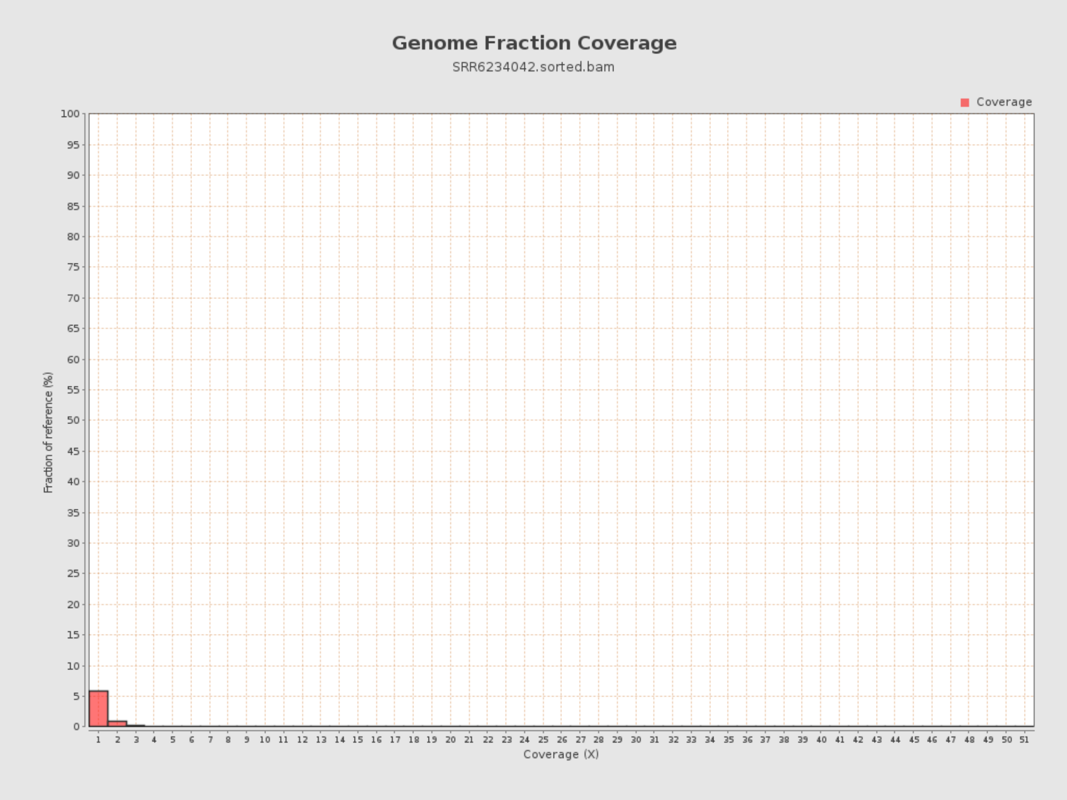
4. Results : Coverage Histogram



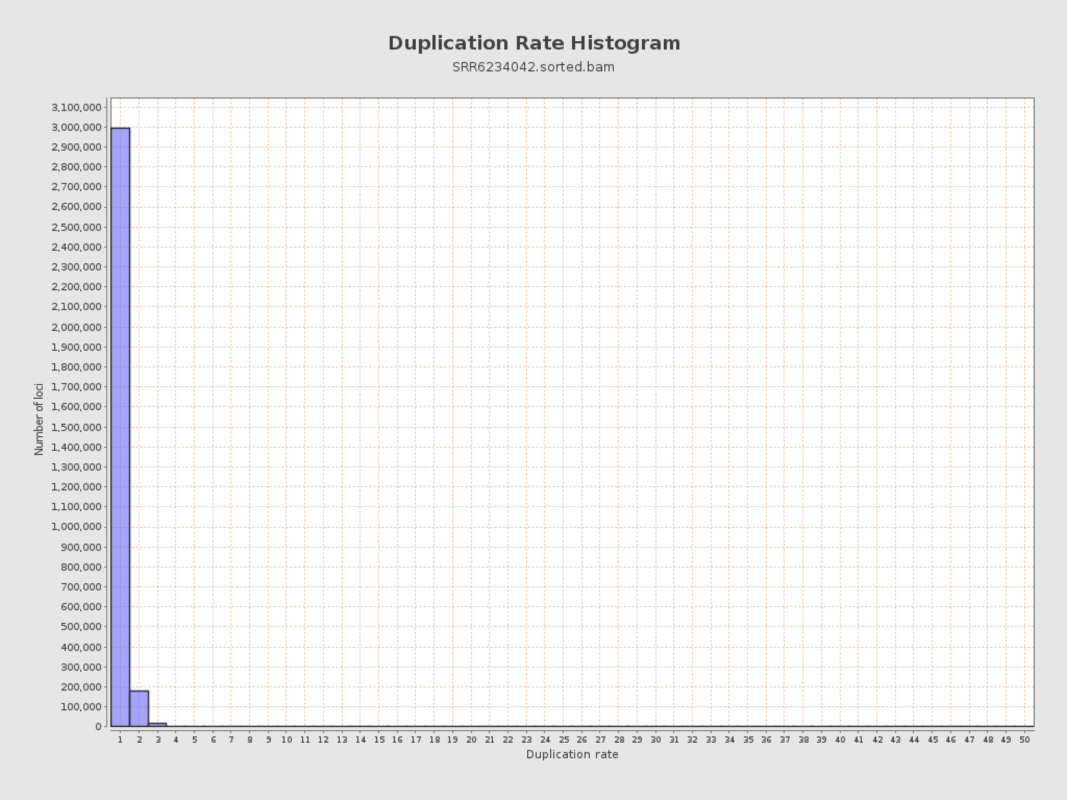
5. Results : Coverage Histogram (0-50X)



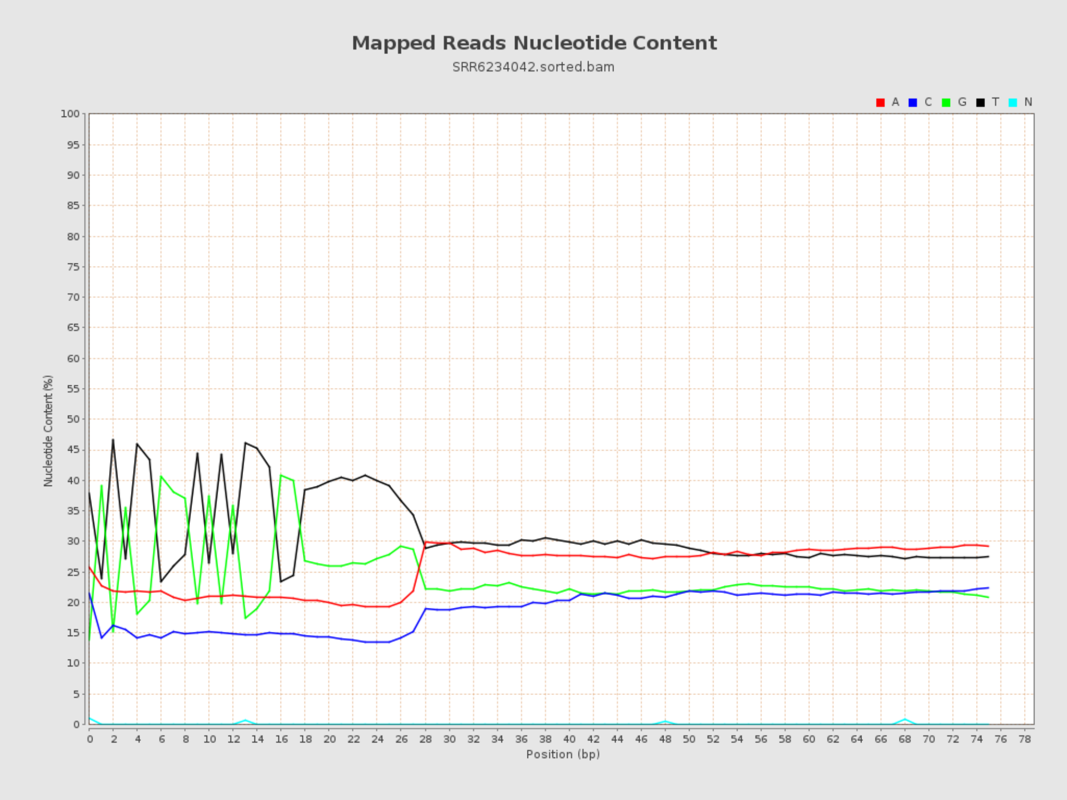
6. Results : Genome Fraction Coverage



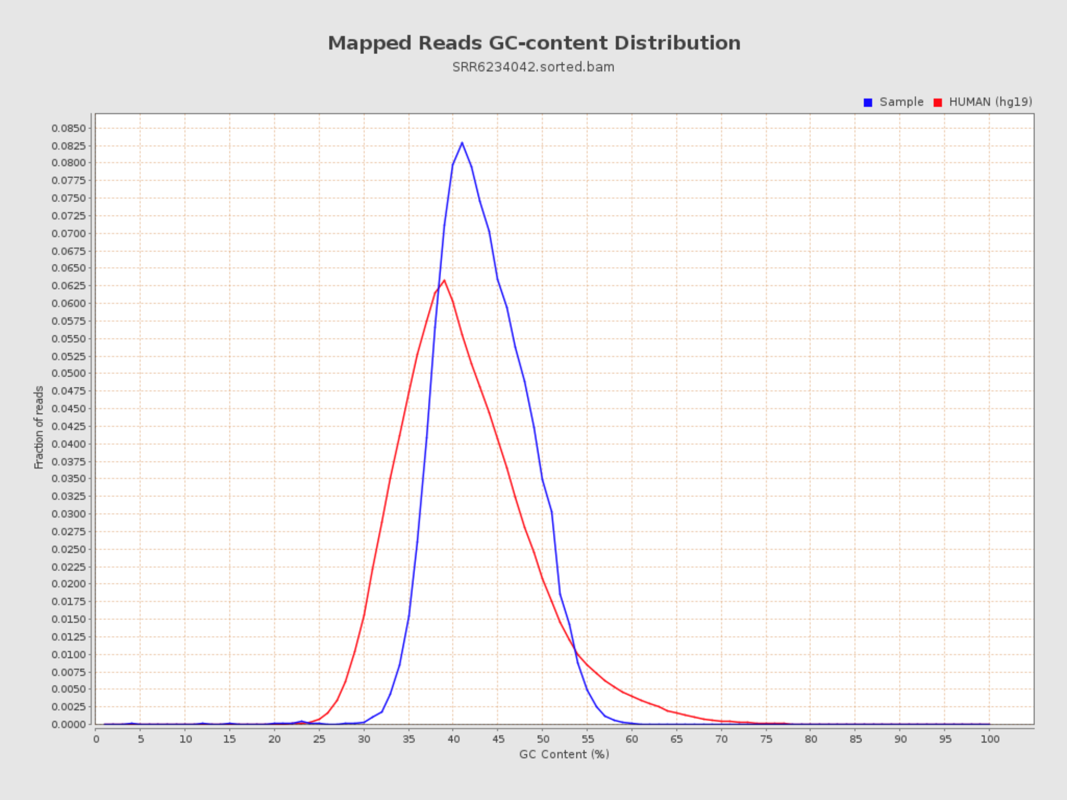
7. Results : Duplication Rate Histogram



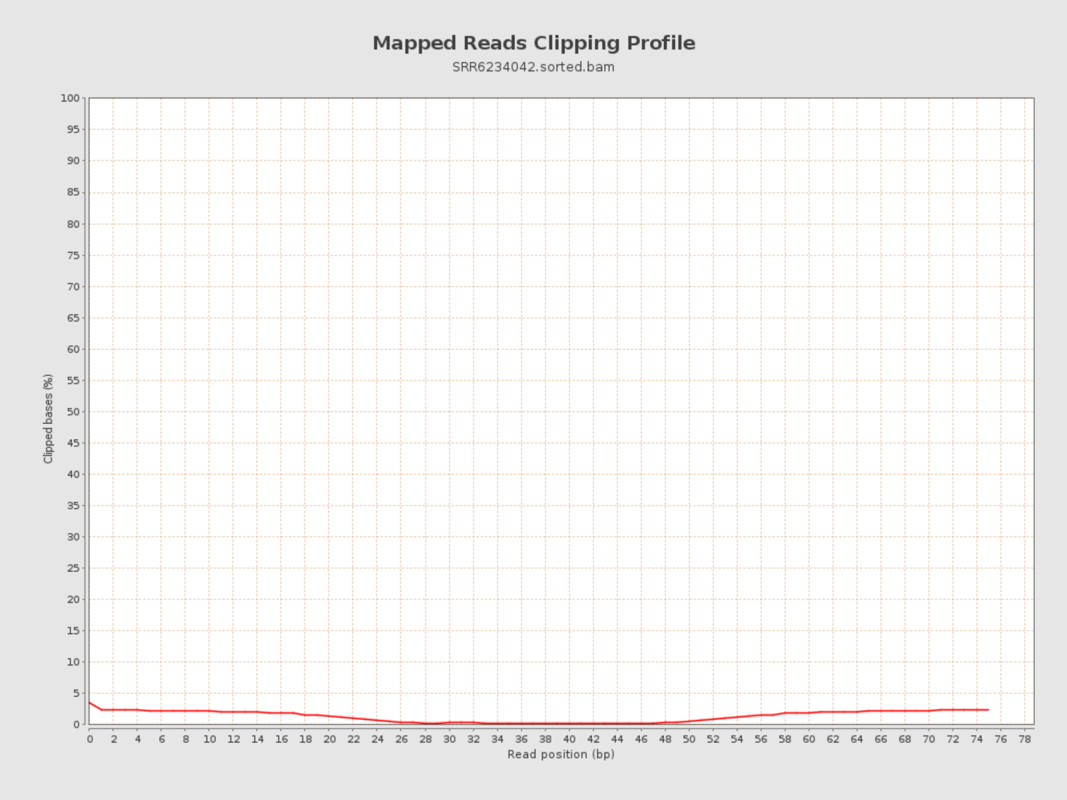
8. Results : Mapped Reads Nucleotide Content



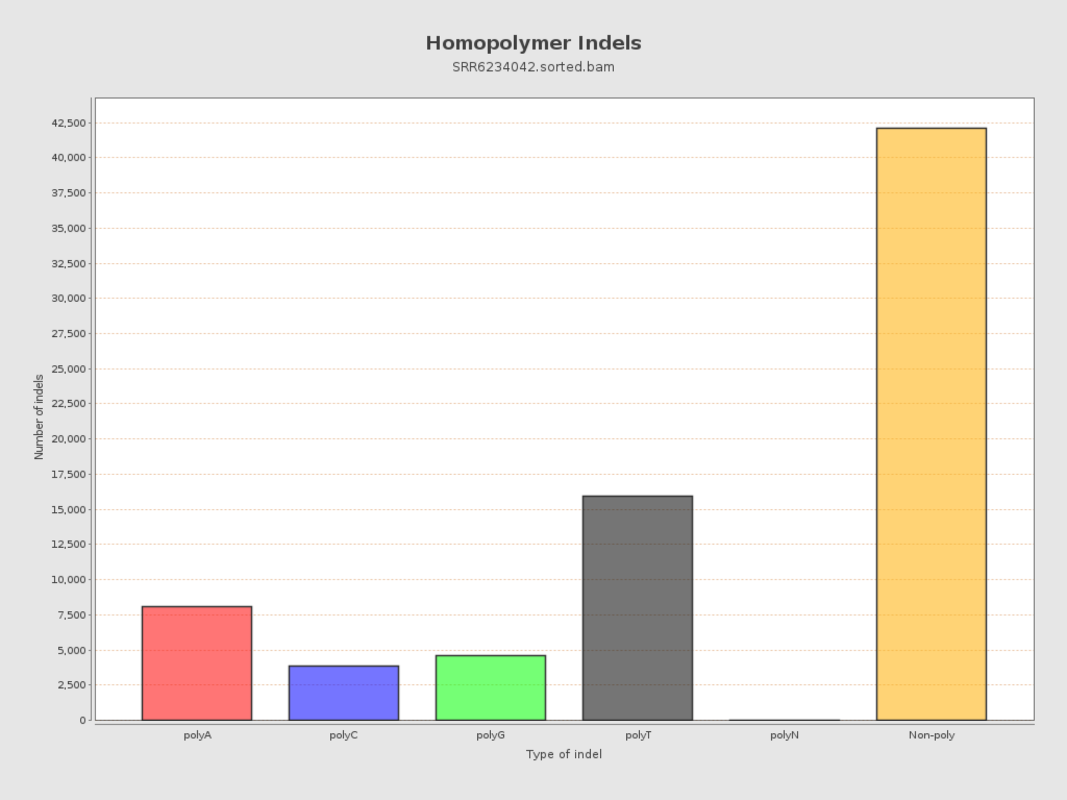
9. Results : Mapped Reads GC-content Distribution



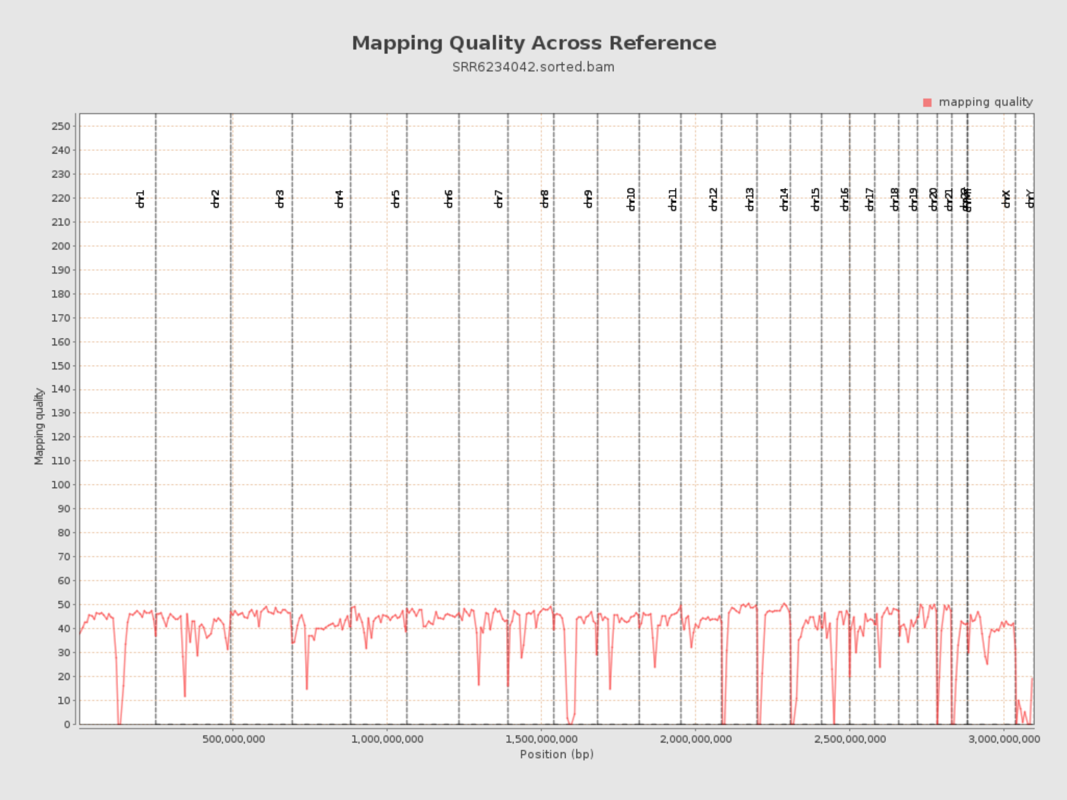
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram