Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:29:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234052.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_SRR6234052 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234052.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:29:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234052.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,579,303
Mapped reads	2,450,314 / 95%
Unmapped reads	128,989 / 5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,194 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	169,705 / 6.58%
Duplication rate	5.62%
Clipped reads	1,031,337 / 39.99%

2.2. ACGT Content

Number/percentage of A's	44,461,958 / 27.09%
Number/percentage of C's	30,547,442 / 18.61%
Number/percentage of T's	52,201,166 / 31.8%
Number/percentage of G's	36,909,430 / 22.49%
Number/percentage of N's	16,207 / 0.01%
GC Percentage	41.1%

2.3. Coverage

Mean	0.053

Standard Deviation	0.6231

2.4. Mapping Quality

Mean Mapping Quality	43.78

2.5. Mismatches and indels

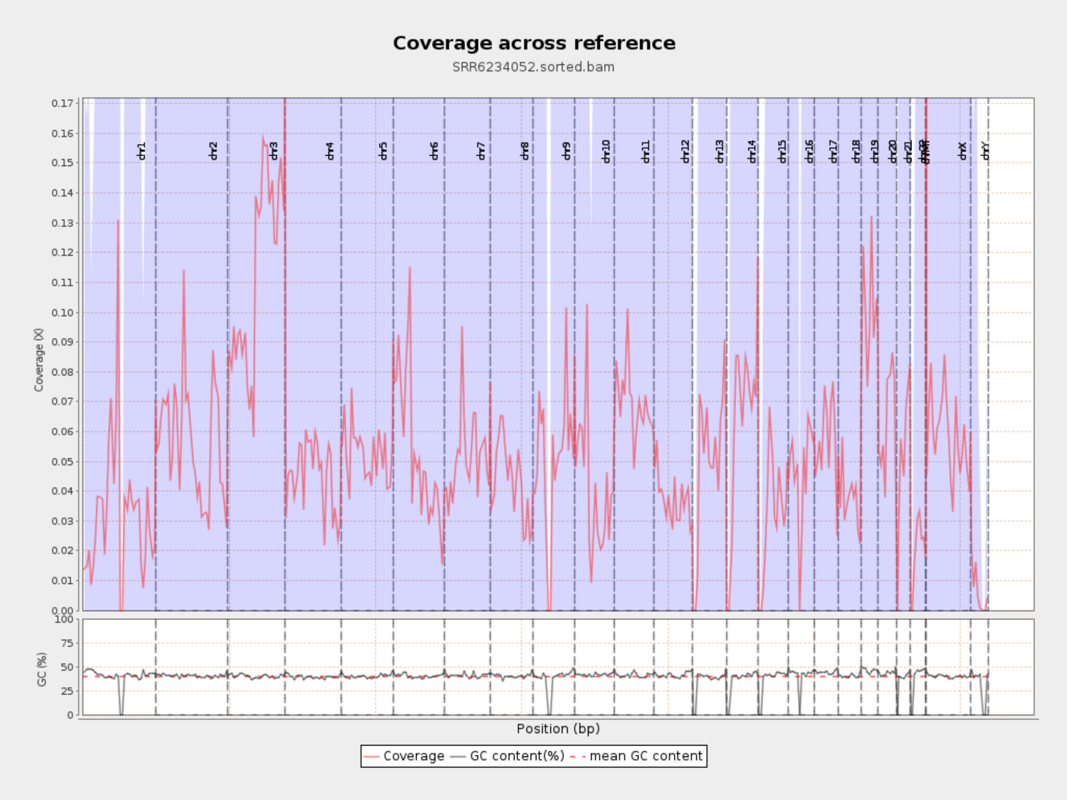
General error rate	0.66%
Mismatches	1,065,392
Insertions	12,911
Mapped reads with at least one insertion	0.52%
Deletions	48,820
Mapped reads with at least one deletion	1.97%
Homopolymer indels	45.14%

2.6. Chromosome stats

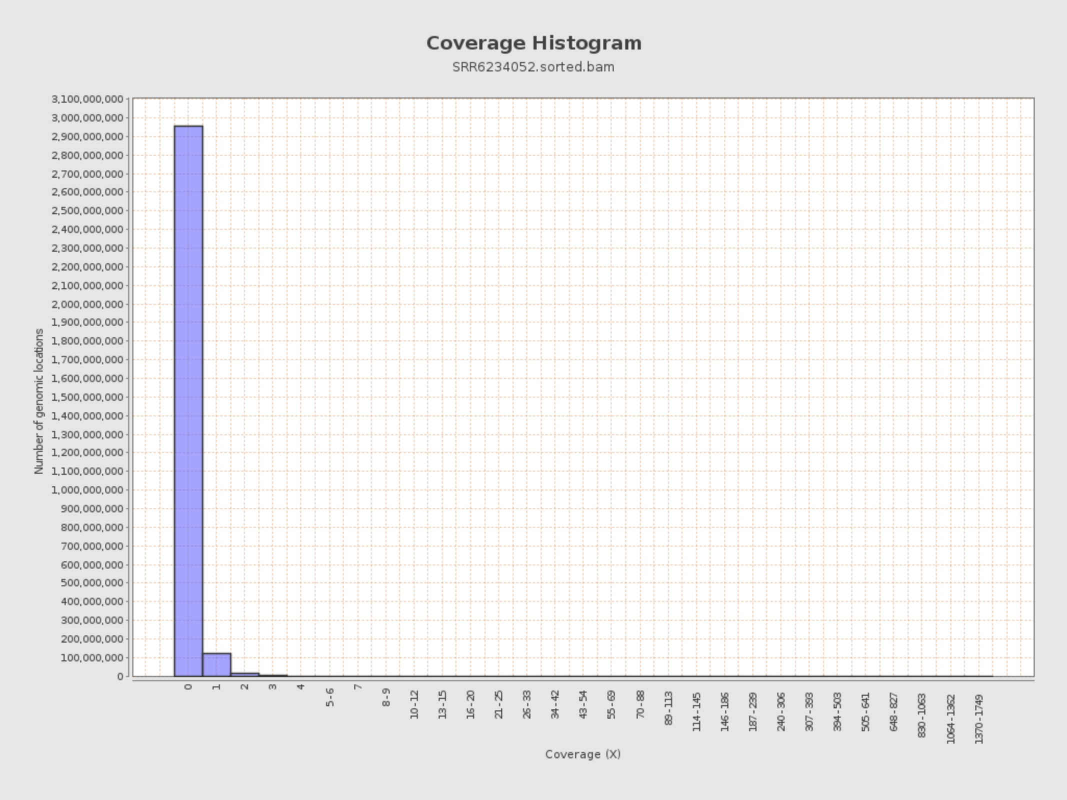
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8144895	0.0327	1.5145
chr2	243199373	13778061	0.0567	0.622
chr3	198022430	22327476	0.1128	0.3817
chr4	191154276	8643158	0.0452	0.2505
chr5	180915260	9631103	0.0532	0.2641
chr6	171115067	9288973	0.0543	0.4551
chr7	159138663	8220778	0.0517	0.6375

chr8	146364022	6355428	0.0434	0.7723
chr9	141213431	7203575	0.051	0.4239
chr10	135534747	5449832	0.0402	0.5619
chr11	135006516	9405425	0.0697	0.537
chr12	133851895	5019062	0.0375	0.2341
chr13	115169878	5858182	0.0509	0.2612
chr14	107349540	6634791	0.0618	0.3063
chr15	102531392	3213754	0.0313	0.2081
chr16	90354753	4131384	0.0457	0.2957
chr17	81195210	4687675	0.0577	0.3476
chr18	78077248	2964800	0.038	0.8956
chr19	59128983	5990328	0.1013	0.8728
chr20	63025520	4034107	0.064	0.2987
chr21	48129895	2532148	0.0526	0.2787
chr22	51304566	1028922	0.0201	0.1576
chrMT	16571	157696	9.5164	6.108
chrX	155270560	9149680	0.0589	0.3398
chrY	59373566	368195	0.0062	0.1265

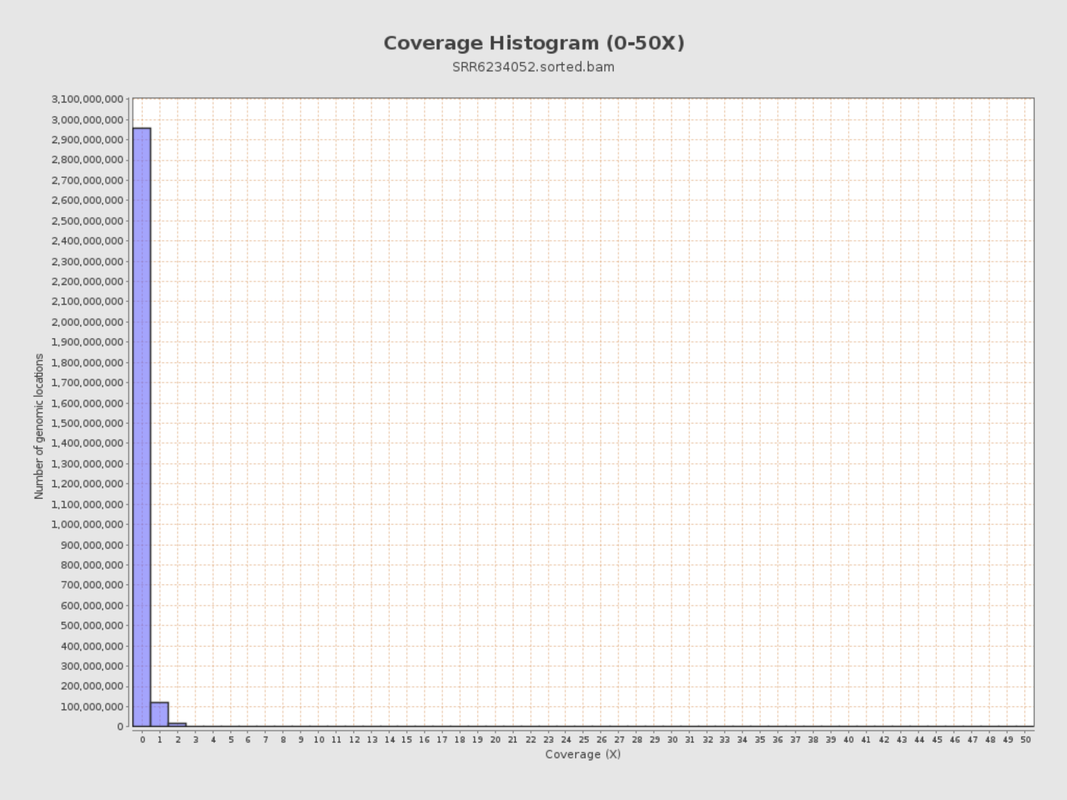
3. Results : Coverage across reference



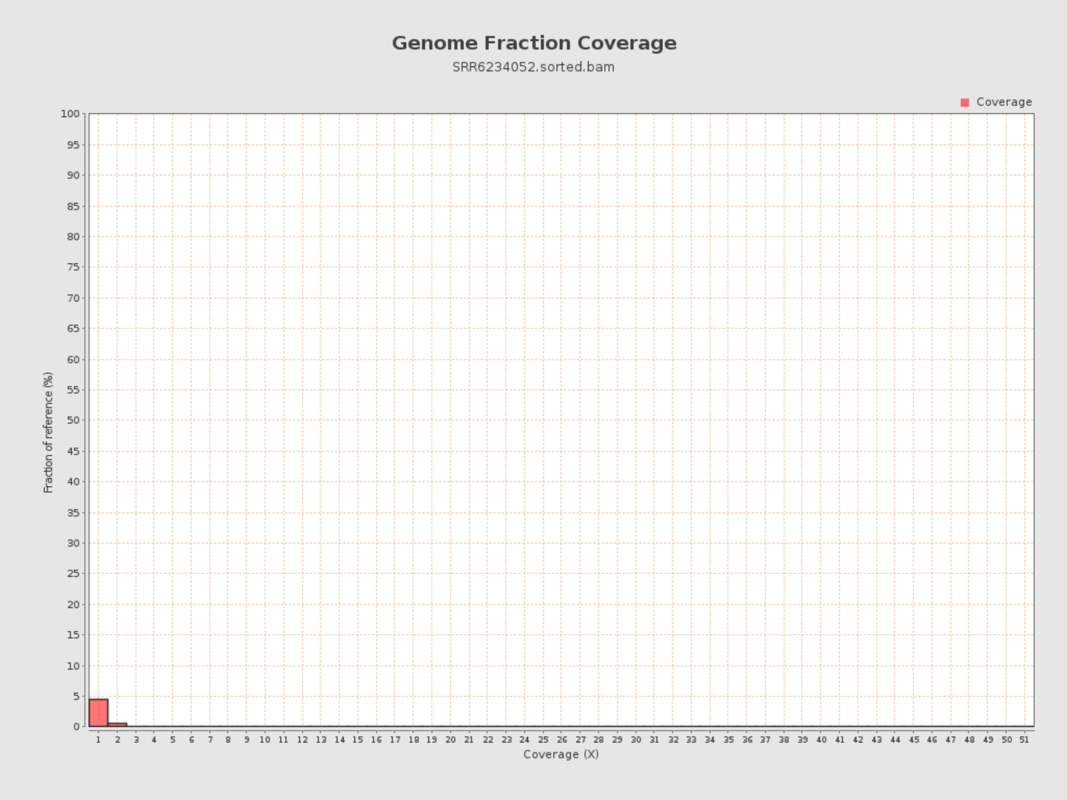
4. Results : Coverage Histogram



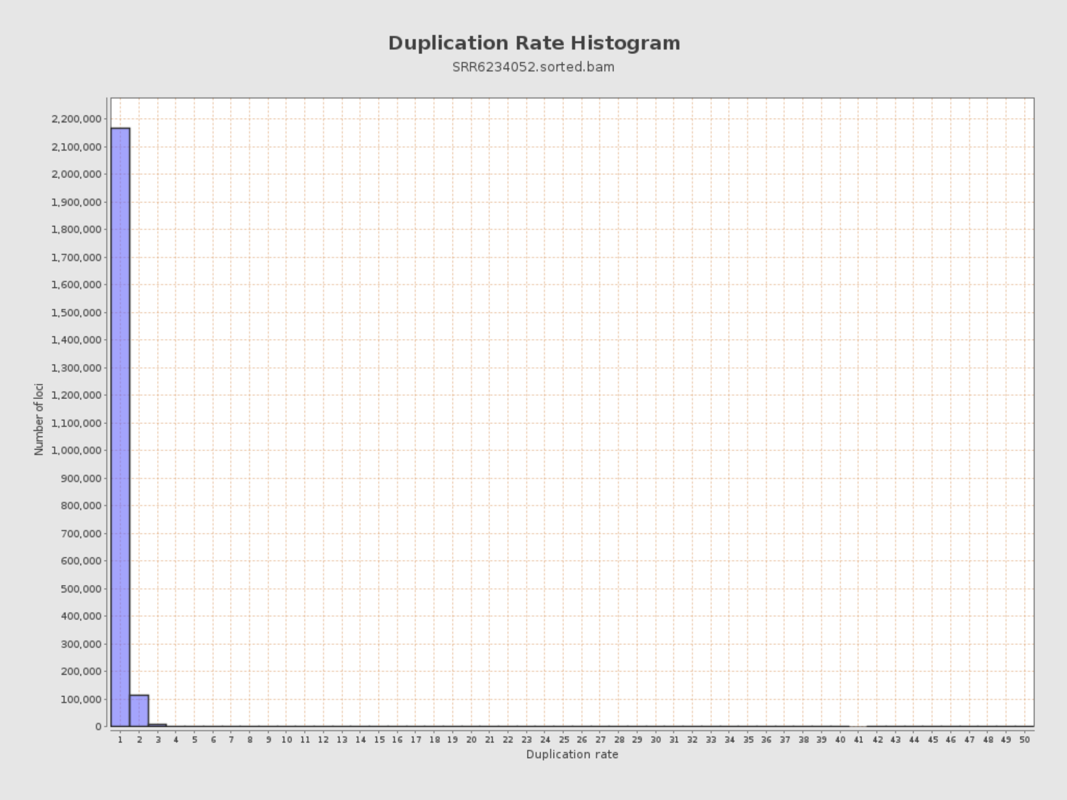
5. Results : Coverage Histogram (0-50X)



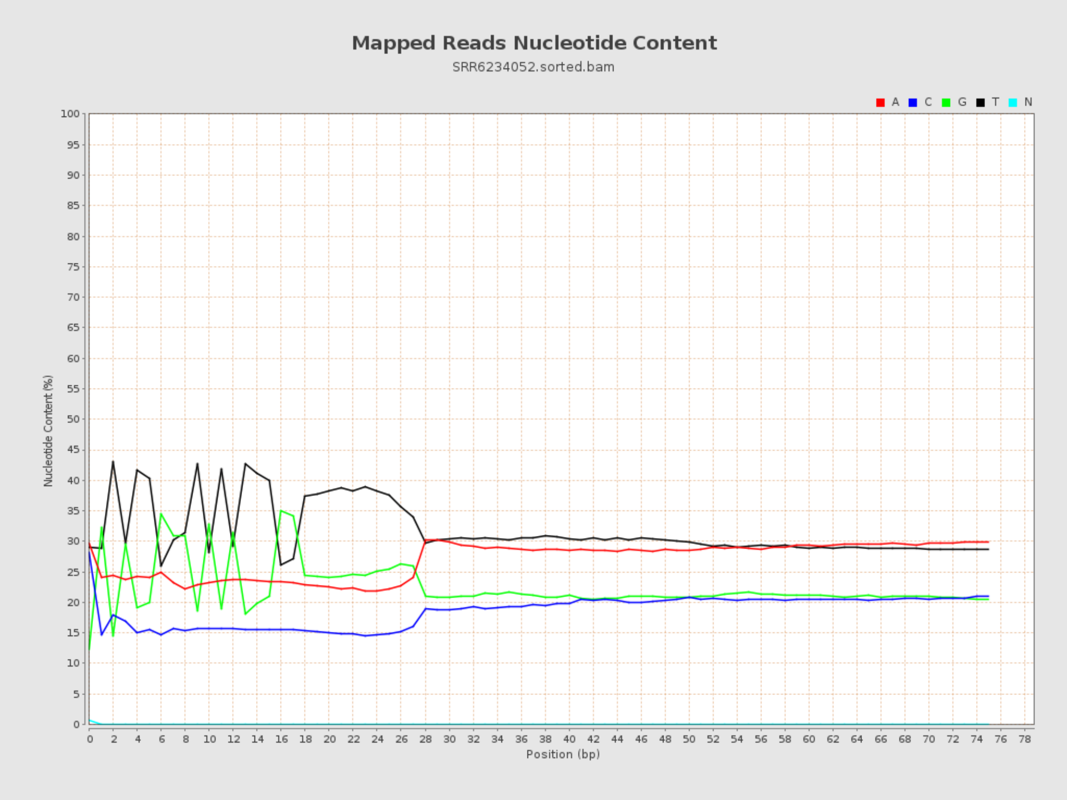
6. Results : Genome Fraction Coverage



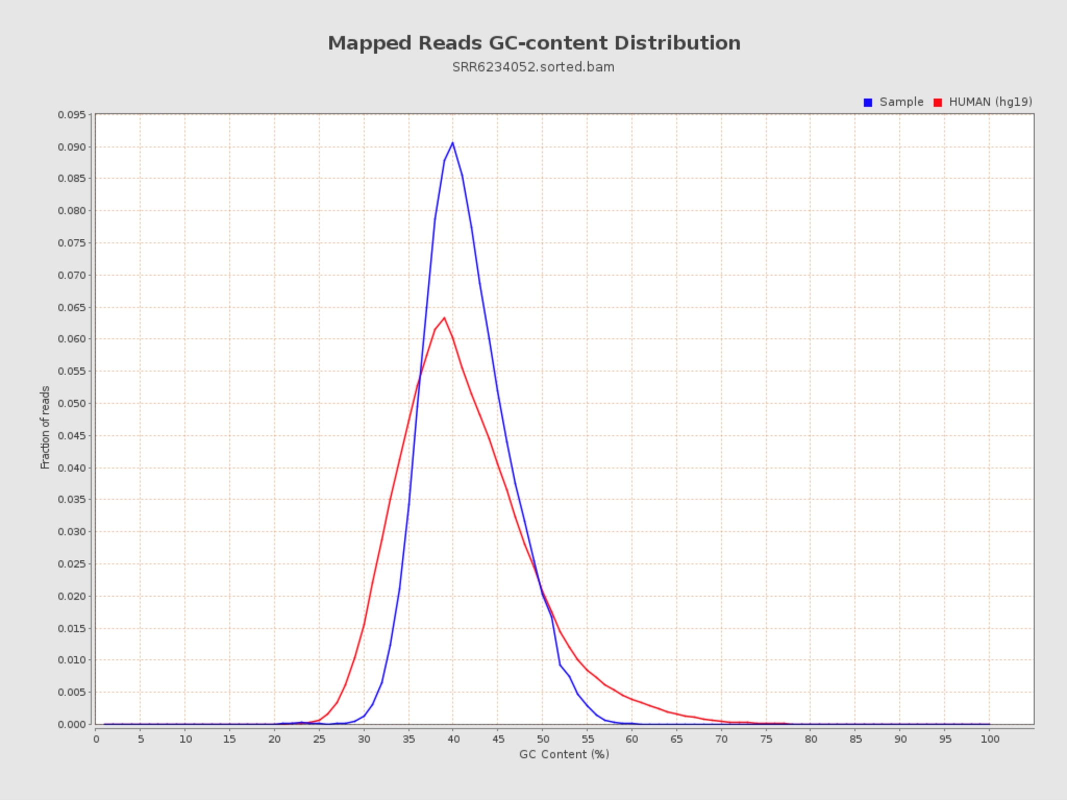
7. Results : Duplication Rate Histogram



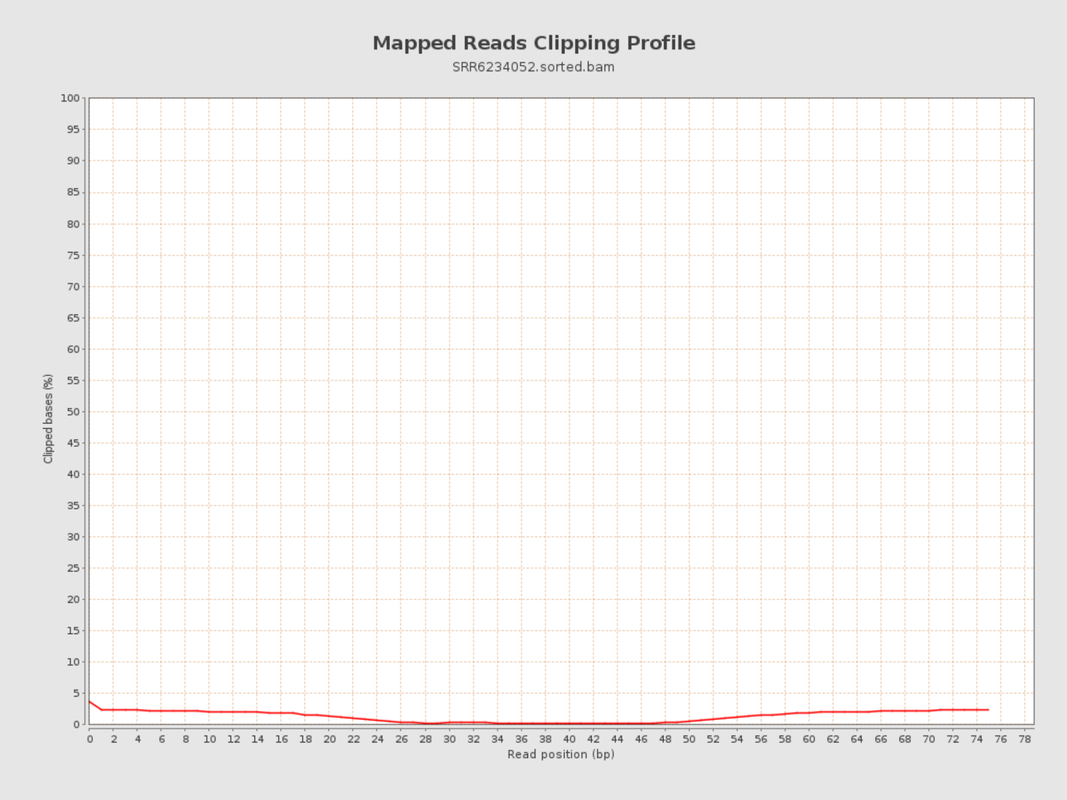
8. Results : Mapped Reads Nucleotide Content



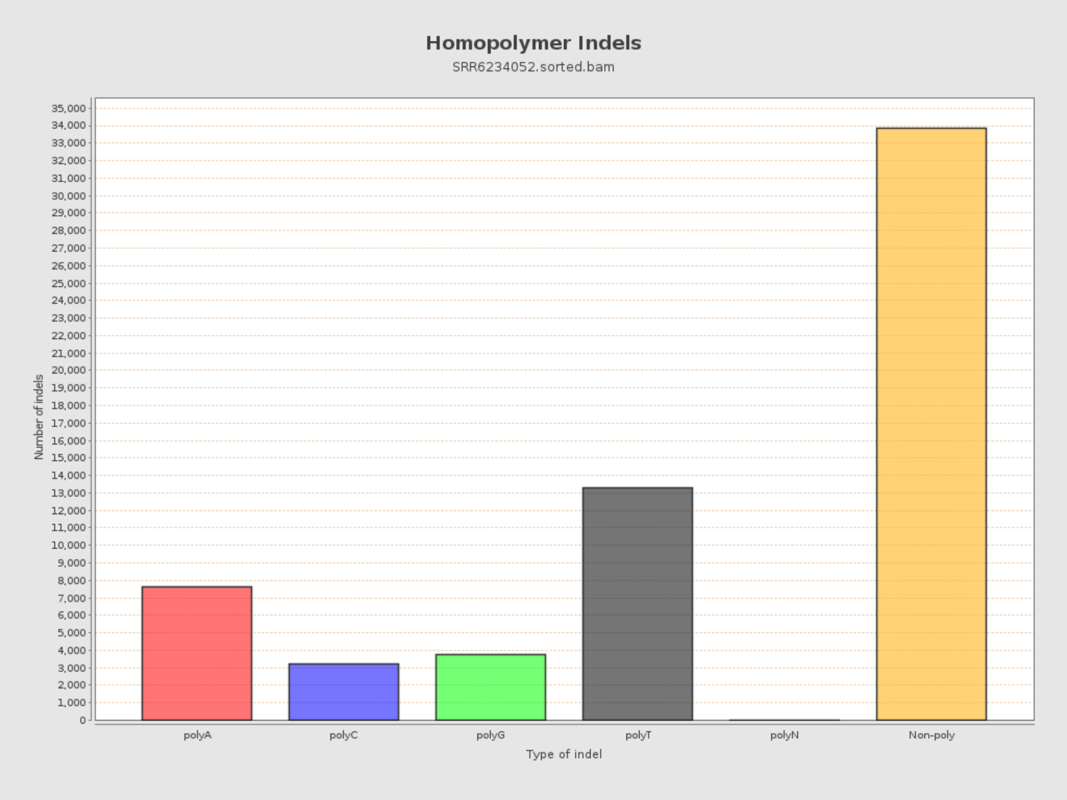
9. Results : Mapped Reads GC-content Distribution



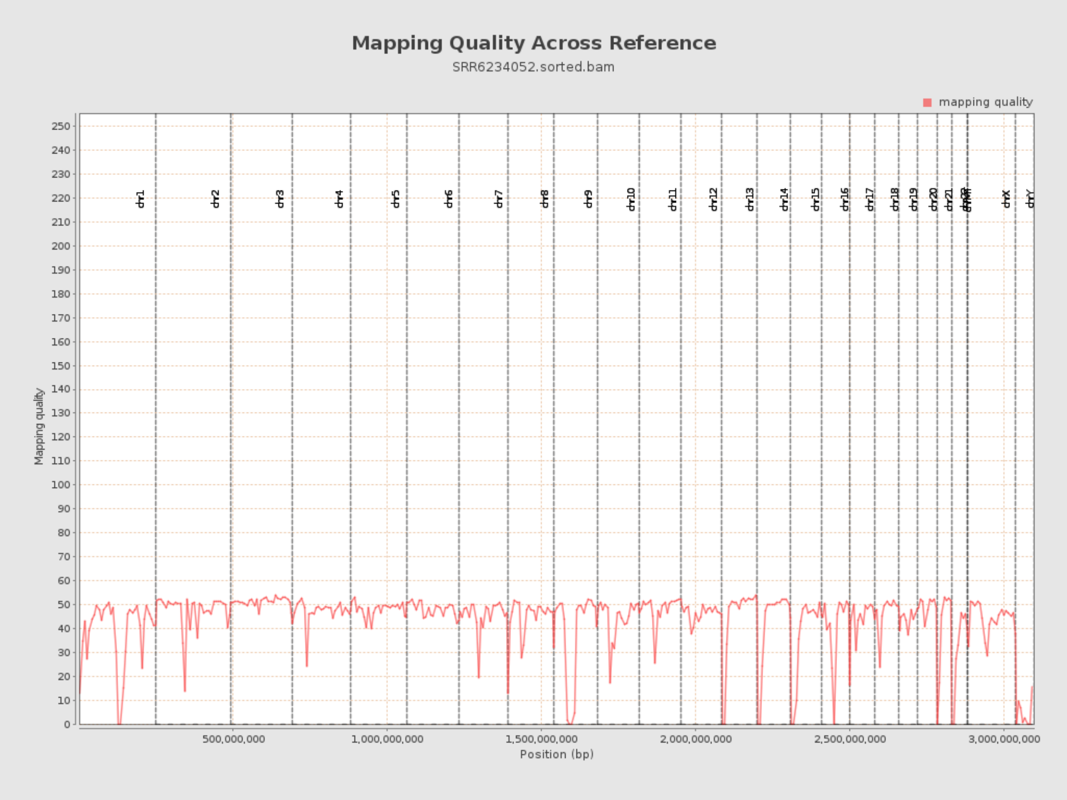
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram