Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:18:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238500.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_SRR6238500 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238500.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:18:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238500.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,297,535
Mapped reads	2,060,537 / 89.68%
Unmapped reads	236,998 / 10.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,083 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	362,463 / 15.78%
Duplication rate	13.93%
Clipped reads	1,279,731 / 55.7%

2.2. ACGT Content

Number/percentage of A's	31,259,772 / 24.52%
Number/percentage of C's	22,948,337 / 18%
Number/percentage of T's	42,194,622 / 33.1%
Number/percentage of G's	31,053,122 / 24.36%
Number/percentage of N's	9,271 / 0.01%
GC Percentage	42.37%

2.3. Coverage

Mean	0.0412

Standard Deviation	0.555

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Mismatches and indels

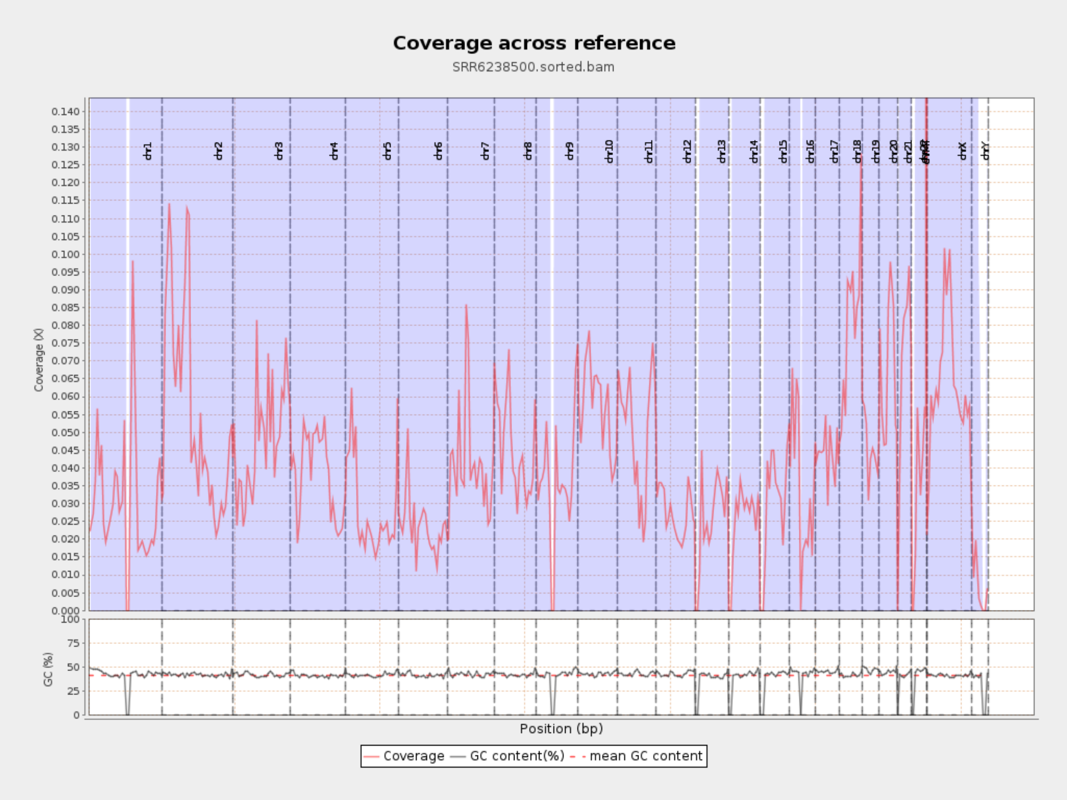
General error rate	0.65%
Mismatches	813,497
Insertions	8,661
Mapped reads with at least one insertion	0.42%
Deletions	45,243
Mapped reads with at least one deletion	2.17%
Homopolymer indels	41.11%

2.6. Chromosome stats

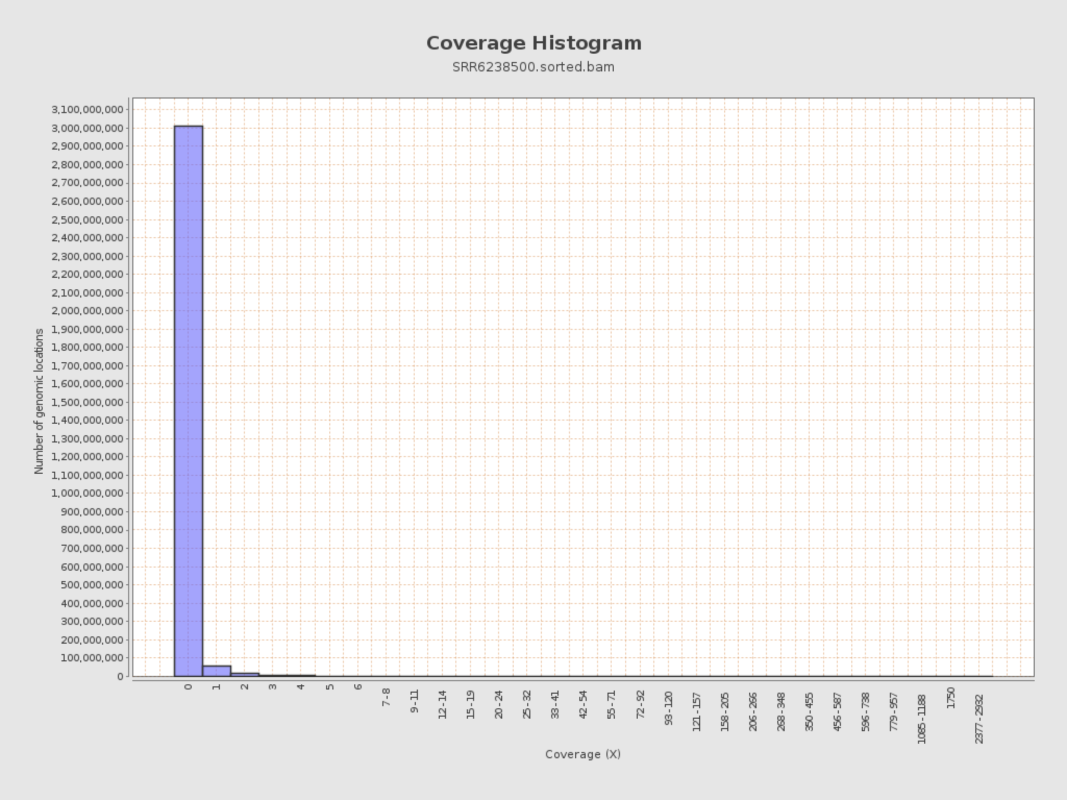
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7616584	0.0306	0.512
chr2	243199373	13720568	0.0564	1.3462
chr3	198022430	9520940	0.0481	0.3238
chr4	191154276	7276969	0.0381	0.2912
chr5	180915260	5093882	0.0282	0.2519
chr6	171115067	4032156	0.0236	0.424
chr7	159138663	6671208	0.0419	0.5506

chr8	146364022	6624792	0.0453	0.5998
chr9	141213431	4919914	0.0348	0.4055
chr10	135534747	7763571	0.0573	0.4204
chr11	135006516	6814374	0.0505	0.392
chr12	133851895	3628159	0.0271	0.2546
chr13	115169878	2963778	0.0257	0.3331
chr14	107349540	2703302	0.0252	0.2679
chr15	102531392	3075935	0.03	0.316
chr16	90354753	3120156	0.0345	0.3078
chr17	81195210	3581377	0.0441	0.3203
chr18	78077248	6184633	0.0792	1.0133
chr19	59128983	2679371	0.0453	0.4725
chr20	63025520	4233892	0.0672	0.4007
chr21	48129895	3261105	0.0678	0.4022
chr22	51304566	1693788	0.033	0.2626
chrMT	16571	71454	4.312	3.7425
chrX	155270560	9891953	0.0637	0.3971
chrY	59373566	398967	0.0067	0.2164

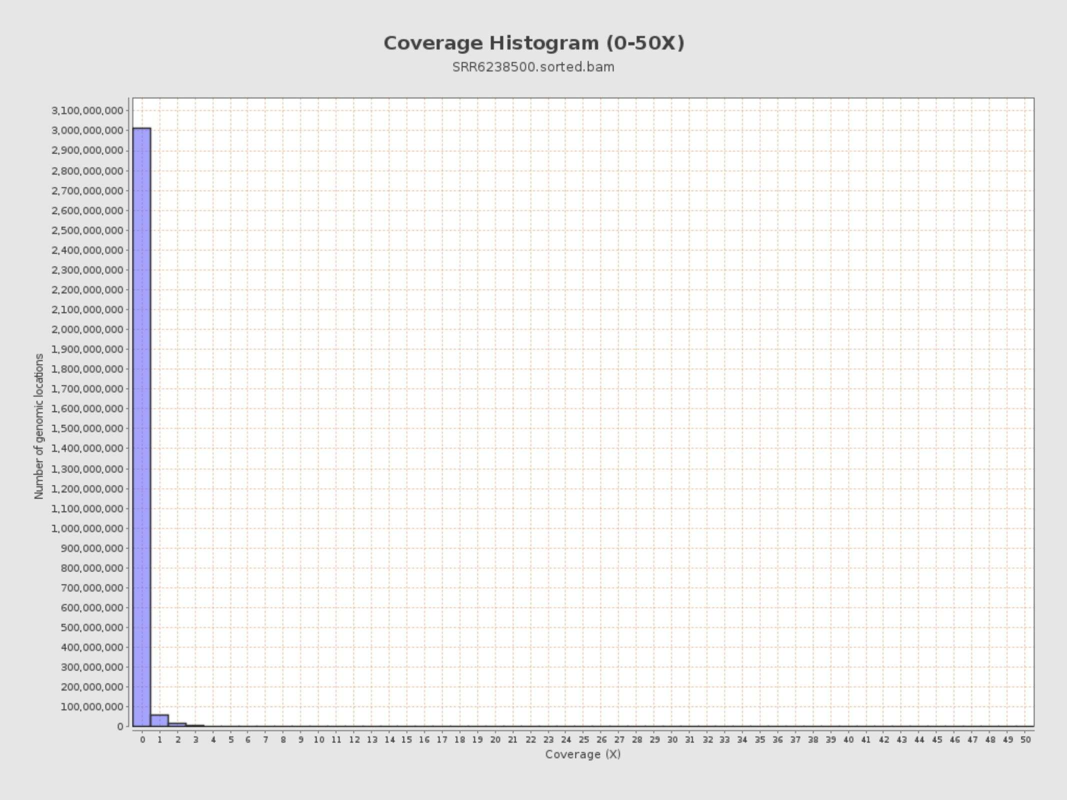
3. Results : Coverage across reference



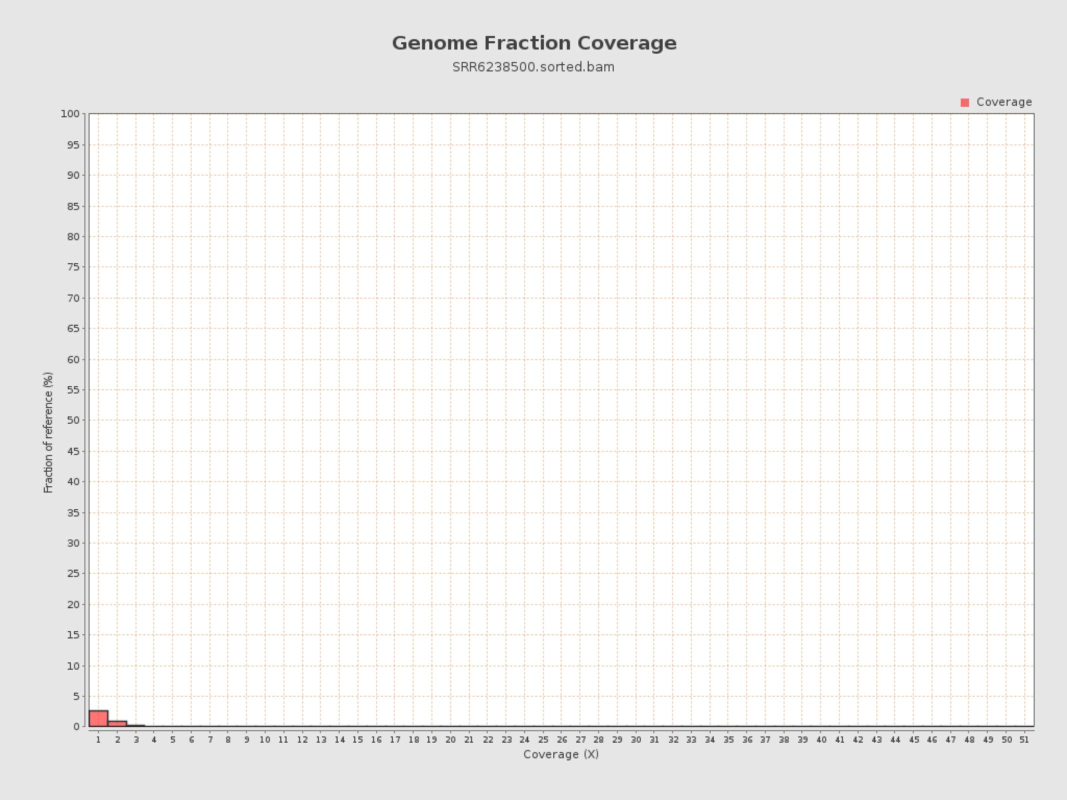
4. Results : Coverage Histogram



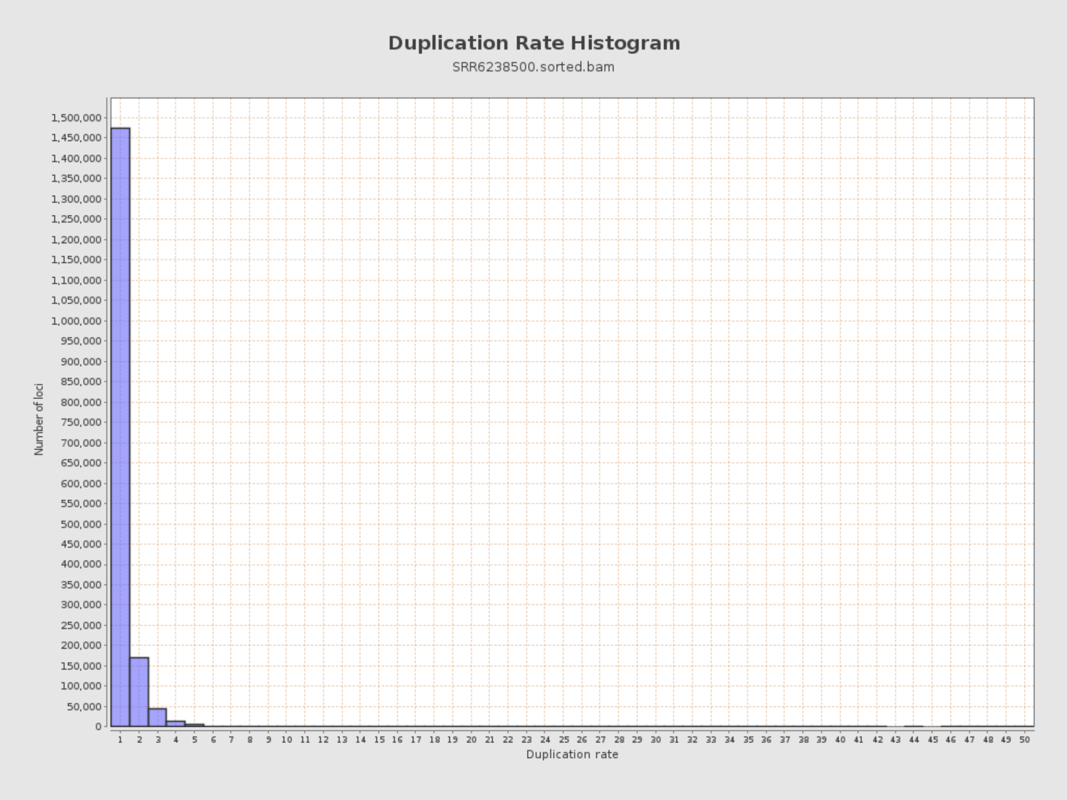
5. Results : Coverage Histogram (0-50X)



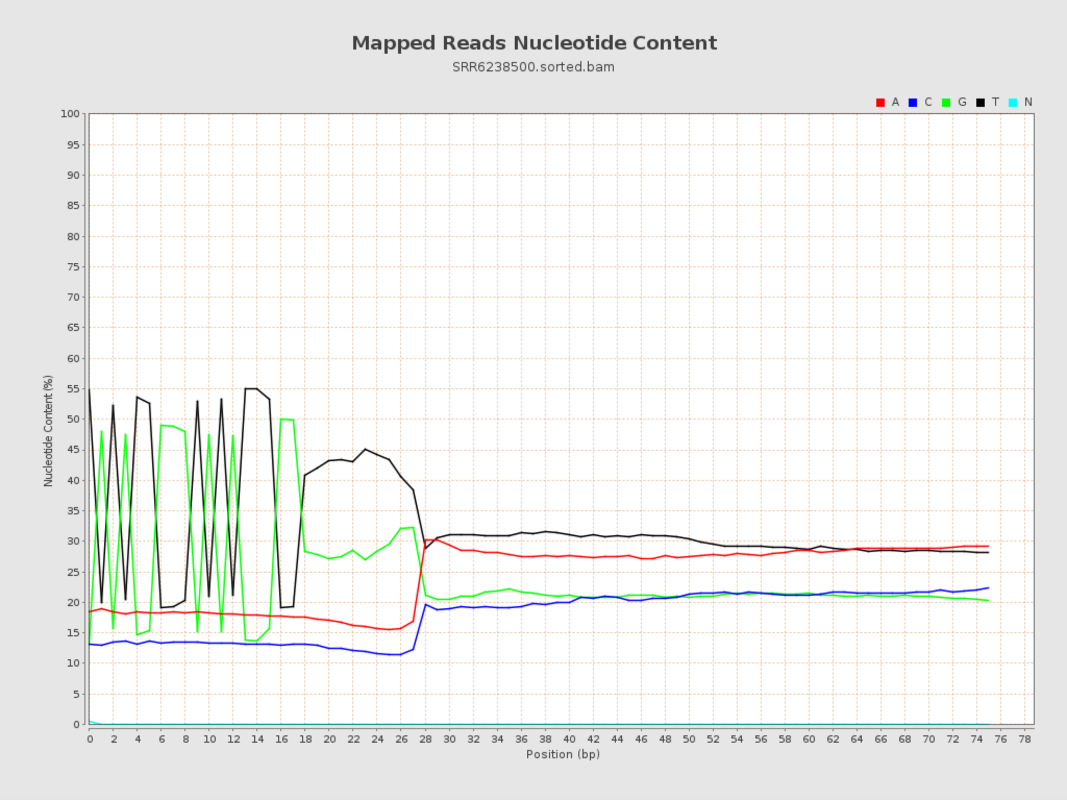
6. Results : Genome Fraction Coverage



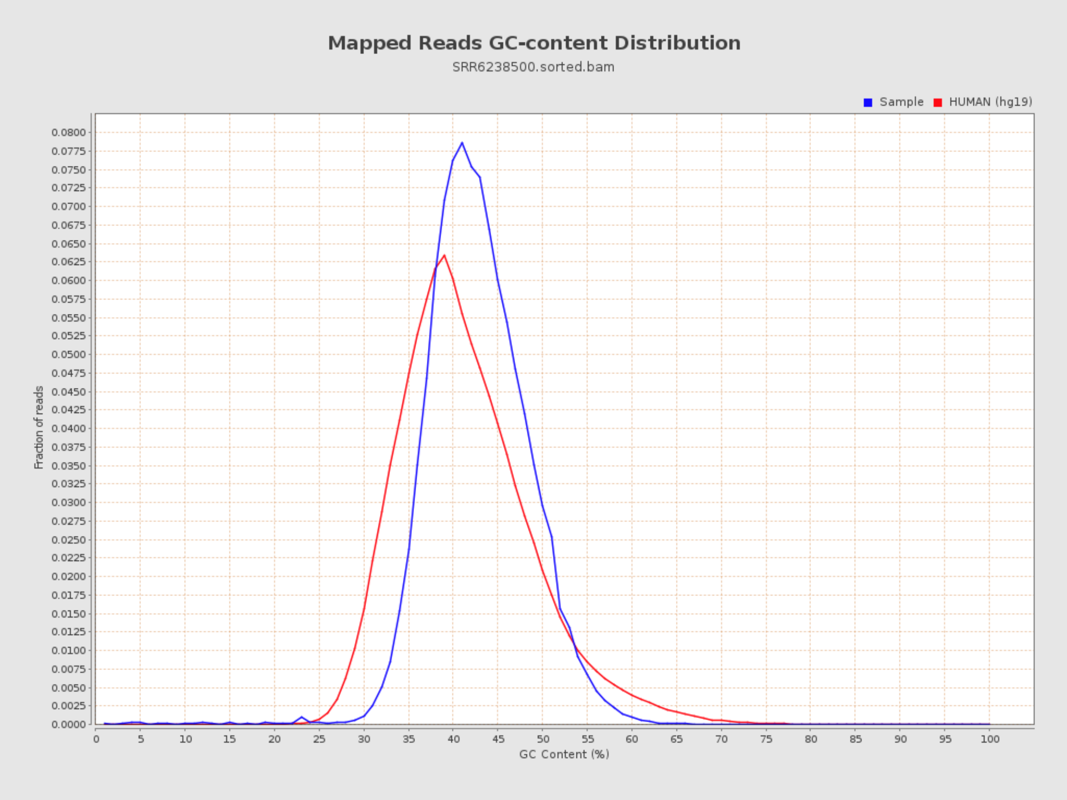
7. Results : Duplication Rate Histogram



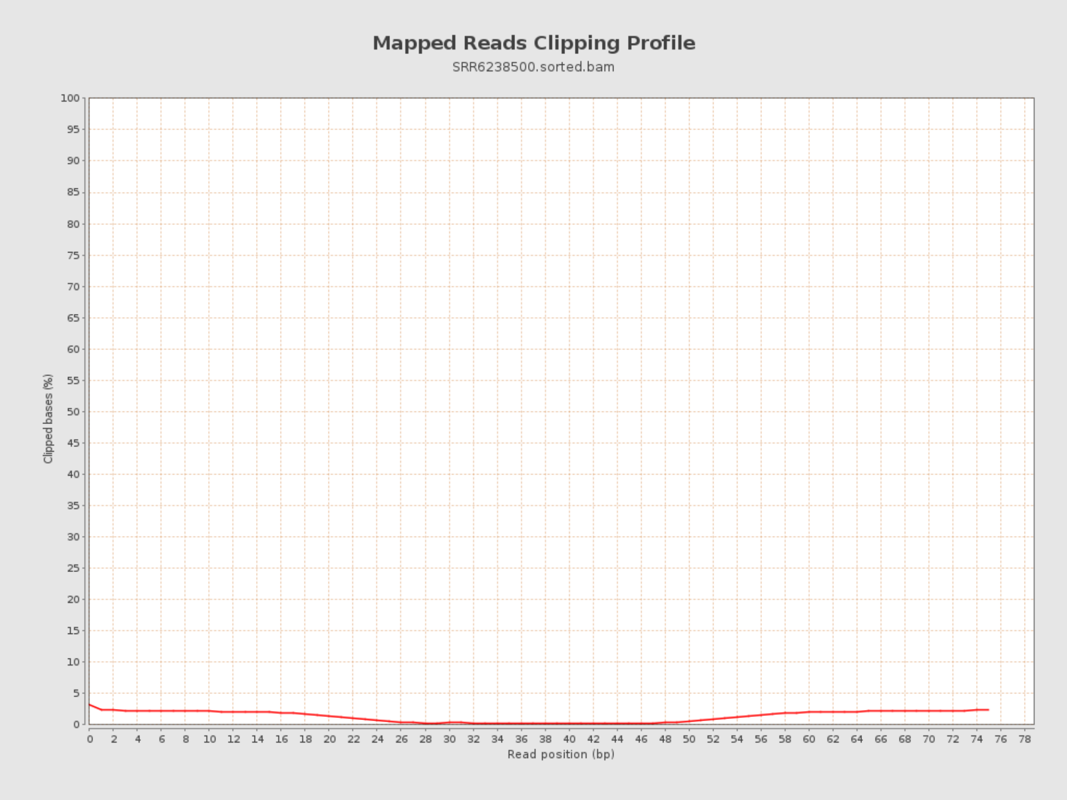
8. Results : Mapped Reads Nucleotide Content



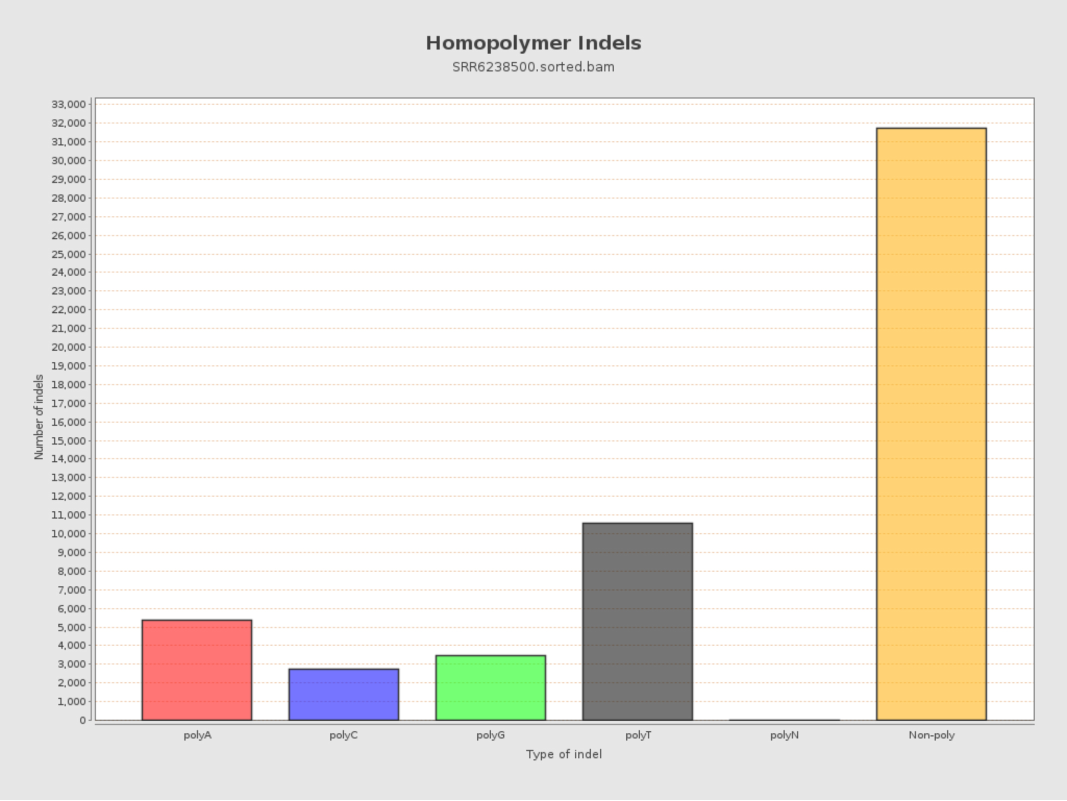
9. Results : Mapped Reads GC-content Distribution



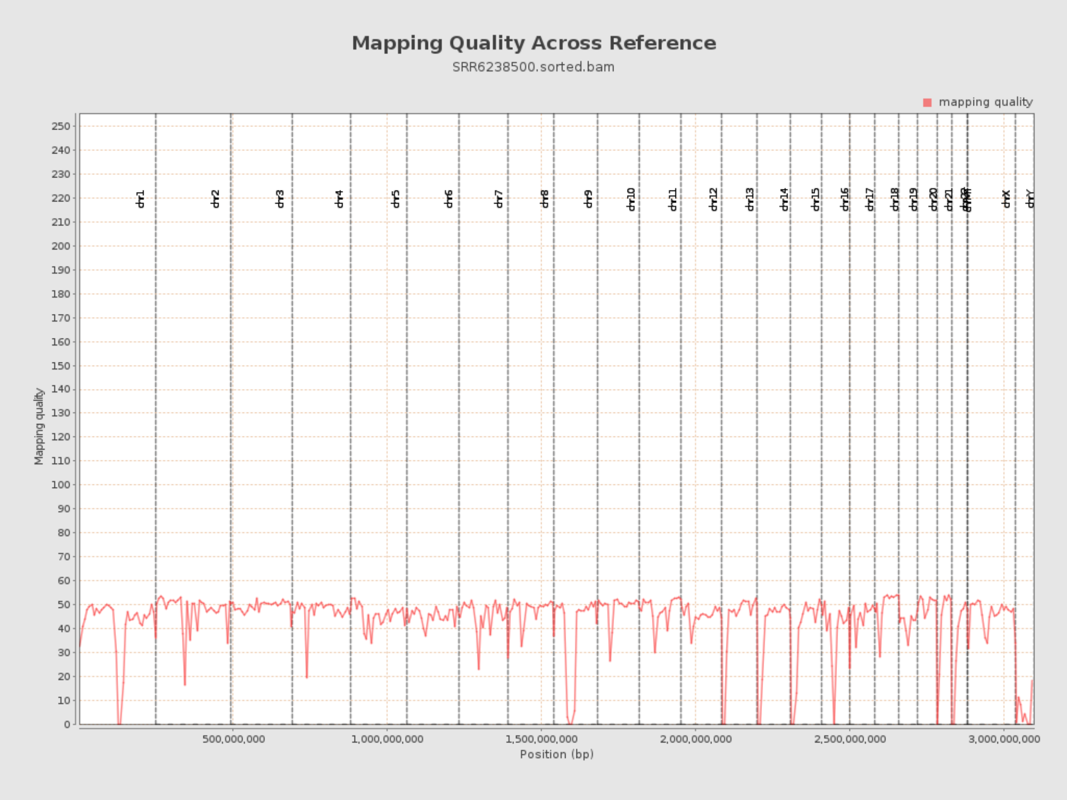
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram