Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:00:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238032.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_SRR6238032 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238032.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:00:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238032.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,780,741
Mapped reads	2,520,297 / 90.63%
Unmapped reads	260,444 / 9.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,874 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	158,352 / 5.69%
Duplication rate	5.1%
Clipped reads	1,016,362 / 36.55%

2.2. ACGT Content

Number/percentage of A's	46,276,052 / 27.21%
Number/percentage of C's	33,053,483 / 19.44%
Number/percentage of T's	52,234,605 / 30.72%
Number/percentage of G's	38,457,369 / 22.62%
Number/percentage of N's	24,690 / 0.01%
GC Percentage	42.05%

2.3. Coverage

Mean	0.055

Standard Deviation	0.4868

2.4. Mapping Quality

Mean Mapping Quality	40.89

2.5. Mismatches and indels

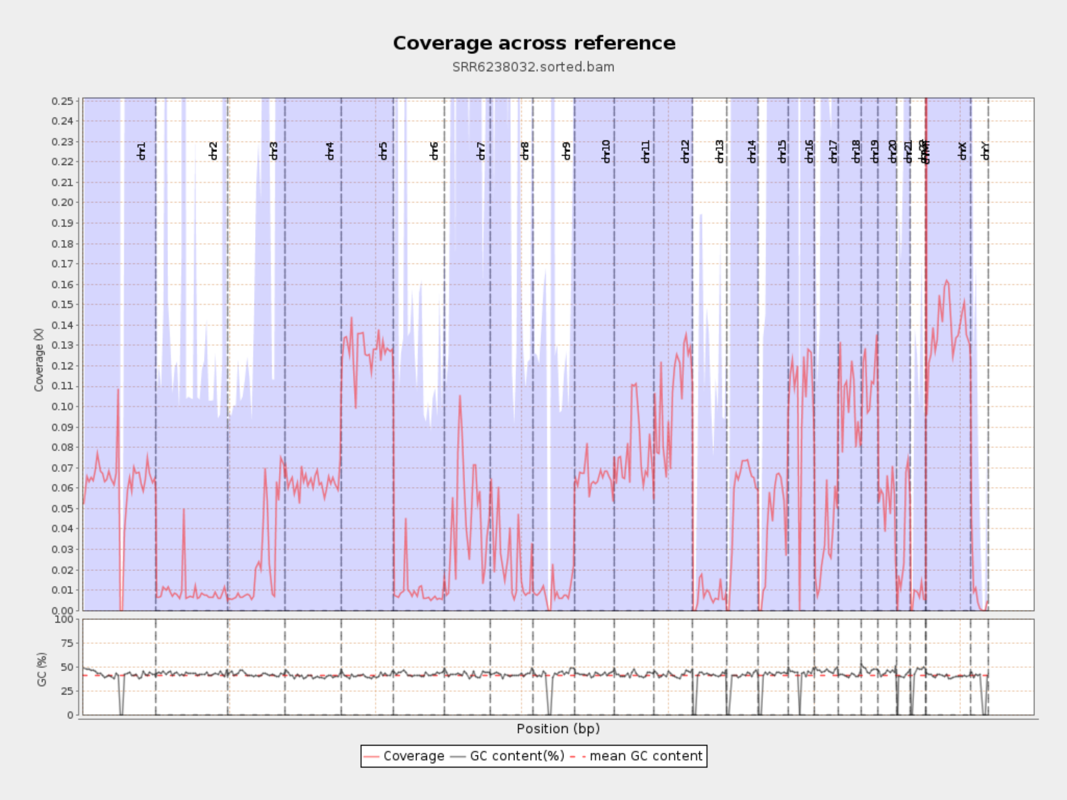
General error rate	0.71%
Mismatches	1,193,134
Insertions	10,923
Mapped reads with at least one insertion	0.43%
Deletions	40,535
Mapped reads with at least one deletion	1.59%
Homopolymer indels	48.1%

2.6. Chromosome stats

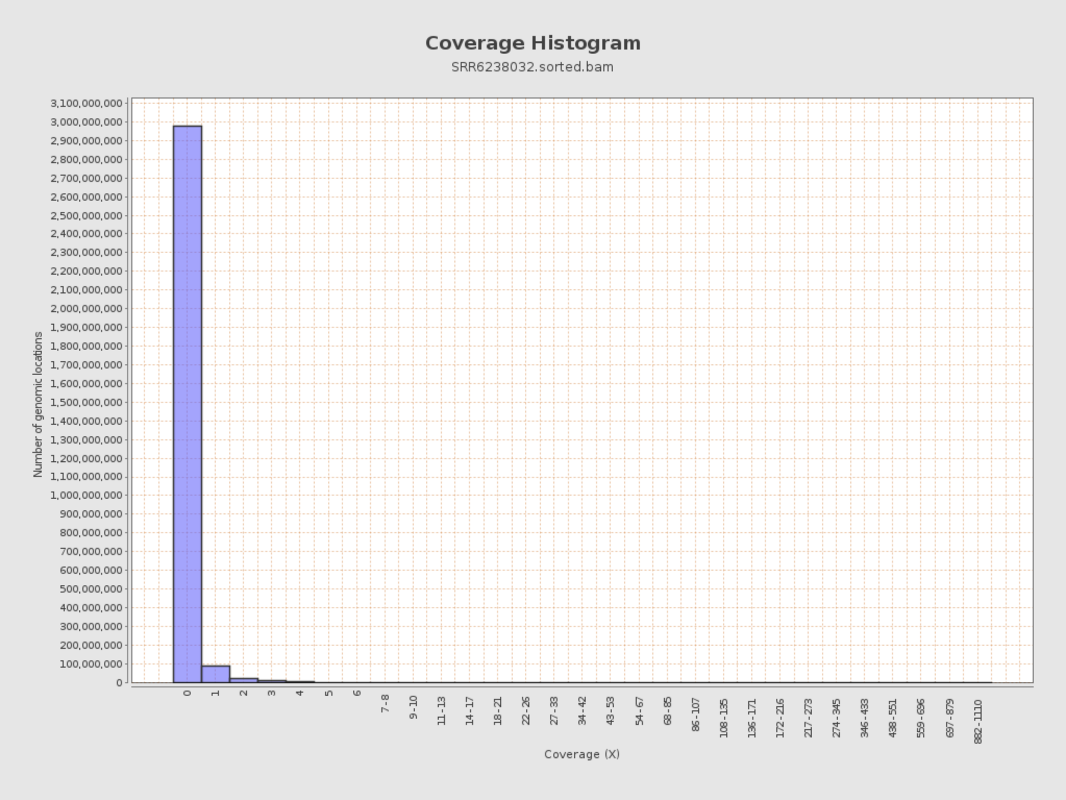
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15362064	0.0616	1.083
chr2	243199373	2232322	0.0092	0.3895
chr3	198022430	4869049	0.0246	0.208
chr4	191154276	12074898	0.0632	0.3413
chr5	180915260	23081257	0.1276	0.4875
chr6	171115067	1591014	0.0093	0.1566
chr7	159138663	7284192	0.0458	0.5357

chr8	146364022	3585495	0.0245	0.283
chr9	141213431	1300659	0.0092	0.2338
chr10	135534747	8859537	0.0654	0.5004
chr11	135006516	10547741	0.0781	0.4819
chr12	133851895	14112339	0.1054	0.4451
chr13	115169878	876170	0.0076	0.114
chr14	107349540	6011200	0.056	0.3201
chr15	102531392	4092078	0.0399	0.2669
chr16	90354753	9345307	0.1034	0.444
chr17	81195210	2581337	0.0318	0.2596
chr18	78077248	8028628	0.1028	0.5355
chr19	59128983	6697912	0.1133	0.8073
chr20	63025520	3447996	0.0547	0.3176
chr21	48129895	1766997	0.0367	0.2629
chr22	51304566	360329	0.007	0.1056
chrMT	16571	78551	4.7403	3.9067
chrX	155270560	21474303	0.1383	0.5594
chrY	59373566	456908	0.0077	0.1121

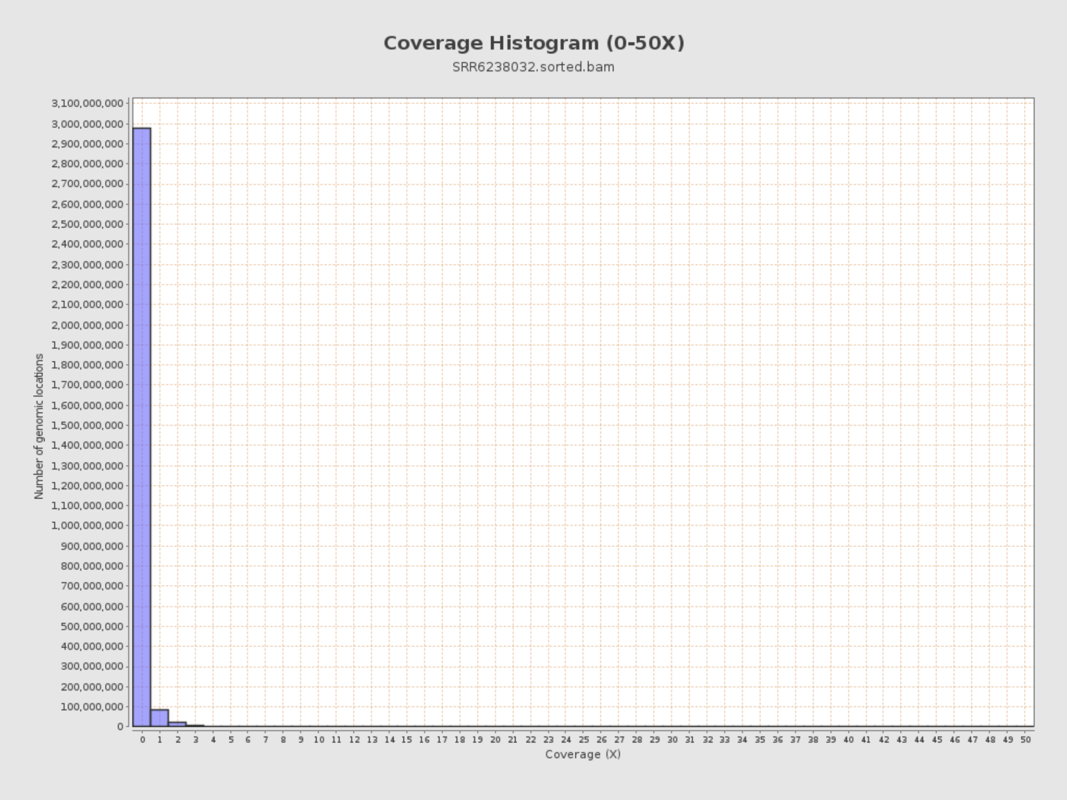
3. Results : Coverage across reference



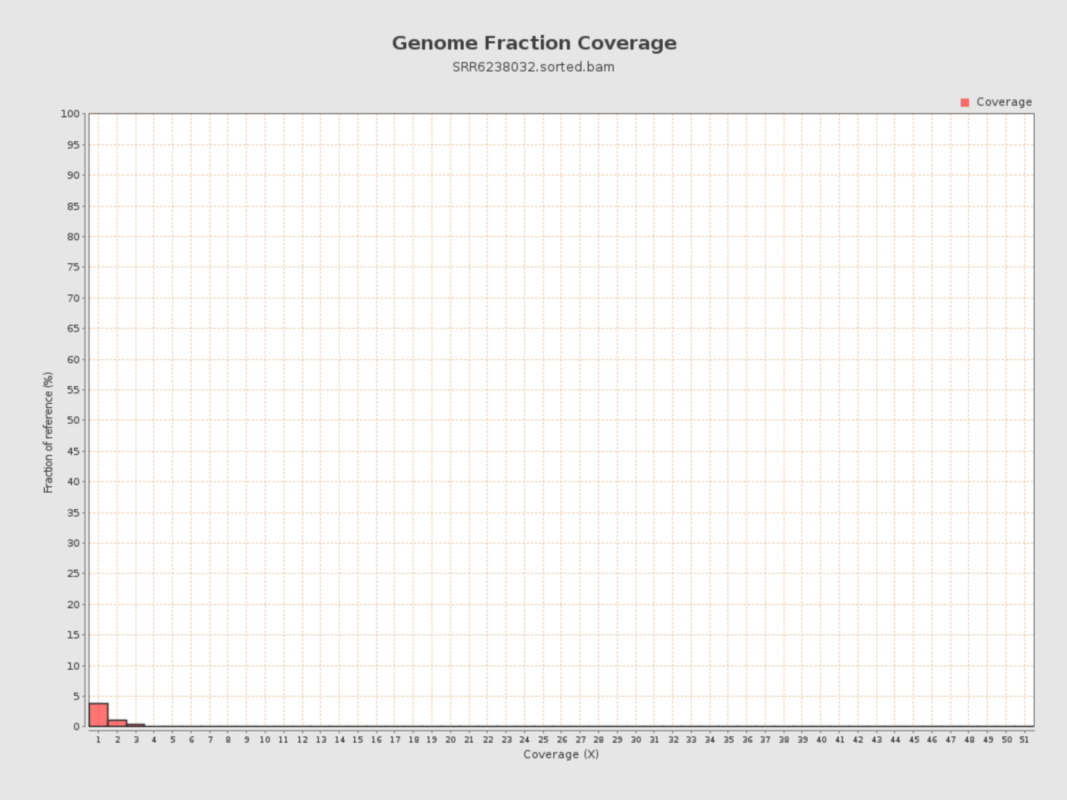
4. Results : Coverage Histogram



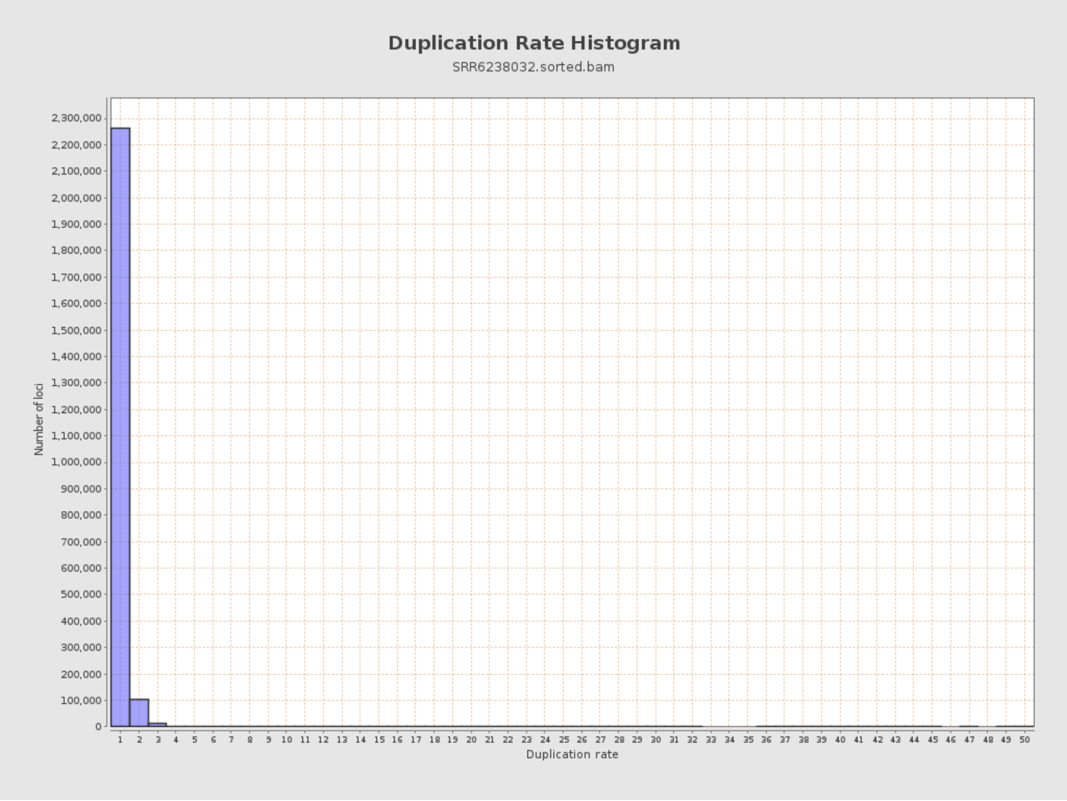
5. Results : Coverage Histogram (0-50X)



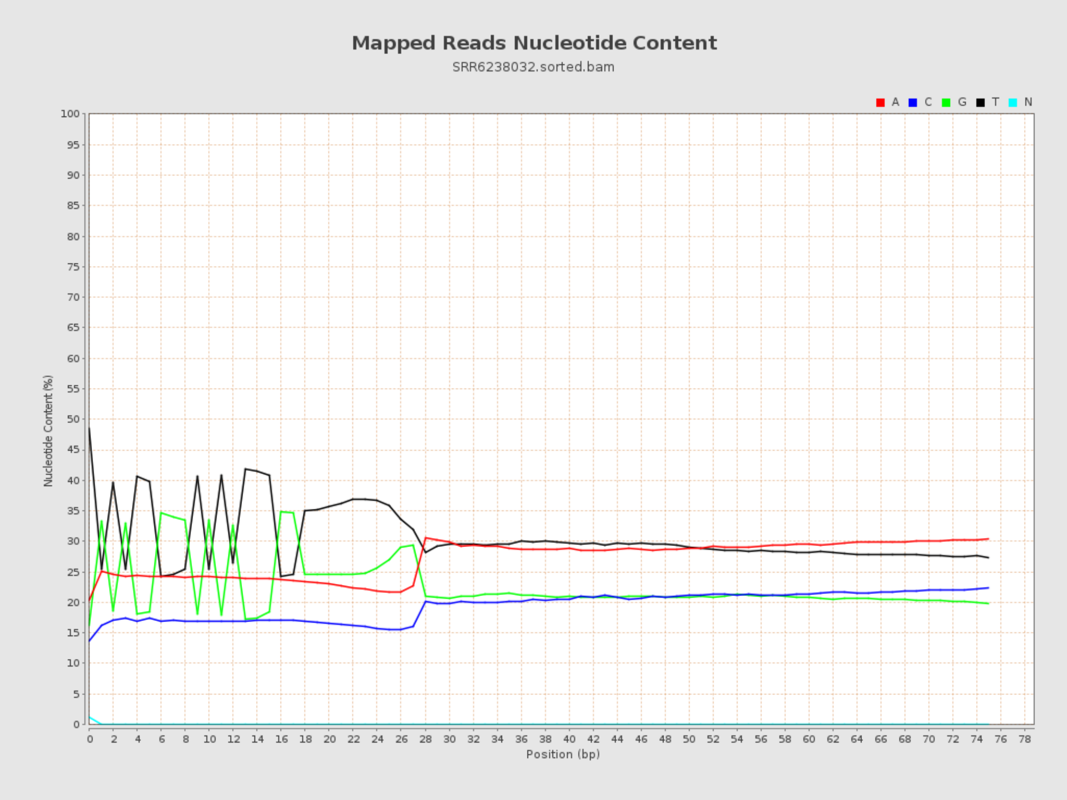
6. Results : Genome Fraction Coverage



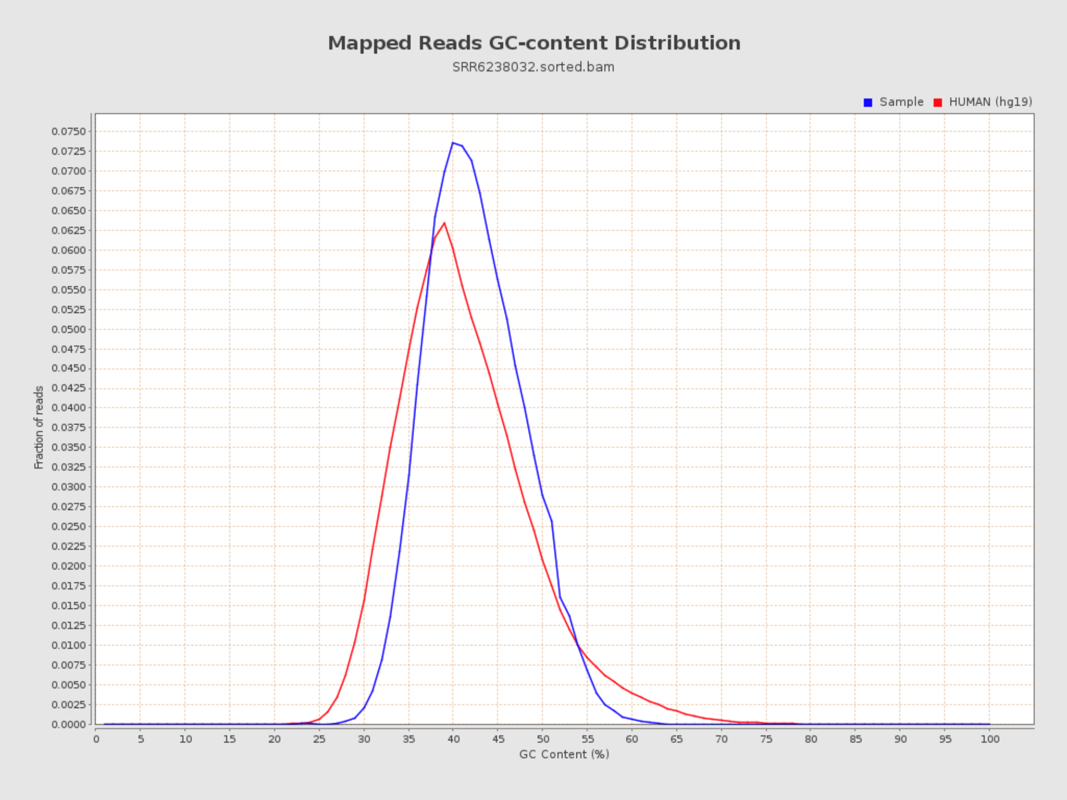
7. Results : Duplication Rate Histogram



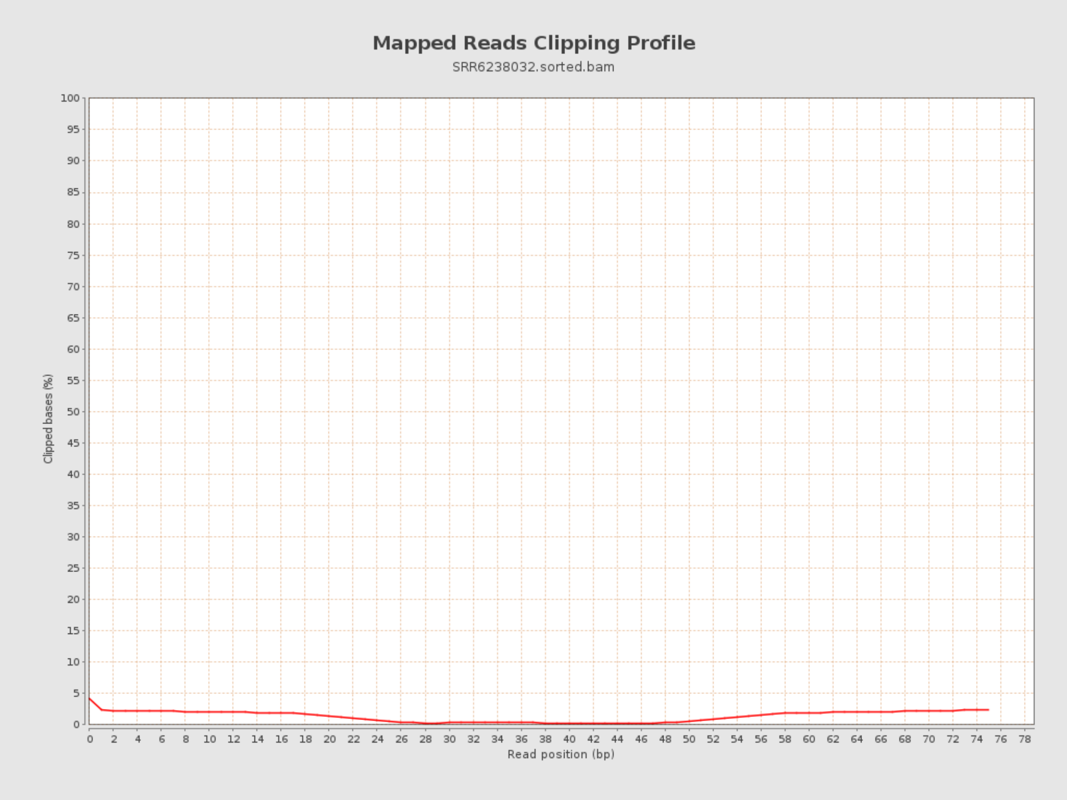
8. Results : Mapped Reads Nucleotide Content



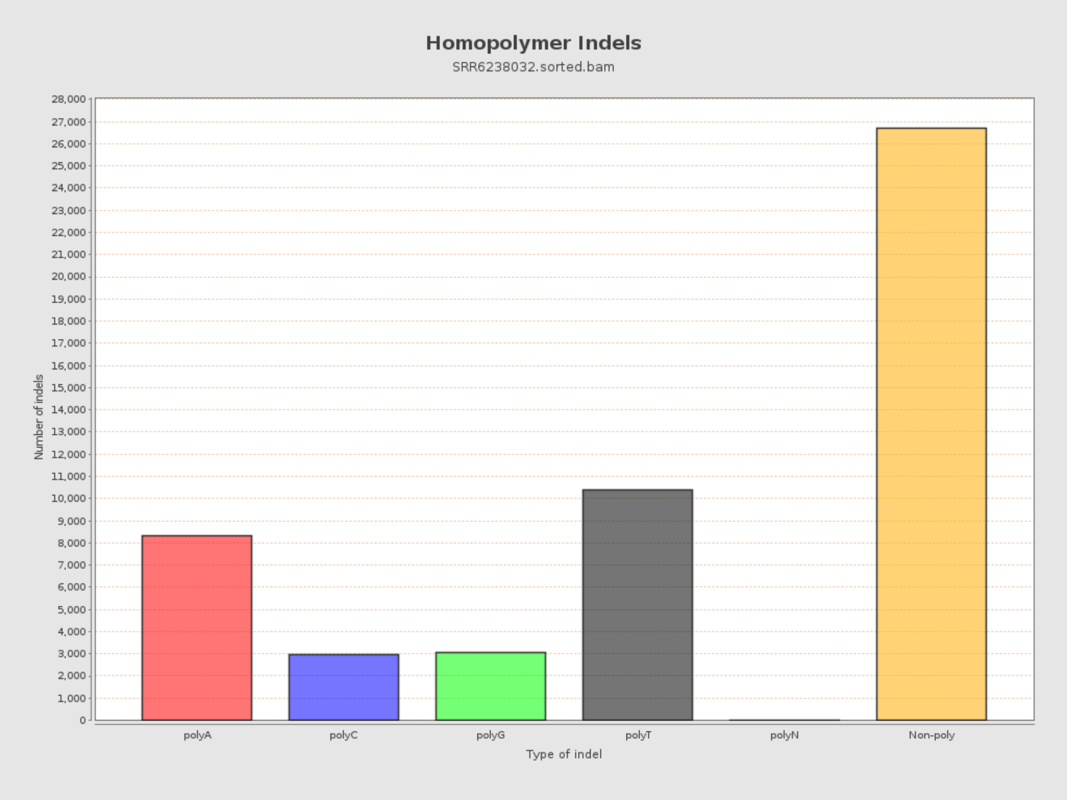
9. Results : Mapped Reads GC-content Distribution



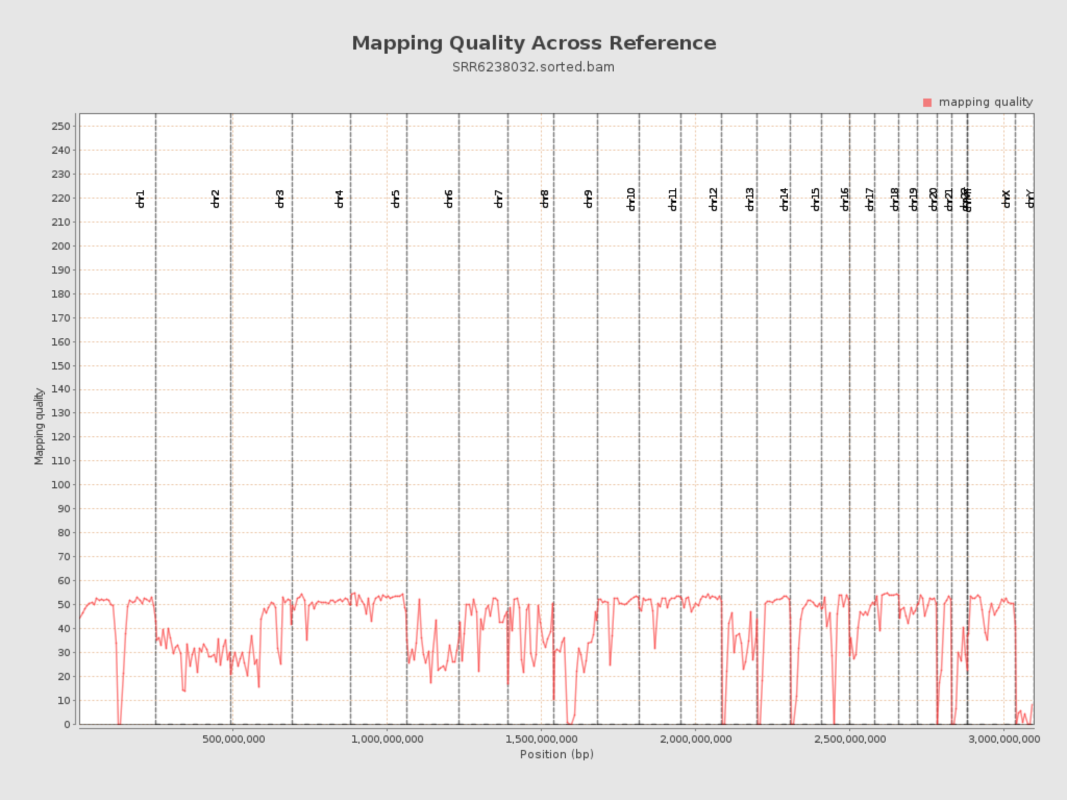
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram