Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:52:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238051.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_SRR6238051 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238051.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:52:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238051.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,011,806
Mapped reads	1,762,230 / 87.59%
Unmapped reads	249,576 / 12.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,600 / 1.02%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	121,082 / 6.02%
Duplication rate	5.4%
Clipped reads	789,797 / 39.26%

2.2. ACGT Content

Number/percentage of A's	31,985,020 / 27.31%
Number/percentage of C's	22,218,640 / 18.97%
Number/percentage of T's	36,622,235 / 31.27%
Number/percentage of G's	26,284,230 / 22.44%
Number/percentage of N's	16,105 / 0.01%
GC Percentage	41.41%

2.3. Coverage

Mean	0.0379

Standard Deviation	0.4052

2.4. Mapping Quality

Mean Mapping Quality	43.95

2.5. Mismatches and indels

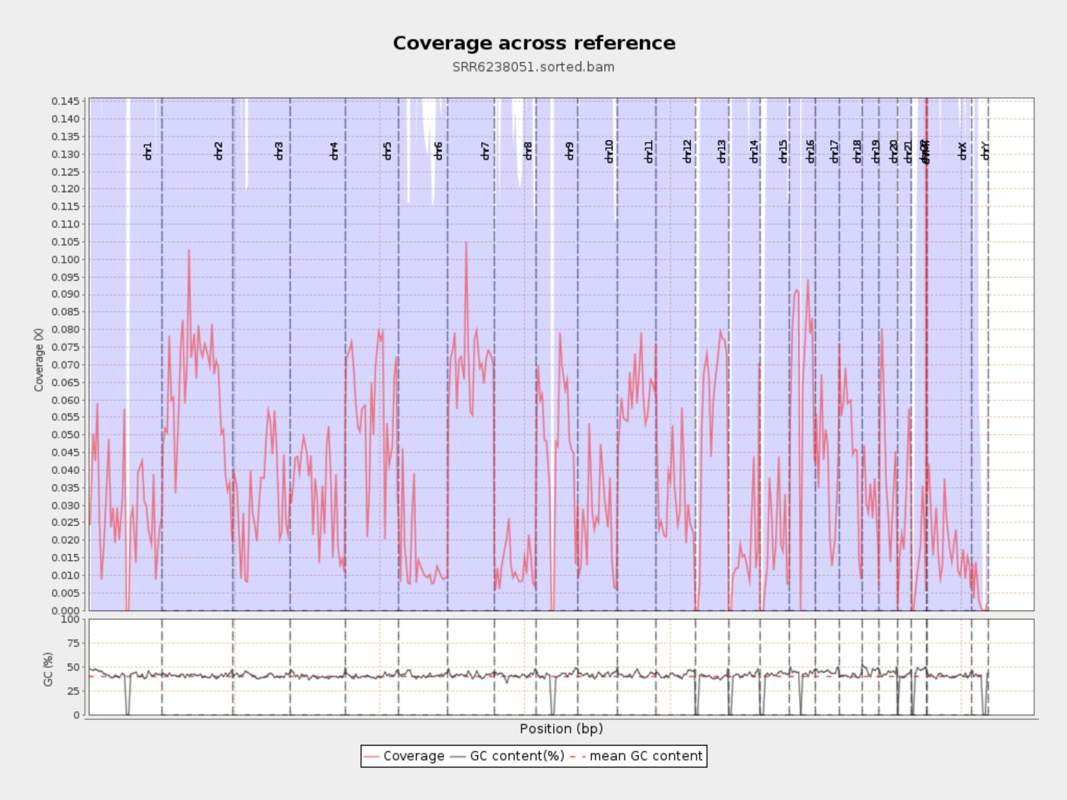
General error rate	0.79%
Mismatches	915,419
Insertions	8,017
Mapped reads with at least one insertion	0.45%
Deletions	33,222
Mapped reads with at least one deletion	1.86%
Homopolymer indels	46.07%

2.6. Chromosome stats

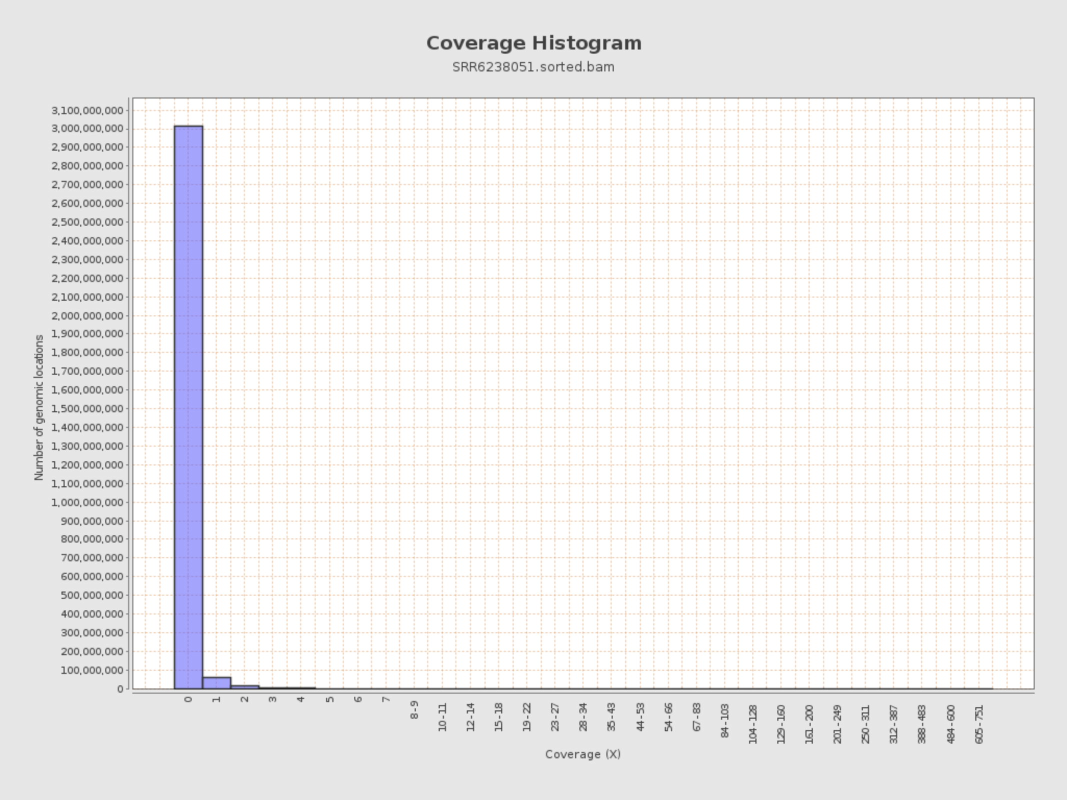
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7021551	0.0282	0.6981
chr2	243199373	15443210	0.0635	0.5237
chr3	198022430	6370333	0.0322	0.2359
chr4	191154276	6331872	0.0331	0.2581
chr5	180915260	10529605	0.0582	0.3207
chr6	171115067	2469071	0.0144	0.1869
chr7	159138663	11343238	0.0713	0.7227

chr8	146364022	1834149	0.0125	0.4104
chr9	141213431	6655529	0.0471	0.3773
chr10	135534747	3455998	0.0255	0.3392
chr11	135006516	8161301	0.0605	0.4462
chr12	133851895	4265904	0.0319	0.2415
chr13	115169878	6371742	0.0553	0.3112
chr14	107349540	1677945	0.0156	0.189
chr15	102531392	1849088	0.018	0.1743
chr16	90354753	6453814	0.0714	0.3748
chr17	81195210	3160462	0.0389	0.3001
chr18	78077248	3818574	0.0489	0.4802
chr19	59128983	1865862	0.0316	0.5575
chr20	63025520	2691472	0.0427	0.281
chr21	48129895	1351501	0.0281	0.2439
chr22	51304566	719661	0.014	0.1561
chrMT	16571	69032	4.1658	3.47
chrX	155270560	3027855	0.0195	0.2169
chrY	59373566	246627	0.0042	0.1328

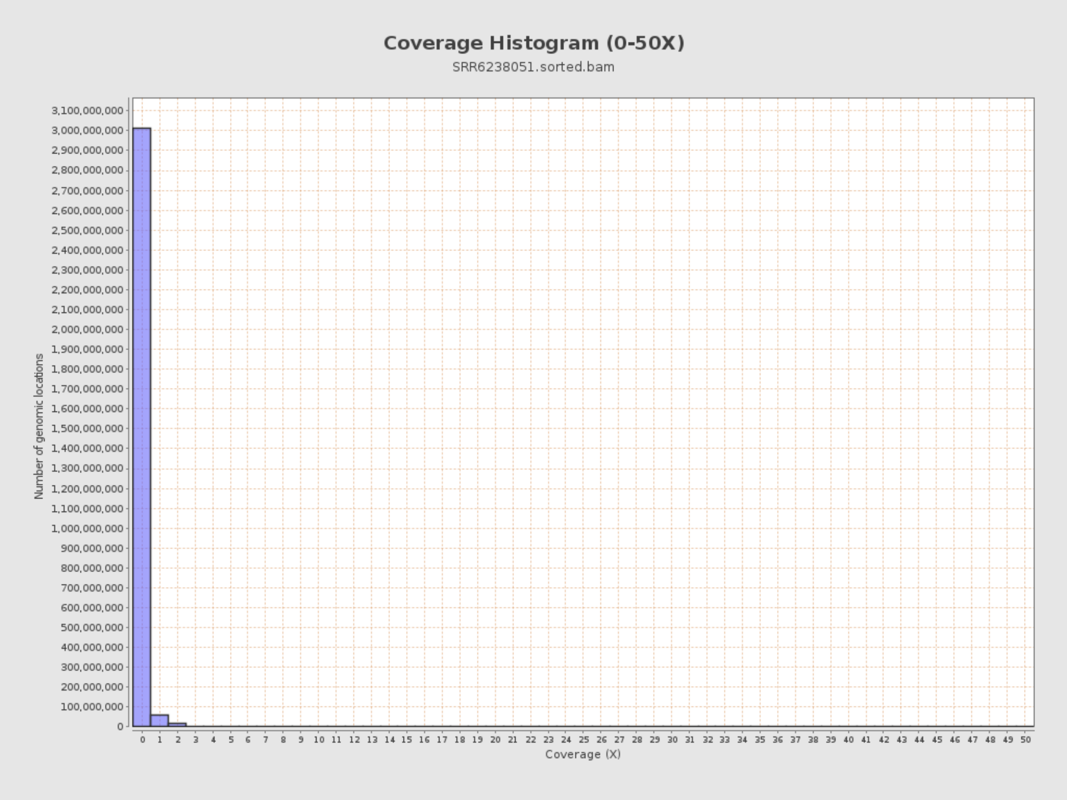
3. Results : Coverage across reference



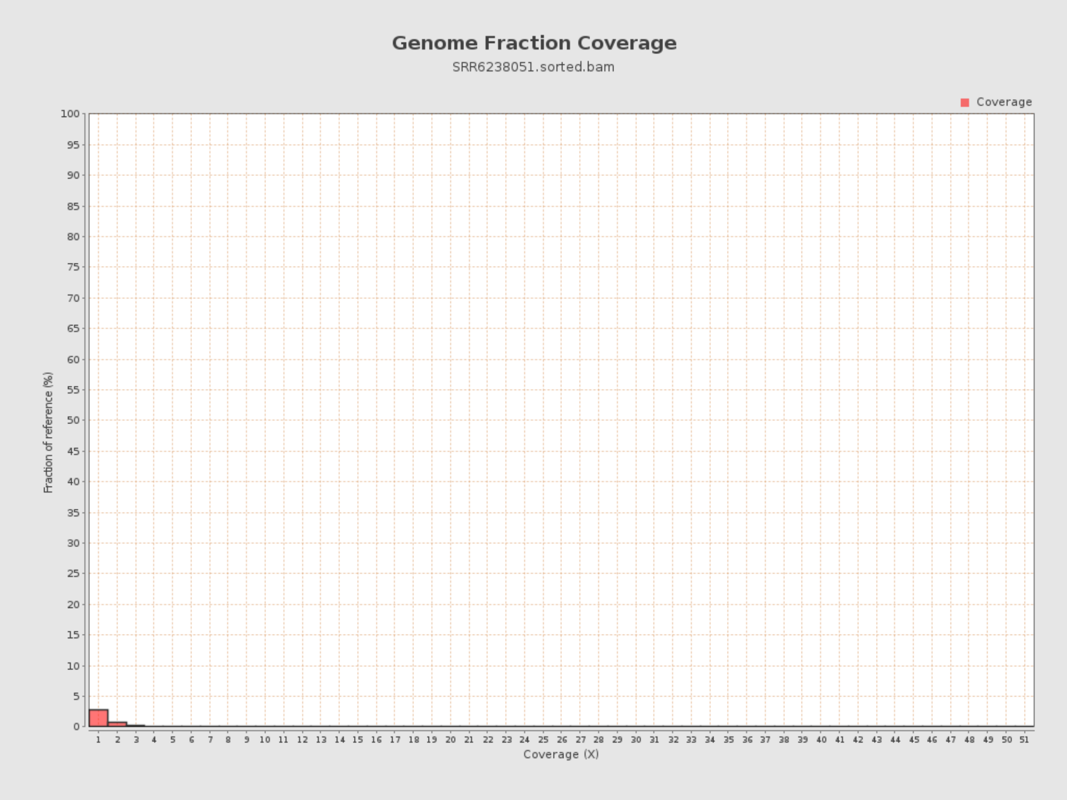
4. Results : Coverage Histogram



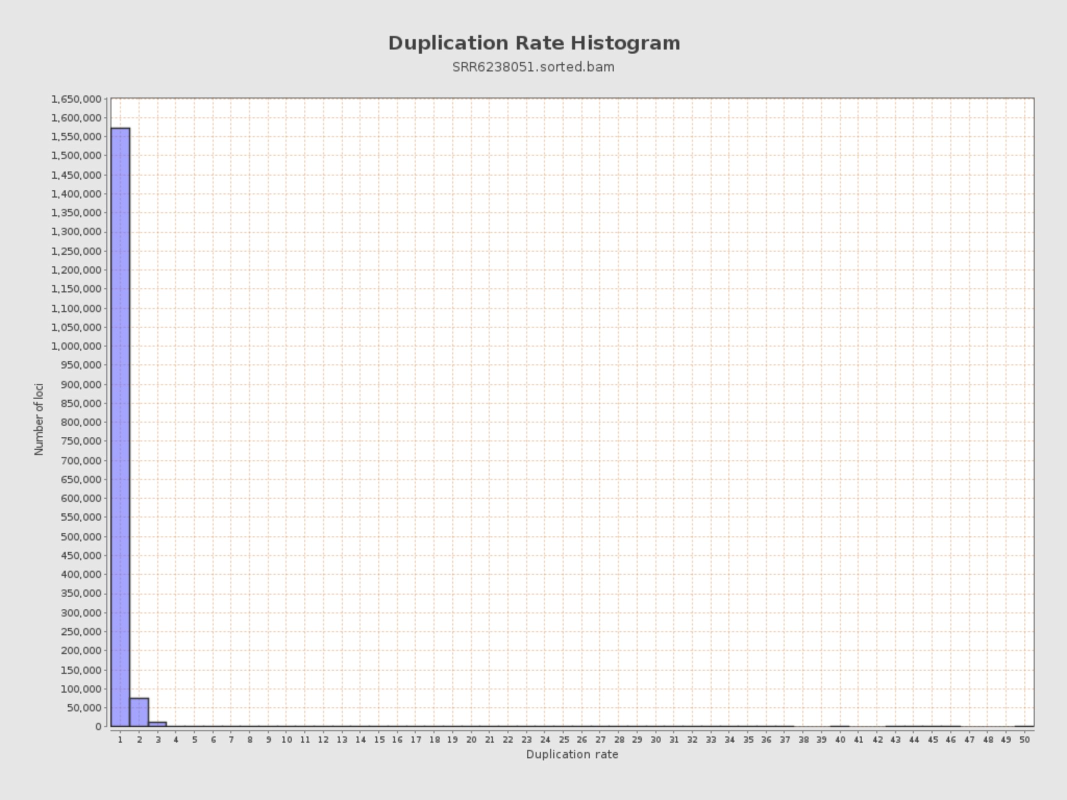
5. Results : Coverage Histogram (0-50X)



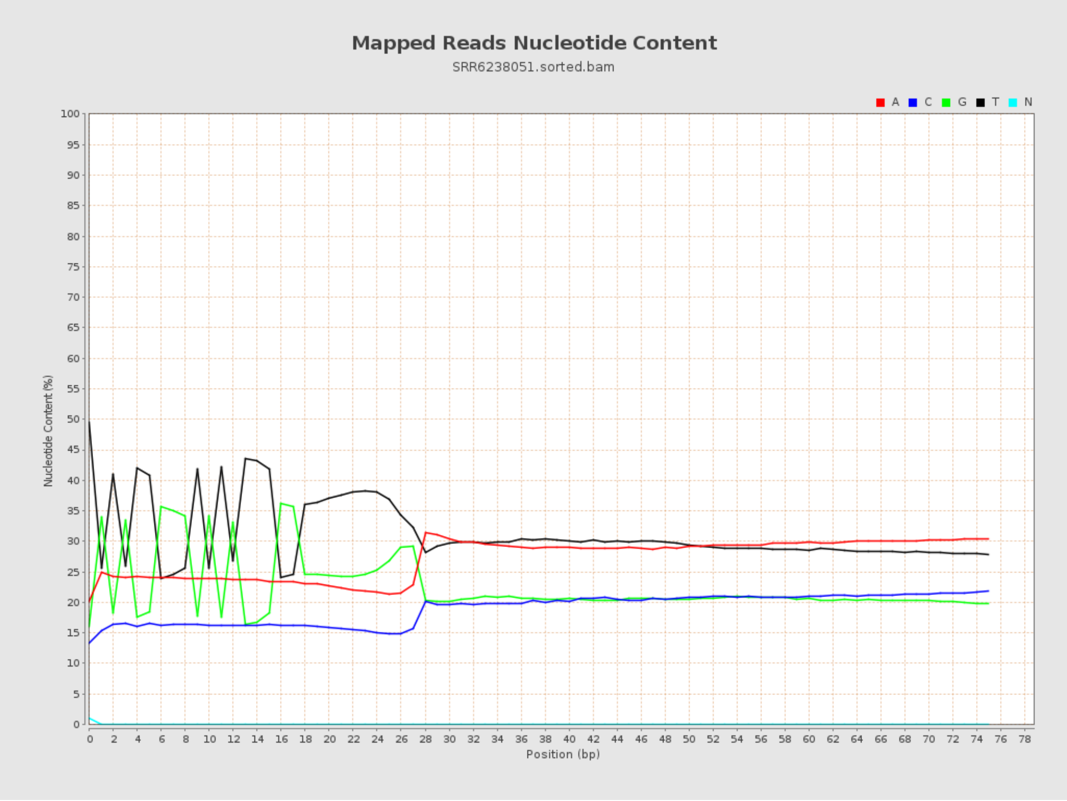
6. Results : Genome Fraction Coverage



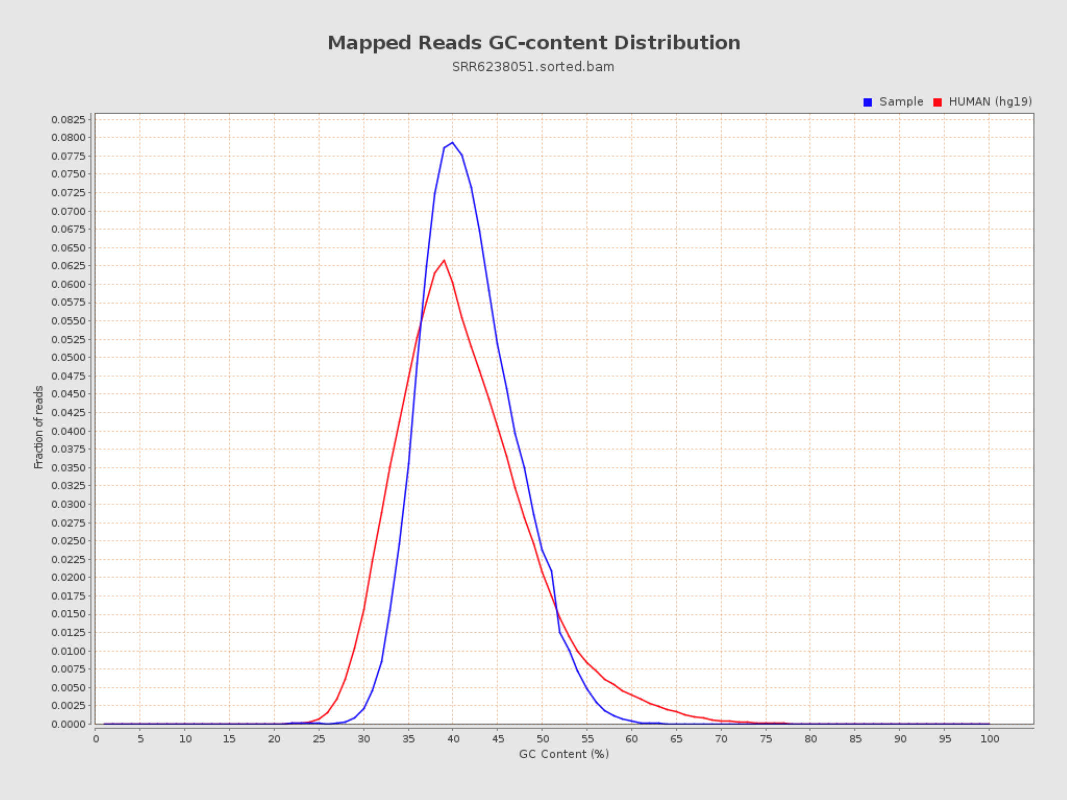
7. Results : Duplication Rate Histogram



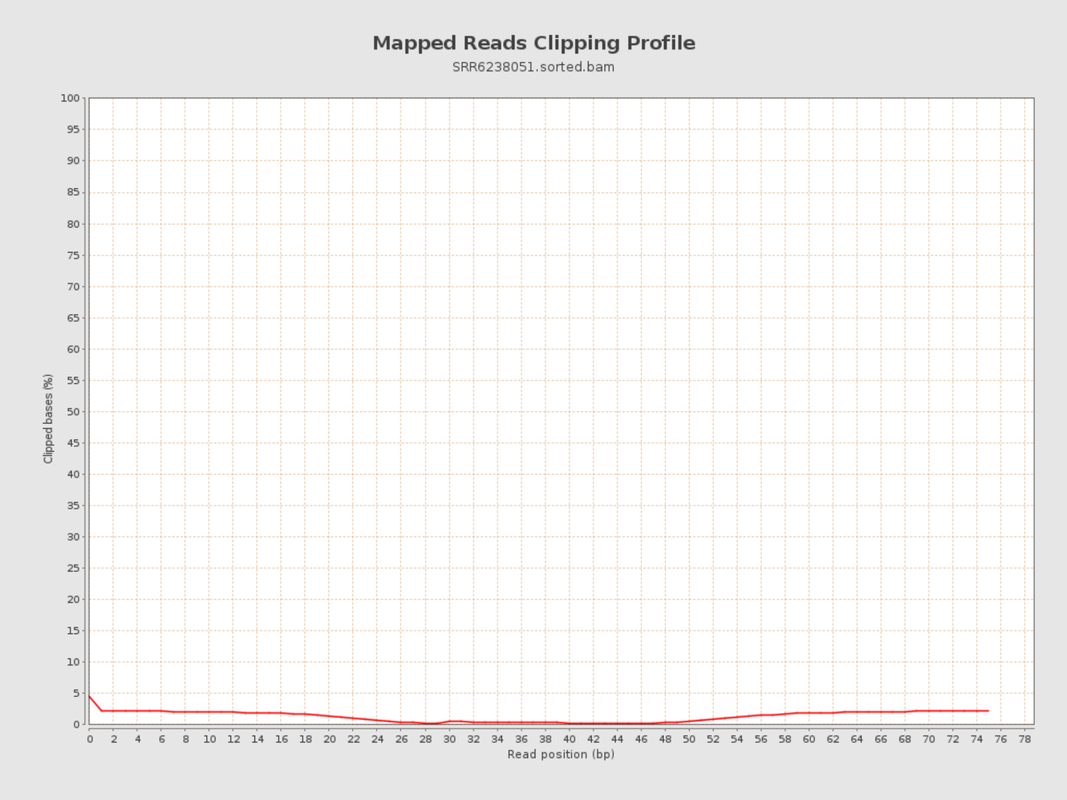
8. Results : Mapped Reads Nucleotide Content



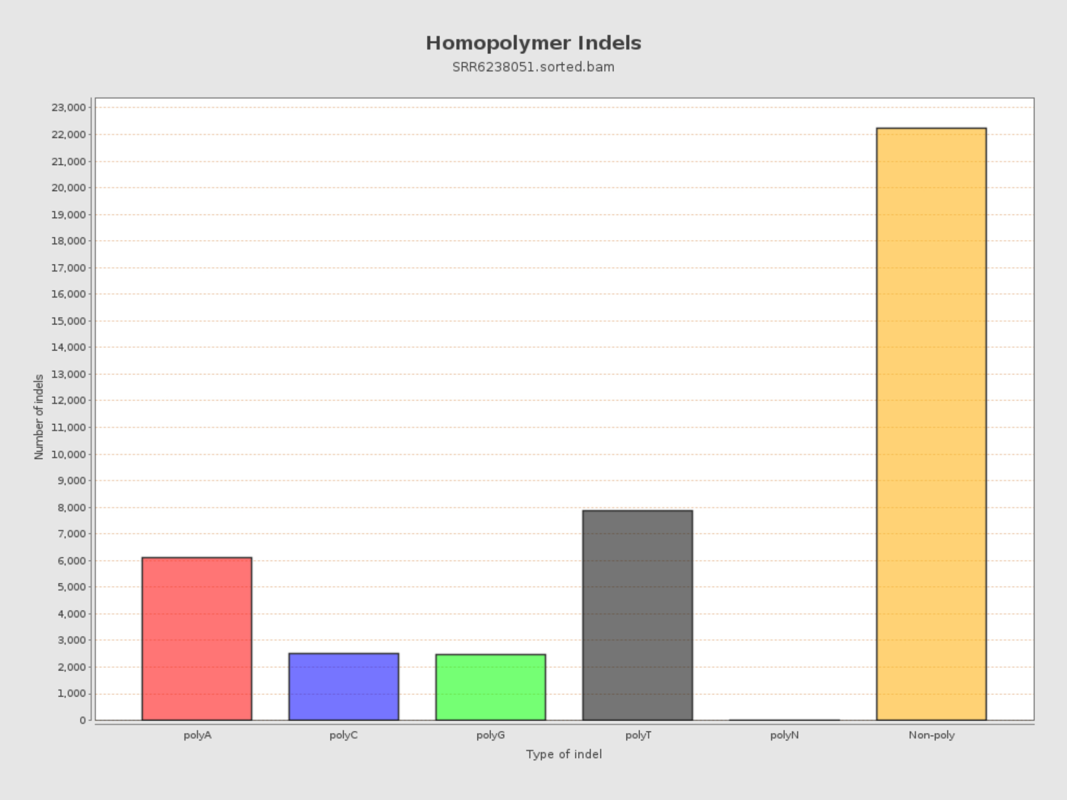
9. Results : Mapped Reads GC-content Distribution



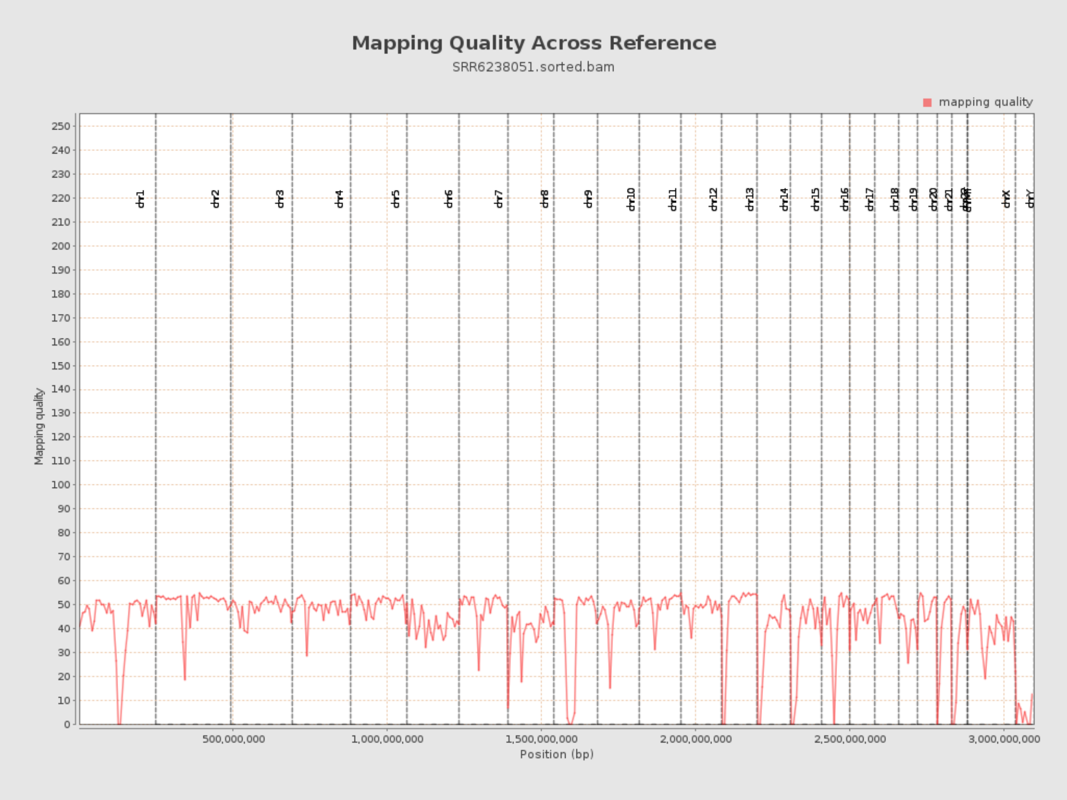
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram