Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:47:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238309.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_SRR6238309 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238309.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:47:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238309.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,370,968
Mapped reads	2,140,426 / 90.28%
Unmapped reads	230,542 / 9.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,014 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	67,712 / 2.86%
Duplication rate	2.14%
Clipped reads	1,202,397 / 50.71%

2.2. ACGT Content

Number/percentage of A's	37,296,094 / 27.05%
Number/percentage of C's	26,902,815 / 19.51%
Number/percentage of T's	41,241,815 / 29.91%
Number/percentage of G's	32,399,368 / 23.5%
Number/percentage of N's	31,664 / 0.02%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0446

Standard Deviation	0.4218

2.4. Mapping Quality

Mean Mapping Quality	42.84

2.5. Mismatches and indels

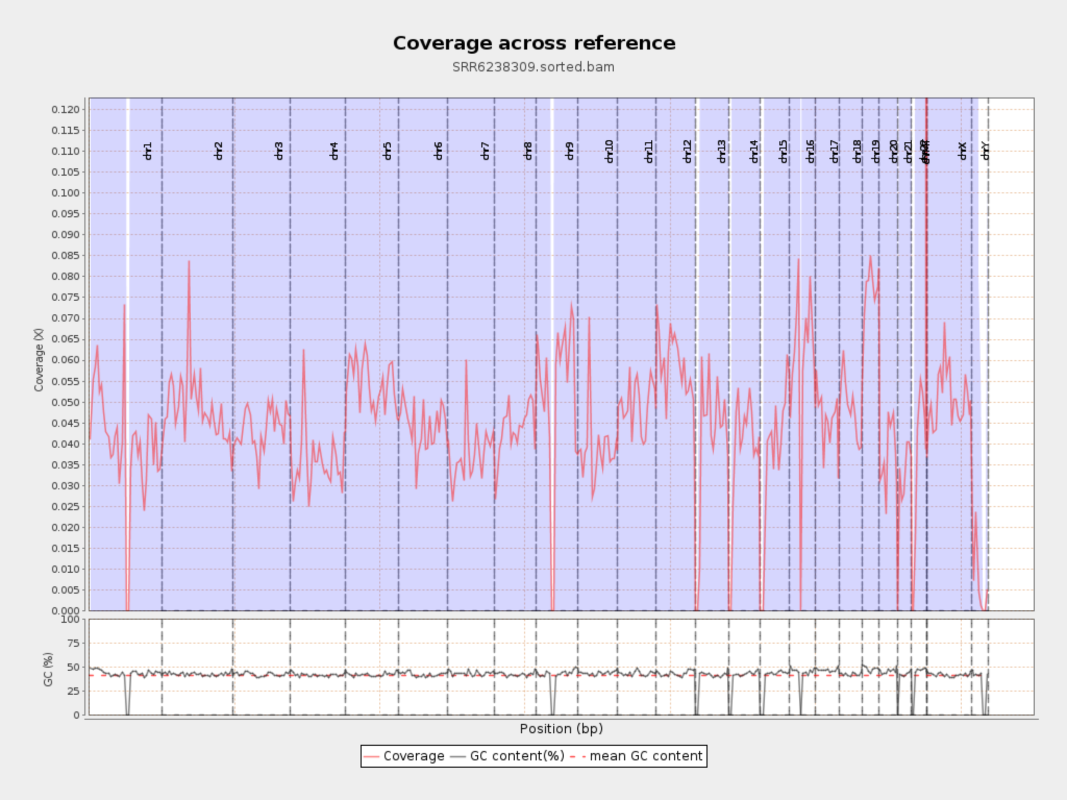
General error rate	0.89%
Mismatches	1,207,842
Insertions	11,676
Mapped reads with at least one insertion	0.54%
Deletions	43,485
Mapped reads with at least one deletion	2.01%
Homopolymer indels	43.69%

2.6. Chromosome stats

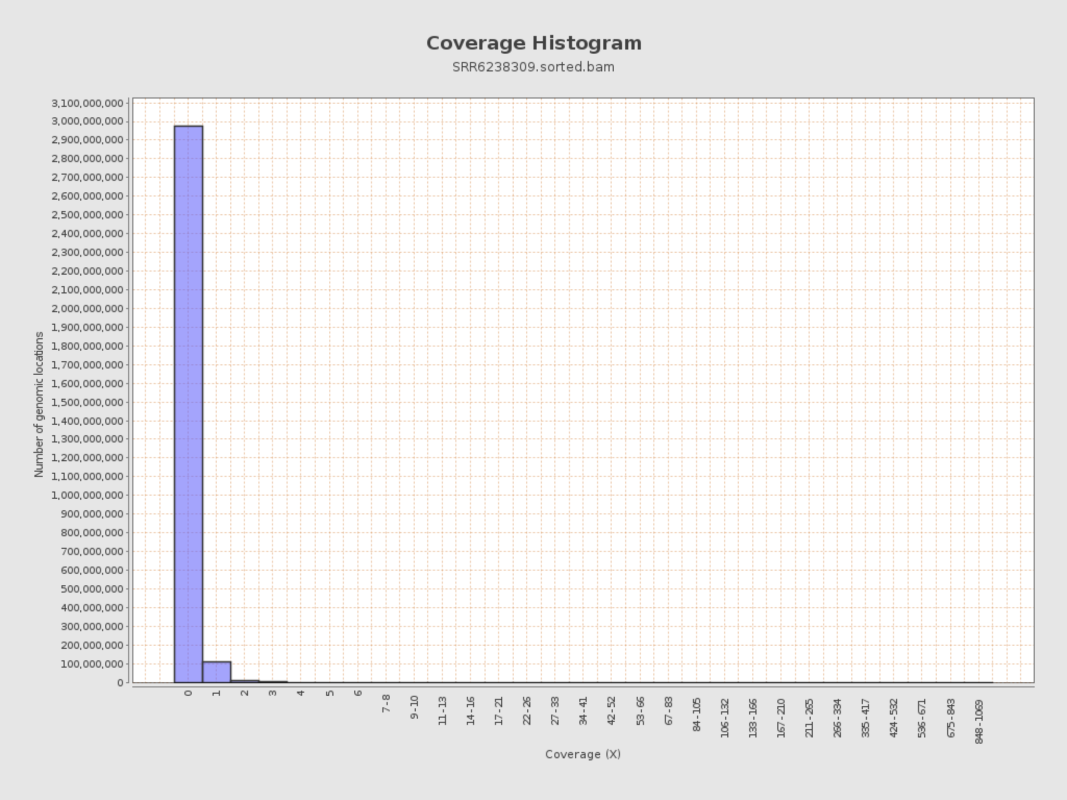
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10005299	0.0401	0.9054
chr2	243199373	11901908	0.0489	0.5059
chr3	198022430	8601174	0.0434	0.2285
chr4	191154276	6780783	0.0355	0.2535
chr5	180915260	9865550	0.0545	0.2642
chr6	171115067	7578512	0.0443	0.281
chr7	159138663	5981832	0.0376	0.3983

chr8	146364022	6326079	0.0432	0.4323
chr9	141213431	7347418	0.052	0.4008
chr10	135534747	5215552	0.0385	0.3875
chr11	135006516	6641251	0.0492	0.3341
chr12	133851895	7891902	0.059	0.2744
chr13	115169878	4622882	0.0401	0.2204
chr14	107349540	4003811	0.0373	0.2617
chr15	102531392	3743575	0.0365	0.2245
chr16	90354753	5447113	0.0603	0.3098
chr17	81195210	3738860	0.046	0.2541
chr18	78077248	3814614	0.0489	0.6772
chr19	59128983	4547041	0.0769	0.6185
chr20	63025520	2349066	0.0373	0.225
chr21	48129895	1490418	0.031	0.2382
chr22	51304566	1736967	0.0339	0.2043
chrMT	16571	10369	0.6257	1.0033
chrX	155270560	7888252	0.0508	0.2928
chrY	59373566	414341	0.007	0.2097

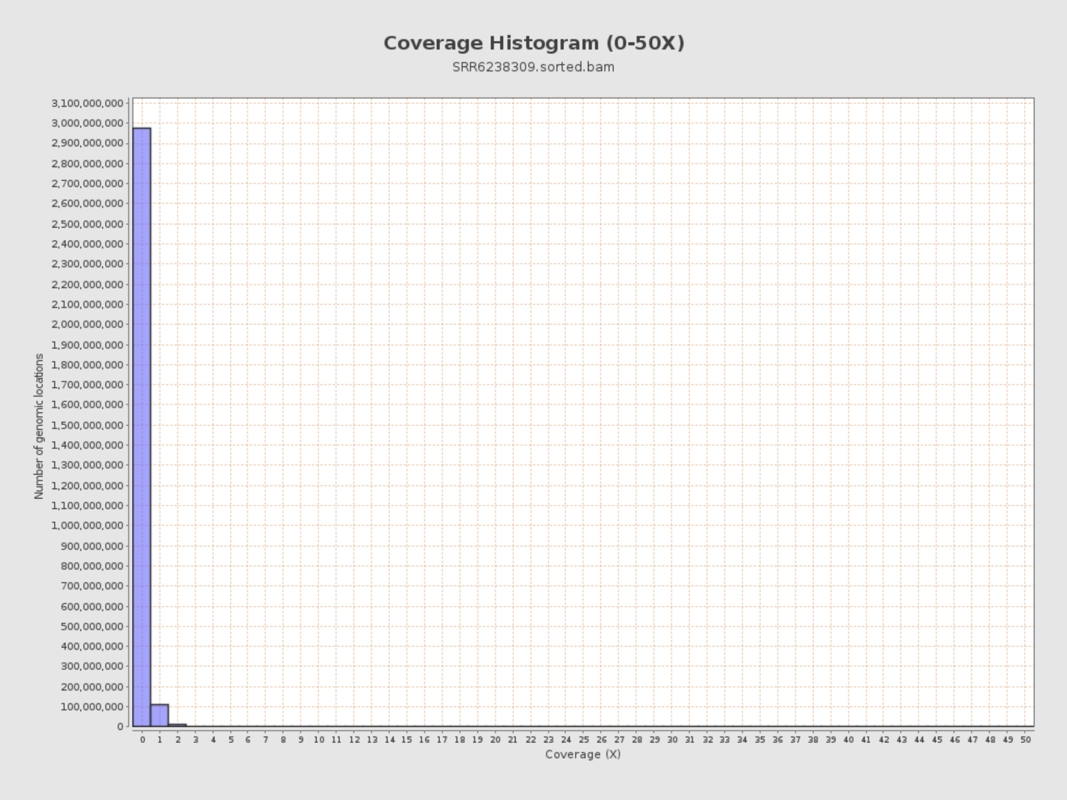
3. Results : Coverage across reference



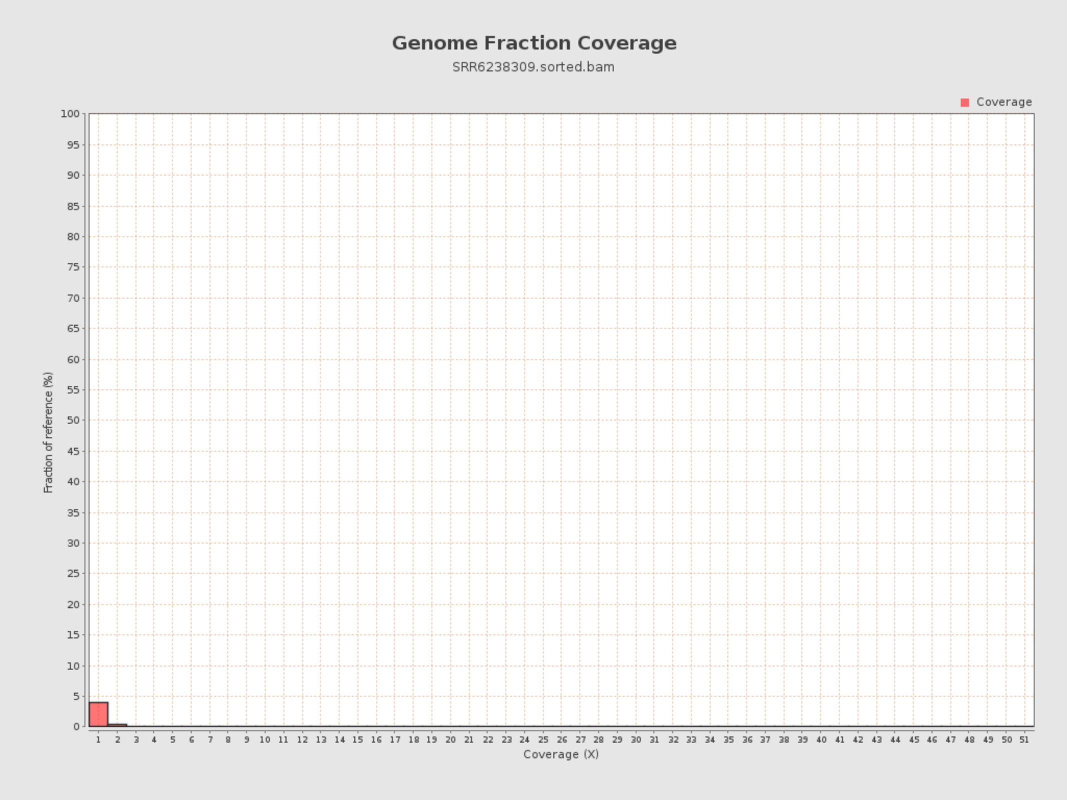
4. Results : Coverage Histogram



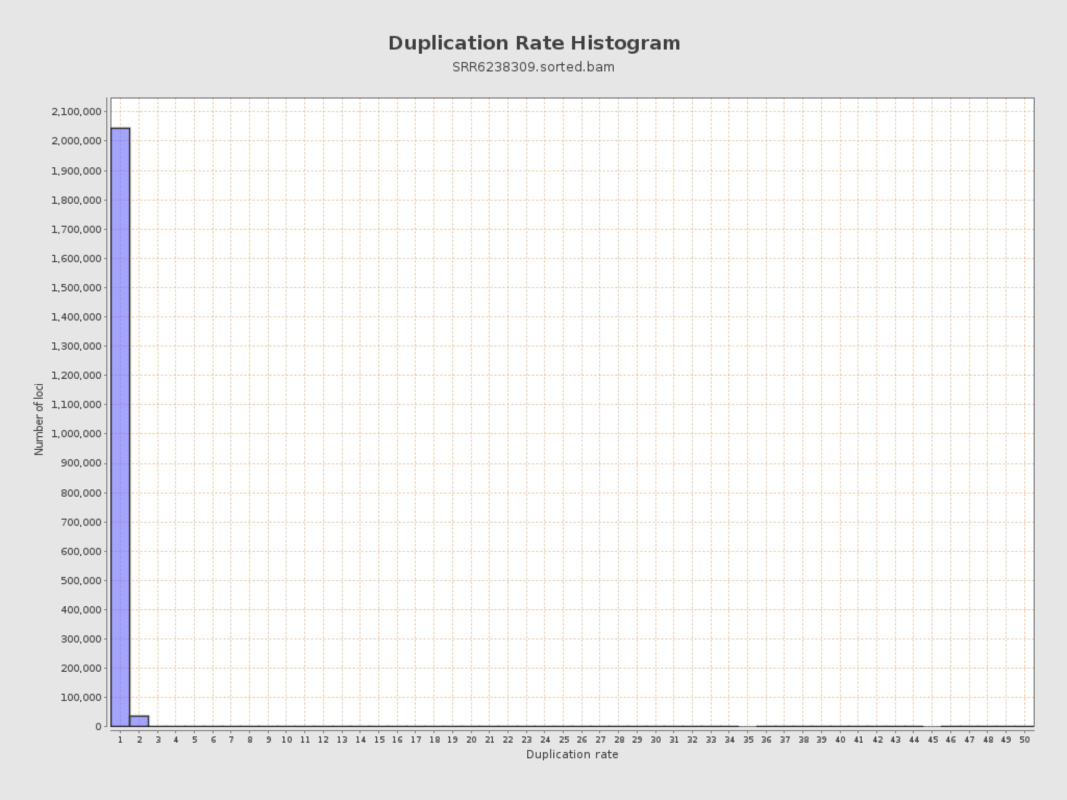
5. Results : Coverage Histogram (0-50X)



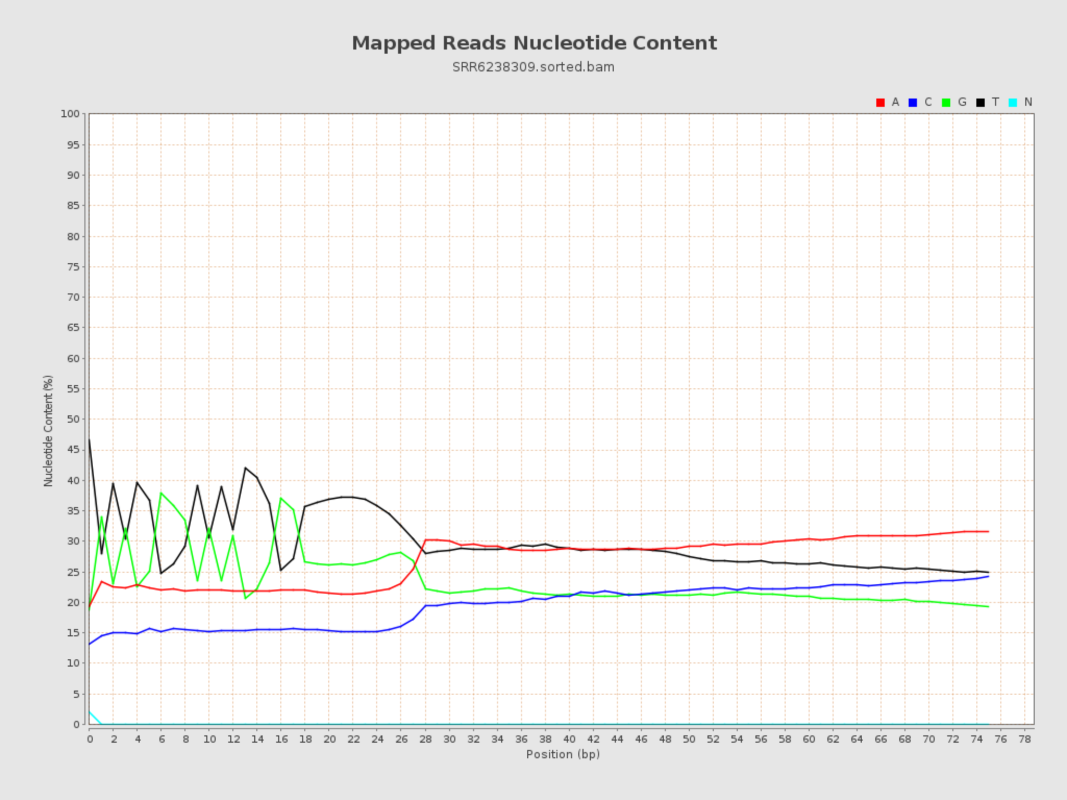
6. Results : Genome Fraction Coverage



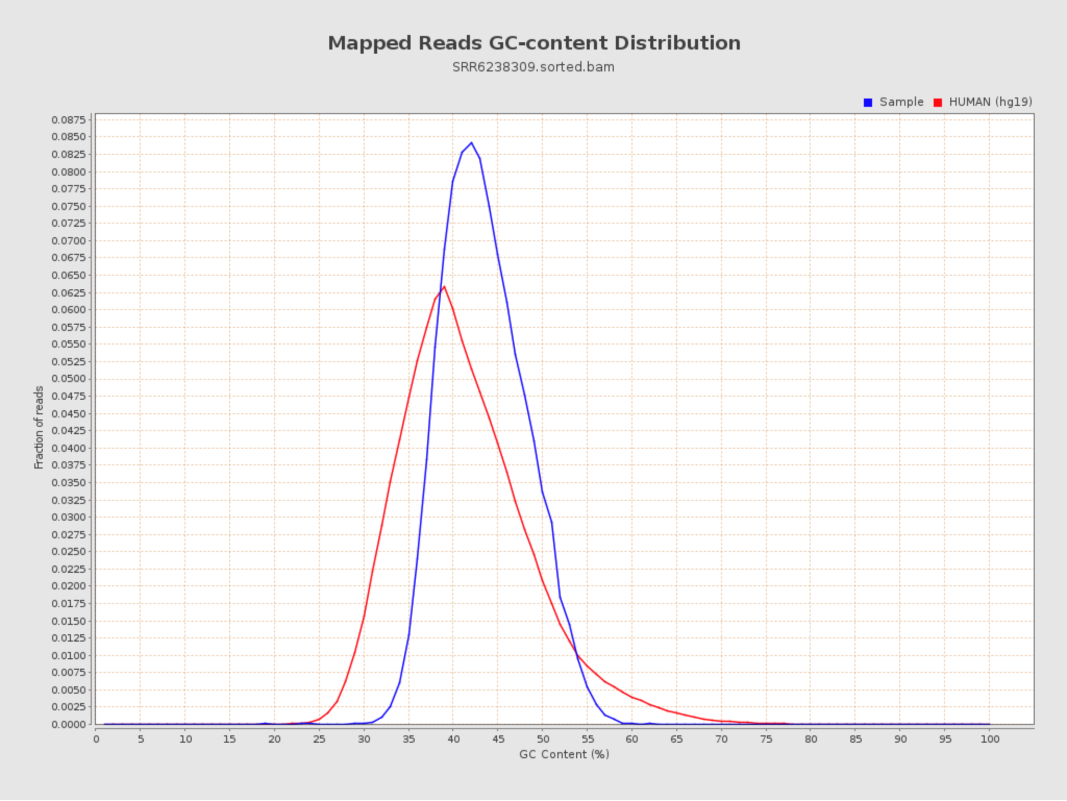
7. Results : Duplication Rate Histogram



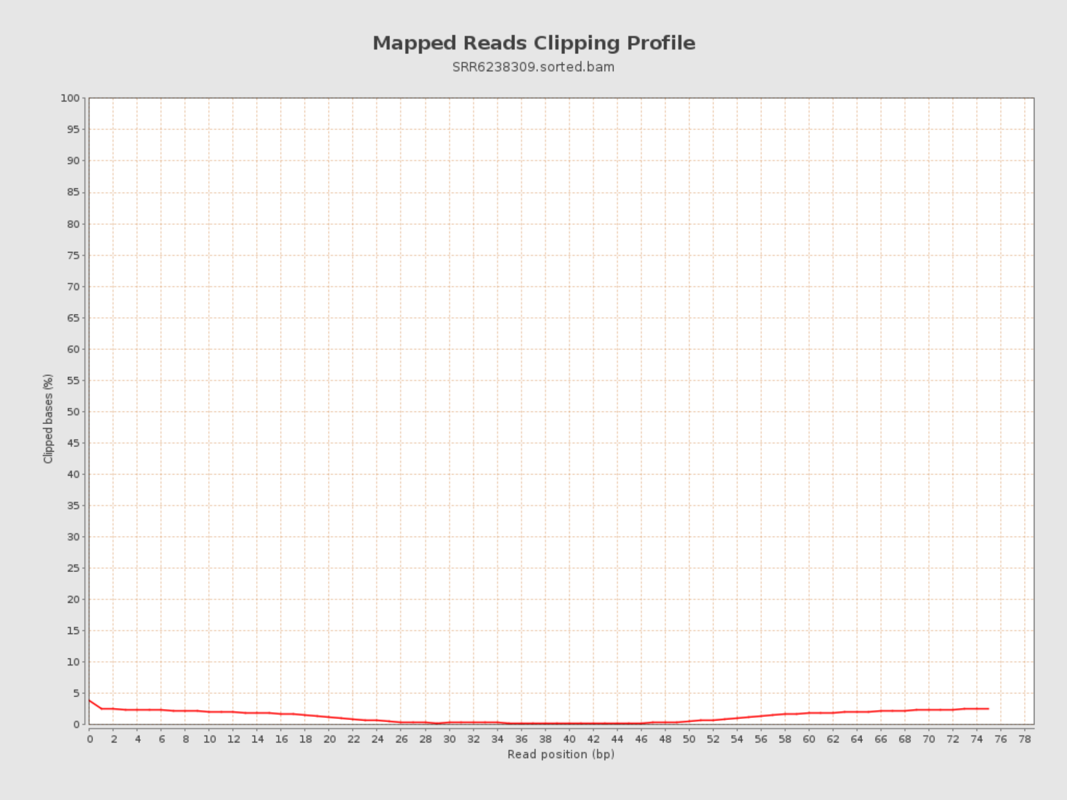
8. Results : Mapped Reads Nucleotide Content



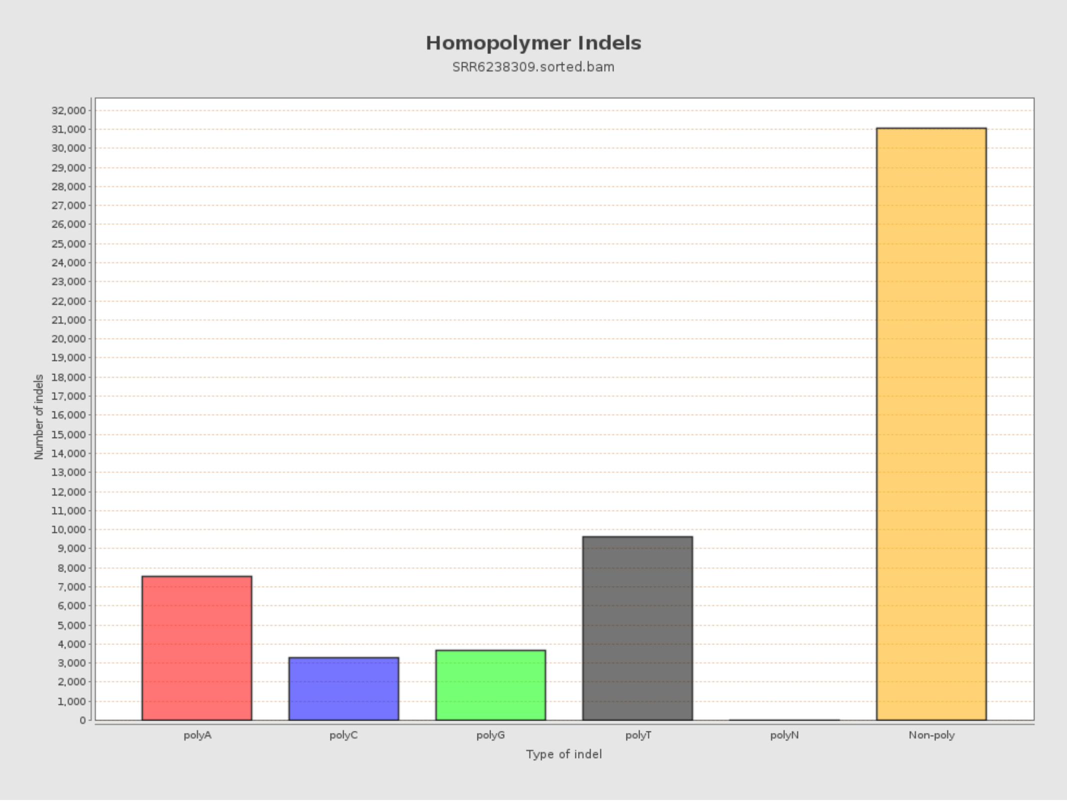
9. Results : Mapped Reads GC-content Distribution



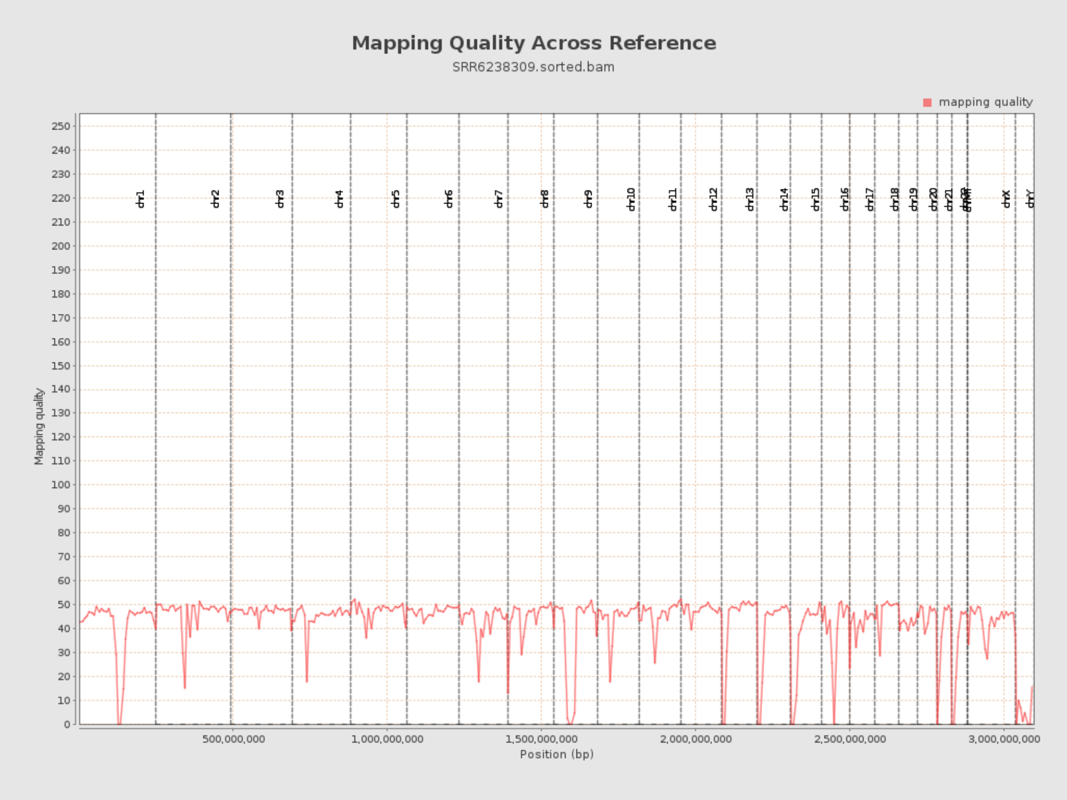
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram