Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:50:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238508.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_SRR6238508 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238508.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:50:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238508.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,372,557
Mapped reads	3,145,610 / 93.27%
Unmapped reads	226,947 / 6.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,899 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	293,595 / 8.71%
Duplication rate	7.85%
Clipped reads	1,842,294 / 54.63%

2.2. ACGT Content

Number/percentage of A's	49,044,129 / 24.78%
Number/percentage of C's	35,584,380 / 17.98%
Number/percentage of T's	64,960,508 / 32.82%
Number/percentage of G's	48,334,270 / 24.42%
Number/percentage of N's	14,078 / 0.01%
GC Percentage	42.4%

2.3. Coverage

Mean	0.064

Standard Deviation	0.6437

2.4. Mapping Quality

Mean Mapping Quality	42.98

2.5. Mismatches and indels

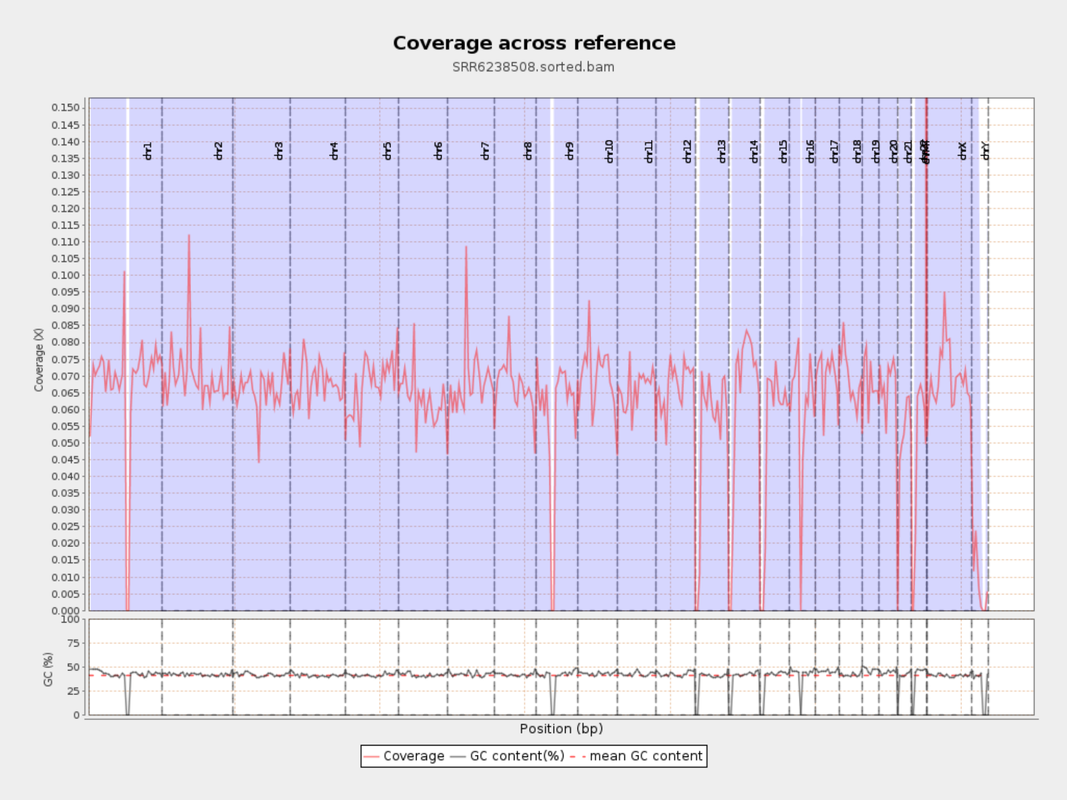
General error rate	0.56%
Mismatches	1,073,197
Insertions	14,094
Mapped reads with at least one insertion	0.44%
Deletions	48,689
Mapped reads with at least one deletion	1.53%
Homopolymer indels	43.55%

2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16766078	0.0673	1.0086
chr2	243199373	17121731	0.0704	1.3709
chr3	198022430	13091423	0.0661	0.3215
chr4	191154276	12954367	0.0678	0.3409
chr5	180915260	12211106	0.0675	0.3226
chr6	171115067	10788771	0.063	0.5283
chr7	159138663	10934526	0.0687	0.7974

chr8	146364022	9818196	0.0671	0.5369
chr9	141213431	8069972	0.0571	0.4615
chr10	135534747	9506894	0.0701	0.4923
chr11	135006516	8898579	0.0659	0.4269
chr12	133851895	8962827	0.067	0.3291
chr13	115169878	6032719	0.0524	0.3546
chr14	107349540	6719364	0.0626	0.3285
chr15	102531392	5389469	0.0526	0.3696
chr16	90354753	5488732	0.0607	0.3667
chr17	81195210	5640767	0.0695	0.3497
chr18	78077248	5458881	0.0699	1.0831
chr19	59128983	4005494	0.0677	0.6438
chr20	63025520	4221537	0.067	0.3276
chr21	48129895	2382597	0.0495	0.3059
chr22	51304566	2236542	0.0436	0.2505
chrMT	16571	16376	0.9882	1.1985
chrX	155270560	10794133	0.0695	0.3696
chrY	59373566	510189	0.0086	0.2363

3. Results : Coverage across reference



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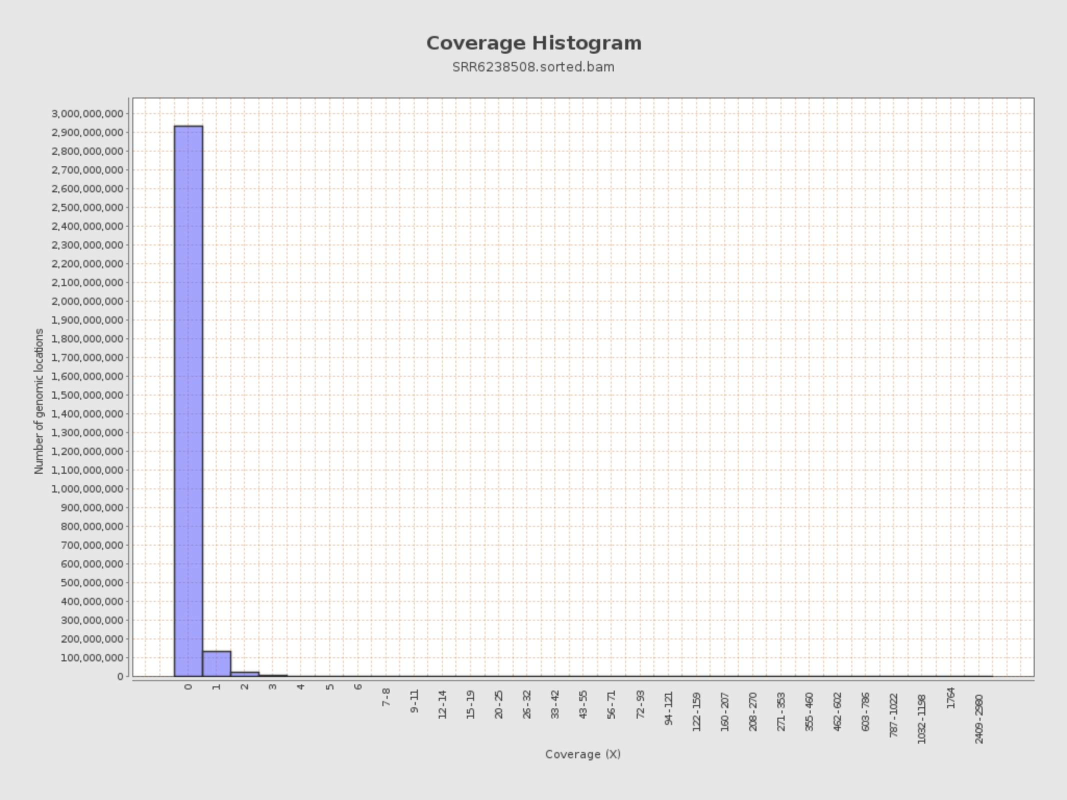
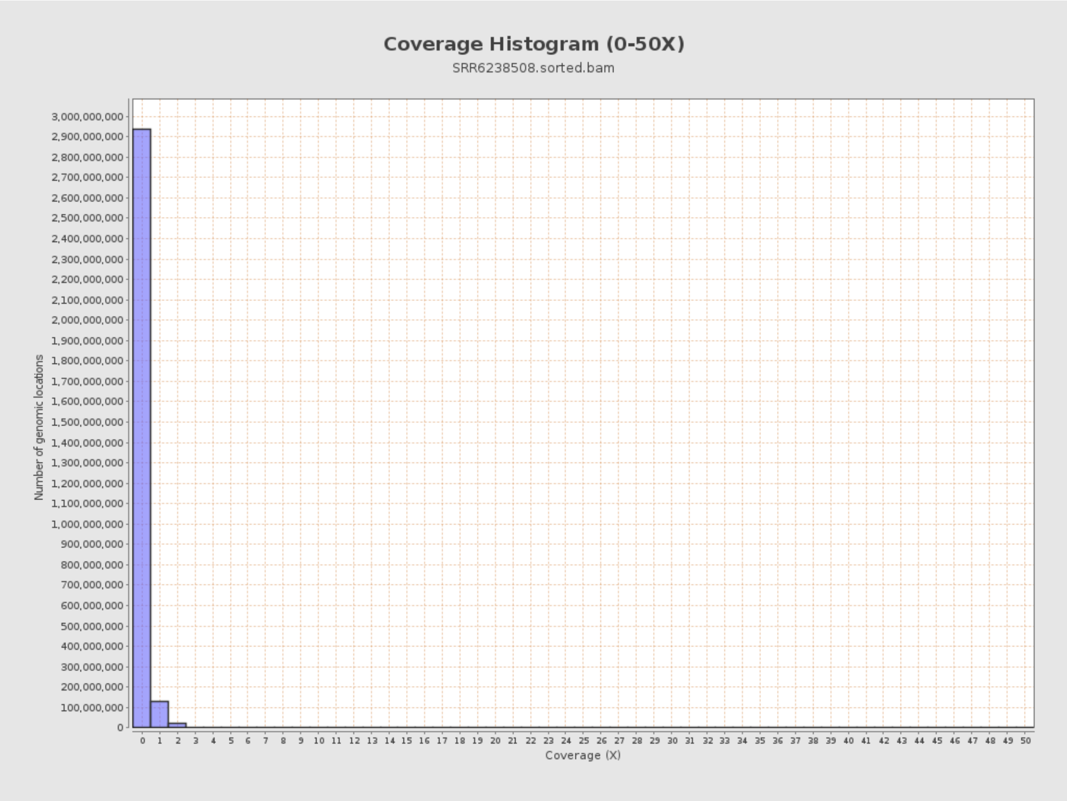
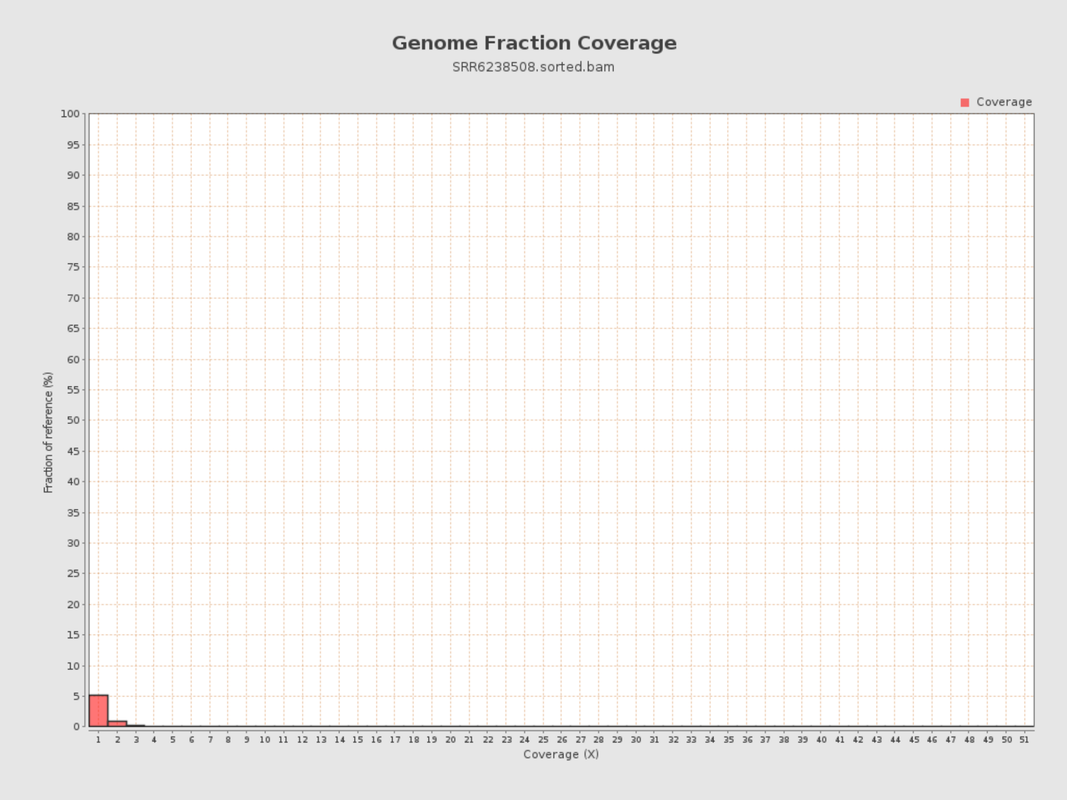
4. Results : Coverage Histogram



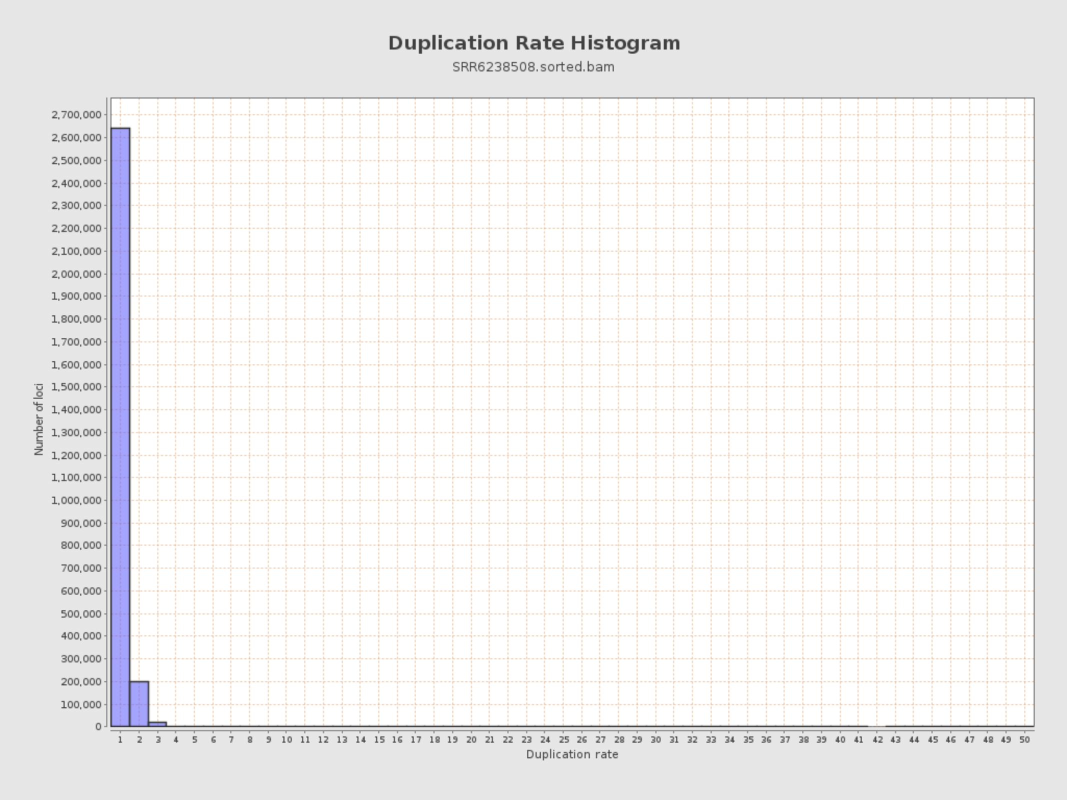
5. Results : Coverage Histogram (0-50X)



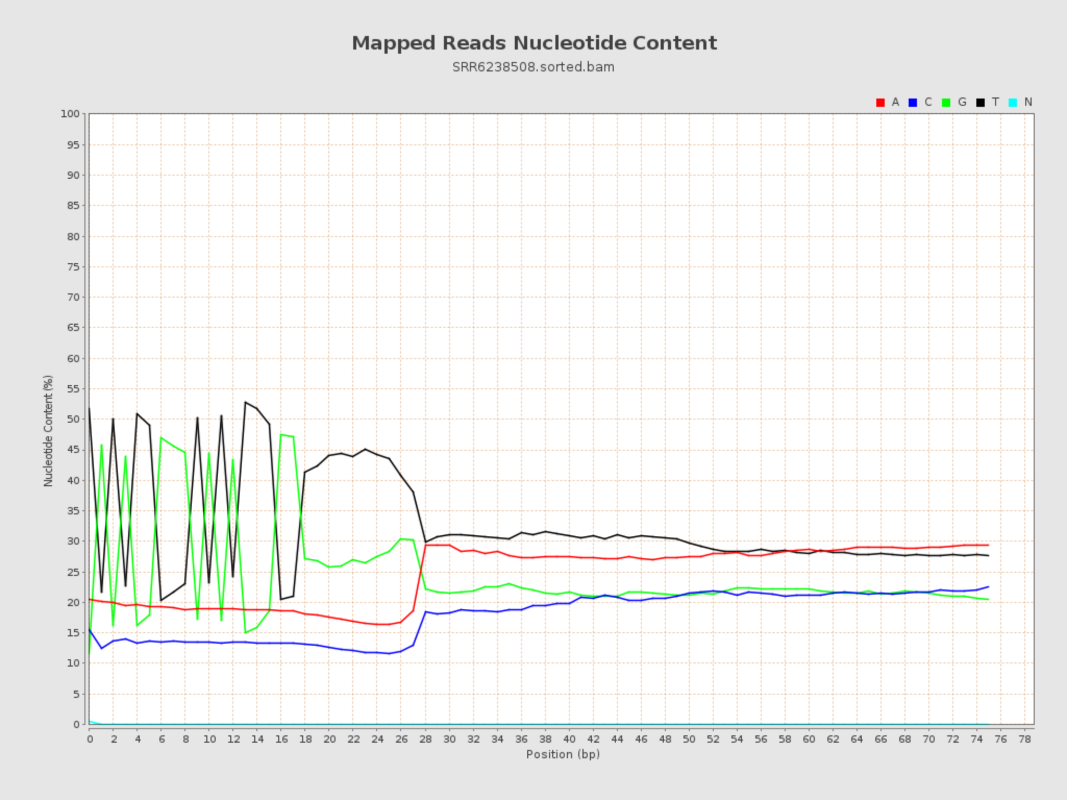
6. Results : Genome Fraction Coverage



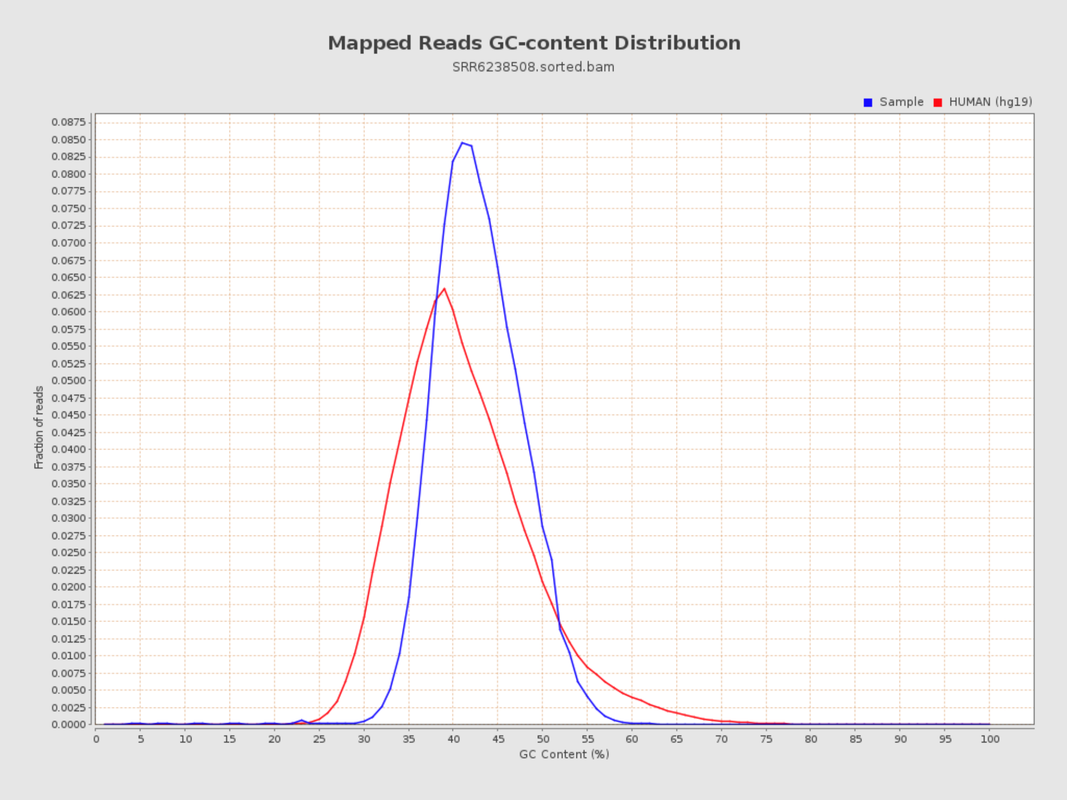
7. Results : Duplication Rate Histogram



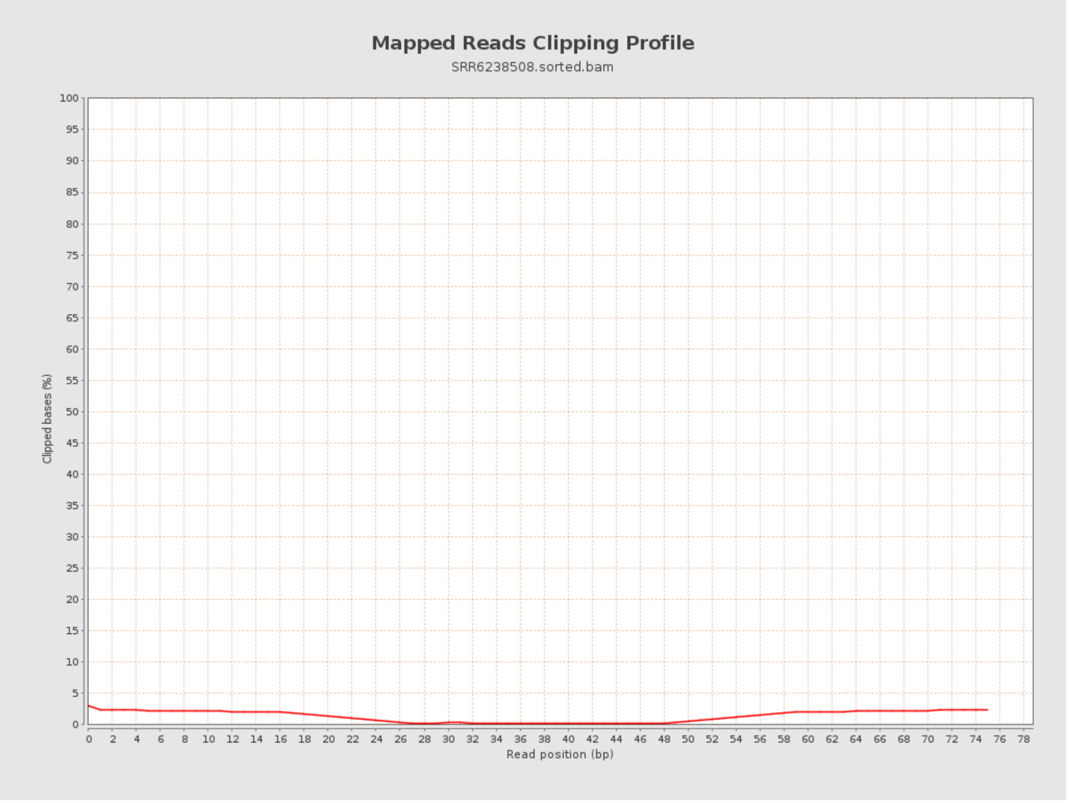
8. Results : Mapped Reads Nucleotide Content



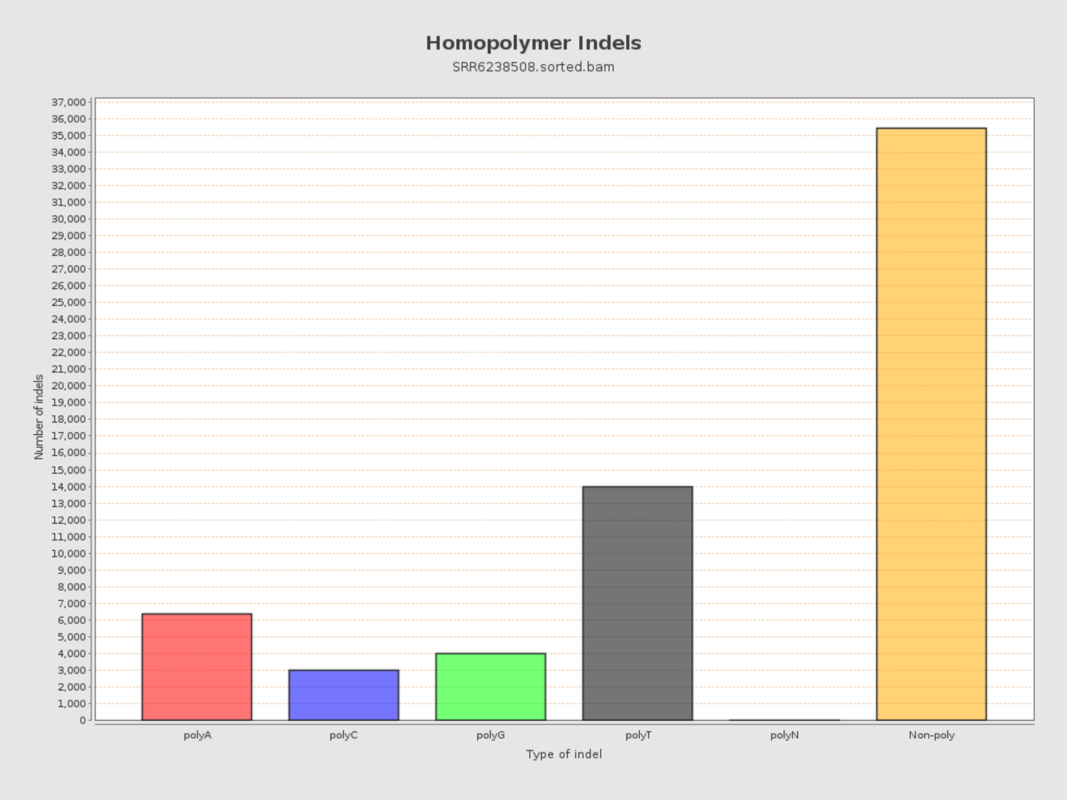
9. Results : Mapped Reads GC-content Distribution



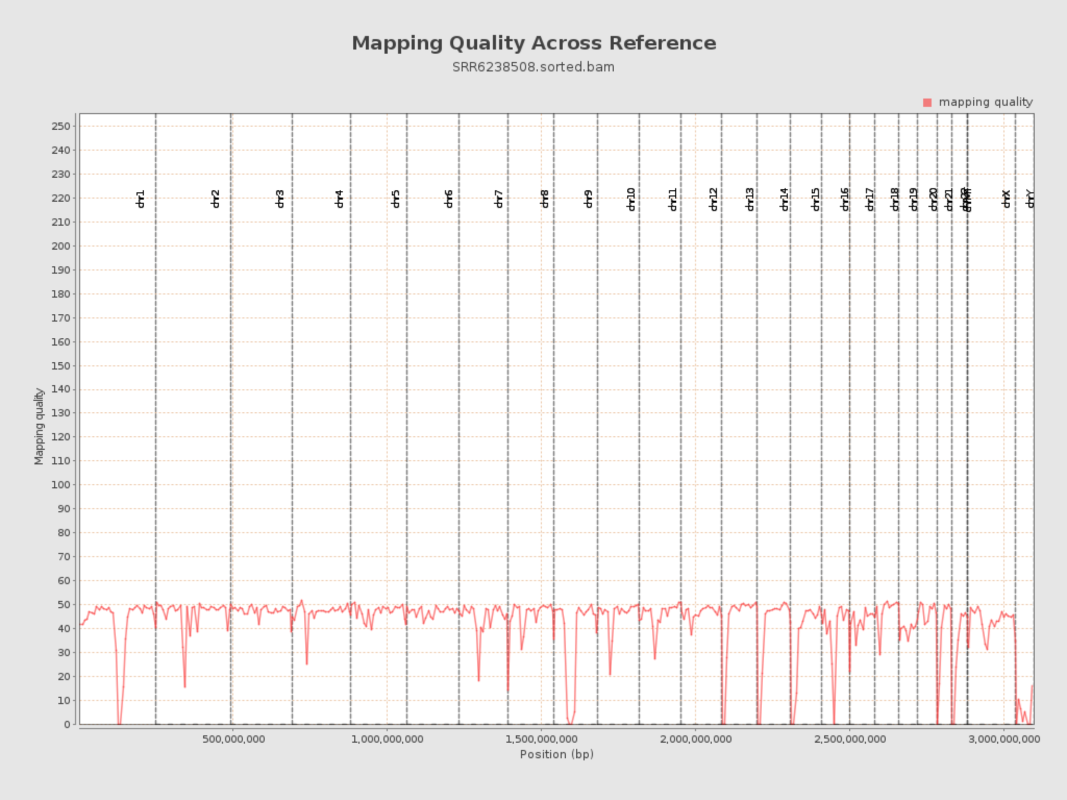
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram