Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:17:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238258.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_SRR6238258 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238258.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:17:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238258.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,599,766
Mapped reads	2,324,533 / 89.41%
Unmapped reads	275,233 / 10.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,173 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	78,162 / 3.01%
Duplication rate	2.09%
Clipped reads	1,265,332 / 48.67%

2.2. ACGT Content

Number/percentage of A's	41,548,549 / 27.66%
Number/percentage of C's	30,770,587 / 20.48%
Number/percentage of T's	43,292,757 / 28.82%
Number/percentage of G's	34,585,370 / 23.02%
Number/percentage of N's	34,696 / 0.02%
GC Percentage	43.5%

2.3. Coverage

Mean	0.0486

Standard Deviation	0.4578

2.4. Mapping Quality

Mean Mapping Quality	41.15

2.5. Mismatches and indels

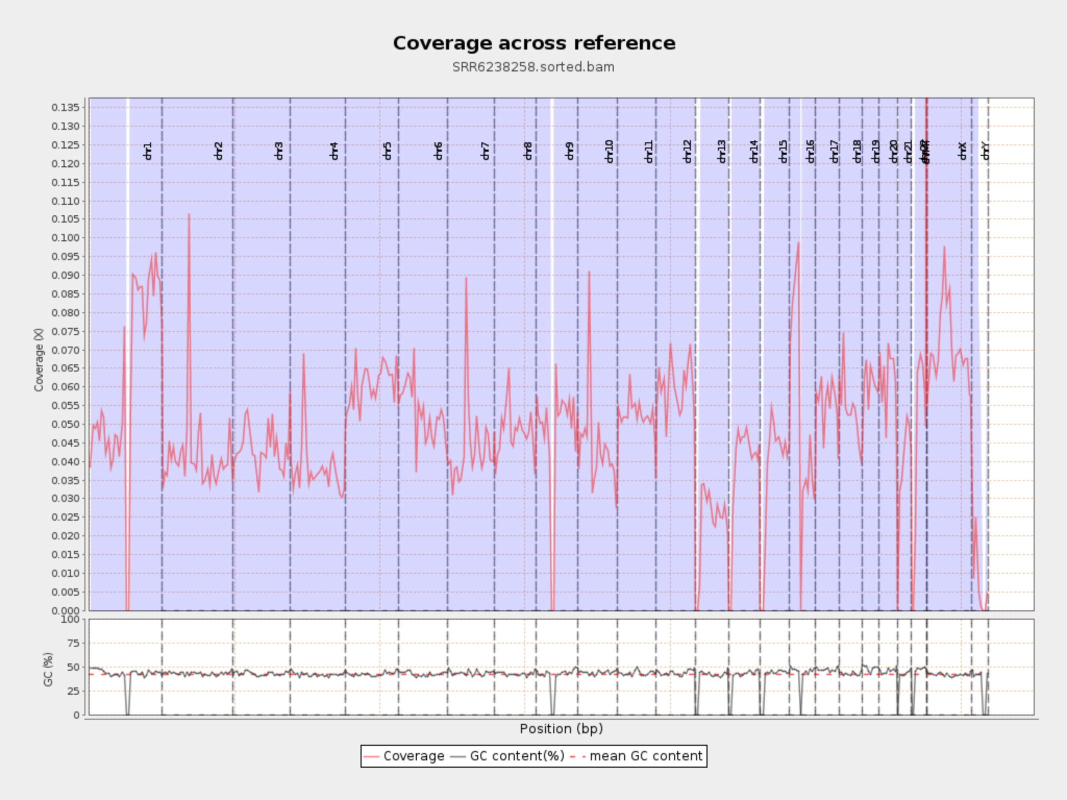
General error rate	0.93%
Mismatches	1,364,919
Insertions	13,604
Mapped reads with at least one insertion	0.58%
Deletions	41,970
Mapped reads with at least one deletion	1.78%
Homopolymer indels	43.51%

2.6. Chromosome stats

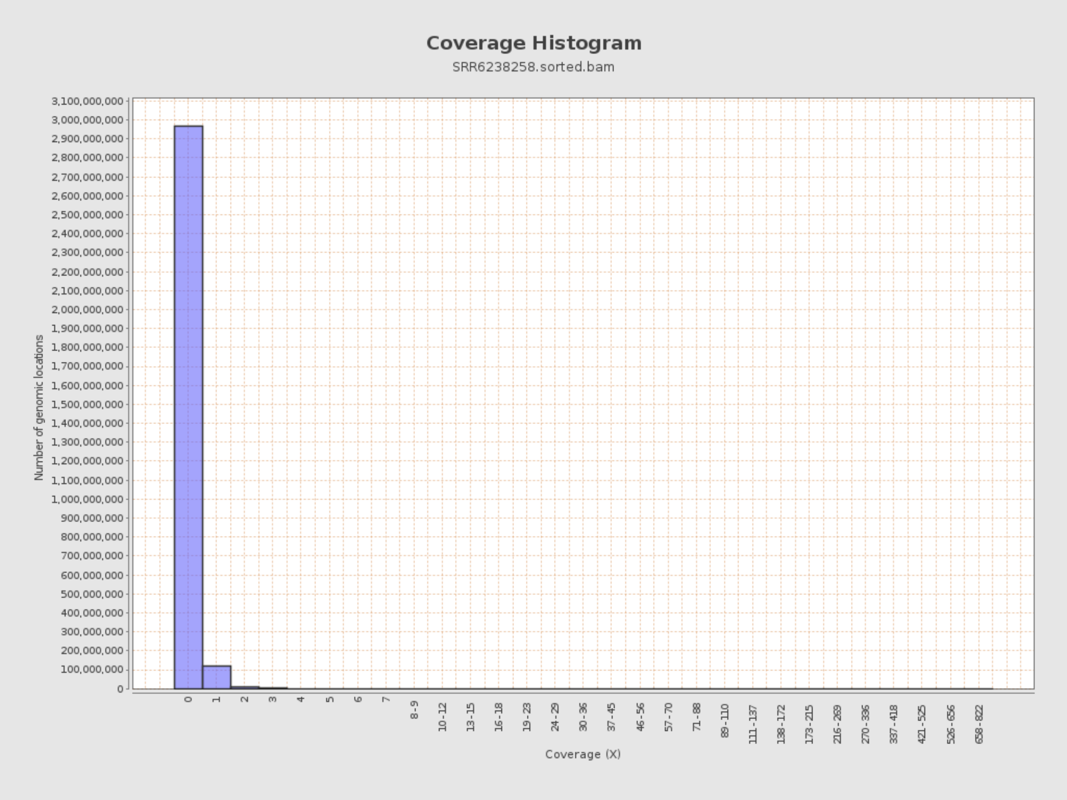
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15271274	0.0613	0.7199
chr2	243199373	10270462	0.0422	0.6564
chr3	198022430	8531877	0.0431	0.2325
chr4	191154276	7230805	0.0378	0.2633
chr5	180915260	11049383	0.0611	0.2785
chr6	171115067	9092675	0.0531	0.3439
chr7	159138663	6993235	0.0439	0.6496

chr8	146364022	7016841	0.0479	0.4845
chr9	141213431	6583463	0.0466	0.4982
chr10	135534747	5975399	0.0441	0.4768
chr11	135006516	7078220	0.0524	0.4287
chr12	133851895	8068017	0.0603	0.2837
chr13	115169878	2674069	0.0232	0.1678
chr14	107349540	4050875	0.0377	0.3005
chr15	102531392	3781153	0.0369	0.2245
chr16	90354753	4808986	0.0532	0.3219
chr17	81195210	4519663	0.0557	0.3115
chr18	78077248	4236830	0.0543	0.8808
chr19	59128983	3592719	0.0608	0.5973
chr20	63025520	3910964	0.0621	0.2886
chr21	48129895	1848855	0.0384	0.2743
chr22	51304566	2249205	0.0438	0.2365
chrMT	16571	7040	0.4248	0.6985
chrX	155270560	10969224	0.0706	0.3758
chrY	59373566	490237	0.0083	0.2104

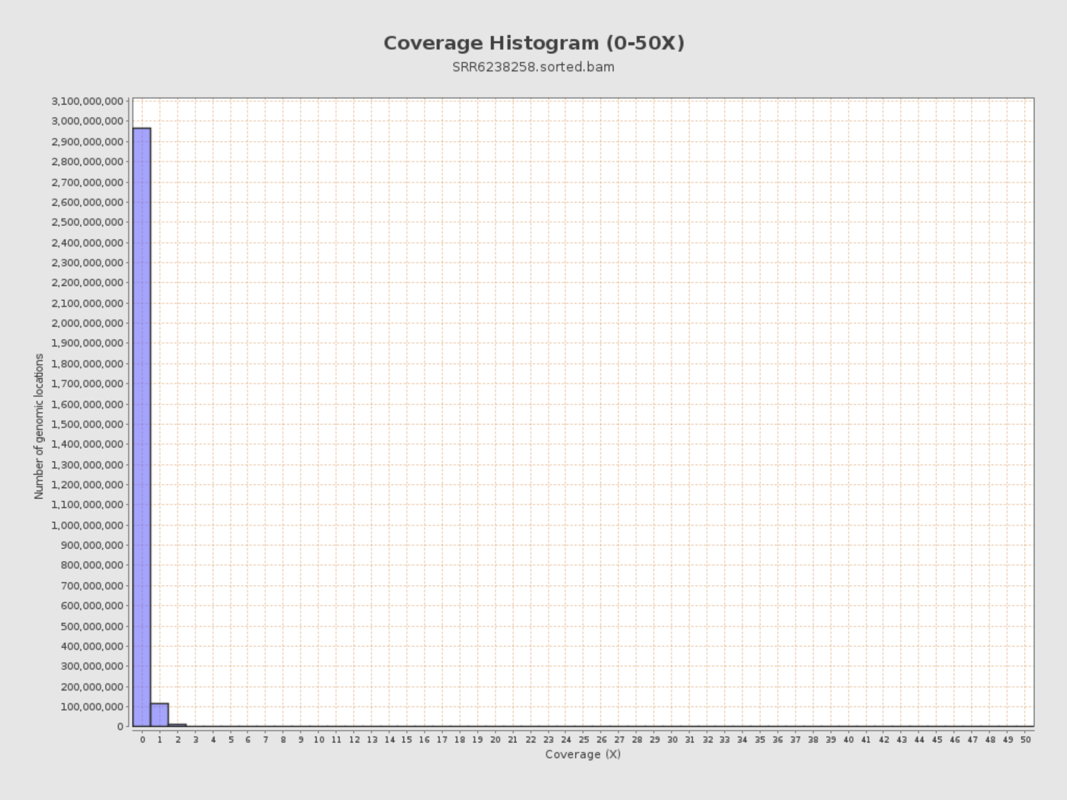
3. Results : Coverage across reference



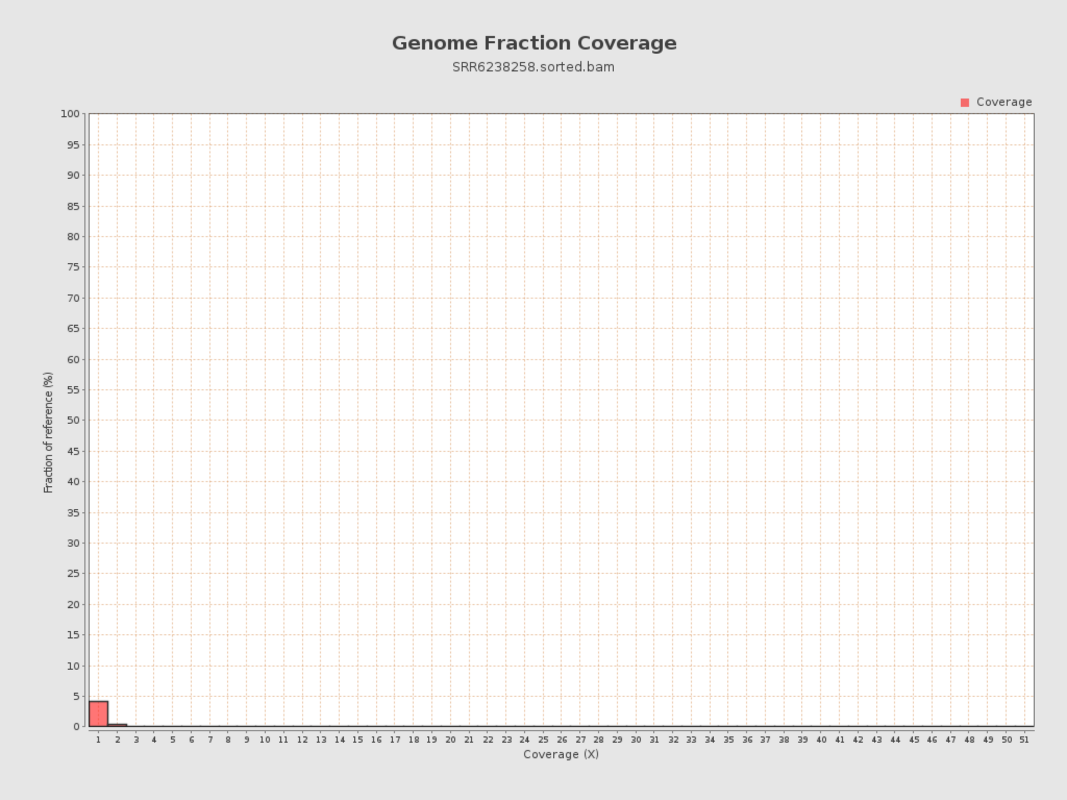
4. Results : Coverage Histogram



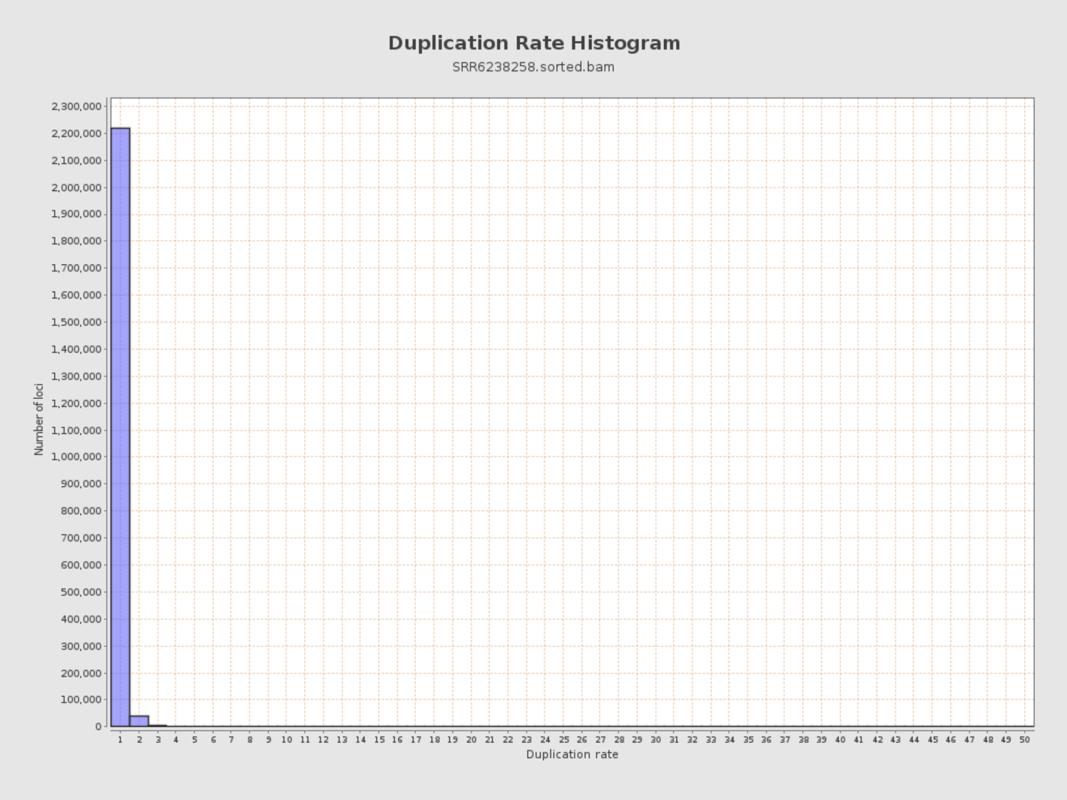
5. Results : Coverage Histogram (0-50X)



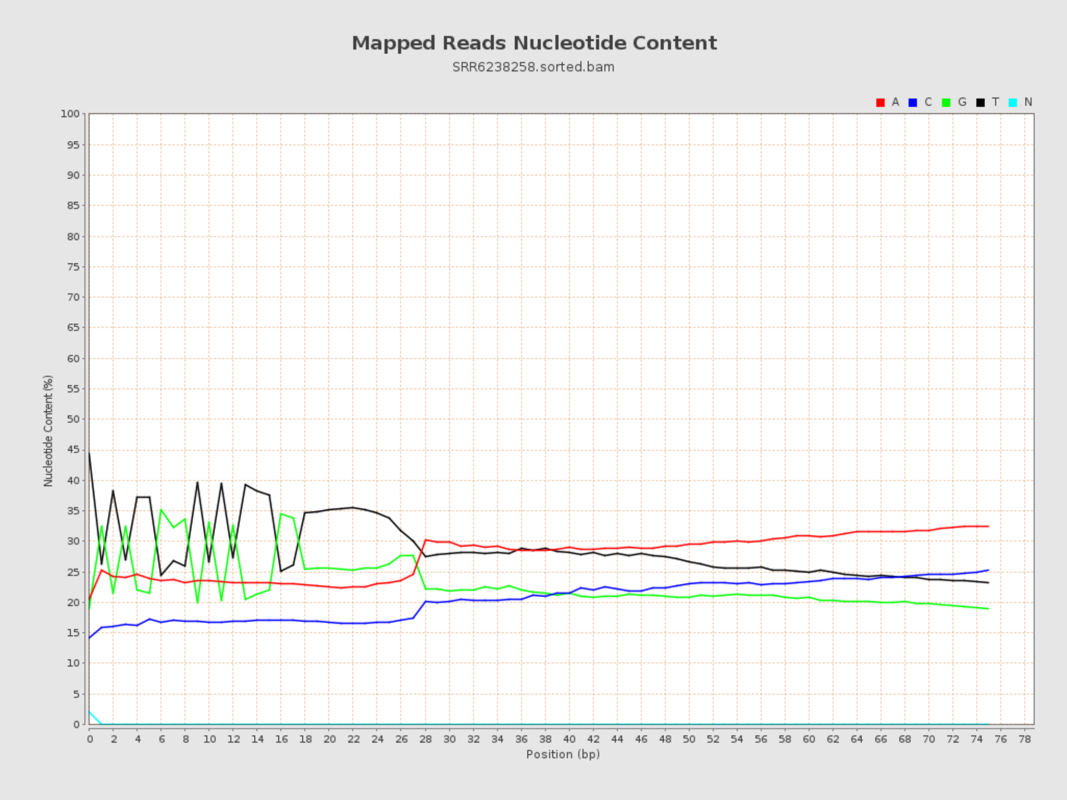
6. Results : Genome Fraction Coverage



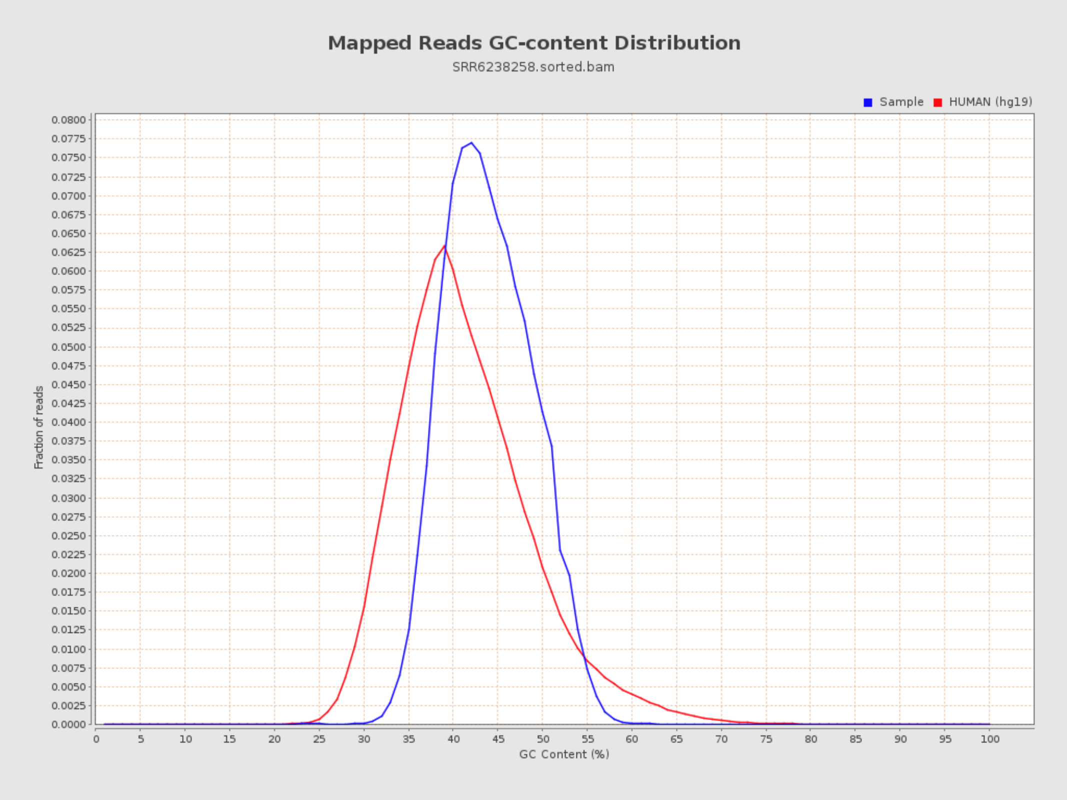
7. Results : Duplication Rate Histogram



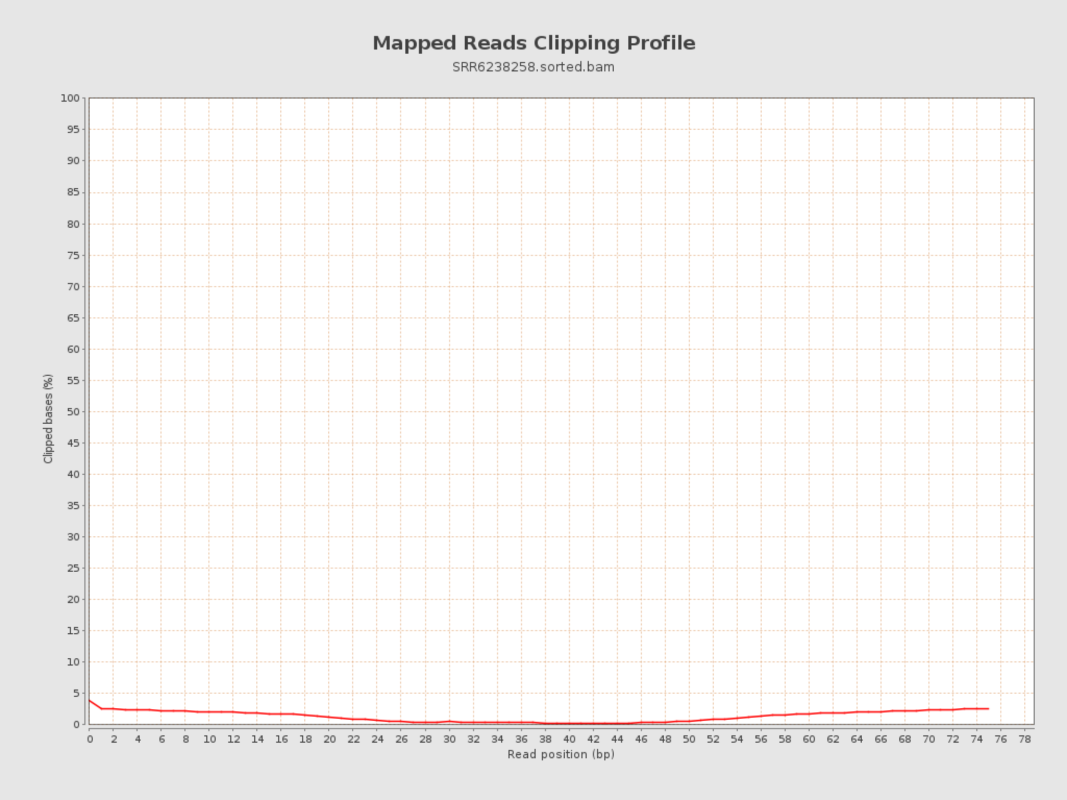
8. Results : Mapped Reads Nucleotide Content



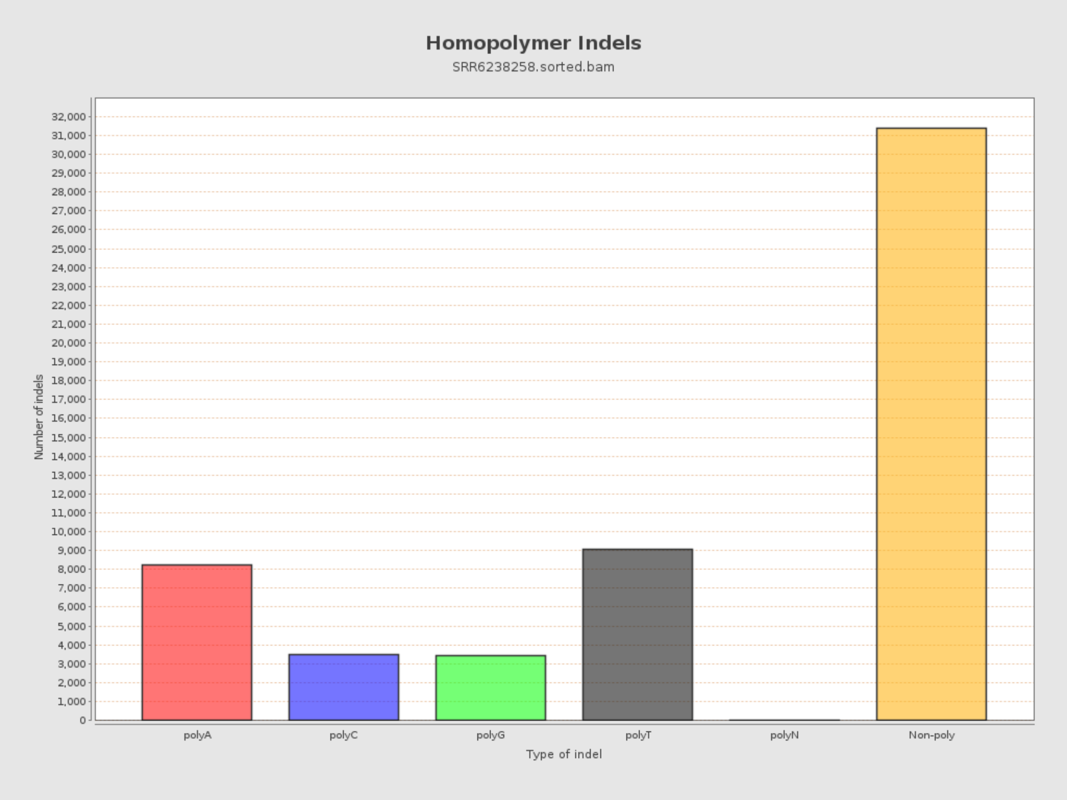
9. Results : Mapped Reads GC-content Distribution



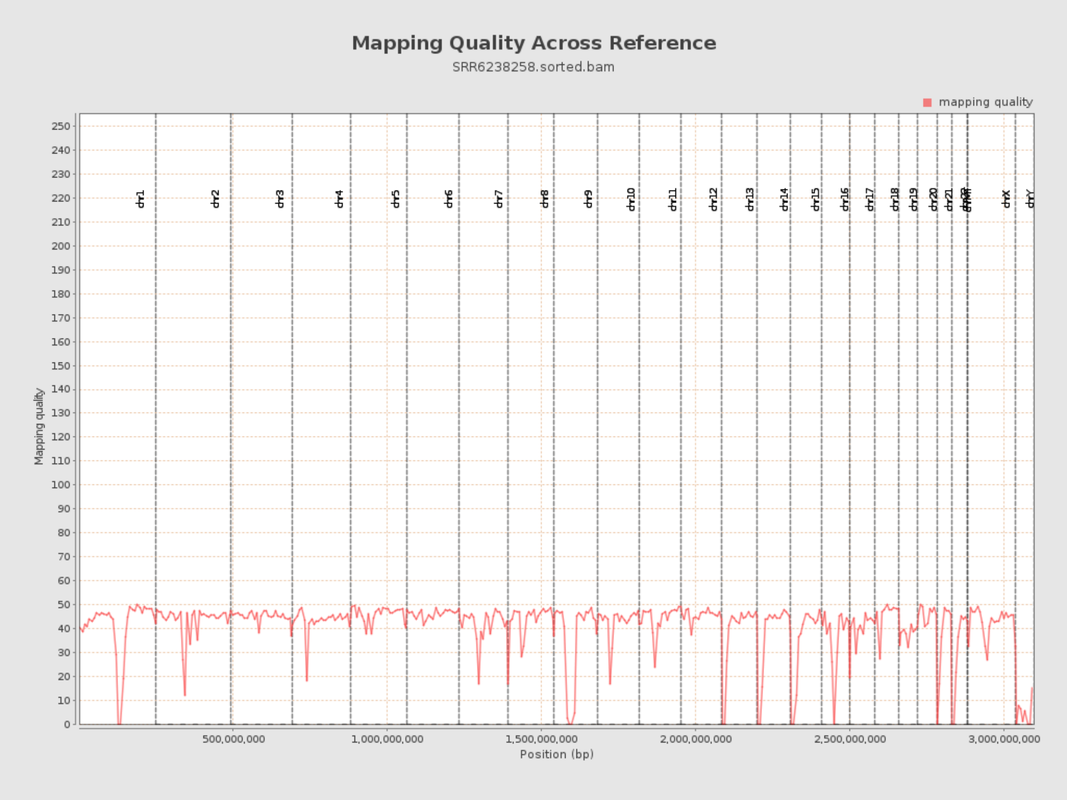
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram