Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:35:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238044.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_SRR6238044 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238044.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:35:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238044.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,874,908
Mapped reads	2,077,984 / 72.28%
Unmapped reads	796,924 / 27.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,832 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	352,014 / 12.24%
Duplication rate	12.48%
Clipped reads	1,067,707 / 37.14%

2.2. ACGT Content

Number/percentage of A's	38,552,330 / 28.56%
Number/percentage of C's	25,286,508 / 18.74%
Number/percentage of T's	42,008,754 / 31.12%
Number/percentage of G's	28,858,437 / 21.38%
Number/percentage of N's	262,507 / 0.19%
GC Percentage	40.12%

2.3. Coverage

Mean	0.0436

Standard Deviation	0.6578

2.4. Mapping Quality

Mean Mapping Quality	47.24

2.5. Mismatches and indels

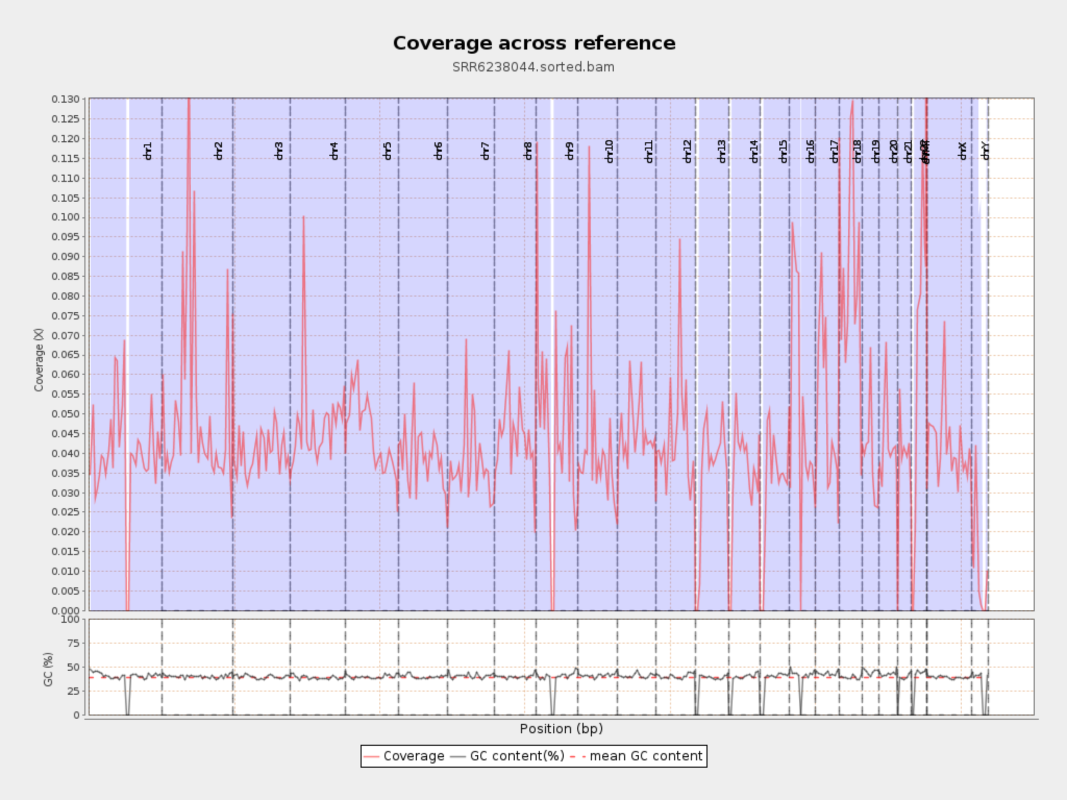
General error rate	0.98%
Mismatches	1,292,002
Insertions	13,105
Mapped reads with at least one insertion	0.62%
Deletions	39,269
Mapped reads with at least one deletion	1.87%
Homopolymer indels	45.96%

2.6. Chromosome stats

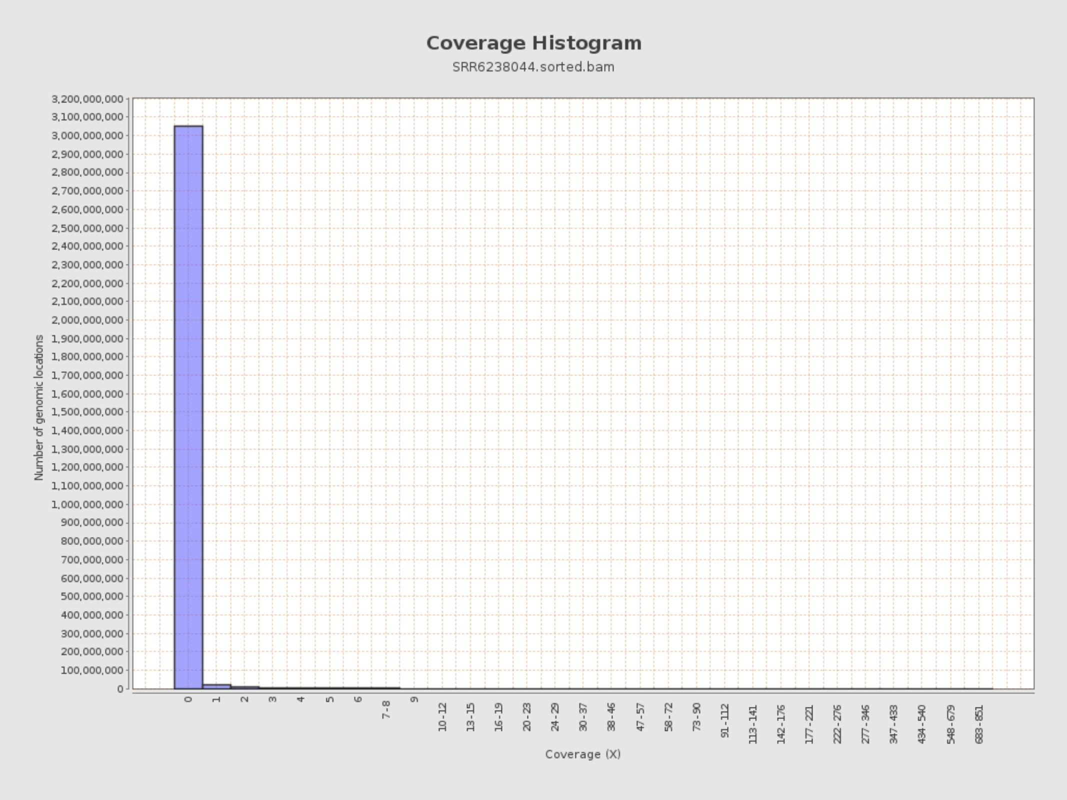
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9916581	0.0398	0.8083
chr2	243199373	12579846	0.0517	0.8527
chr3	198022430	8088481	0.0408	0.5016
chr4	191154276	9120771	0.0477	0.604
chr5	180915260	8226272	0.0455	0.5354
chr6	171115067	6672338	0.039	0.5196
chr7	159138663	5990996	0.0376	0.6054

chr8	146364022	6451884	0.0441	0.734
chr9	141213431	6286792	0.0445	0.6956
chr10	135534747	5640841	0.0416	0.7491
chr11	135006516	6128300	0.0454	0.5948
chr12	133851895	6035505	0.0451	0.535
chr13	115169878	3950154	0.0343	0.451
chr14	107349540	3564765	0.0332	0.4838
chr15	102531392	3291038	0.0321	0.4551
chr16	90354753	4747978	0.0525	0.613
chr17	81195210	4060184	0.05	0.6479
chr18	78077248	6776669	0.0868	1.2888
chr19	59128983	2359493	0.0399	0.7409
chr20	63025520	2758423	0.0438	0.5296
chr21	48129895	1826150	0.0379	0.5309
chr22	51304566	3200024	0.0624	0.6386
chrMT	16571	195708	11.8103	9.3889
chrX	155270560	6553588	0.0422	0.5517
chrY	59373566	611113	0.0103	0.4345

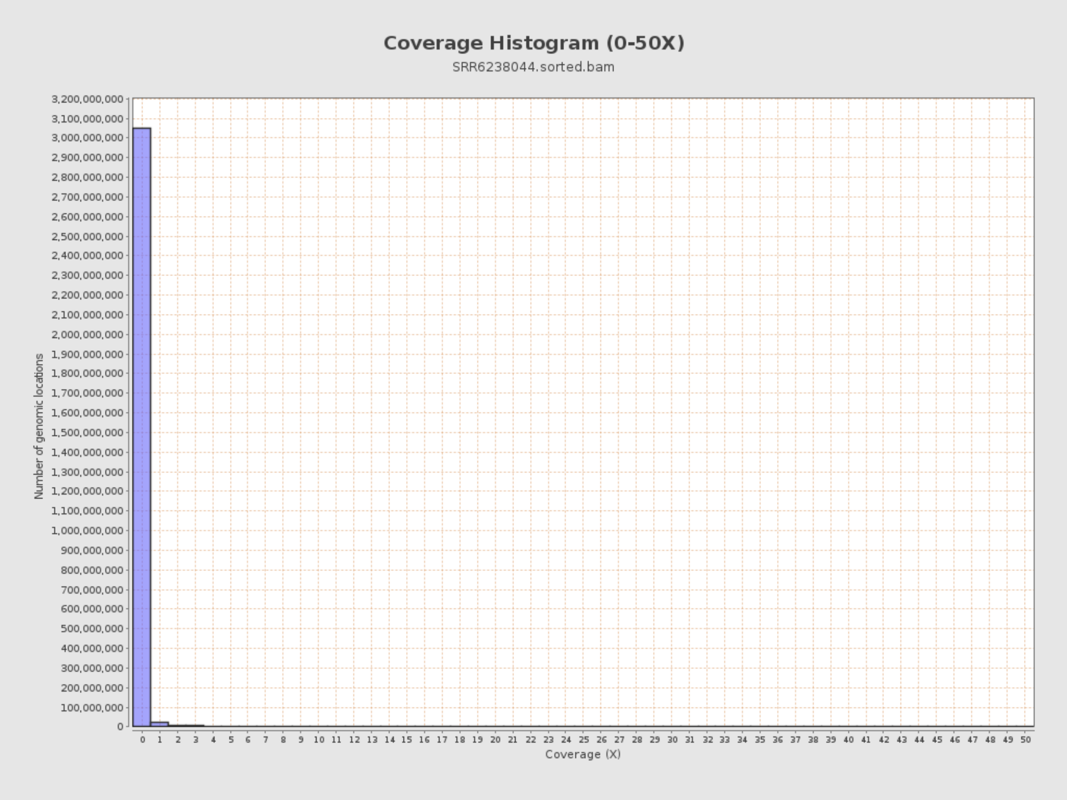
3. Results : Coverage across reference



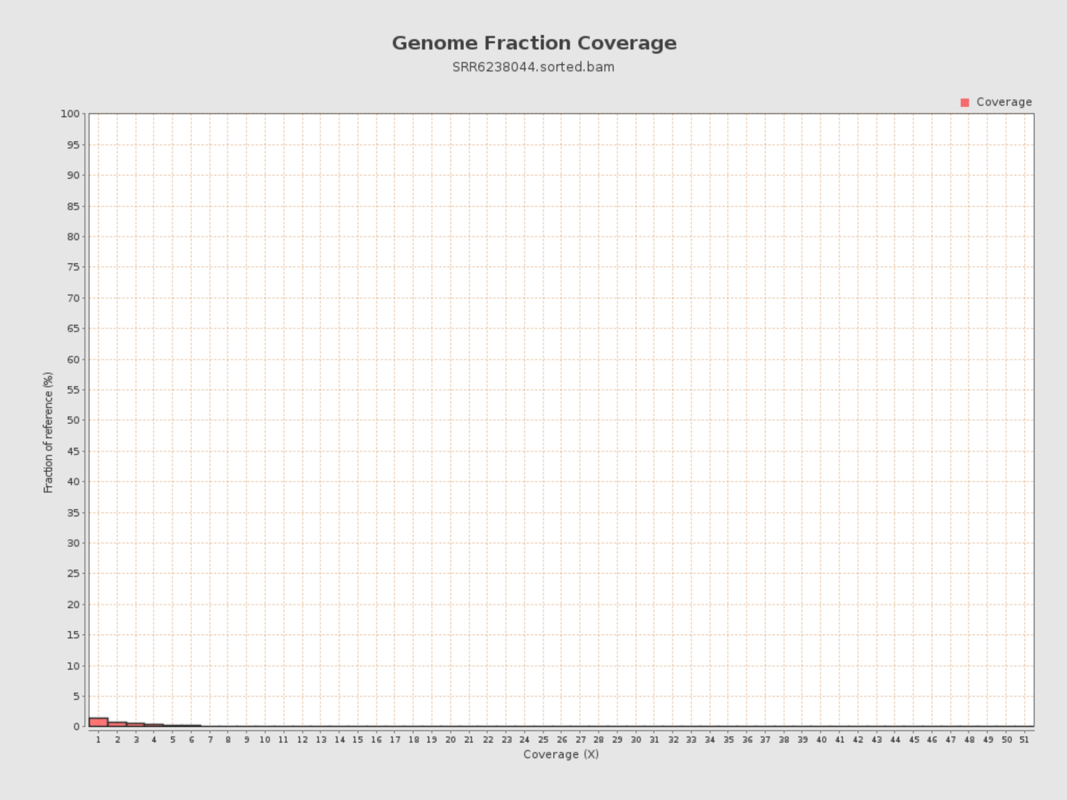
4. Results : Coverage Histogram



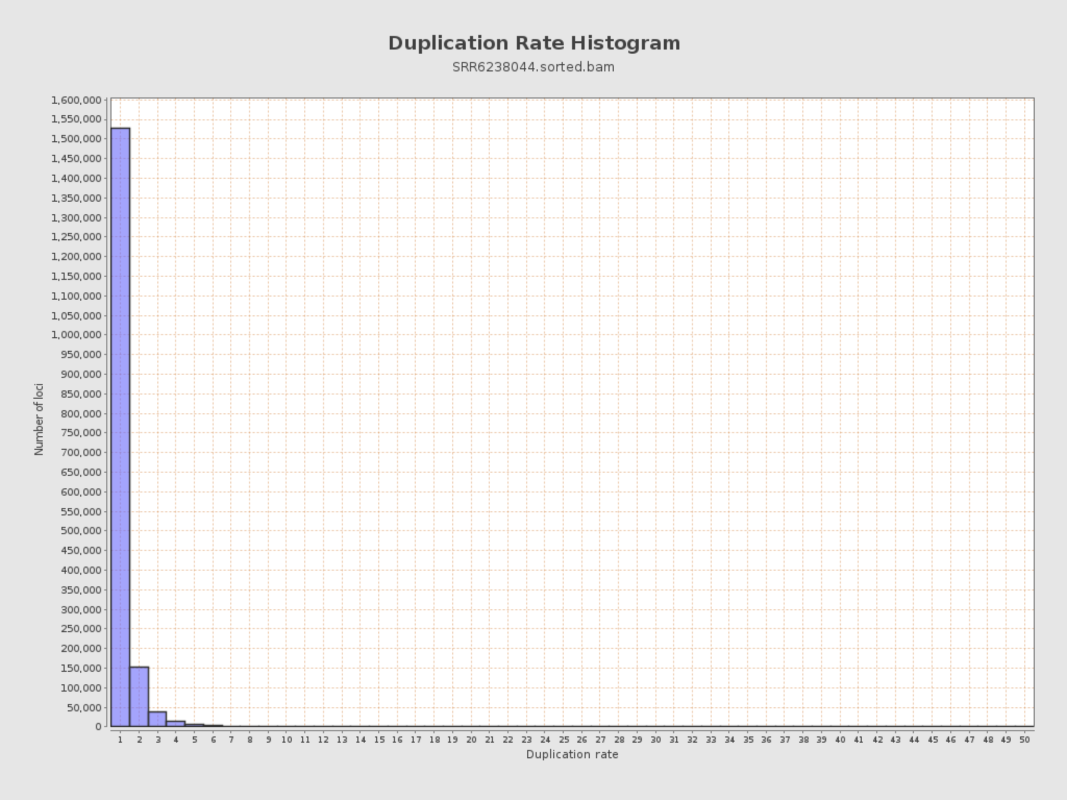
5. Results : Coverage Histogram (0-50X)



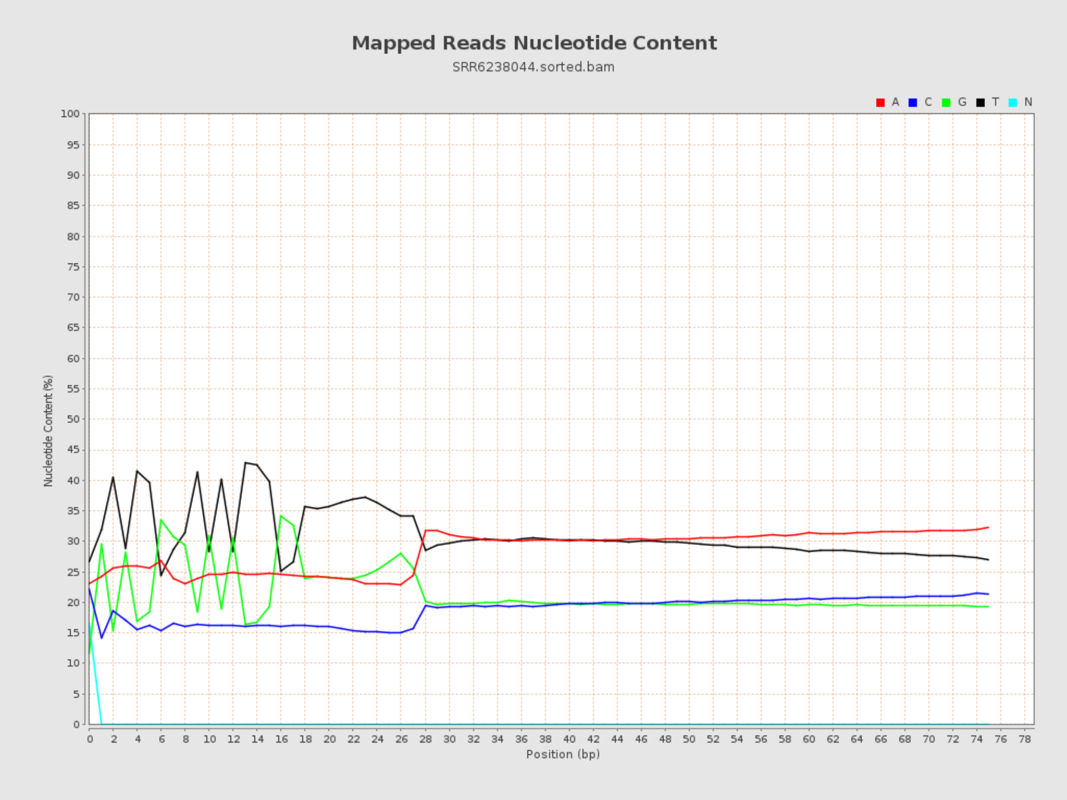
6. Results : Genome Fraction Coverage



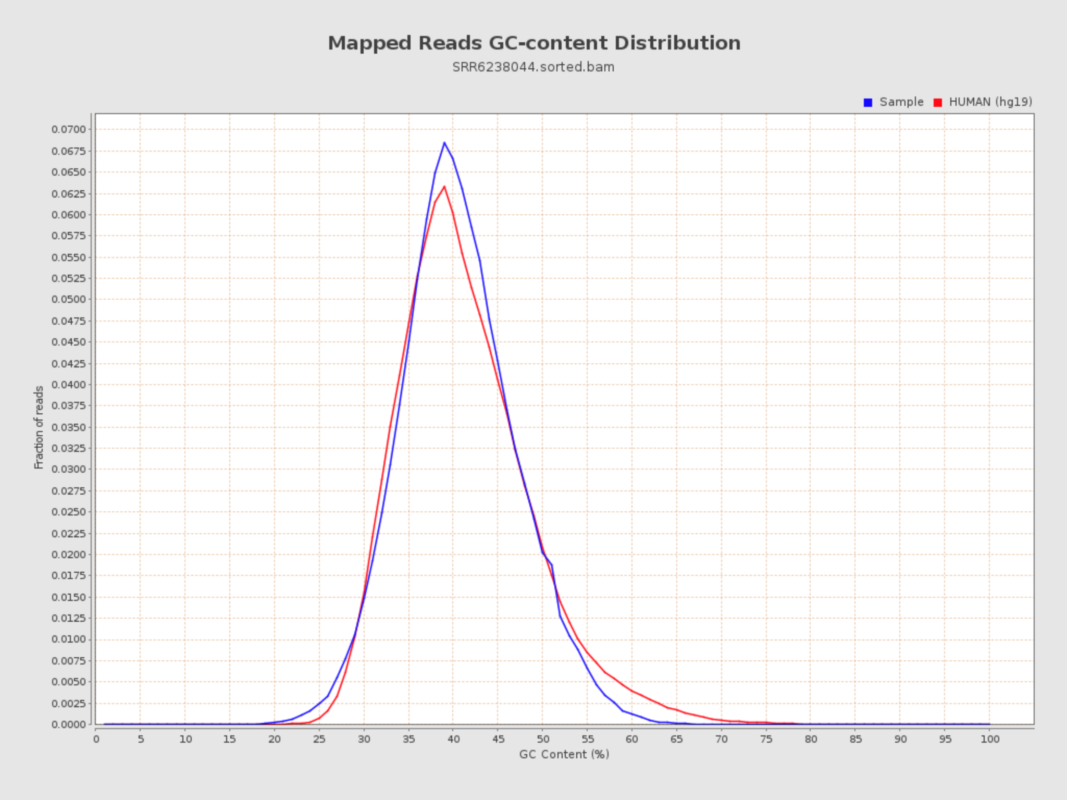
7. Results : Duplication Rate Histogram



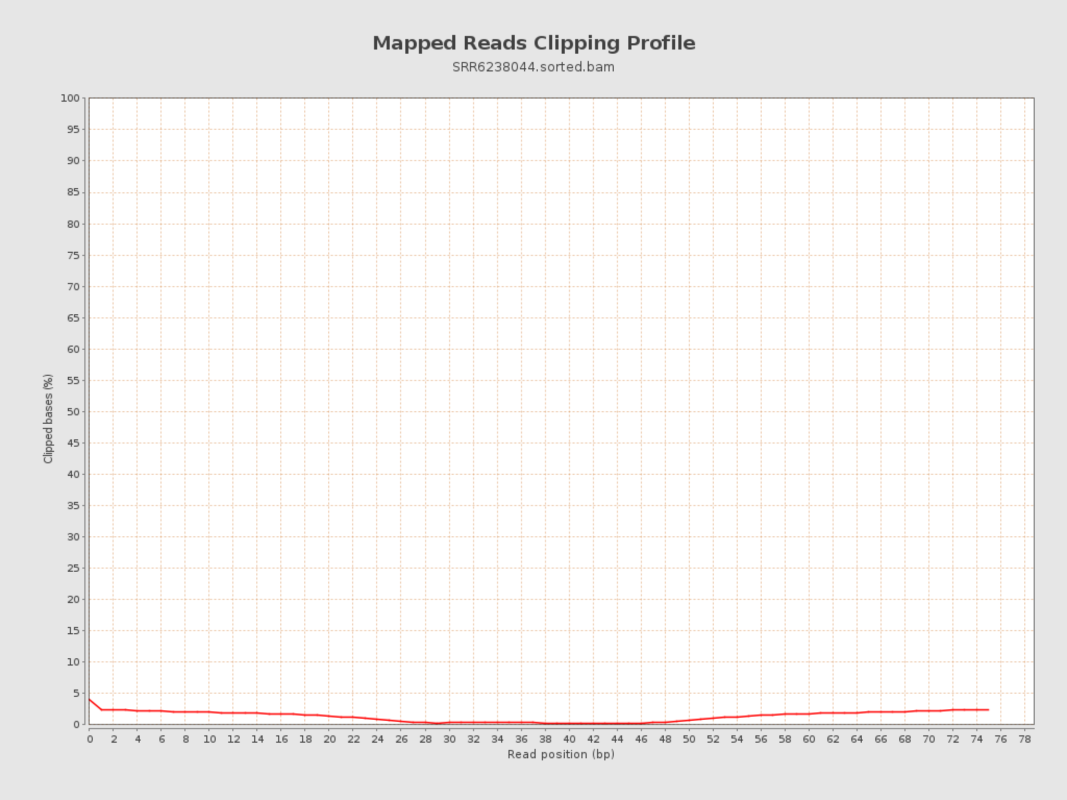
8. Results : Mapped Reads Nucleotide Content



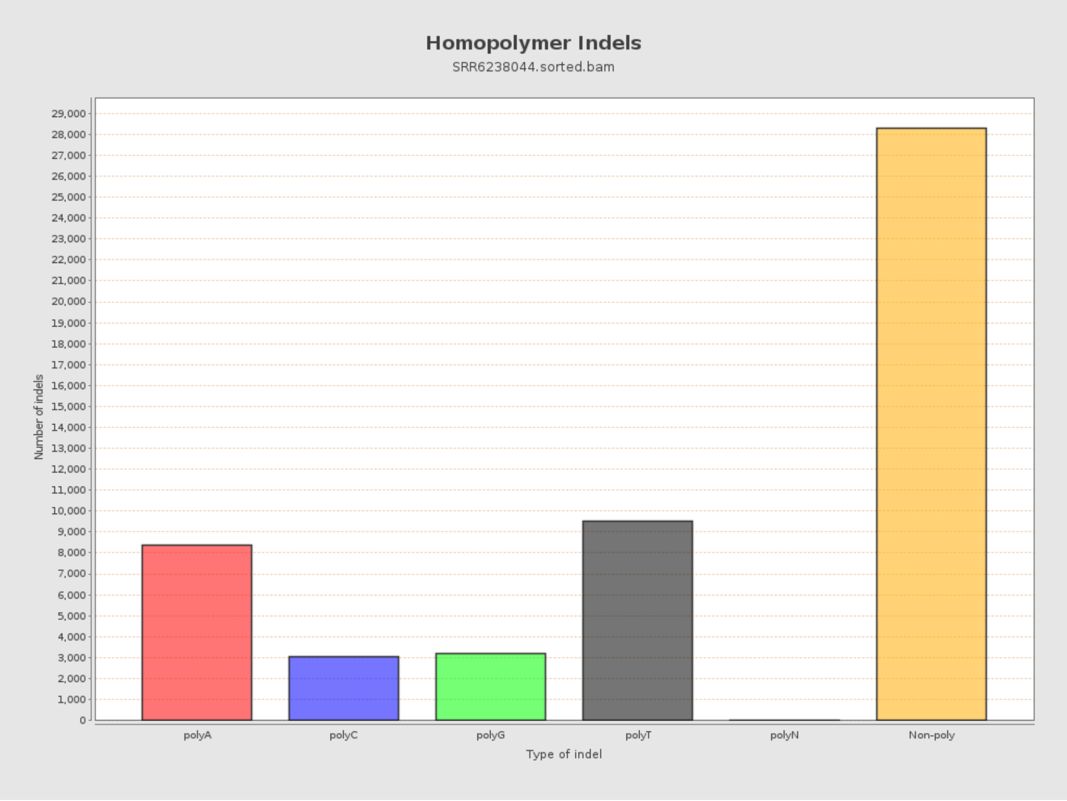
9. Results : Mapped Reads GC-content Distribution



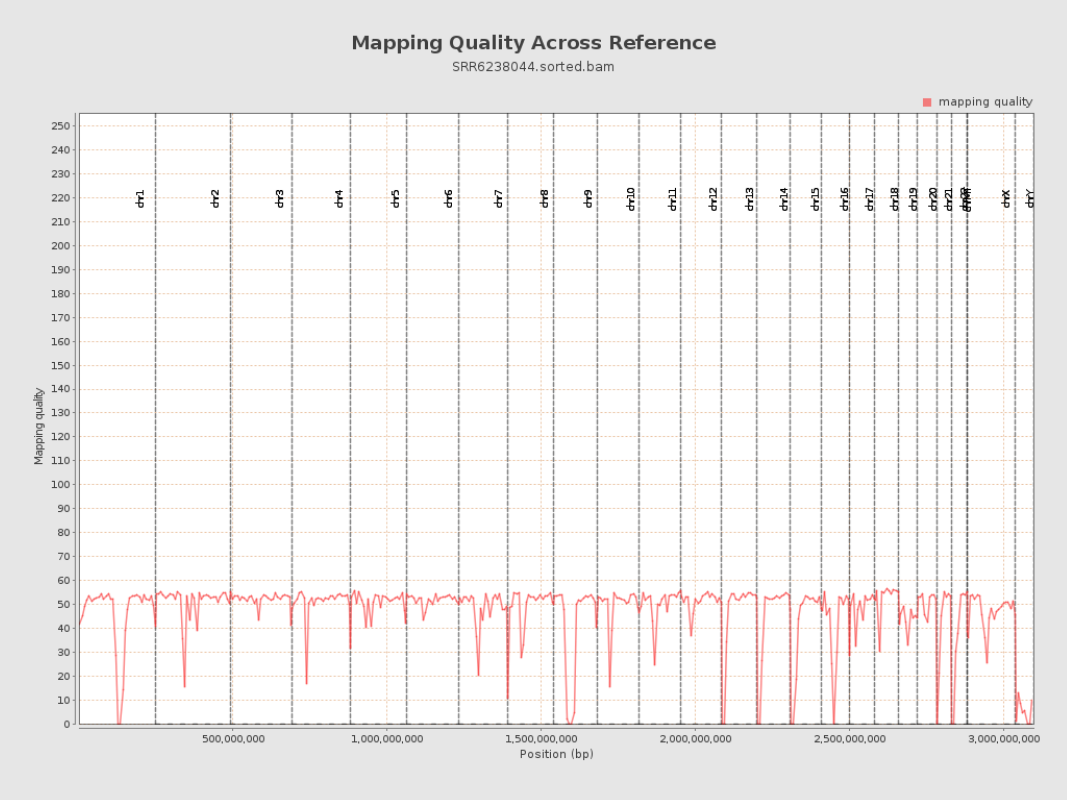
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram