Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 22:16:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238611.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_SRR6238611 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238611.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 22:16:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238611.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,730,340
Mapped reads	2,997,125 / 80.34%
Unmapped reads	733,215 / 19.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,622 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	1,333,257 / 35.74%
Duplication rate	20.58%
Clipped reads	1,821,507 / 48.83%

2.2. ACGT Content

Number/percentage of A's	47,187,429 / 25.35%
Number/percentage of C's	32,676,338 / 17.55%
Number/percentage of T's	62,672,765 / 33.67%
Number/percentage of G's	43,623,195 / 23.43%
Number/percentage of N's	4,404 / 0%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0602

Standard Deviation	1.4008

2.4. Mapping Quality

Mean Mapping Quality	41.88

2.5. Mismatches and indels

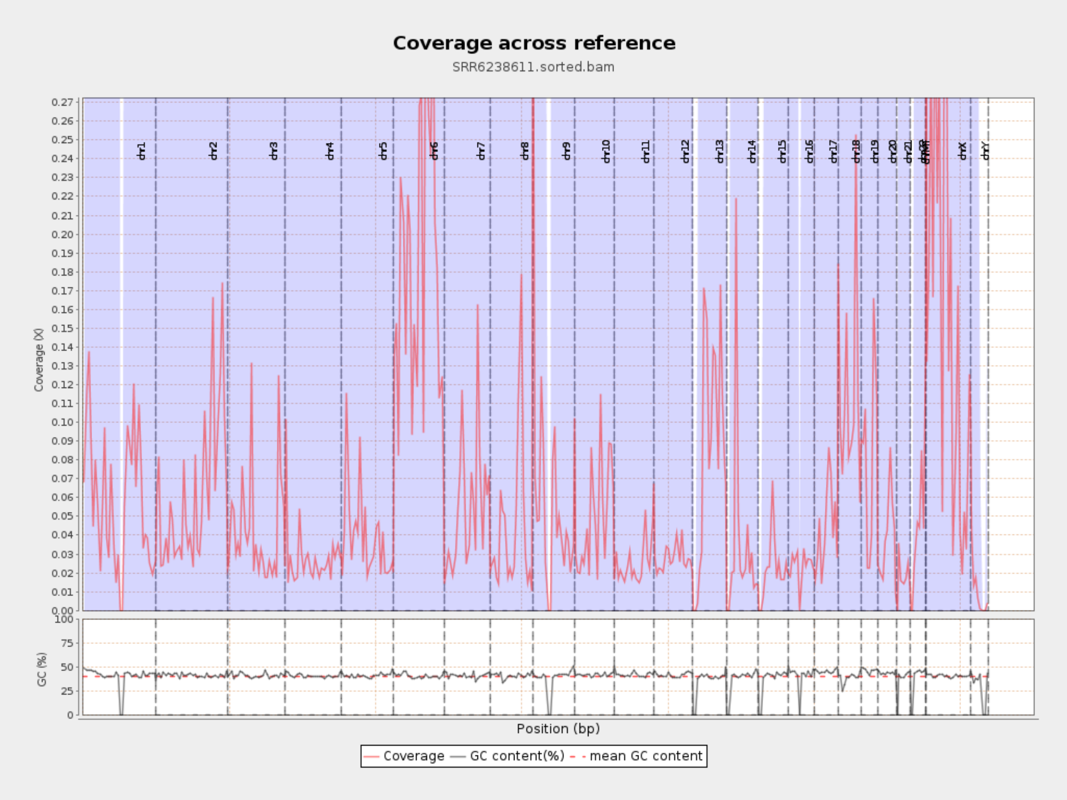
General error rate	0.52%
Mismatches	946,757
Insertions	11,351
Mapped reads with at least one insertion	0.38%
Deletions	40,460
Mapped reads with at least one deletion	1.34%
Homopolymer indels	43.2%

2.6. Chromosome stats

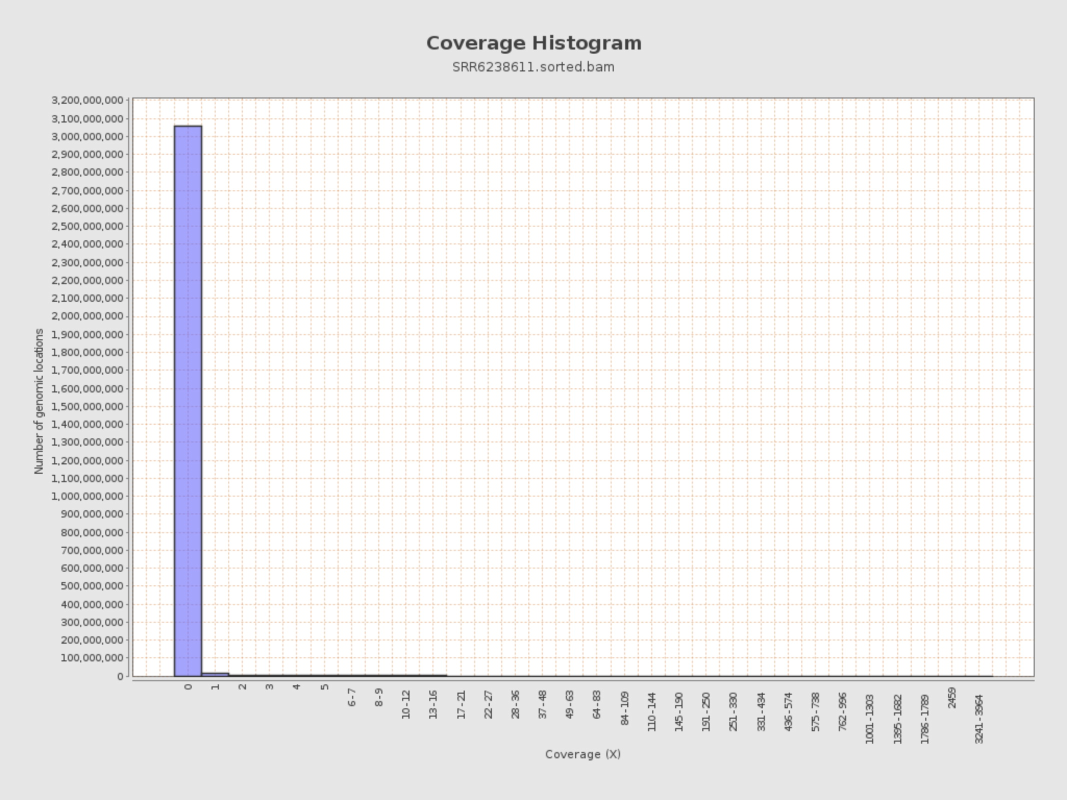
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14499569	0.0582	0.9279
chr2	243199373	15496739	0.0637	2.0099
chr3	198022430	8390087	0.0424	0.7701
chr4	191154276	5310032	0.0278	0.5861
chr5	180915260	6980312	0.0386	0.7109
chr6	171115067	32264218	0.1886	1.9621
chr7	159138663	9010350	0.0566	1.6306

chr8	146364022	6302151	0.0431	1.1988
chr9	141213431	7149385	0.0506	0.9032
chr10	135534747	6704071	0.0495	0.8514
chr11	135006516	3428208	0.0254	0.5589
chr12	133851895	3713751	0.0277	0.6199
chr13	115169878	9898385	0.0859	1.3669
chr14	107349540	3852629	0.0359	0.7894
chr15	102531392	2246256	0.0219	0.6513
chr16	90354753	2084454	0.0231	0.572
chr17	81195210	3685324	0.0454	0.771
chr18	78077248	9182305	0.1176	5.0927
chr19	59128983	4640892	0.0785	1.1272
chr20	63025520	2494072	0.0396	0.7492
chr21	48129895	896858	0.0186	0.4679
chr22	51304566	2183542	0.0426	0.7539
chrMT	16571	35953	2.1696	4.7342
chrX	155270560	25236142	0.1625	1.6076
chrY	59373566	547757	0.0092	0.531

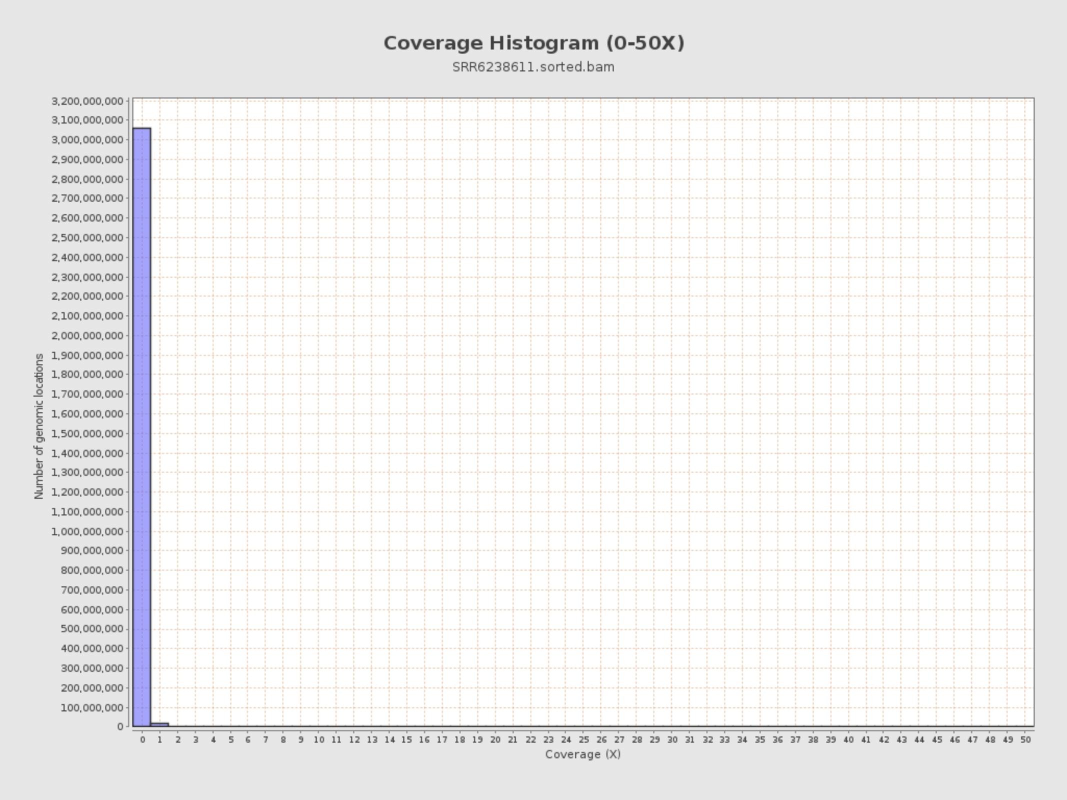
3. Results : Coverage across reference



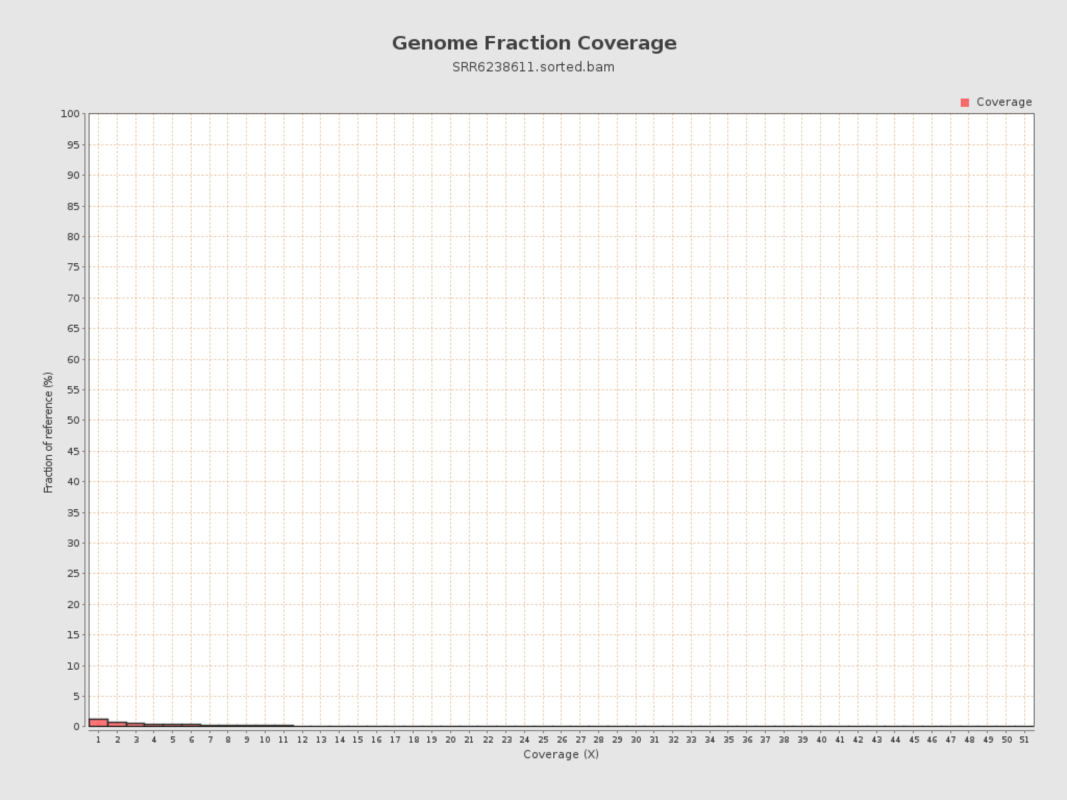
4. Results : Coverage Histogram



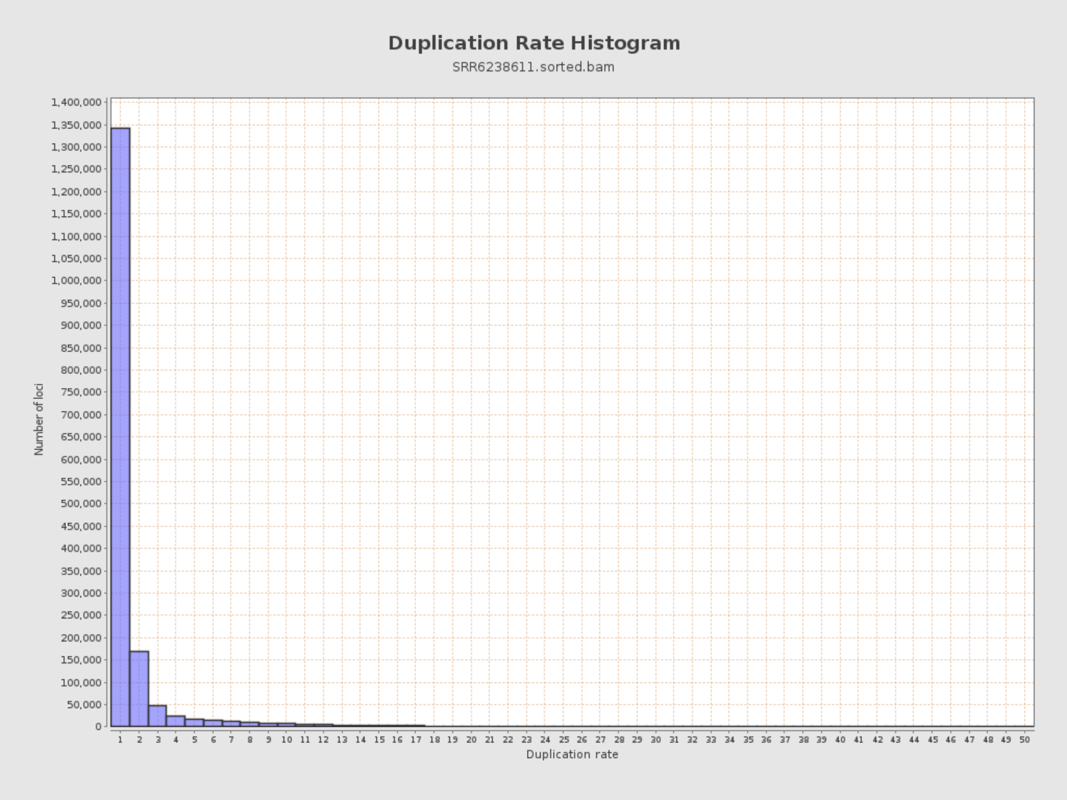
5. Results : Coverage Histogram (0-50X)



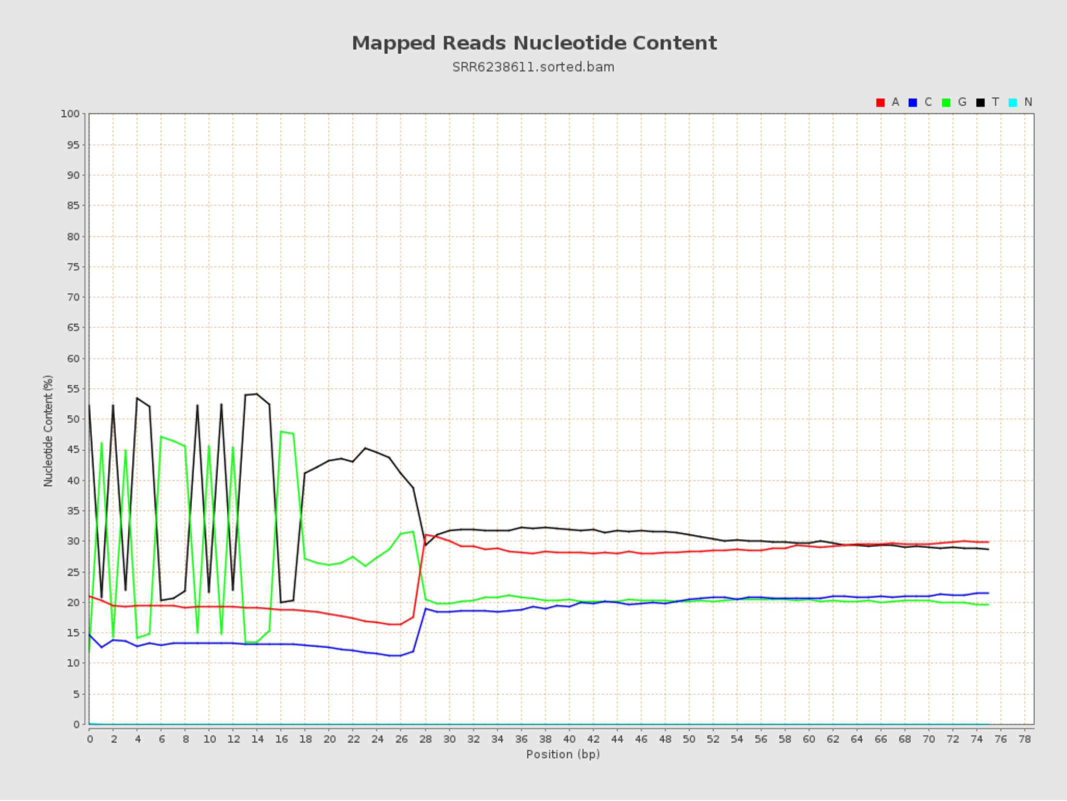
6. Results : Genome Fraction Coverage



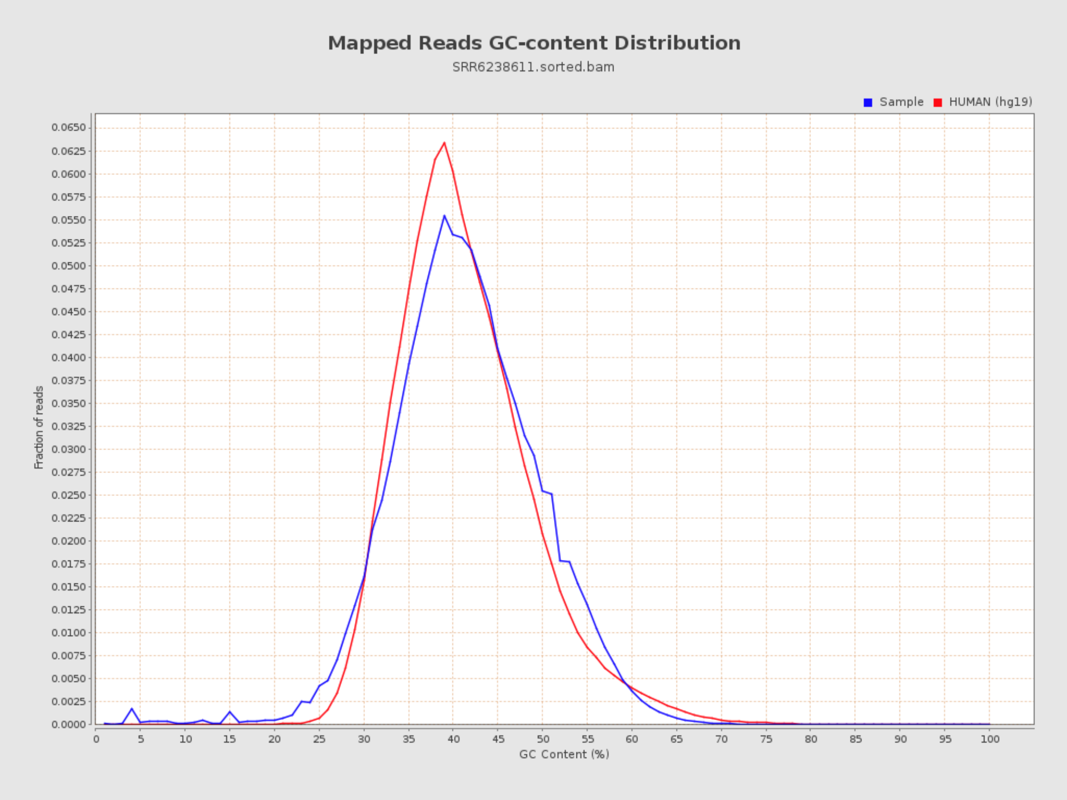
7. Results : Duplication Rate Histogram



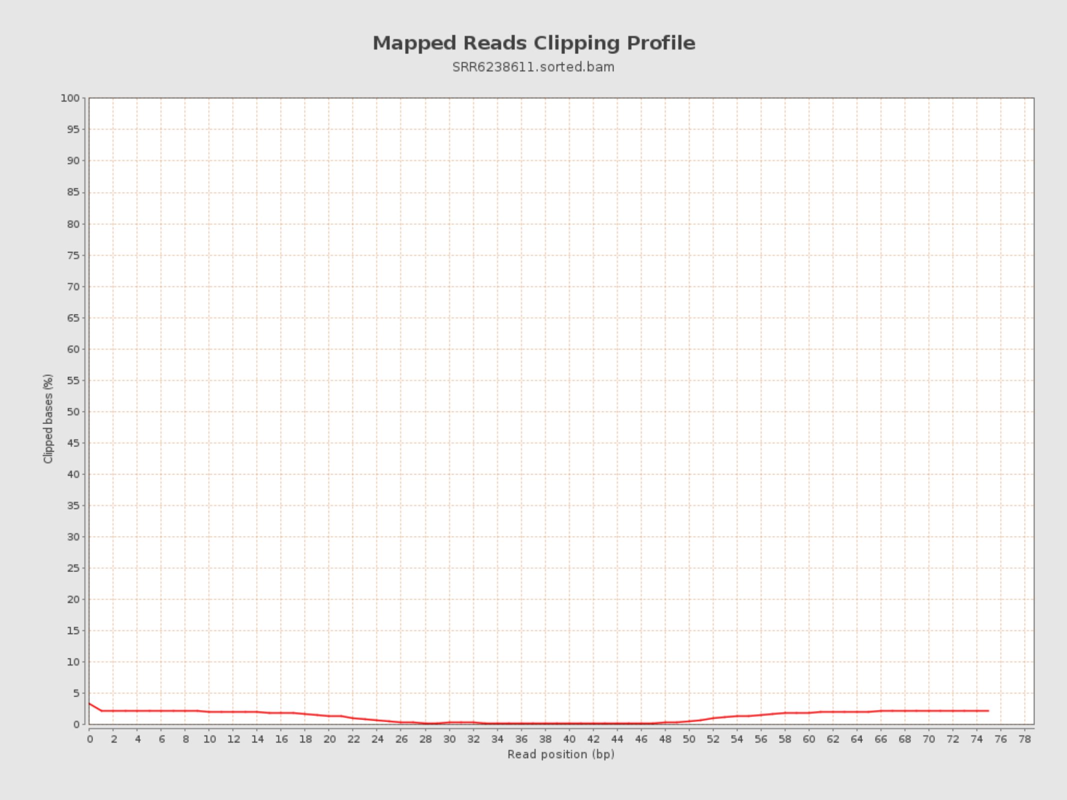
8. Results : Mapped Reads Nucleotide Content



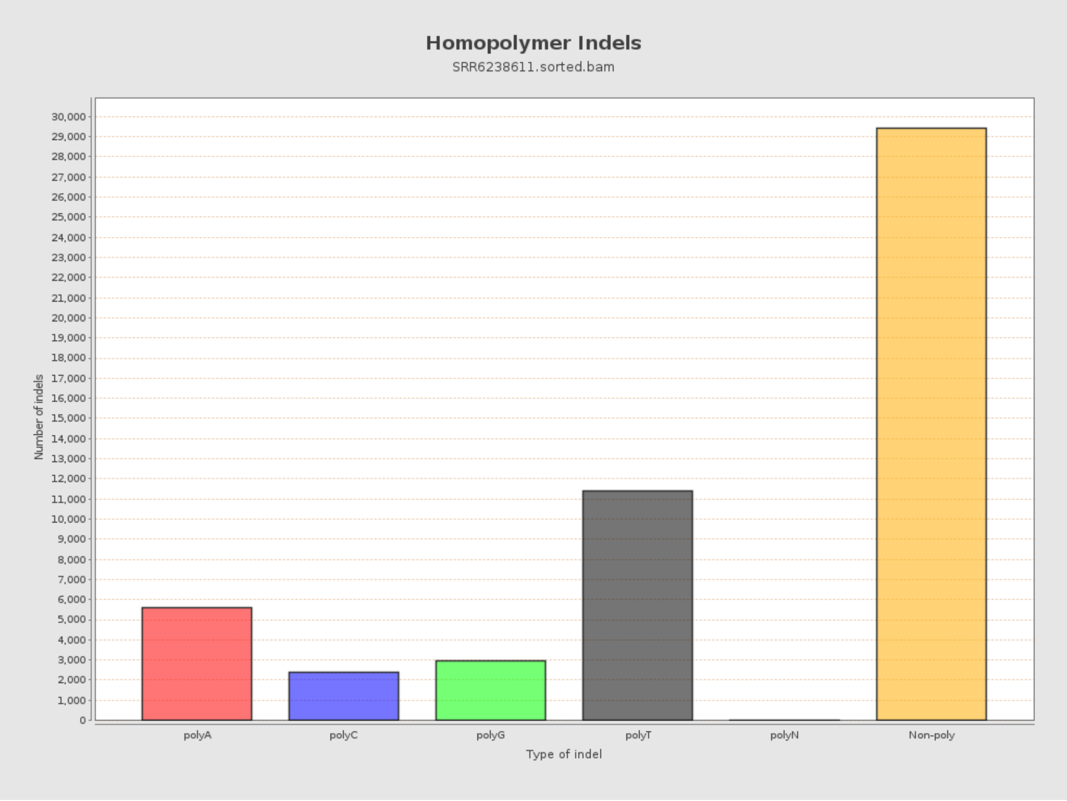
9. Results : Mapped Reads GC-content Distribution



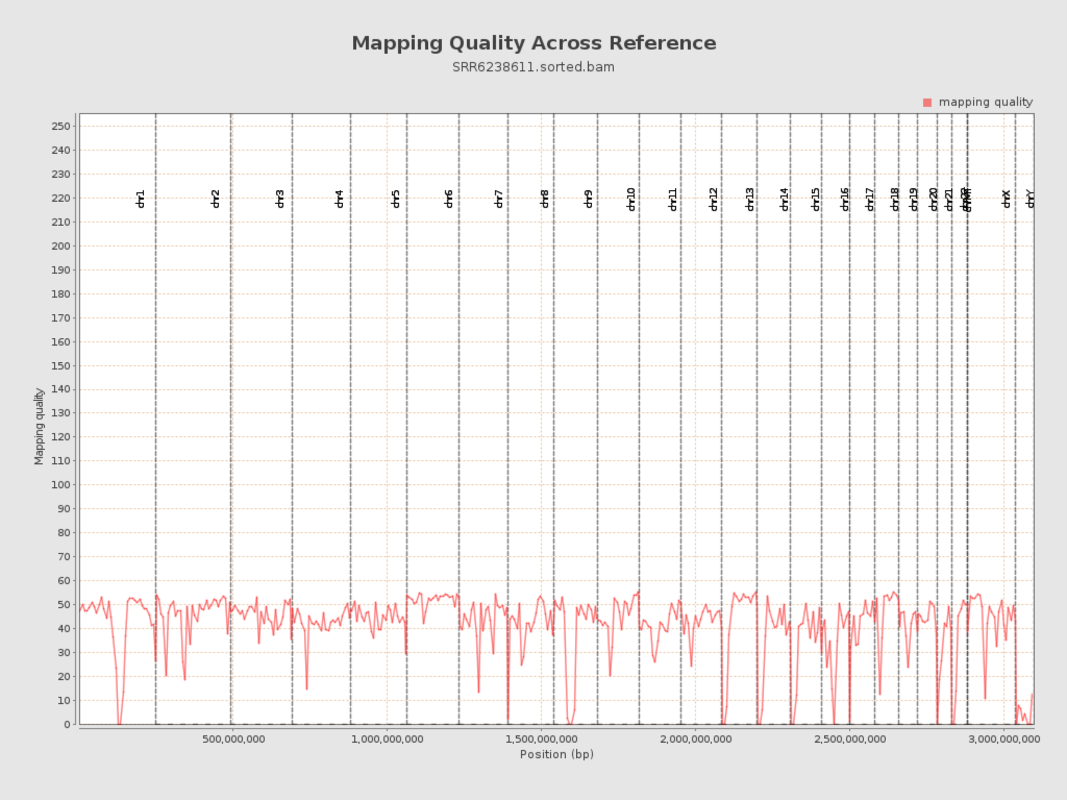
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram