Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 22:12:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238610.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_SRR6238610 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238610.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 22:12:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238610.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,643,979
Mapped reads	2,114,377 / 45.53%
Unmapped reads	2,529,602 / 54.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,566 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	772,260 / 16.63%
Duplication rate	21.07%
Clipped reads	1,392,559 / 29.99%

2.2. ACGT Content

Number/percentage of A's	32,064,561 / 24.81%
Number/percentage of C's	23,014,332 / 17.81%
Number/percentage of T's	43,292,765 / 33.49%
Number/percentage of G's	30,874,391 / 23.89%
Number/percentage of N's	5,885 / 0%
GC Percentage	41.69%

2.3. Coverage

Mean	0.0418

Standard Deviation	0.858

2.4. Mapping Quality

Mean Mapping Quality	42.96

2.5. Mismatches and indels

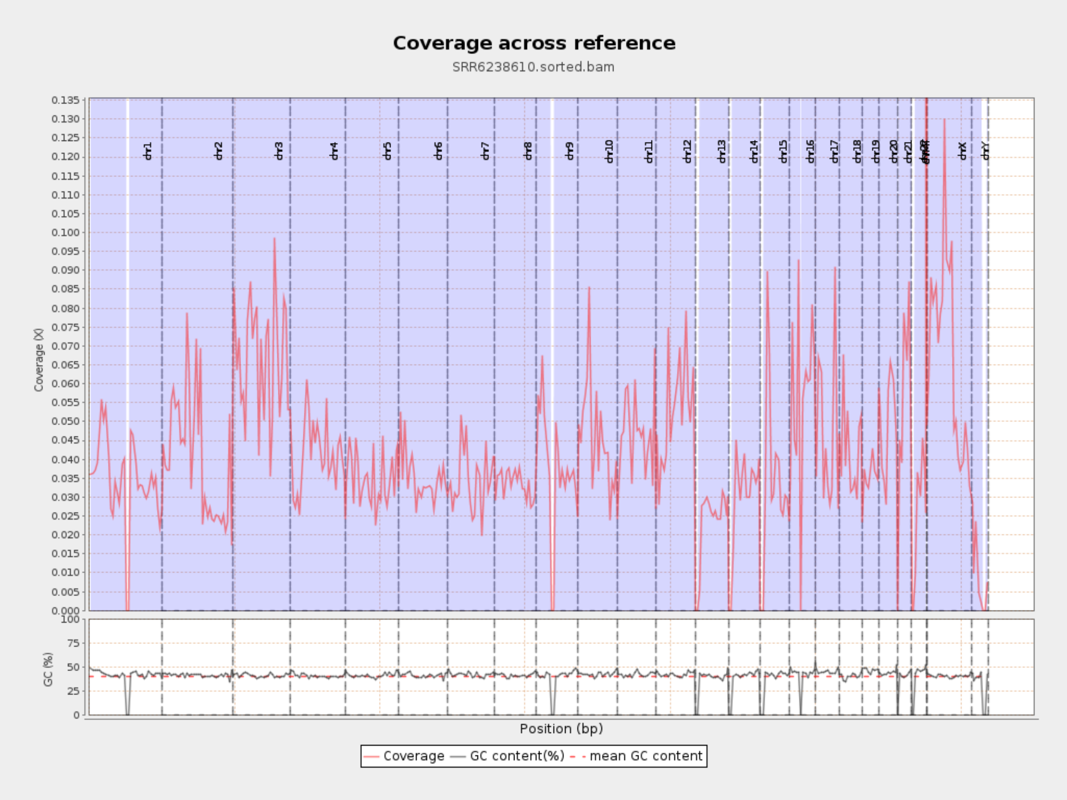
General error rate	0.69%
Mismatches	872,321
Insertions	8,919
Mapped reads with at least one insertion	0.42%
Deletions	42,569
Mapped reads with at least one deletion	1.99%
Homopolymer indels	39.89%

2.6. Chromosome stats

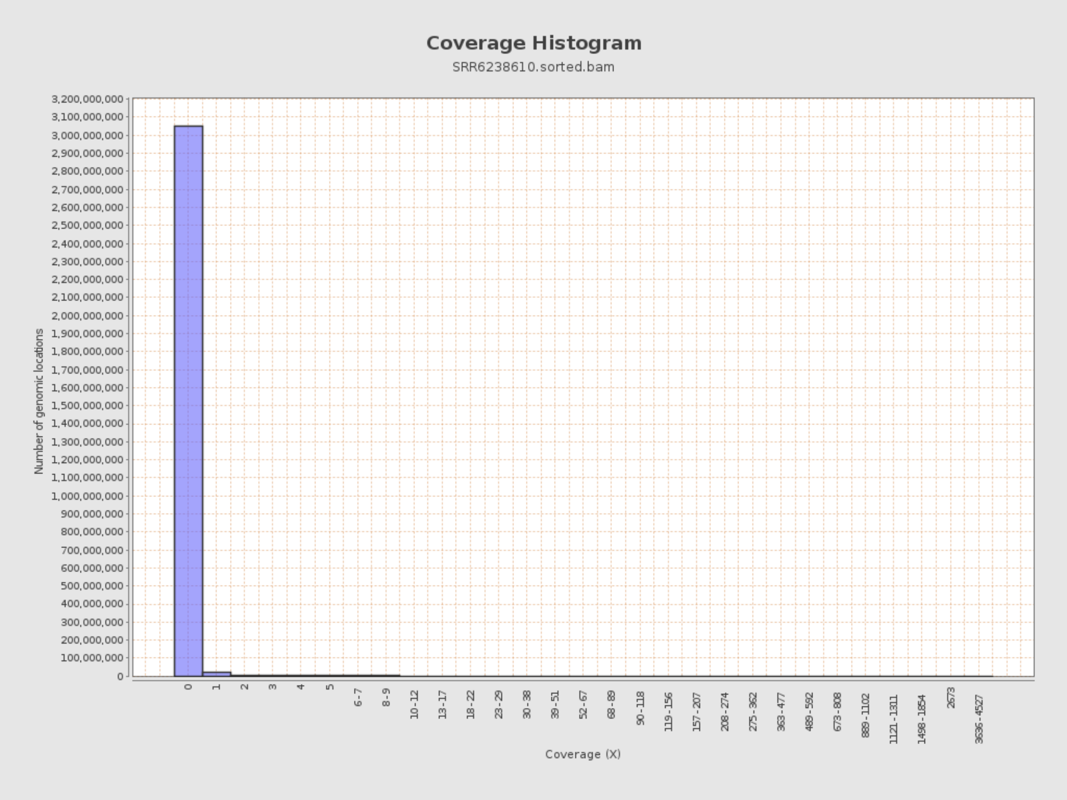
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8546757	0.0343	0.5746
chr2	243199373	9883644	0.0406	2.0175
chr3	198022430	13241213	0.0669	0.6666
chr4	191154276	7853931	0.0411	0.5203
chr5	180915260	6305439	0.0349	0.4775
chr6	171115067	6001334	0.0351	0.8033
chr7	159138663	5419628	0.0341	0.6062

chr8	146364022	4881860	0.0334	0.6045
chr9	141213431	5333683	0.0378	0.5299
chr10	135534747	6248322	0.0461	0.6926
chr11	135006516	6294950	0.0466	0.5502
chr12	133851895	7122336	0.0532	0.623
chr13	115169878	2632033	0.0229	0.5885
chr14	107349540	3184989	0.0297	0.4878
chr15	102531392	3486783	0.034	0.6121
chr16	90354753	5171178	0.0572	0.658
chr17	81195210	3672699	0.0452	0.5619
chr18	78077248	3286627	0.0421	1.7742
chr19	59128983	2164107	0.0366	0.6144
chr20	63025520	3047241	0.0483	0.5849
chr21	48129895	2650721	0.0551	0.6636
chr22	51304566	1285918	0.0251	0.3982
chrMT	16571	672624	40.5904	27.0372
chrX	155270560	10417931	0.0671	0.6775
chrY	59373566	516667	0.0087	0.3494

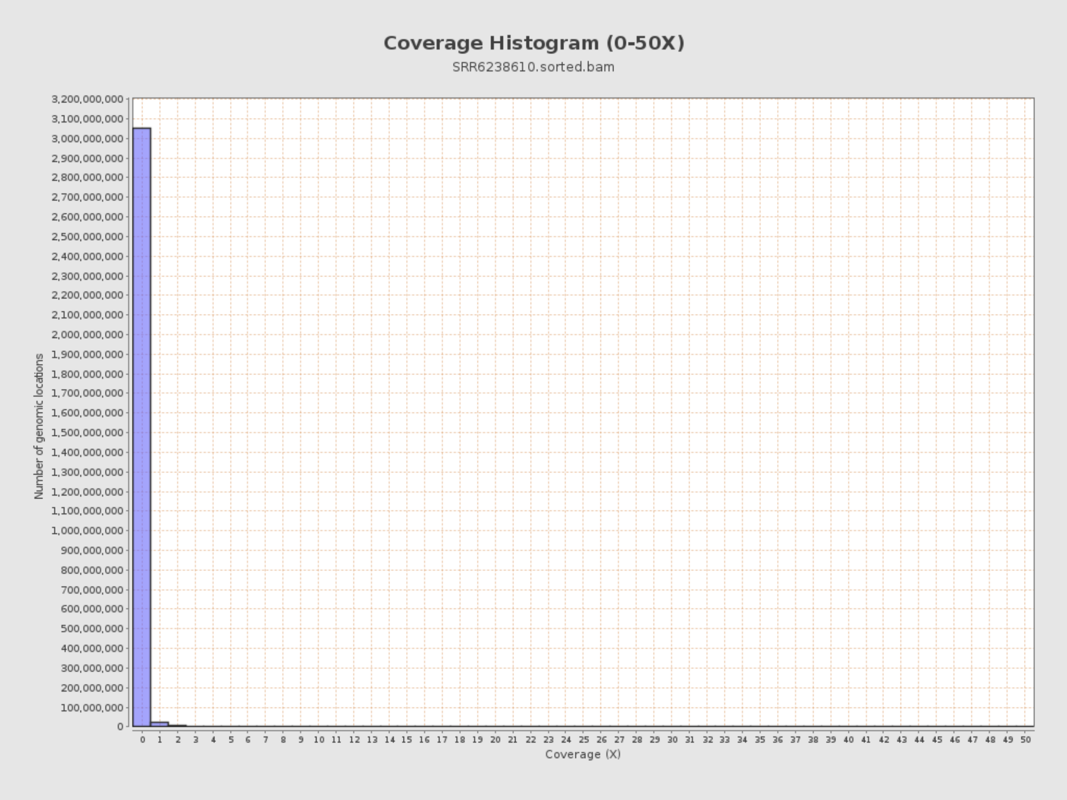
3. Results : Coverage across reference



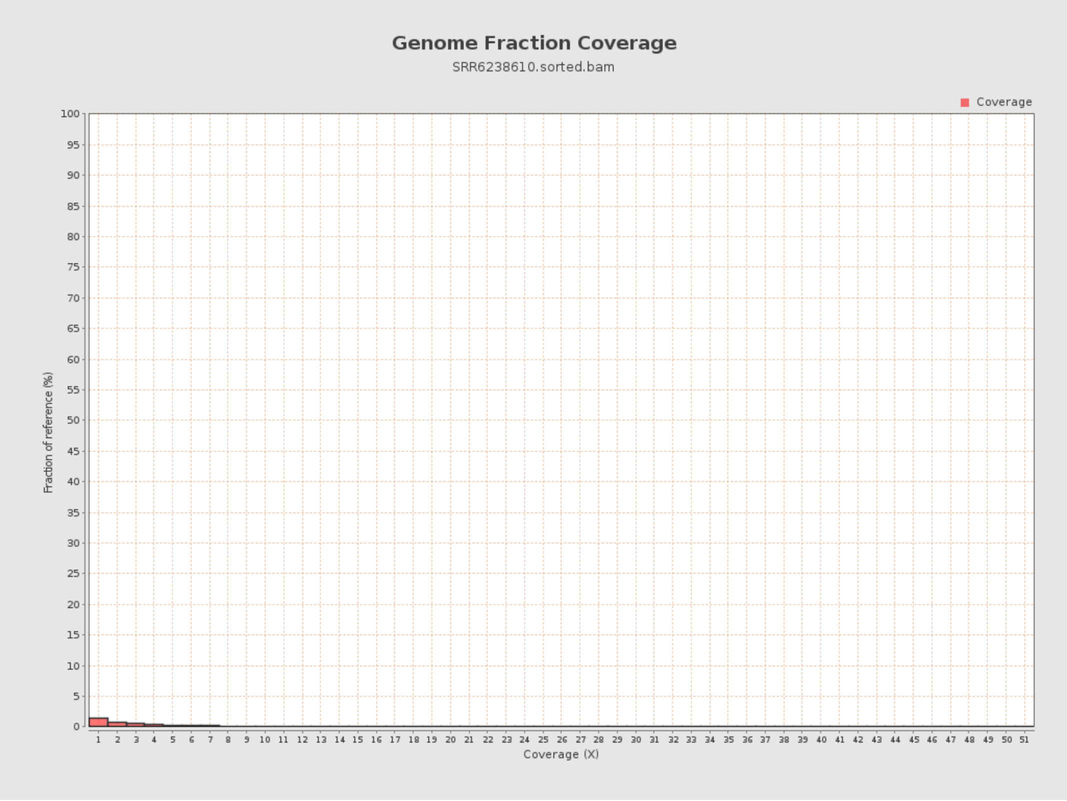
4. Results : Coverage Histogram



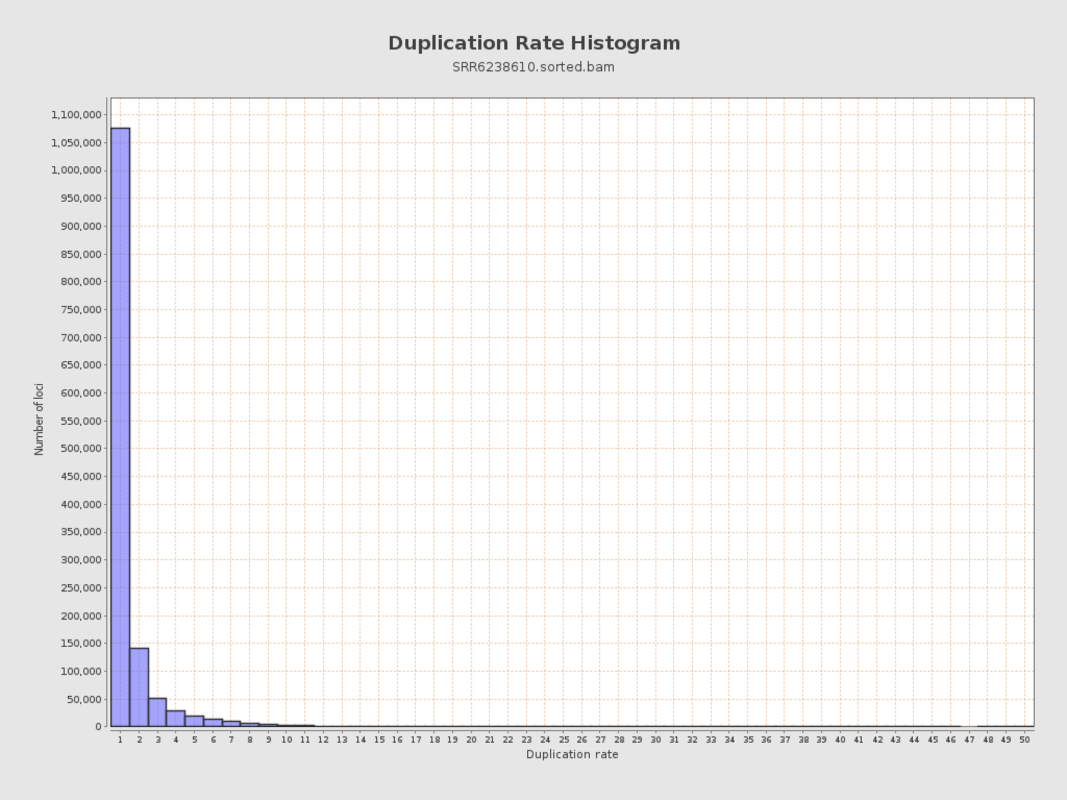
5. Results : Coverage Histogram (0-50X)



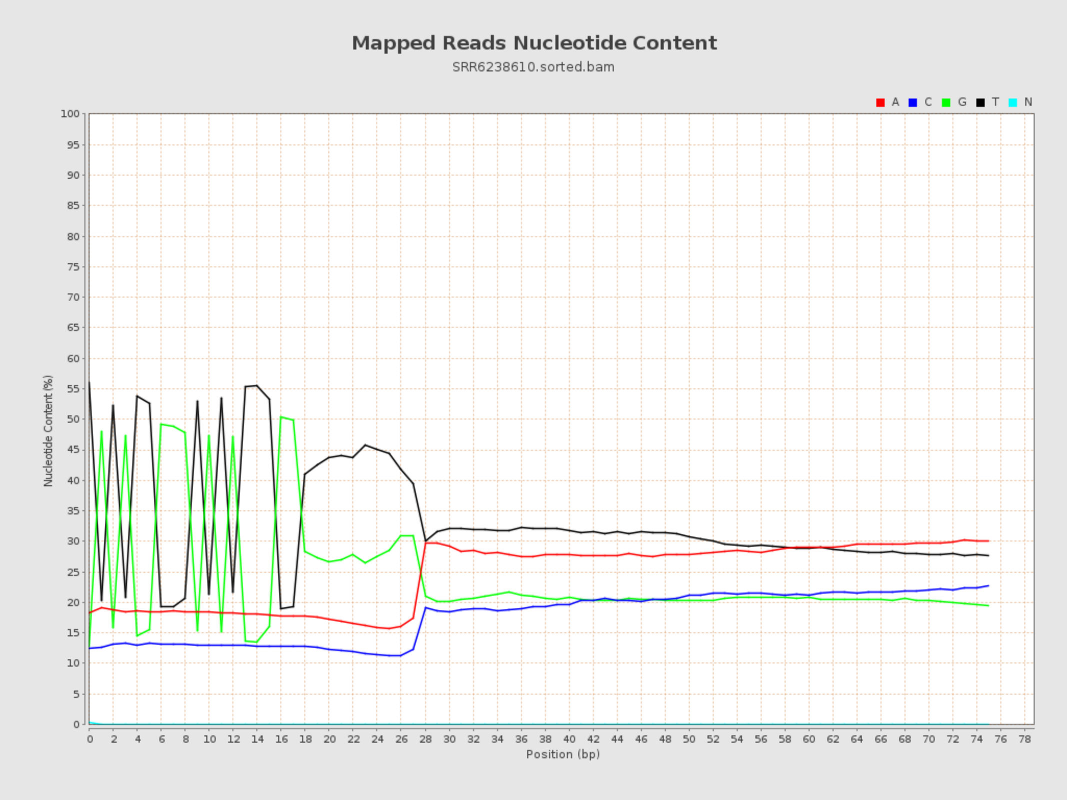
6. Results : Genome Fraction Coverage



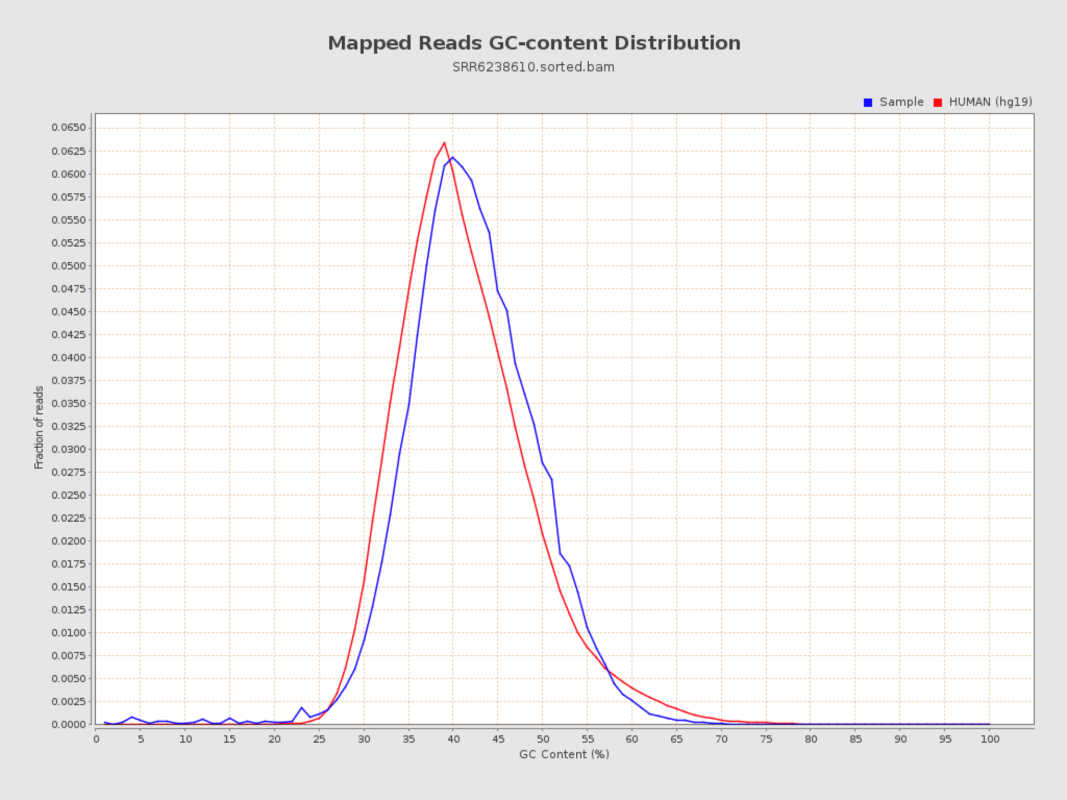
7. Results : Duplication Rate Histogram



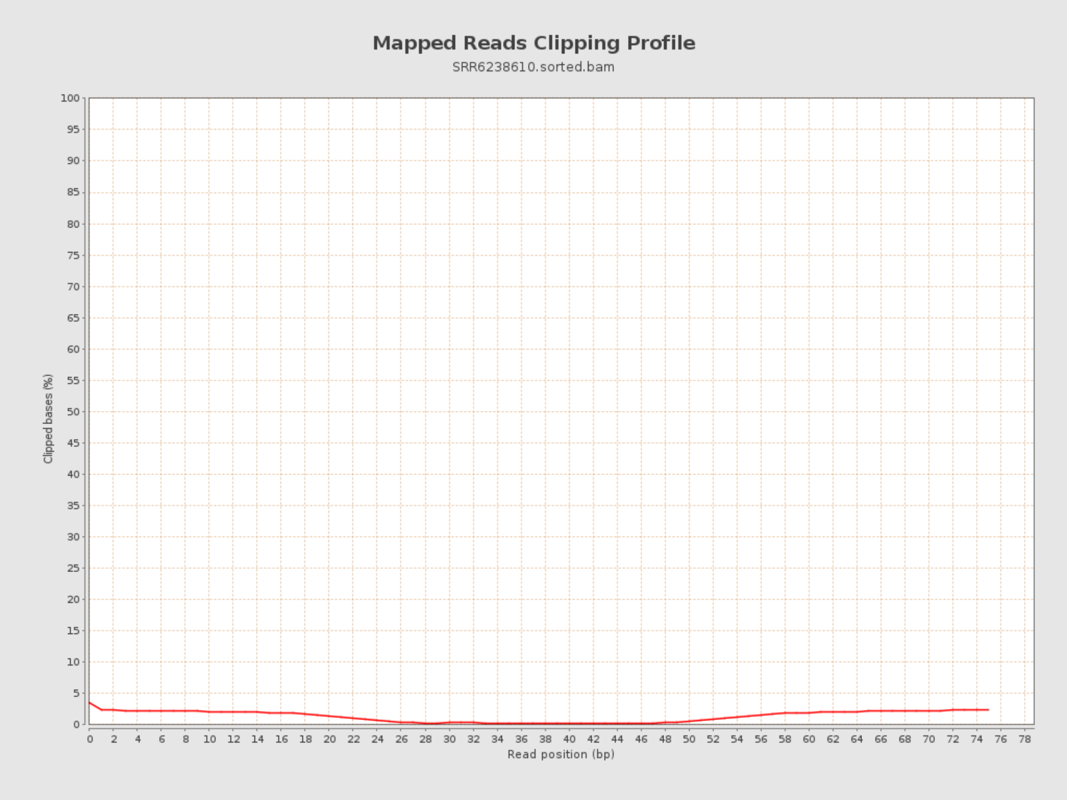
8. Results : Mapped Reads Nucleotide Content



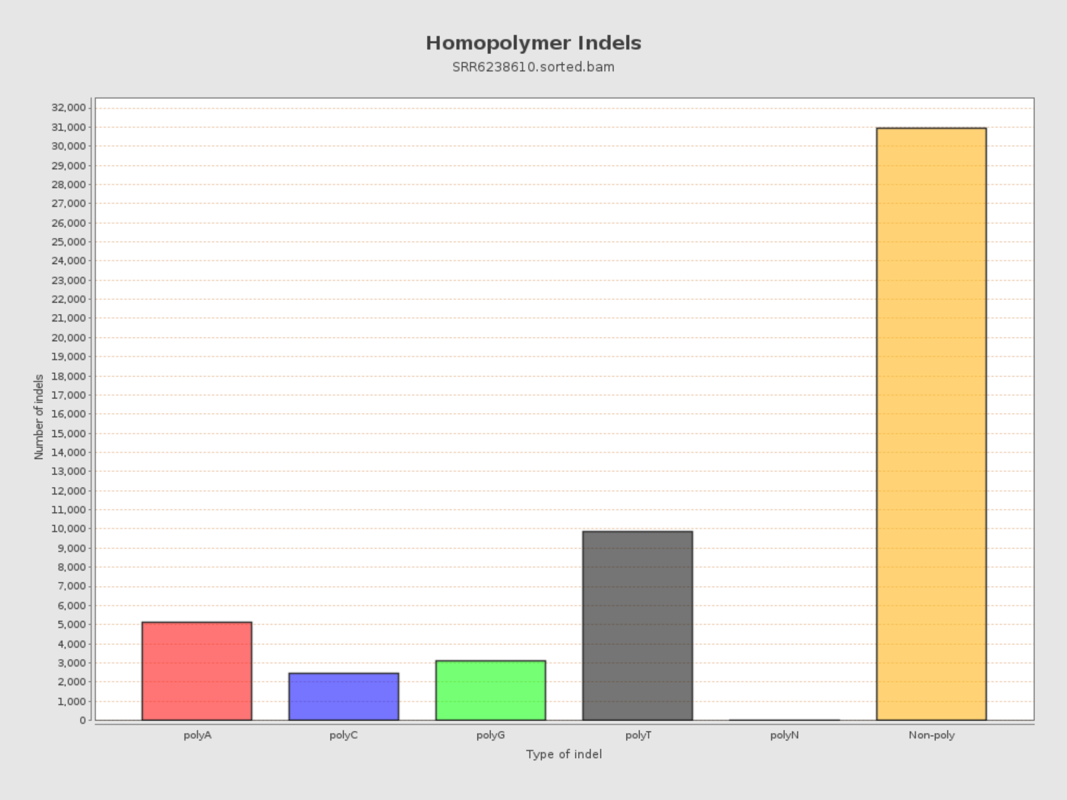
9. Results : Mapped Reads GC-content Distribution



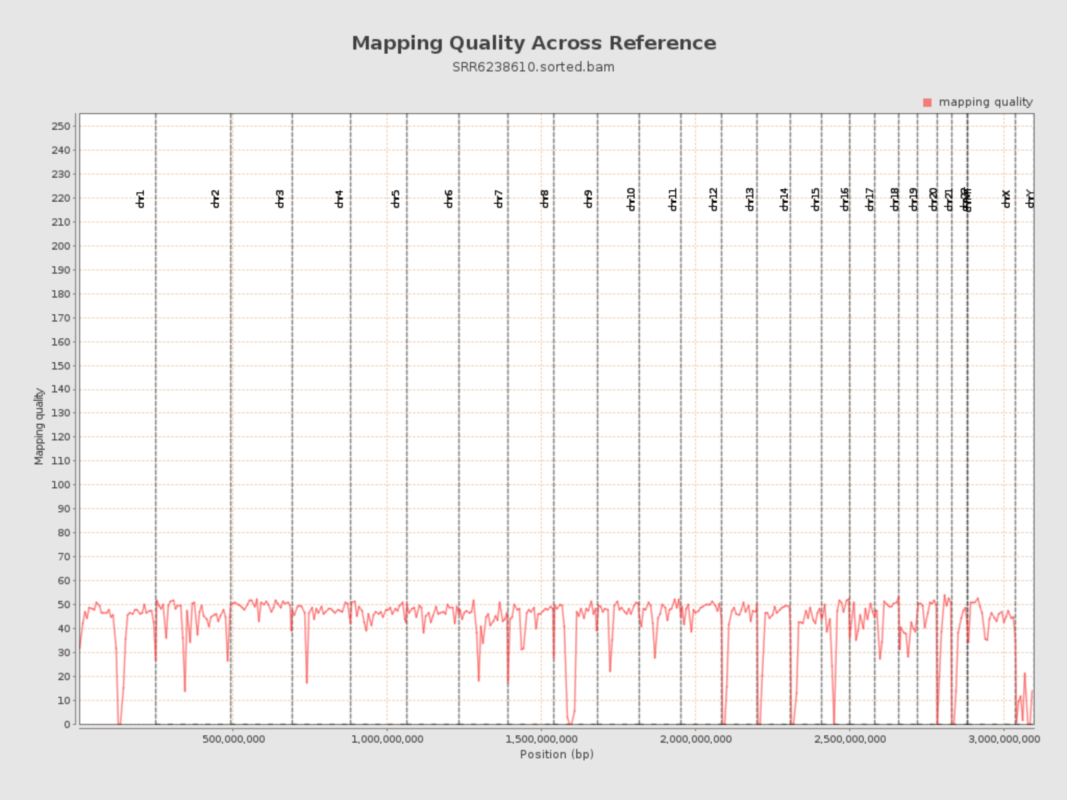
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram