Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 01:56:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238668.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_SRR6238668 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238668.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 01:56:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238668.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,732,887
Mapped reads	1,938,837 / 70.94%
Unmapped reads	794,050 / 29.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,781 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	1,011,878 / 37.03%
Duplication rate	20.68%
Clipped reads	1,316,797 / 48.18%

2.2. ACGT Content

Number/percentage of A's	28,333,633 / 24.23%
Number/percentage of C's	19,613,483 / 16.77%
Number/percentage of T's	41,169,292 / 35.21%
Number/percentage of G's	27,812,227 / 23.79%
Number/percentage of N's	2,421 / 0%
GC Percentage	40.56%

2.3. Coverage

Mean	0.0378

Standard Deviation	1.3211

2.4. Mapping Quality

Mean Mapping Quality	43.11

2.5. Mismatches and indels

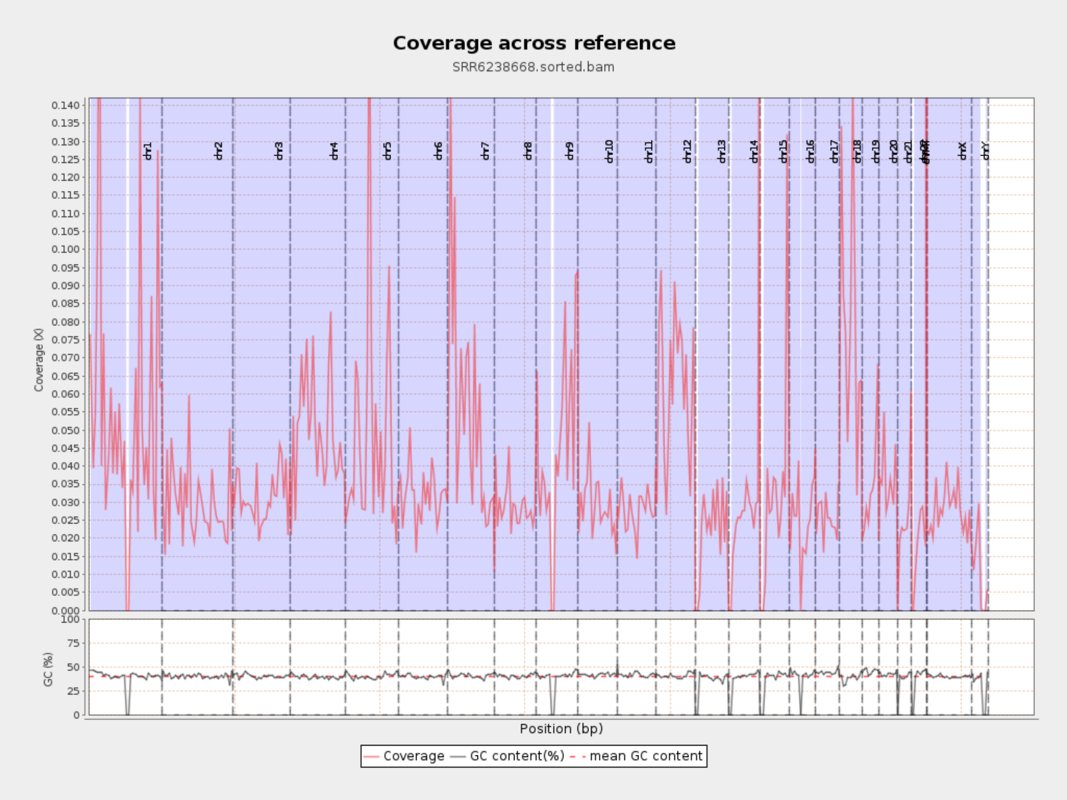
General error rate	0.64%
Mismatches	727,066
Insertions	8,852
Mapped reads with at least one insertion	0.45%
Deletions	30,593
Mapped reads with at least one deletion	1.56%
Homopolymer indels	40.97%

2.6. Chromosome stats

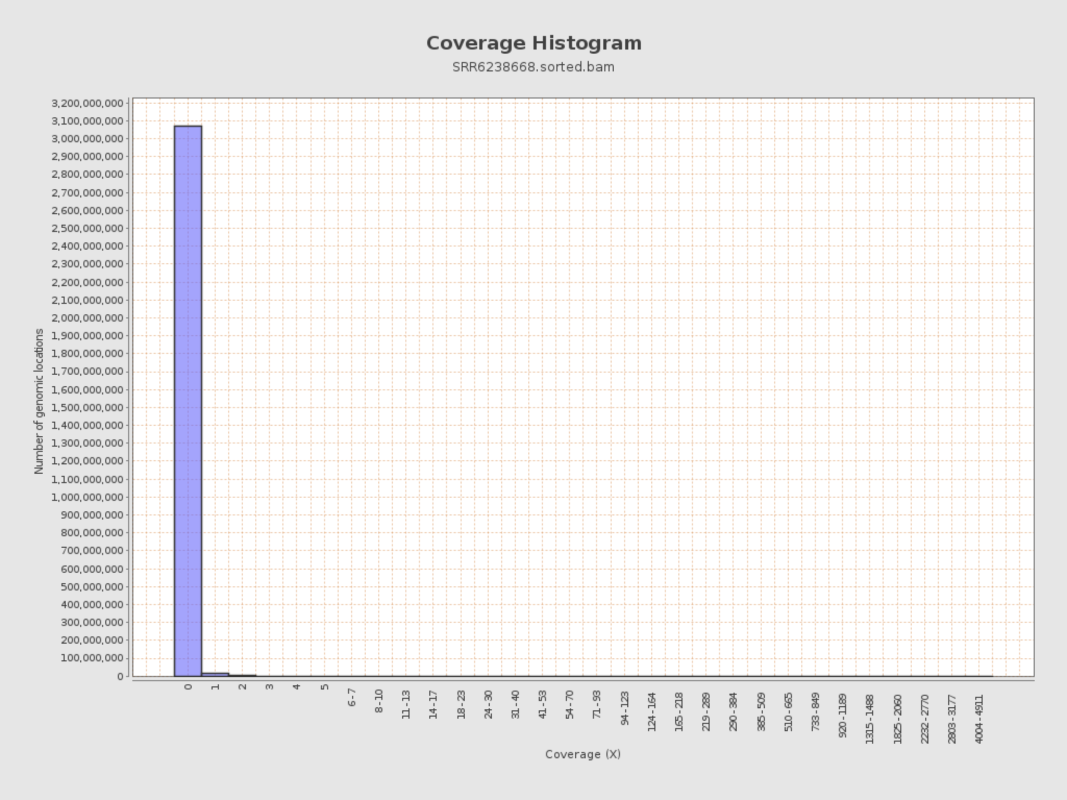
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13883290	0.0557	1.2139
chr2	243199373	7260600	0.0299	2.3136
chr3	198022430	6223612	0.0314	0.898
chr4	191154276	9560757	0.05	1.0713
chr5	180915260	8986353	0.0497	1.0637
chr6	171115067	5496939	0.0321	1.1806
chr7	159138663	8741475	0.0549	1.2907

chr8	146364022	4242380	0.029	0.9459
chr9	141213431	6023781	0.0427	1.0252
chr10	135534747	3933646	0.029	0.7961
chr11	135006516	3725516	0.0276	0.7661
chr12	133851895	8288324	0.0619	1.2851
chr13	115169878	2551198	0.0222	0.9894
chr14	107349540	2650342	0.0247	0.8275
chr15	102531392	3342224	0.0326	0.9586
chr16	90354753	2261073	0.025	0.7954
chr17	81195210	2051736	0.0253	0.7113
chr18	78077248	6341803	0.0812	4.1686
chr19	59128983	2006832	0.0339	0.8602
chr20	63025520	2336221	0.0371	0.8818
chr21	48129895	1214011	0.0252	0.769
chr22	51304566	860901	0.0168	0.5697
chrMT	16571	95003	5.7331	11.0961
chrX	155270560	4327729	0.0279	0.7636
chrY	59373566	575201	0.0097	0.4813

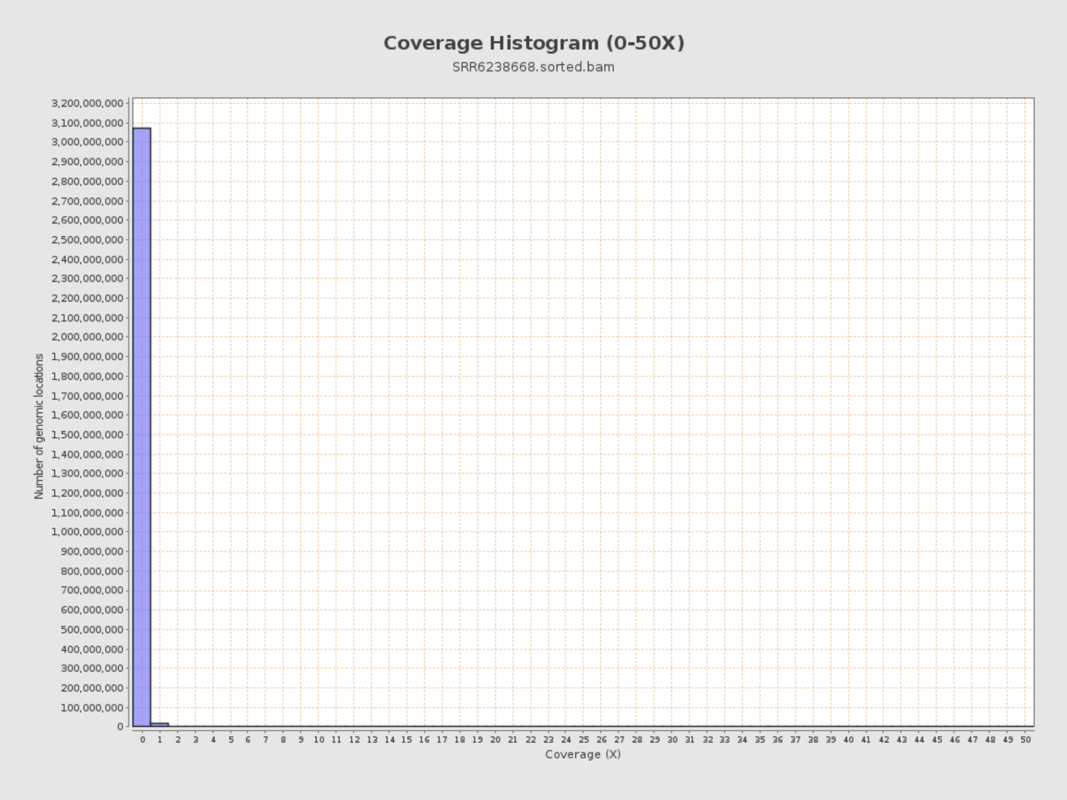
3. Results : Coverage across reference



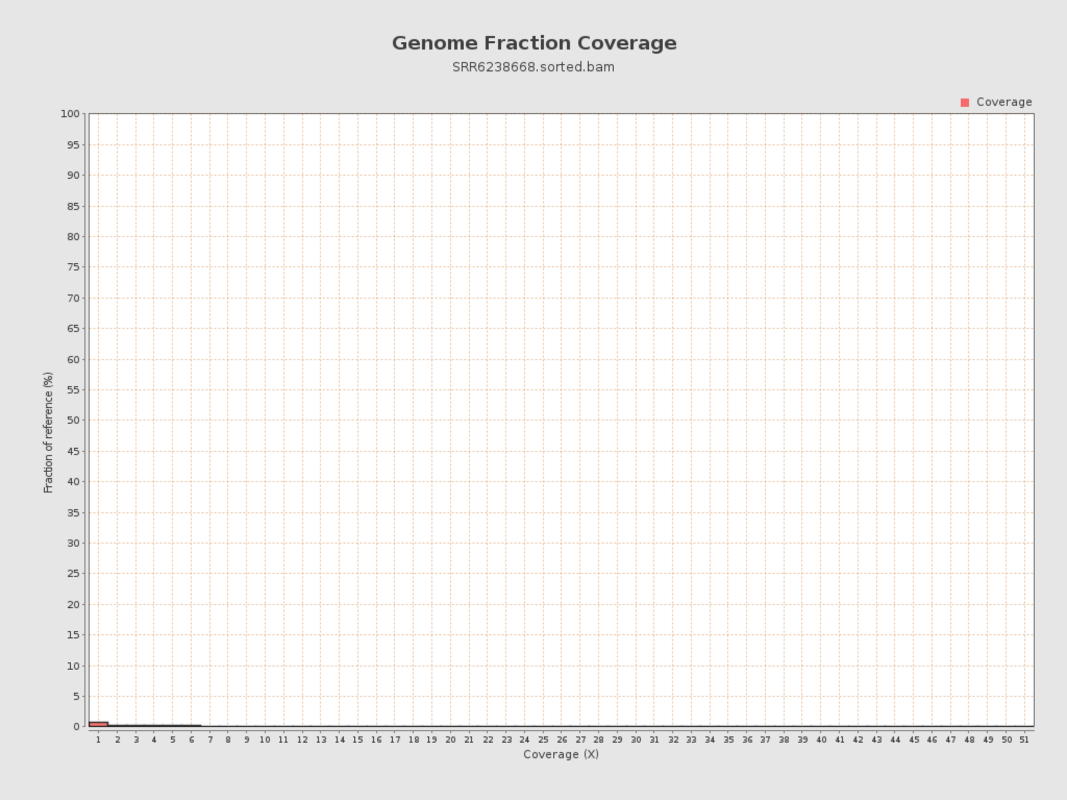
4. Results : Coverage Histogram



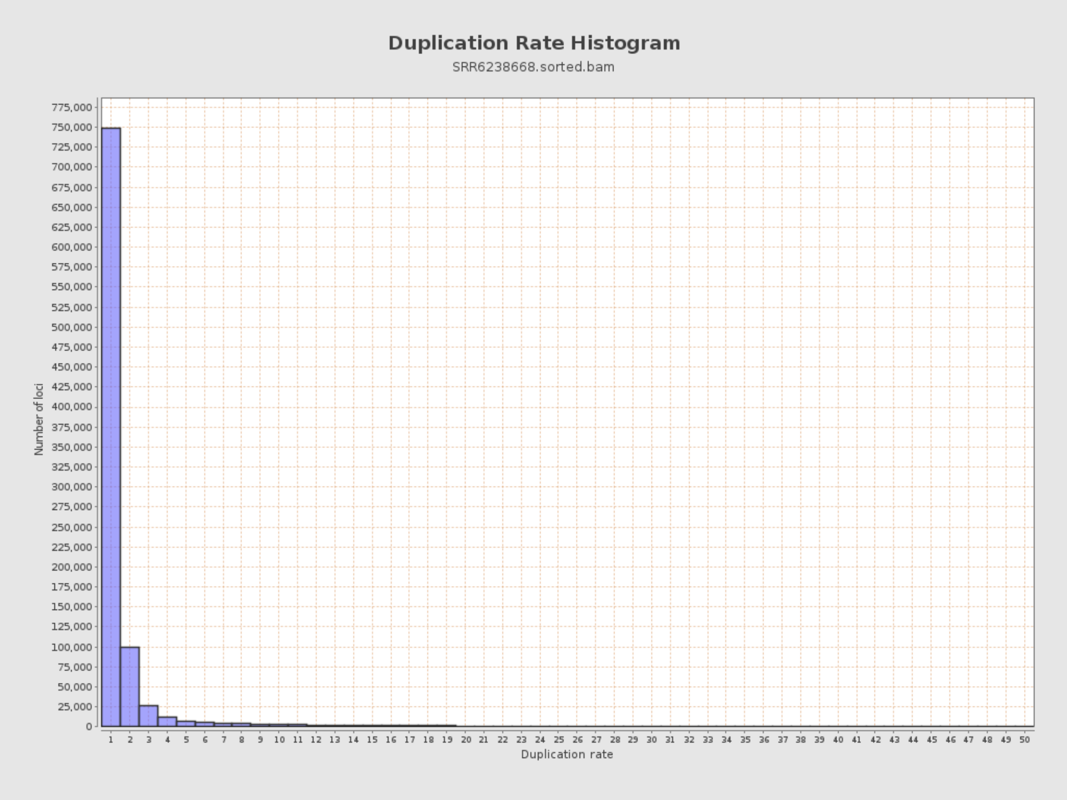
5. Results : Coverage Histogram (0-50X)



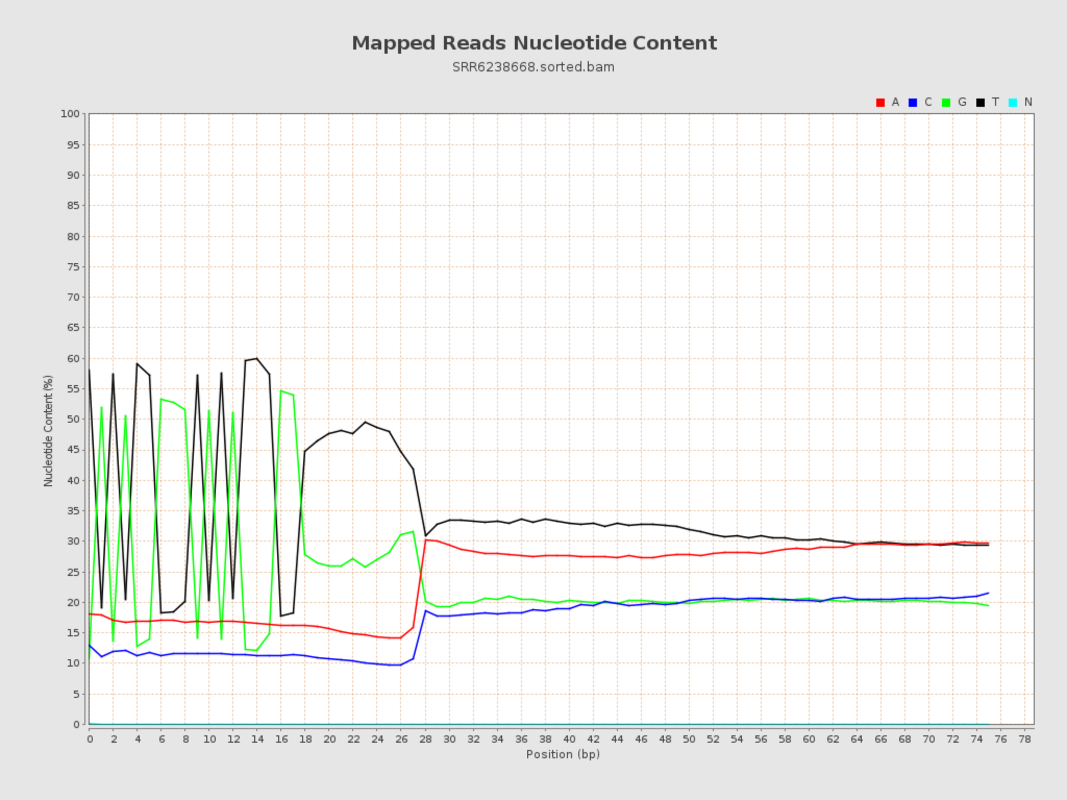
6. Results : Genome Fraction Coverage



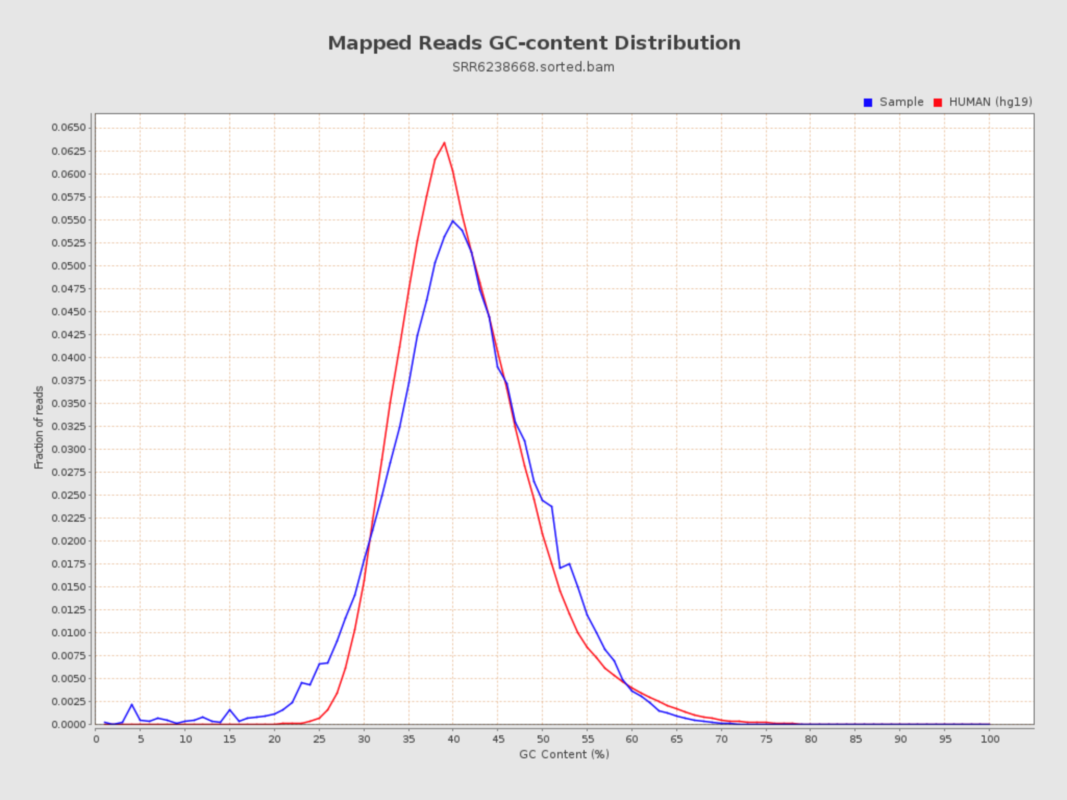
7. Results : Duplication Rate Histogram



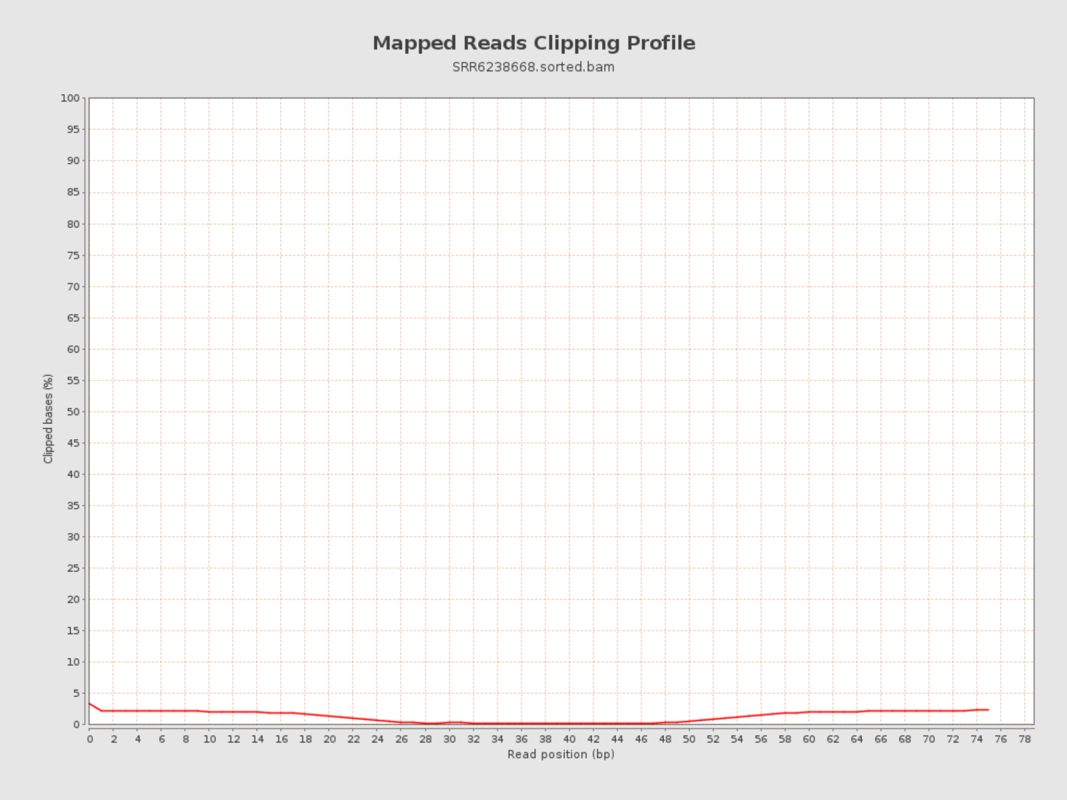
8. Results : Mapped Reads Nucleotide Content



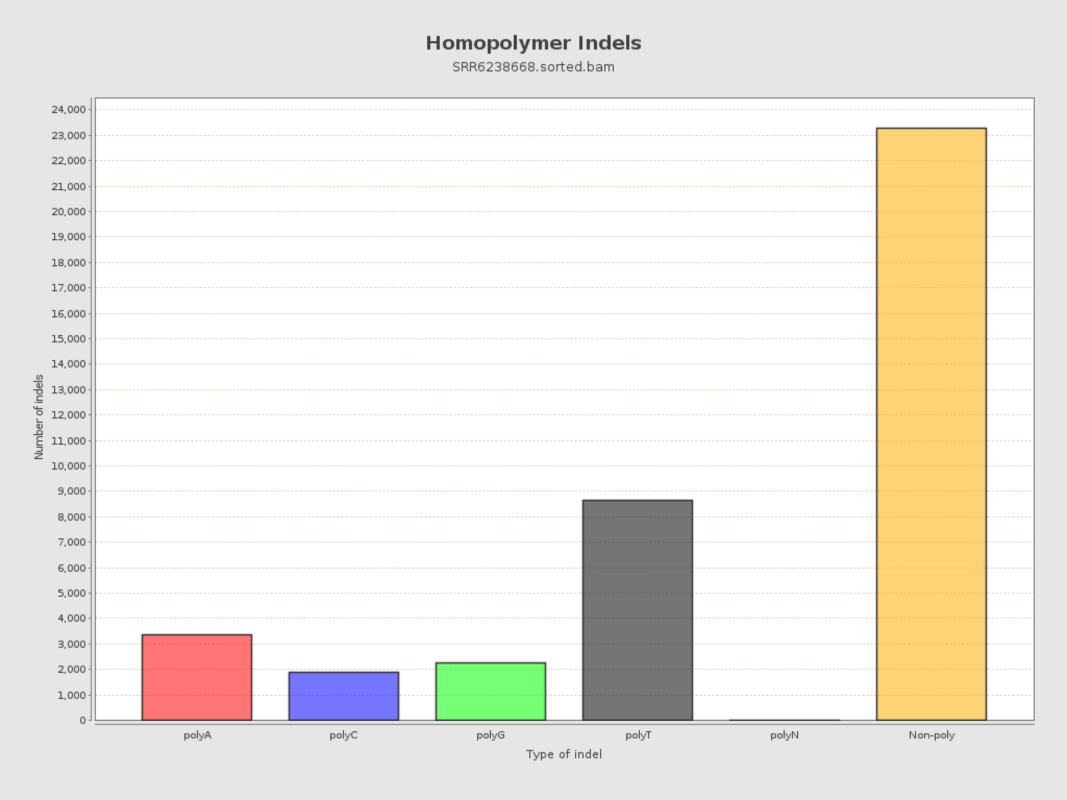
9. Results : Mapped Reads GC-content Distribution



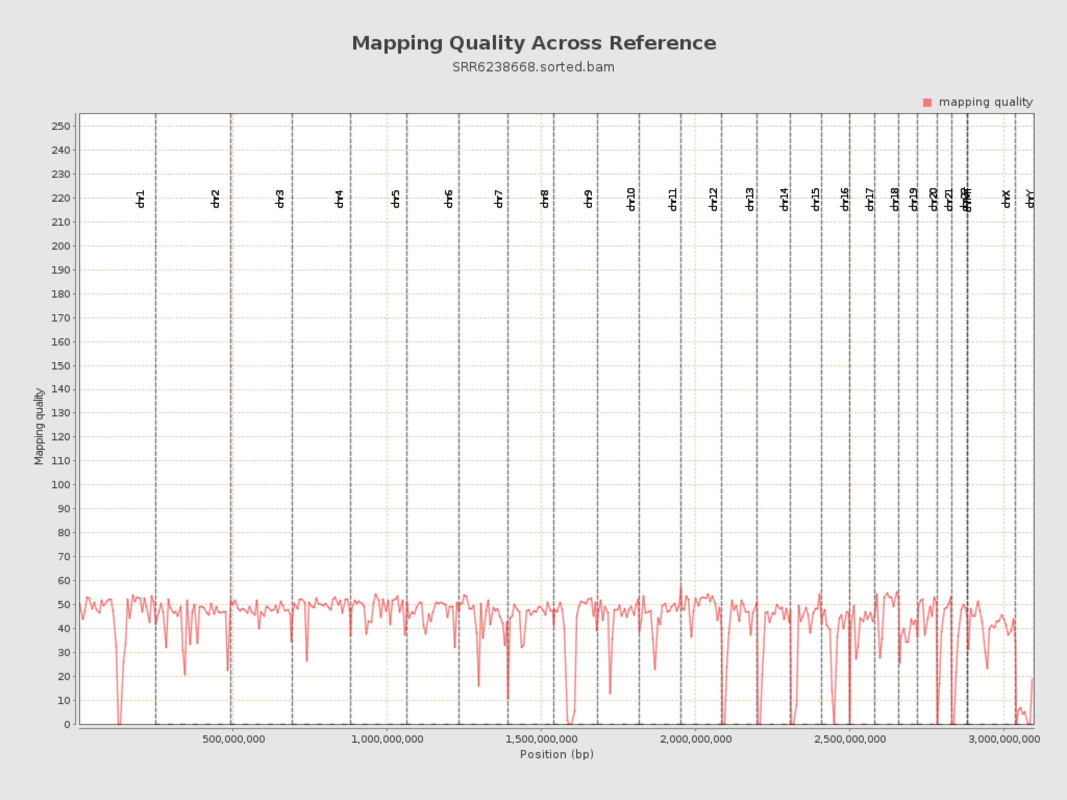
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram