Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 01:49:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238666.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_SRR6238666 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238666.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 01:49:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238666.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,300,199
Mapped reads	1,840,335 / 80.01%
Unmapped reads	459,864 / 19.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,402 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	258,019 / 11.22%
Duplication rate	11.97%
Clipped reads	1,162,318 / 50.53%

2.2. ACGT Content

Number/percentage of A's	27,571,242 / 24.25%
Number/percentage of C's	20,309,151 / 17.86%
Number/percentage of T's	37,798,062 / 33.25%
Number/percentage of G's	28,006,437 / 24.63%
Number/percentage of N's	5,768 / 0.01%
GC Percentage	42.5%

2.3. Coverage

Mean	0.0367

Standard Deviation	0.452

2.4. Mapping Quality

Mean Mapping Quality	44.27

2.5. Mismatches and indels

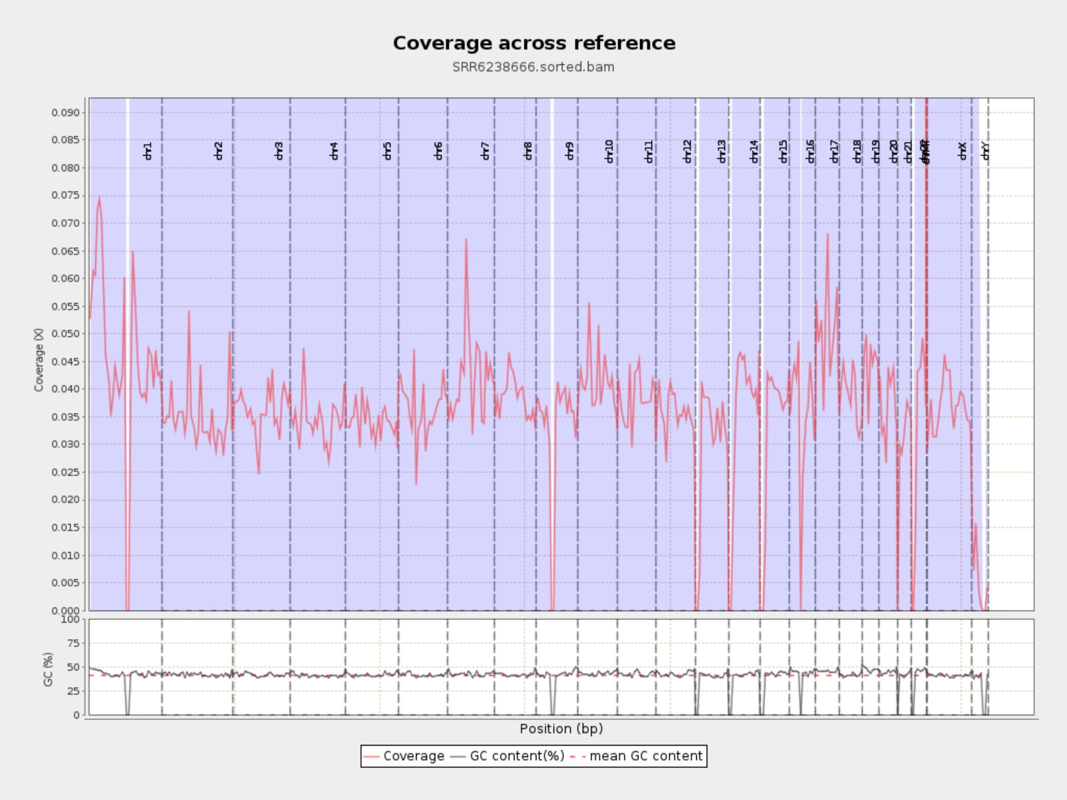
General error rate	0.57%
Mismatches	635,275
Insertions	7,830
Mapped reads with at least one insertion	0.42%
Deletions	29,516
Mapped reads with at least one deletion	1.59%
Homopolymer indels	42.79%

2.6. Chromosome stats

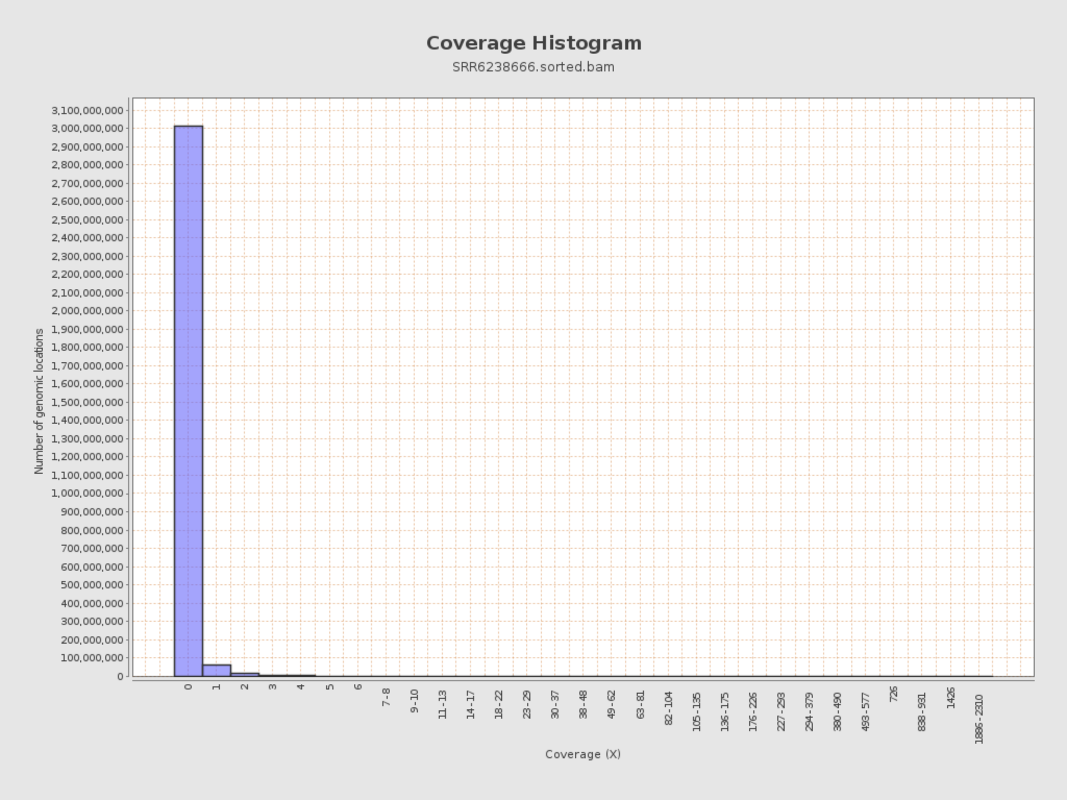
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11382695	0.0457	0.5541
chr2	243199373	8499390	0.0349	1.0353
chr3	198022430	7171058	0.0362	0.2572
chr4	191154276	6537818	0.0342	0.2531
chr5	180915260	6186357	0.0342	0.2464
chr6	171115067	6264827	0.0366	0.4179
chr7	159138663	6715167	0.0422	0.5044

chr8	146364022	5636504	0.0385	0.322
chr9	141213431	4591796	0.0325	0.2921
chr10	135534747	5634626	0.0416	0.3352
chr11	135006516	5171890	0.0383	0.2993
chr12	133851895	4810298	0.0359	0.2552
chr13	115169878	3371745	0.0293	0.292
chr14	107349540	3728936	0.0347	0.2538
chr15	102531392	3283530	0.032	0.3135
chr16	90354753	3184633	0.0352	0.2771
chr17	81195210	4153416	0.0512	0.3103
chr18	78077248	3052045	0.0391	0.7001
chr19	59128983	2615494	0.0442	0.4157
chr20	63025520	2331281	0.037	0.2625
chr21	48129895	1438086	0.0299	0.2463
chr22	51304566	1567863	0.0306	0.2292
chrMT	16571	389511	23.5056	14.208
chrX	155270560	5710371	0.0368	0.2646
chrY	59373566	312043	0.0053	0.1738

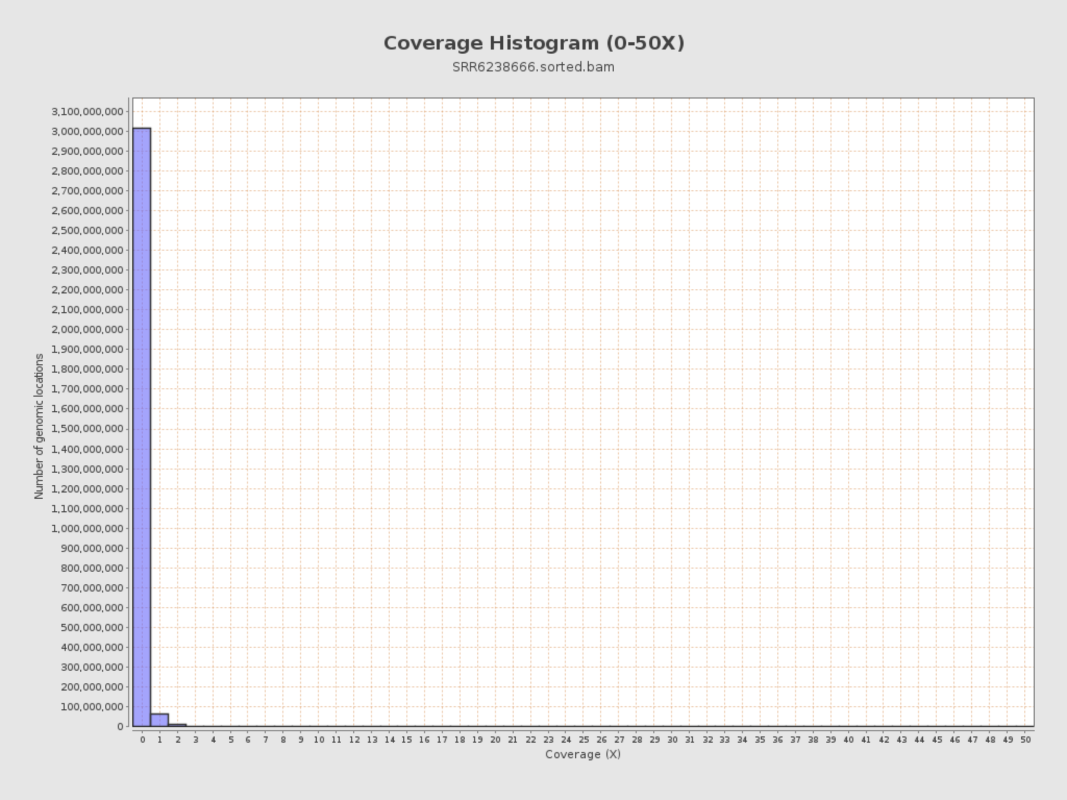
3. Results : Coverage across reference



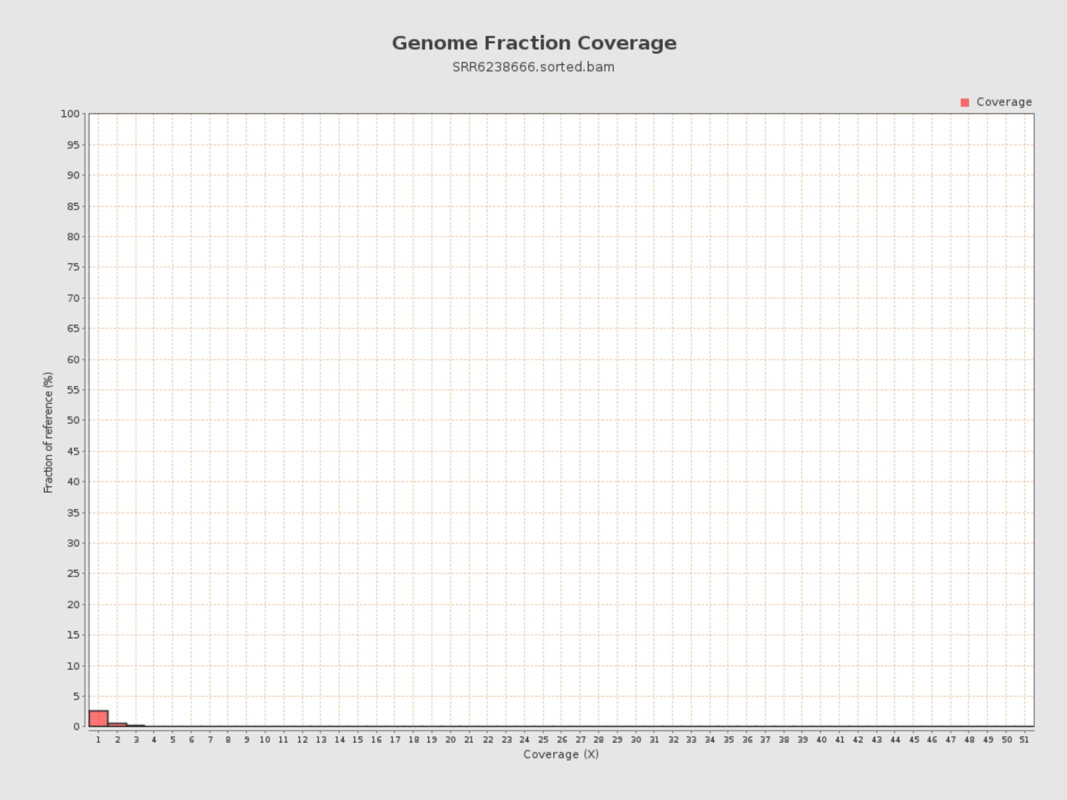
4. Results : Coverage Histogram



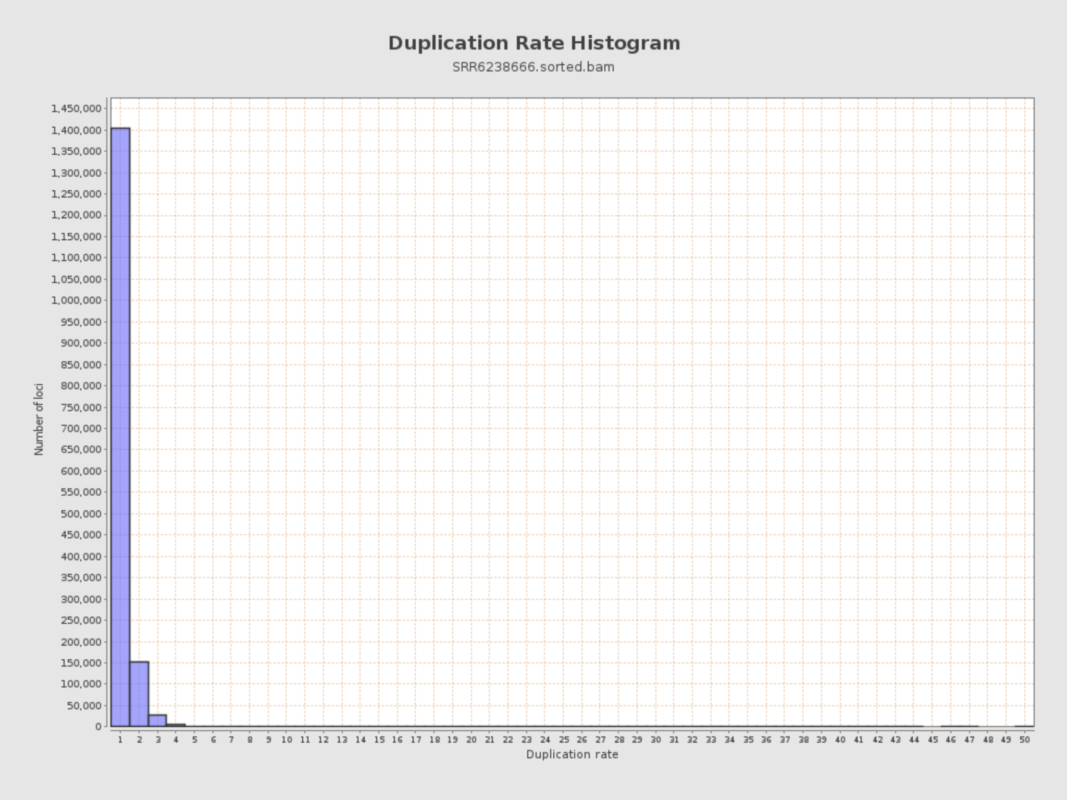
5. Results : Coverage Histogram (0-50X)



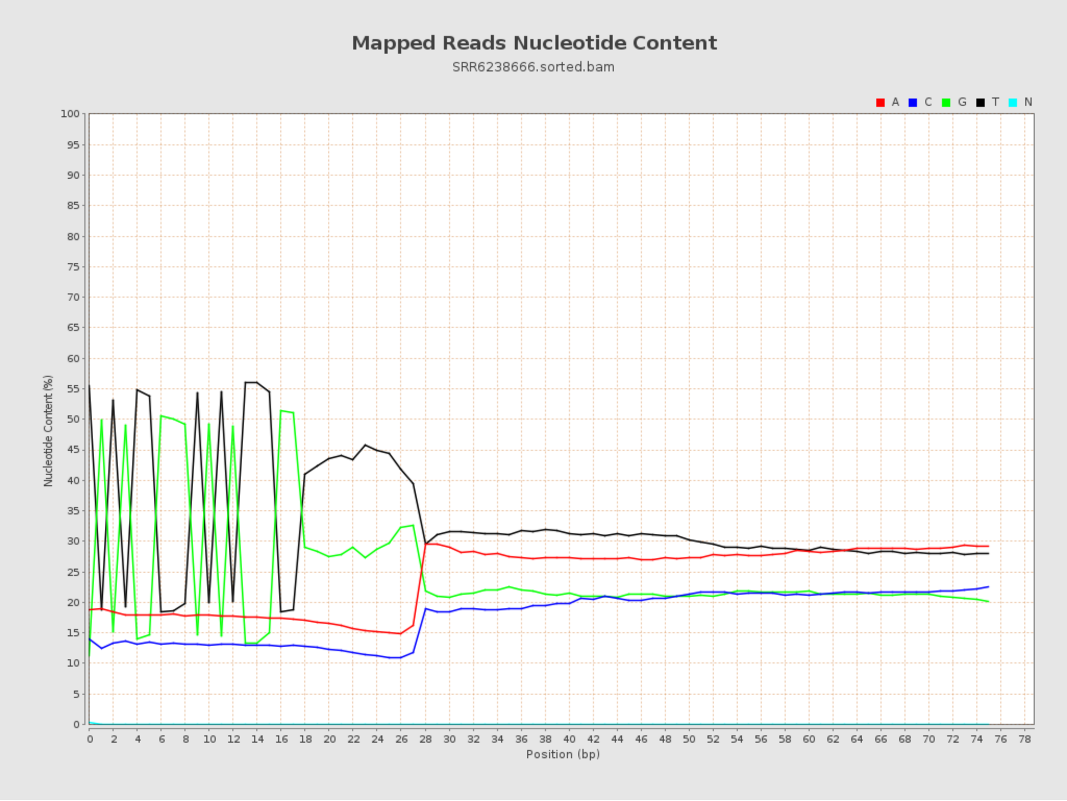
6. Results : Genome Fraction Coverage



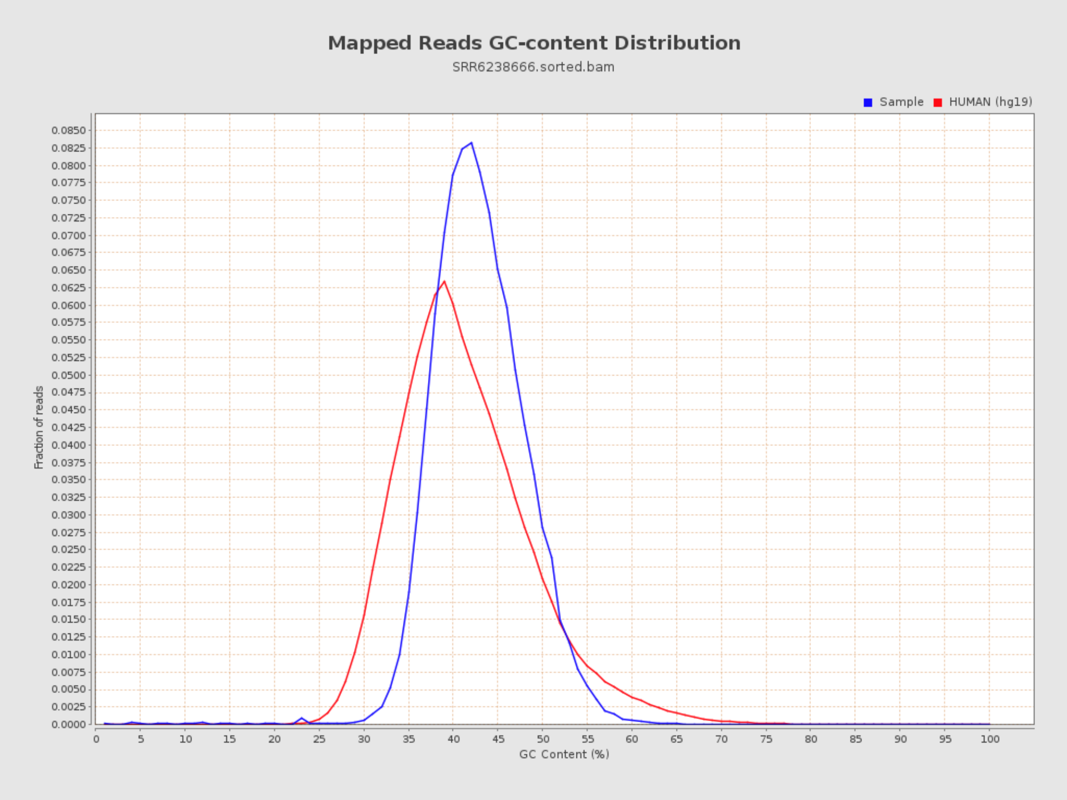
7. Results : Duplication Rate Histogram



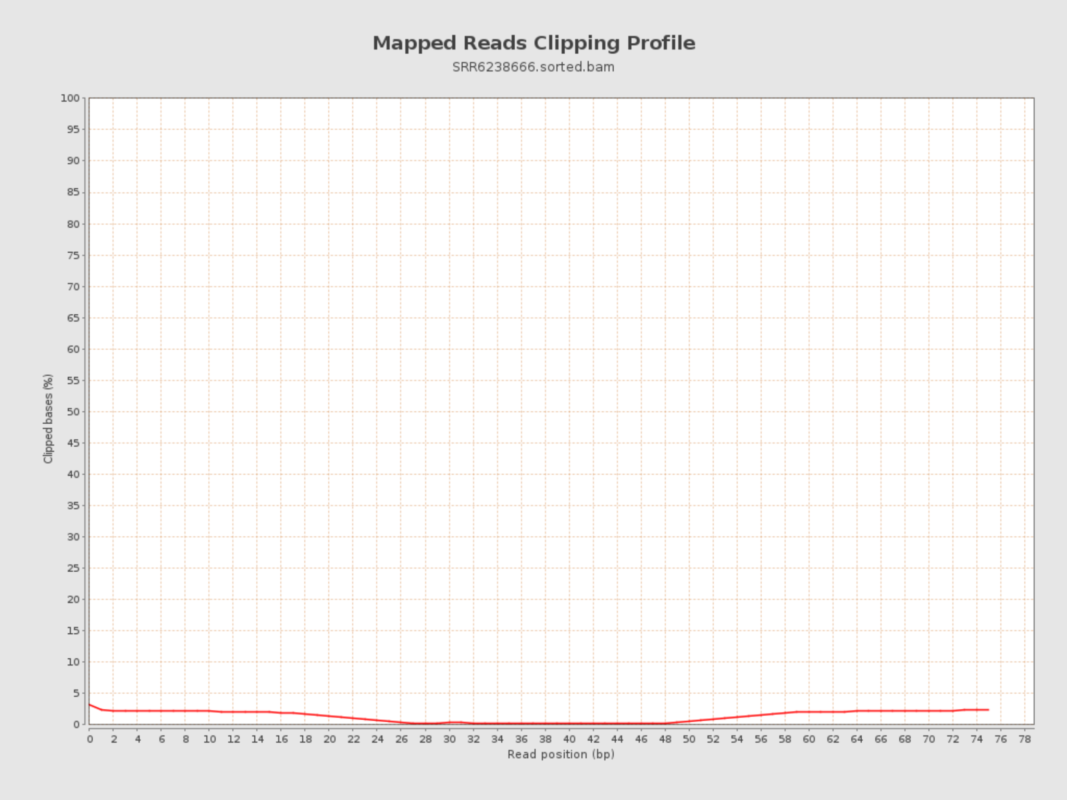
8. Results : Mapped Reads Nucleotide Content



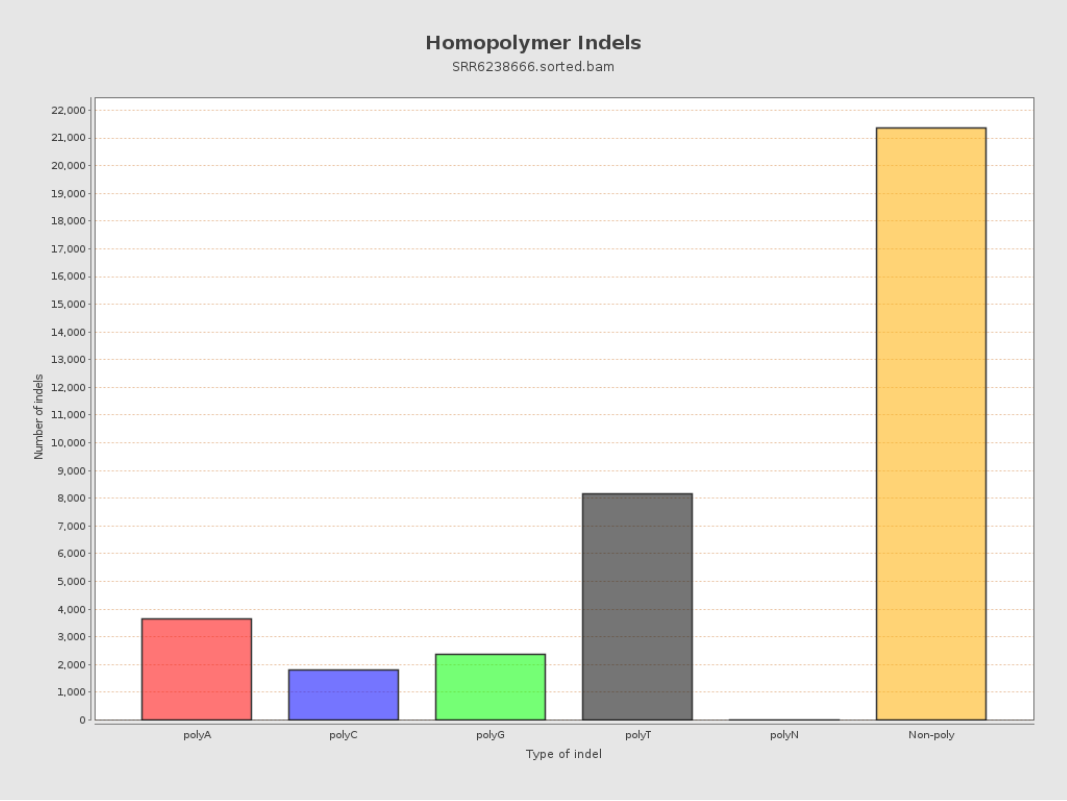
9. Results : Mapped Reads GC-content Distribution



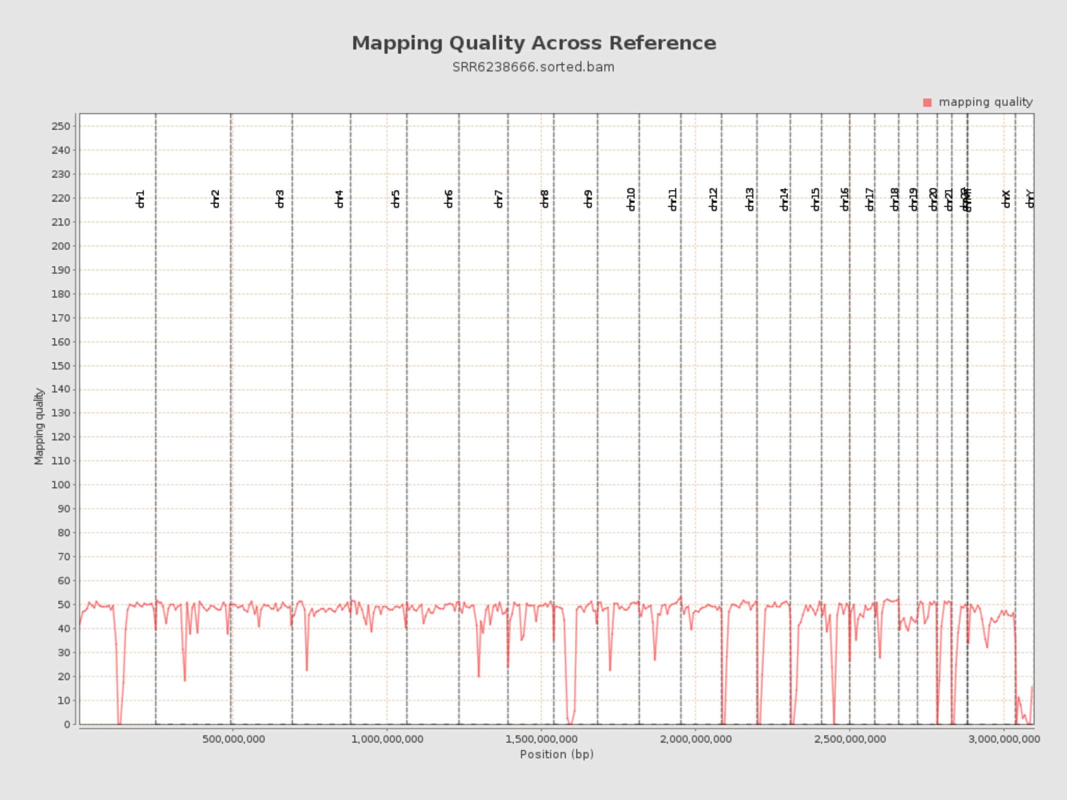
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram