Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 22:35:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238616.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_SRR6238616 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238616.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 22:35:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238616.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,431,370
Mapped reads	1,947,163 / 56.75%
Unmapped reads	1,484,207 / 43.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,126 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	572,139 / 16.67%
Duplication rate	20.5%
Clipped reads	1,305,172 / 38.04%

2.2. ACGT Content

Number/percentage of A's	28,728,615 / 24.33%
Number/percentage of C's	20,854,906 / 17.66%
Number/percentage of T's	39,570,478 / 33.51%
Number/percentage of G's	28,916,771 / 24.49%
Number/percentage of N's	5,693 / 0%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0382

Standard Deviation	0.5678

2.4. Mapping Quality

Mean Mapping Quality	44.06

2.5. Mismatches and indels

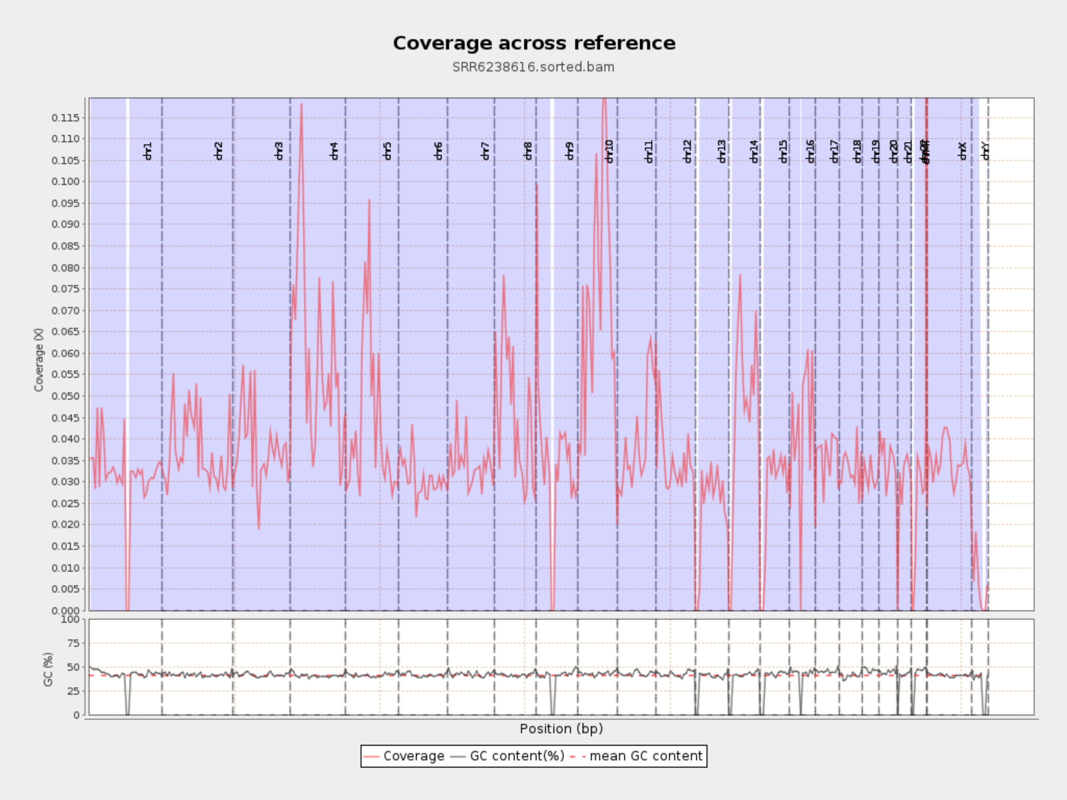
General error rate	0.57%
Mismatches	663,893
Insertions	7,665
Mapped reads with at least one insertion	0.39%
Deletions	29,161
Mapped reads with at least one deletion	1.48%
Homopolymer indels	42.44%

2.6. Chromosome stats

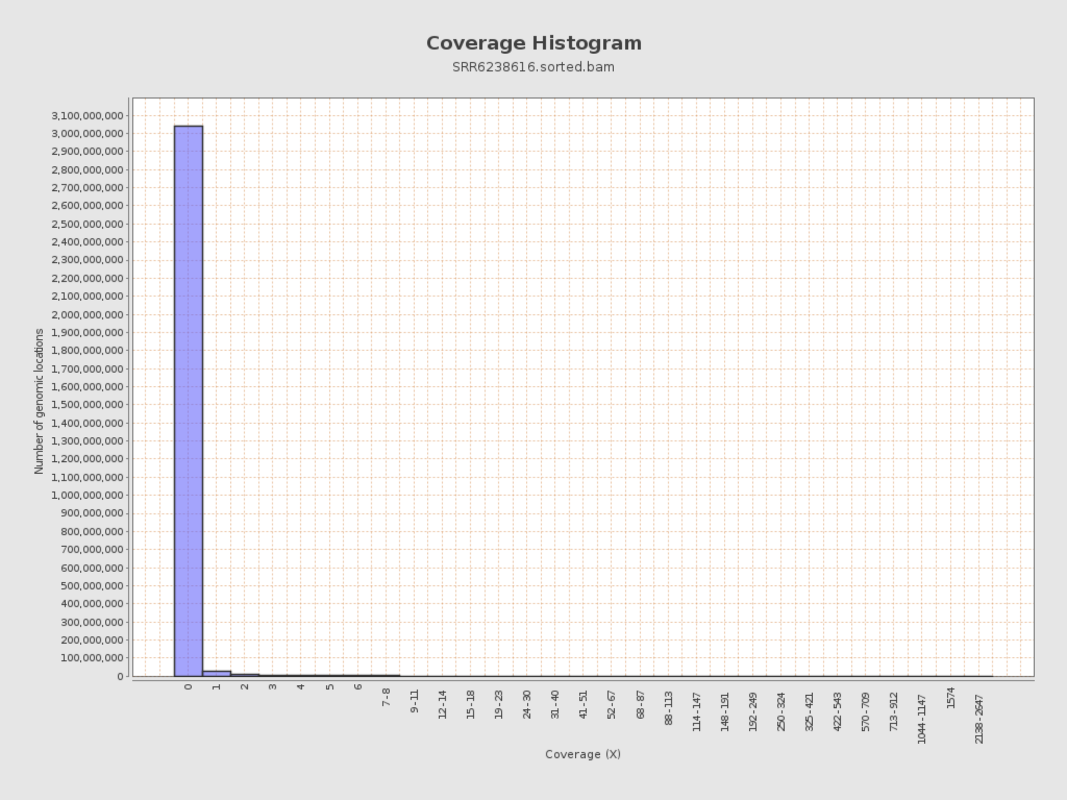
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7807862	0.0313	0.4892
chr2	243199373	9073498	0.0373	1.2174
chr3	198022430	7484736	0.0378	0.3811
chr4	191154276	11440965	0.0599	0.4873
chr5	180915260	7905323	0.0437	0.413
chr6	171115067	5283320	0.0309	0.5552
chr7	159138663	5418923	0.0341	0.4614

chr8	146364022	6704183	0.0458	0.4903
chr9	141213431	4600109	0.0326	0.3669
chr10	135534747	9941294	0.0733	0.5825
chr11	135006516	5326149	0.0395	0.4188
chr12	133851895	4623670	0.0345	0.3799
chr13	115169878	2710740	0.0235	0.407
chr14	107349540	5100790	0.0475	0.4498
chr15	102531392	2796031	0.0273	0.4035
chr16	90354753	3784726	0.0419	0.4535
chr17	81195210	2955559	0.0364	0.3848
chr18	78077248	2594162	0.0332	1.0951
chr19	59128983	1857979	0.0314	0.4386
chr20	63025520	2188579	0.0347	0.3694
chr21	48129895	1397154	0.029	0.3514
chr22	51304566	1138038	0.0222	0.2907
chrMT	16571	287023	17.3208	12.0504
chrX	155270560	5355094	0.0345	0.3607
chrY	59373566	350460	0.0059	0.2323

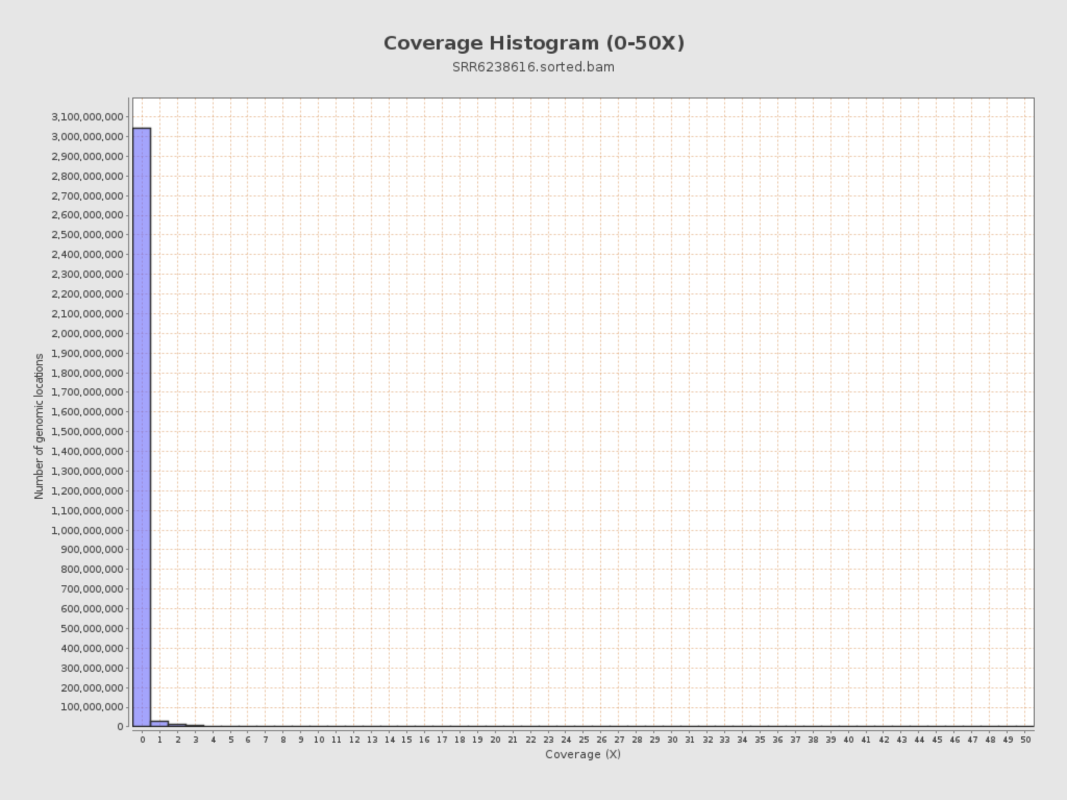
3. Results : Coverage across reference



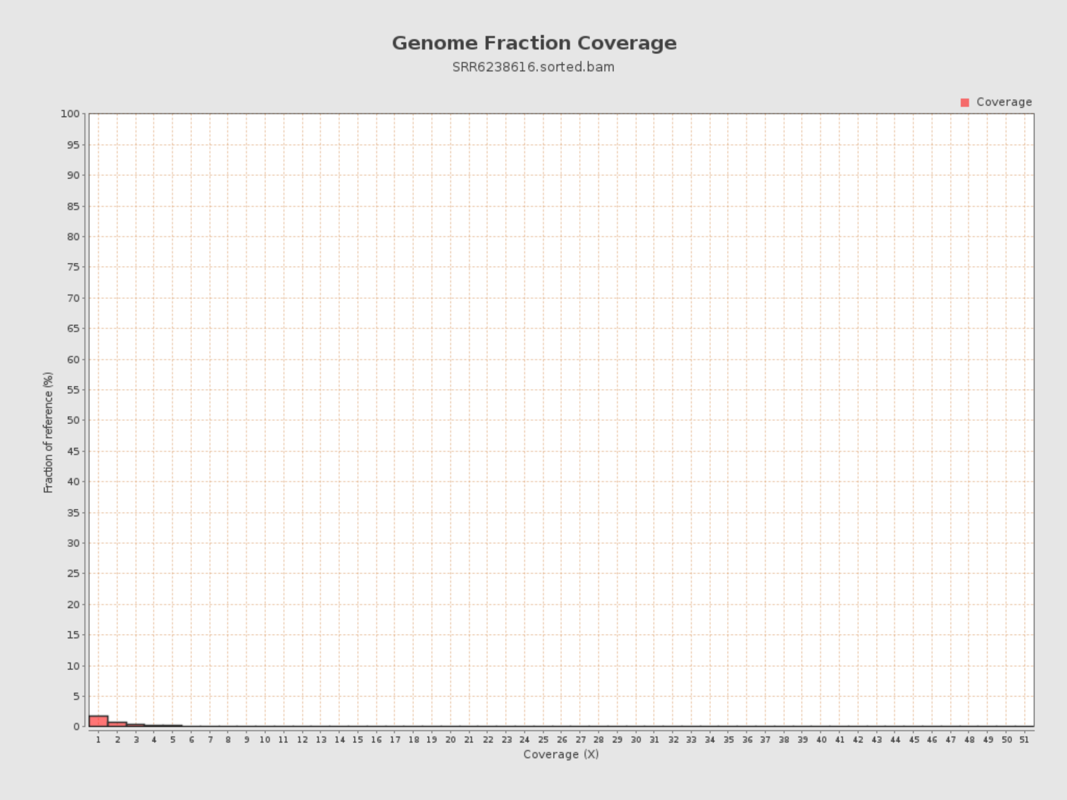
4. Results : Coverage Histogram



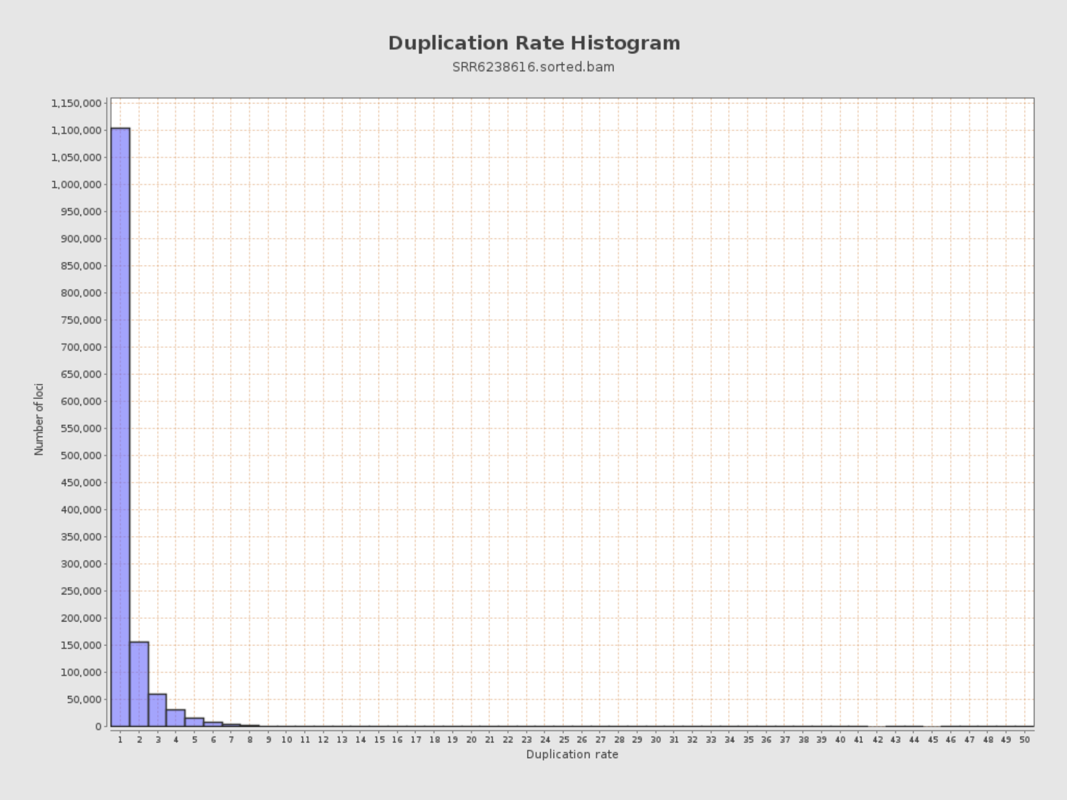
5. Results : Coverage Histogram (0-50X)



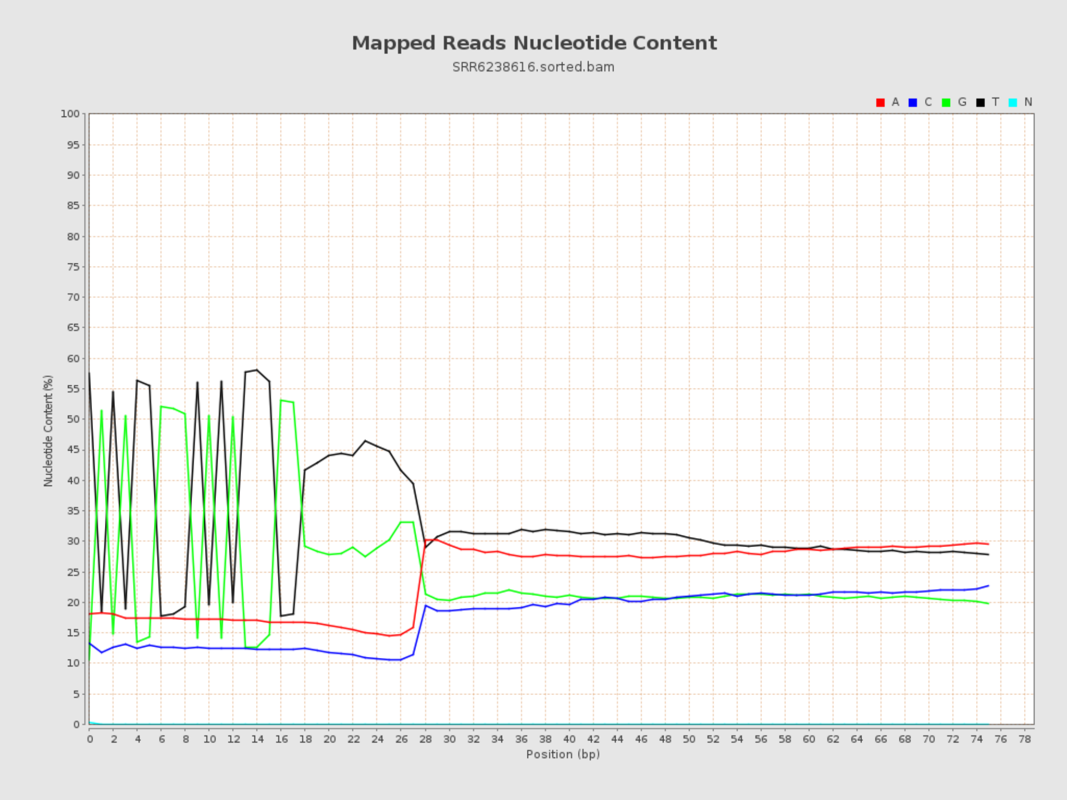
6. Results : Genome Fraction Coverage



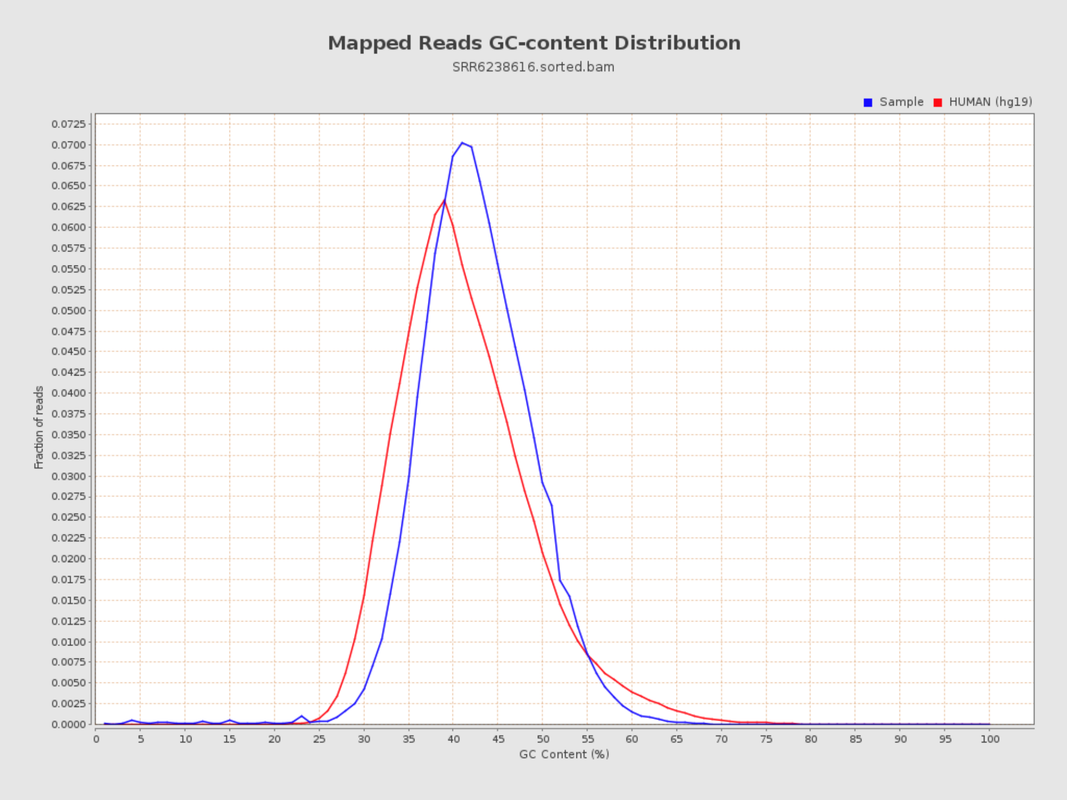
7. Results : Duplication Rate Histogram



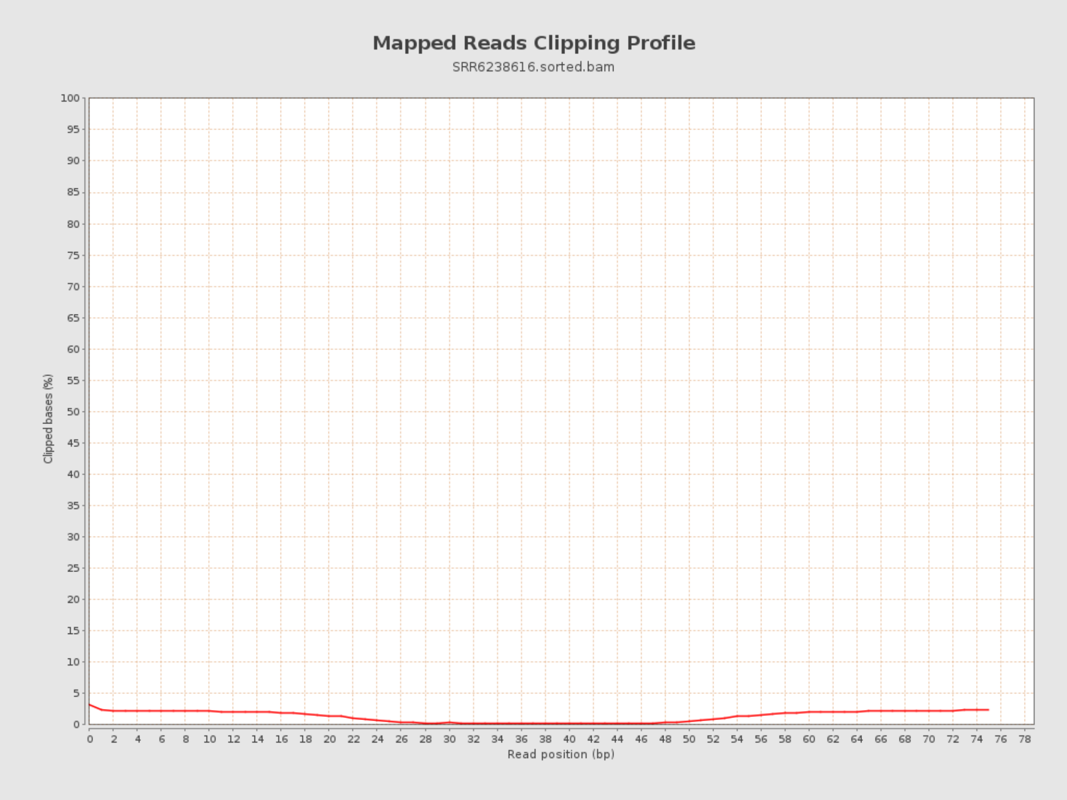
8. Results : Mapped Reads Nucleotide Content



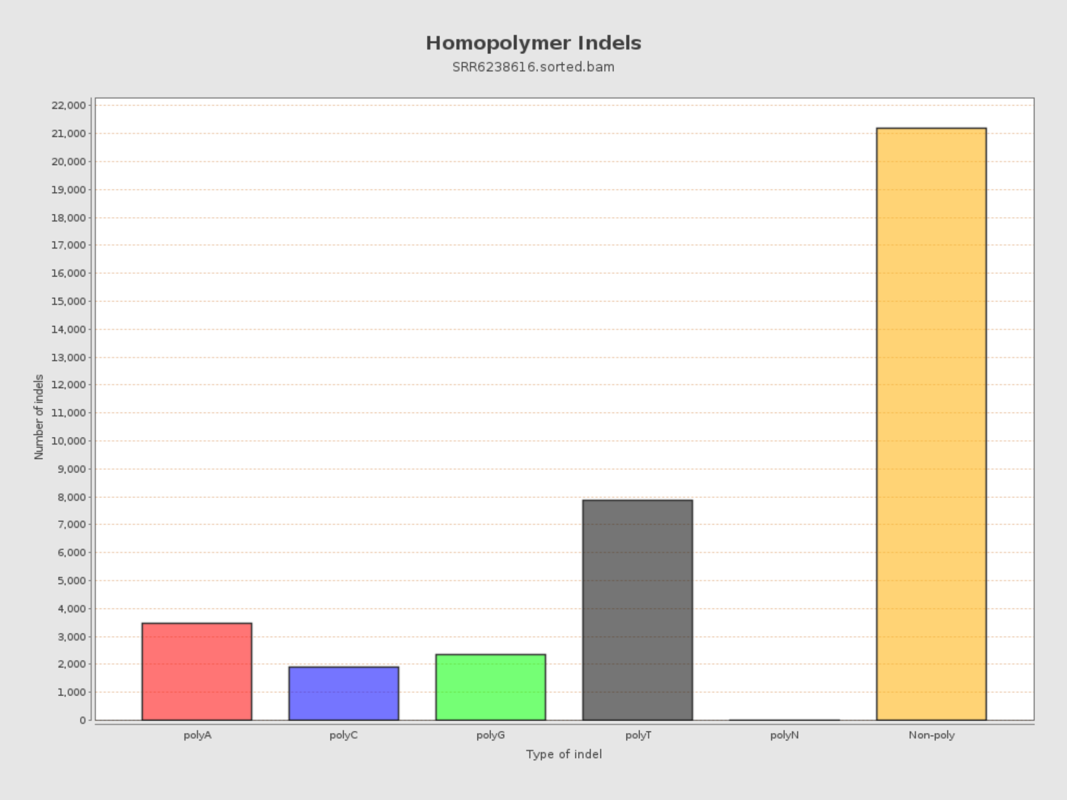
9. Results : Mapped Reads GC-content Distribution



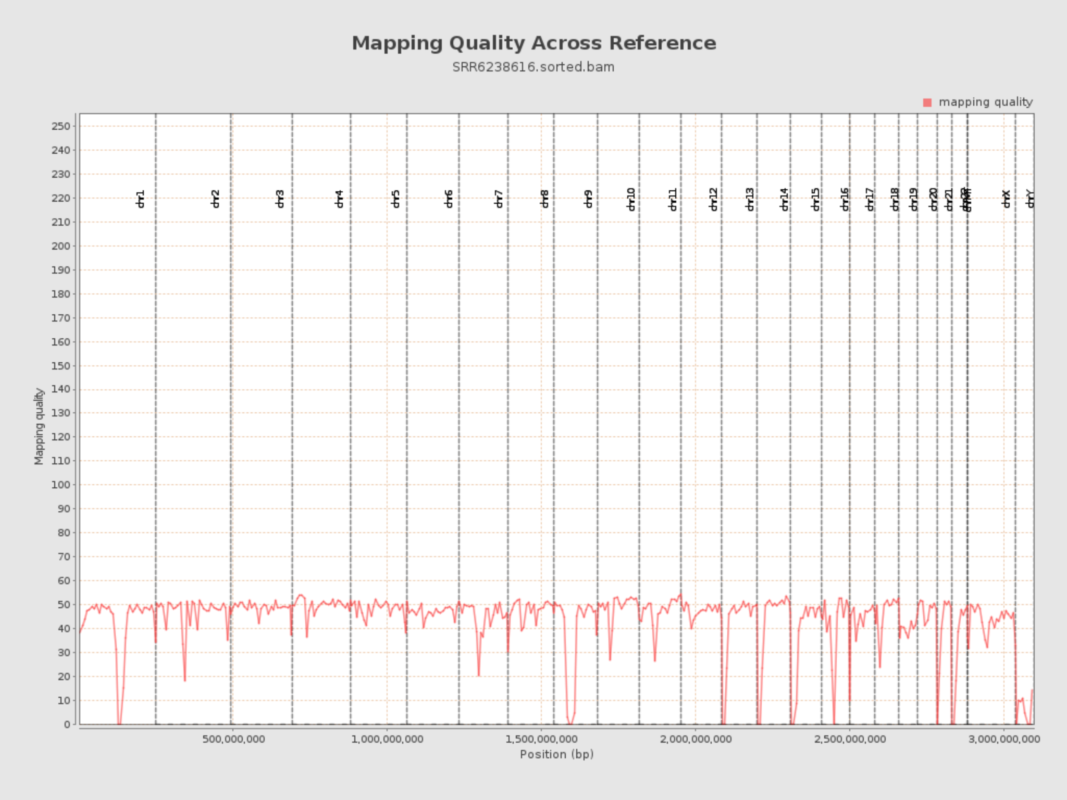
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram