Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 20:15:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238531.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_SRR6238531 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238531.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 20:15:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238531.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,101,226
Mapped reads	1,779,268 / 84.68%
Unmapped reads	321,958 / 15.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,628 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	494,365 / 23.53%
Duplication rate	19.74%
Clipped reads	1,215,286 / 57.84%

2.2. ACGT Content

Number/percentage of A's	27,057,823 / 25.23%
Number/percentage of C's	18,887,318 / 17.61%
Number/percentage of T's	35,855,855 / 33.43%
Number/percentage of G's	25,437,413 / 23.72%
Number/percentage of N's	6,949 / 0.01%
GC Percentage	41.33%

2.3. Coverage

Mean	0.0347

Standard Deviation	0.5979

2.4. Mapping Quality

Mean Mapping Quality	38.49

2.5. Mismatches and indels

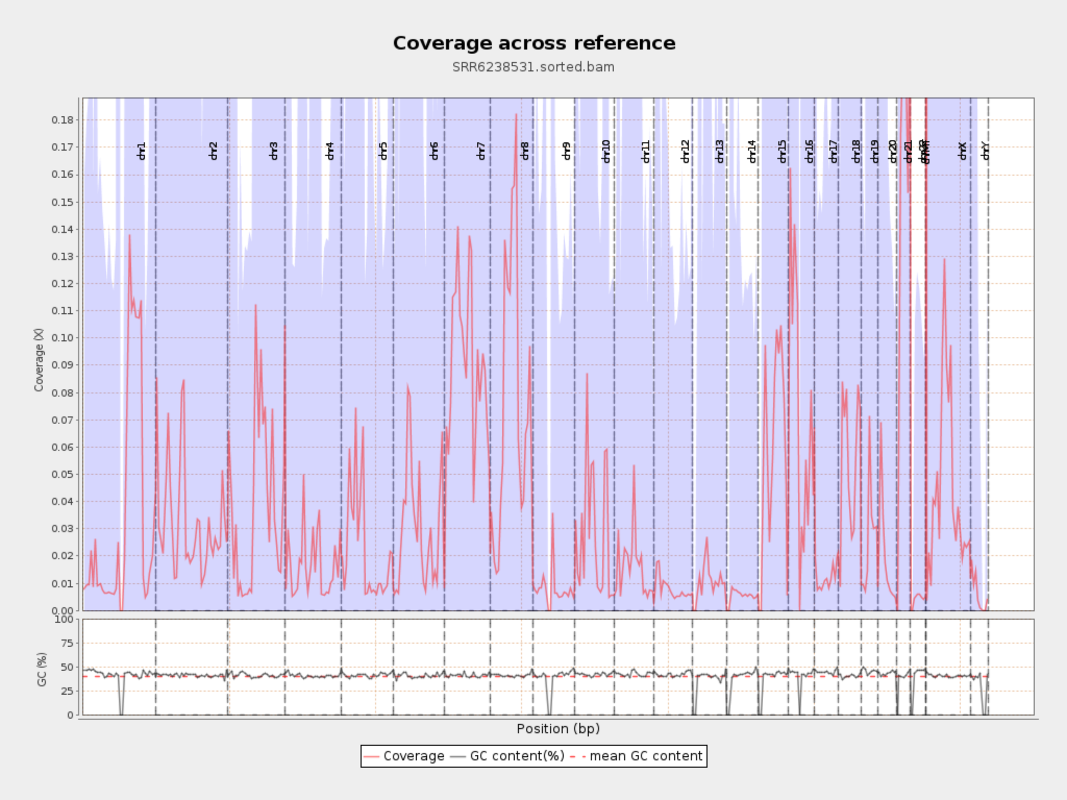
General error rate	0.66%
Mismatches	701,336
Insertions	6,371
Mapped reads with at least one insertion	0.35%
Deletions	32,165
Mapped reads with at least one deletion	1.79%
Homopolymer indels	40.77%

2.6. Chromosome stats

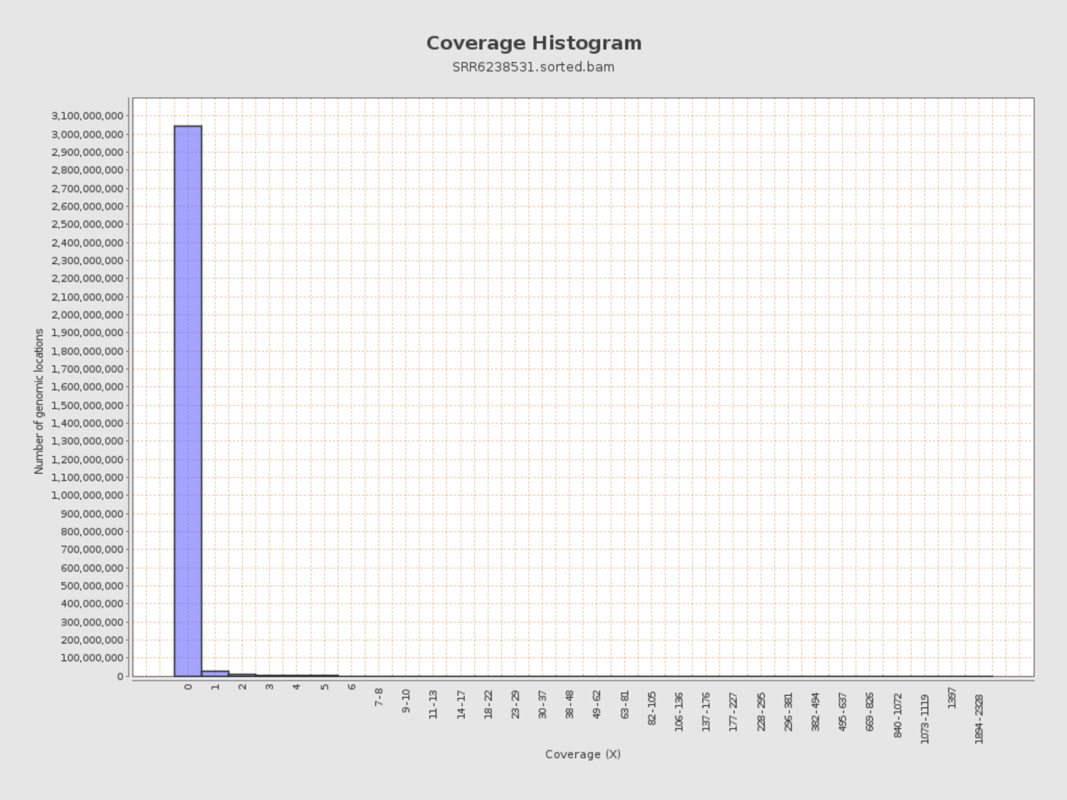
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8337672	0.0335	0.4978
chr2	243199373	8085922	0.0332	1.1065
chr3	198022430	7541059	0.0381	0.3715
chr4	191154276	3267714	0.0171	0.2323
chr5	180915260	3965944	0.0219	0.2778
chr6	171115067	5300980	0.031	0.4716
chr7	159138663	14085628	0.0885	0.8786

chr8	146364022	11224356	0.0767	0.6339
chr9	141213431	1126831	0.008	0.2641
chr10	135534747	3876046	0.0286	0.4036
chr11	135006516	2165439	0.016	0.2601
chr12	133851895	1064159	0.008	0.1727
chr13	115169878	1204260	0.0105	0.3175
chr14	107349540	577653	0.0054	0.2847
chr15	102531392	6191935	0.0604	0.4932
chr16	90354753	6254798	0.0692	0.5489
chr17	81195210	961068	0.0118	0.1859
chr18	78077248	4213427	0.054	1.8132
chr19	59128983	1578520	0.0267	0.5115
chr20	63025520	1307481	0.0207	0.4366
chr21	48129895	7366630	0.1531	0.7527
chr22	51304566	208567	0.0041	0.093
chrMT	16571	25911	1.5636	2.1657
chrX	155270560	7016194	0.0452	0.4992
chrY	59373566	351543	0.0059	0.201

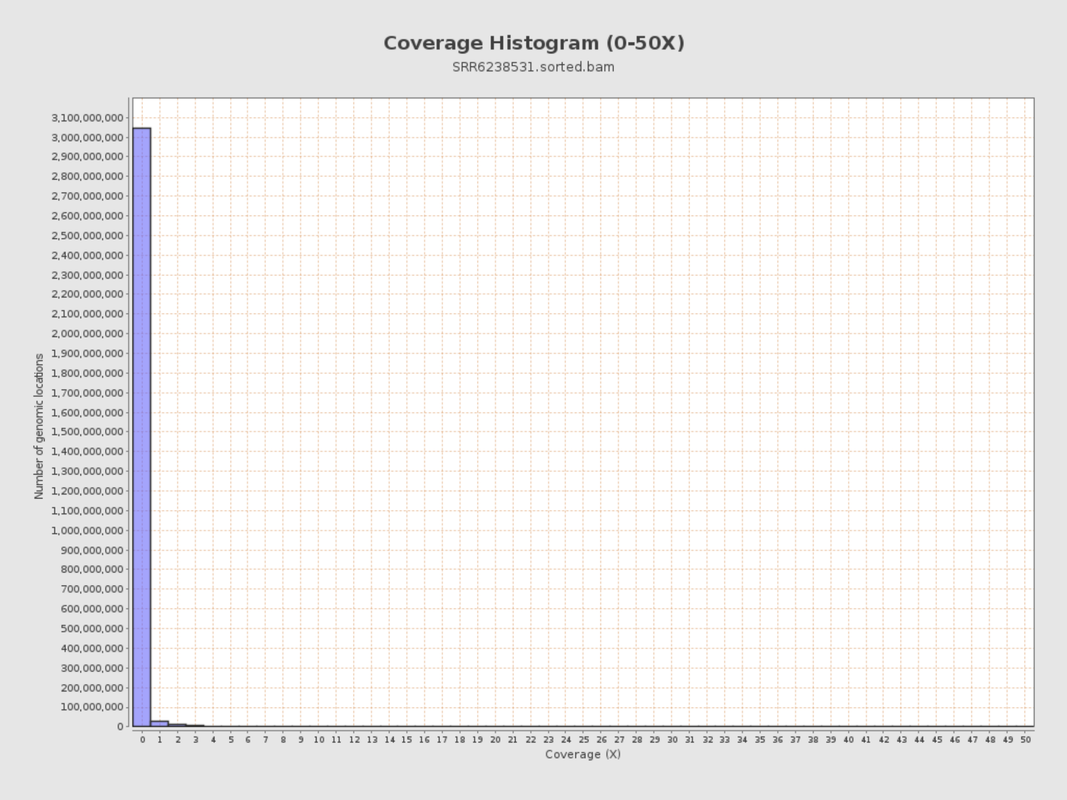
3. Results : Coverage across reference



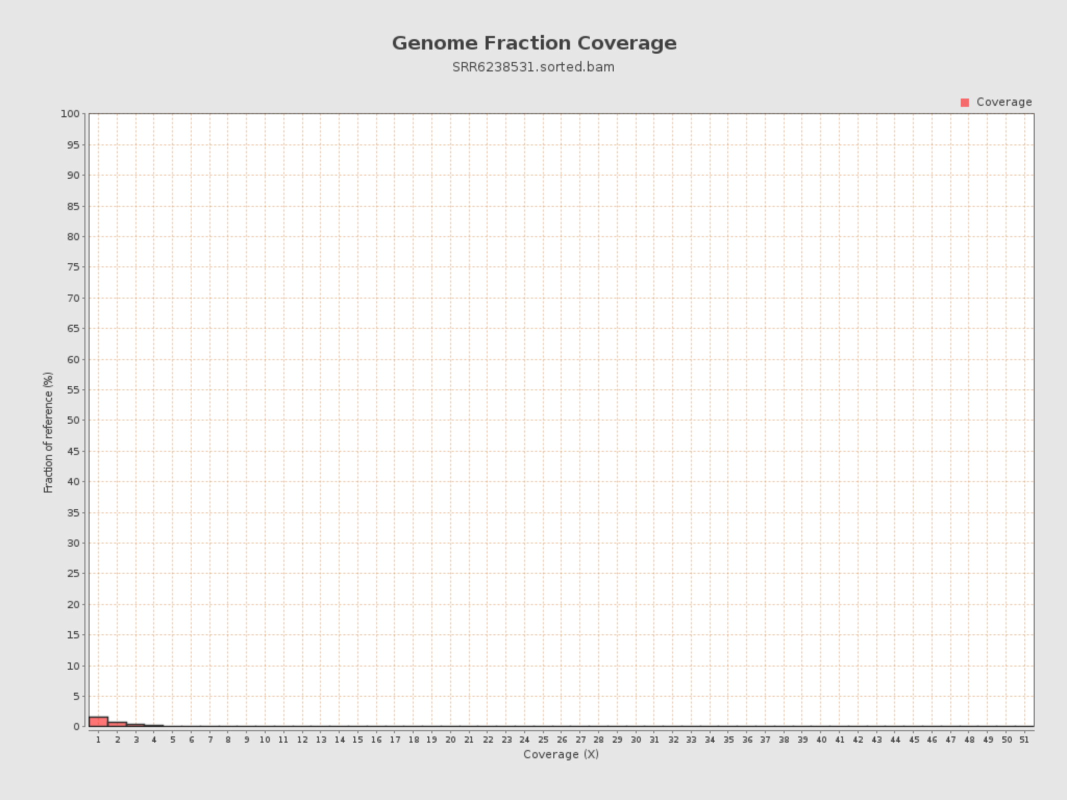
4. Results : Coverage Histogram



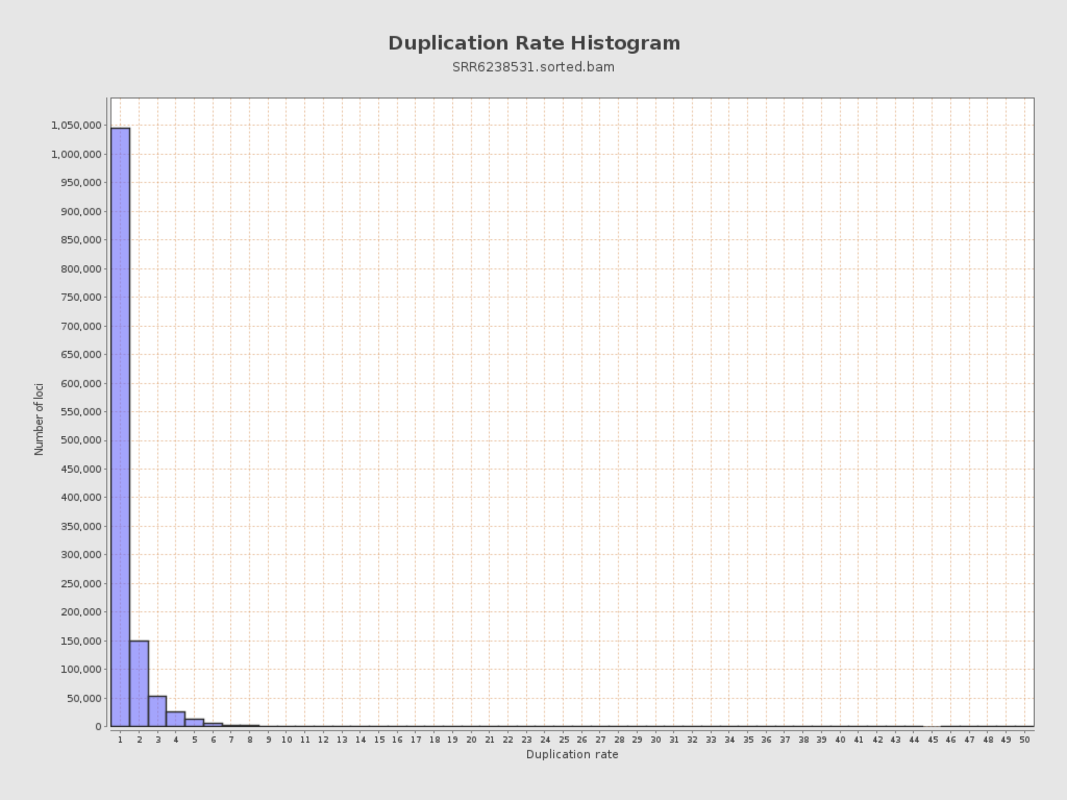
5. Results : Coverage Histogram (0-50X)



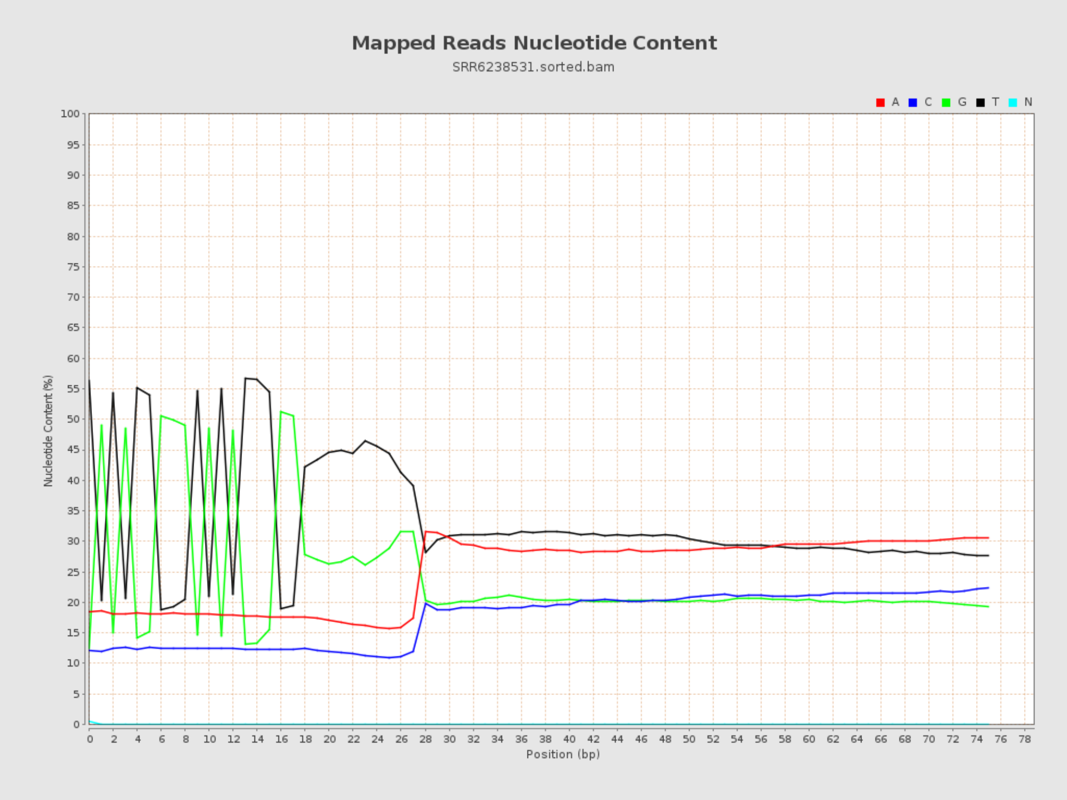
6. Results : Genome Fraction Coverage



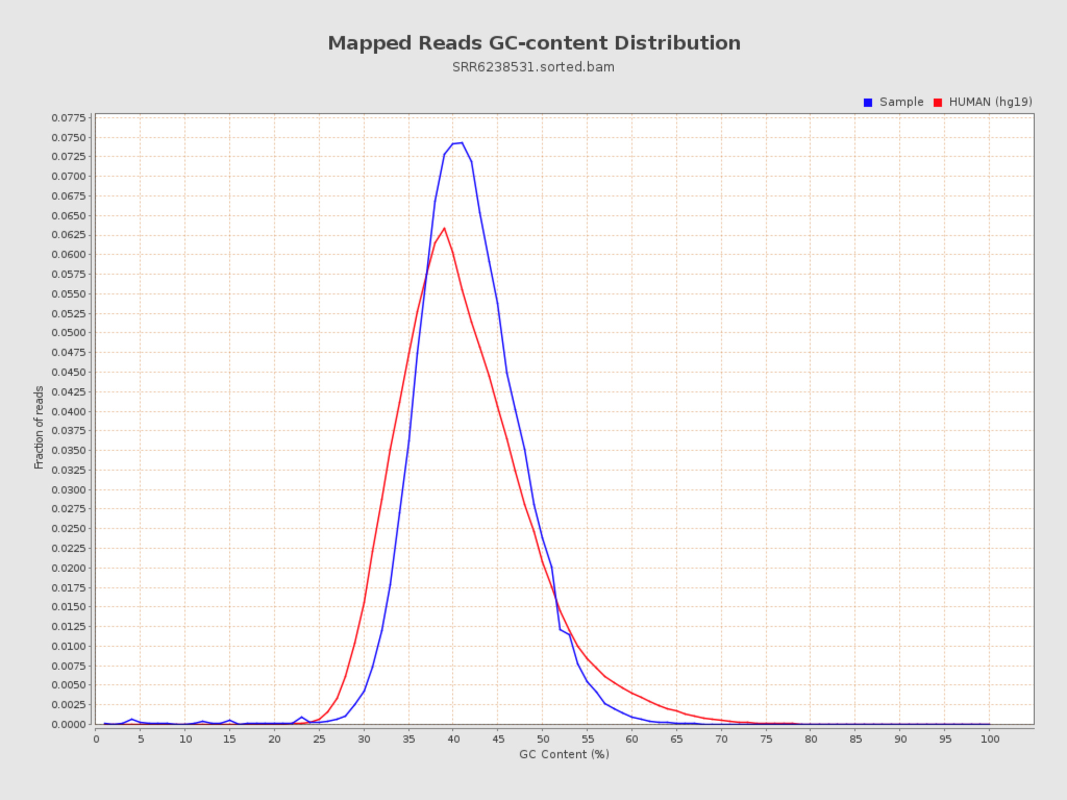
7. Results : Duplication Rate Histogram



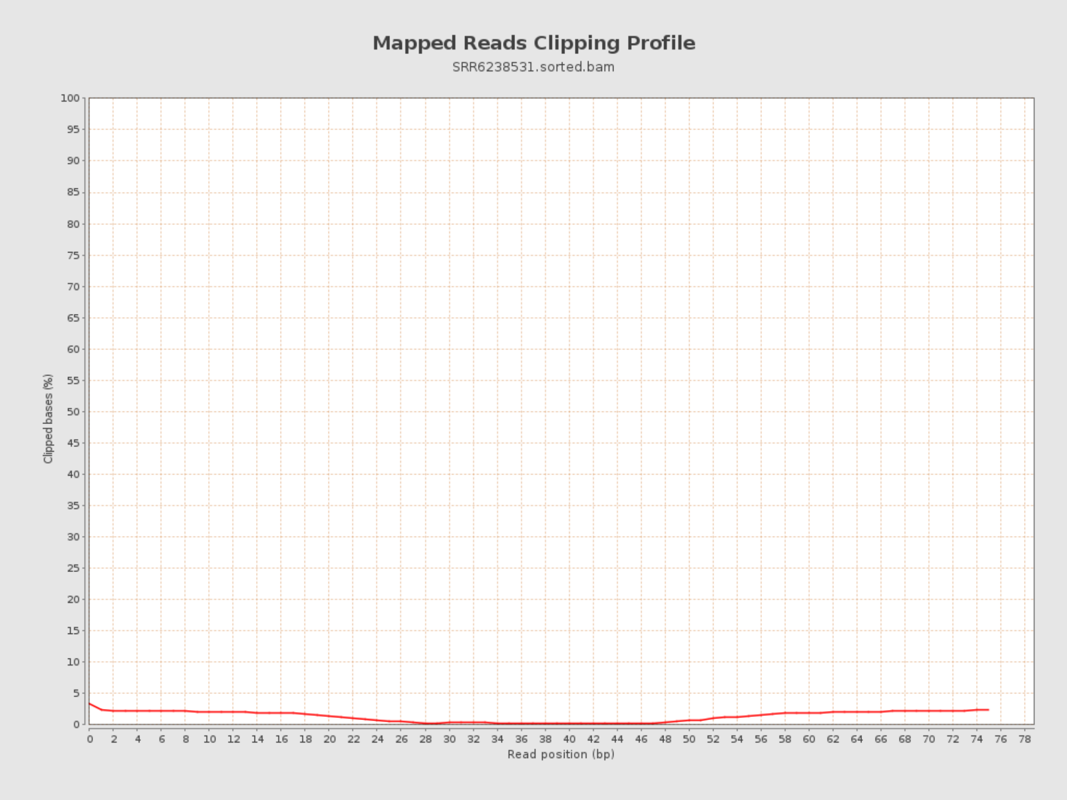
8. Results : Mapped Reads Nucleotide Content



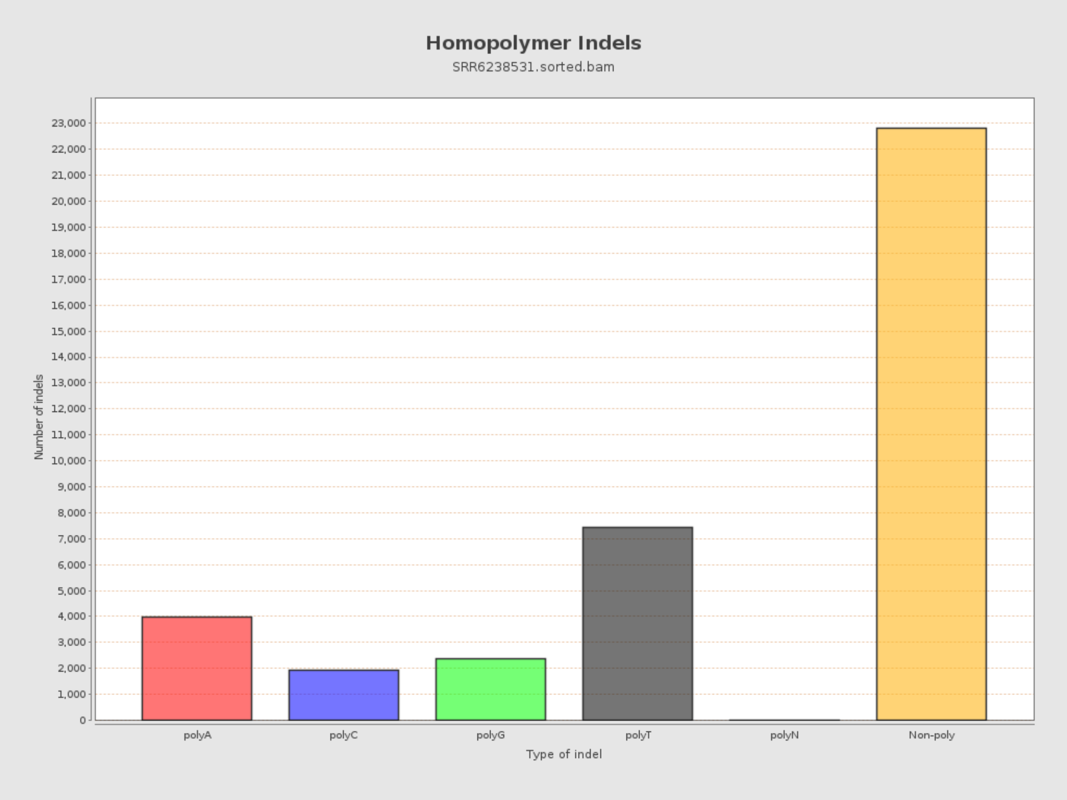
9. Results : Mapped Reads GC-content Distribution



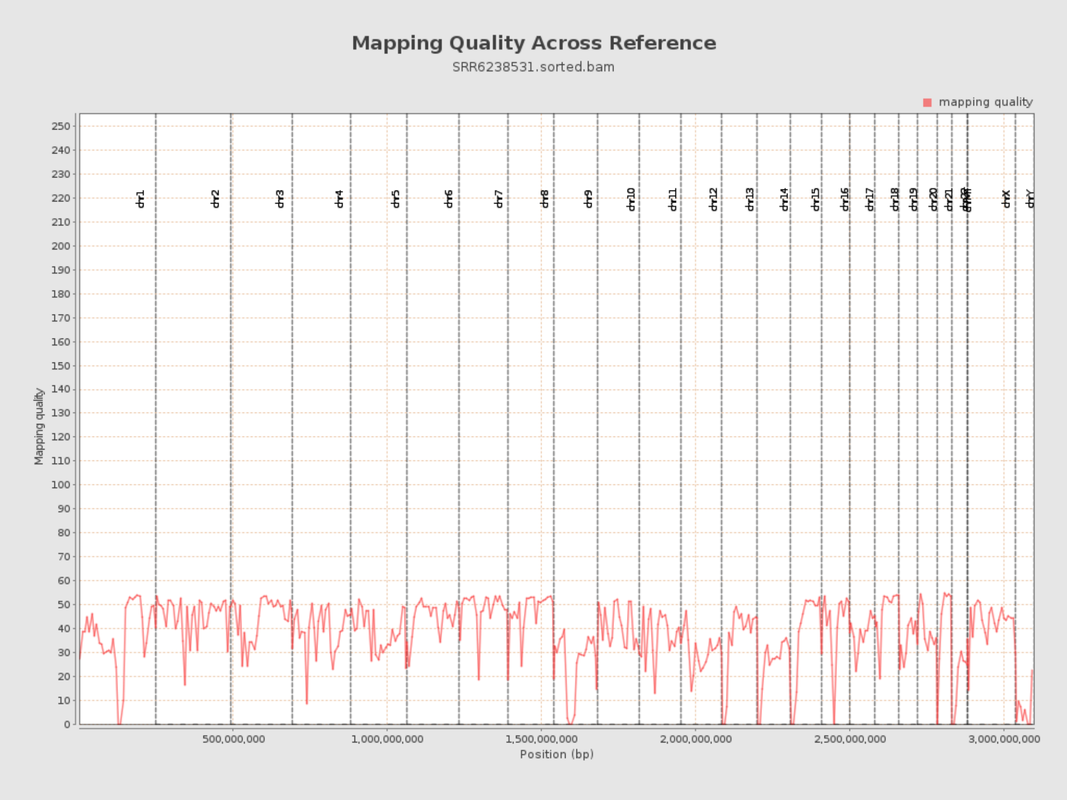
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram