Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:14:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238628.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_SRR6238628 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238628.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:14:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238628.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,279,071
Mapped reads	1,365,065 / 59.9%
Unmapped reads	914,006 / 40.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,720 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	614,379 / 26.96%
Duplication rate	24.9%
Clipped reads	977,259 / 42.88%

2.2. ACGT Content

Number/percentage of A's	19,445,785 / 23.94%
Number/percentage of C's	13,545,698 / 16.68%
Number/percentage of T's	28,388,877 / 34.95%
Number/percentage of G's	19,842,665 / 24.43%
Number/percentage of N's	1,707 / 0%
GC Percentage	41.11%

2.3. Coverage

Mean	0.0263

Standard Deviation	0.62

2.4. Mapping Quality

Mean Mapping Quality	40.52

2.5. Mismatches and indels

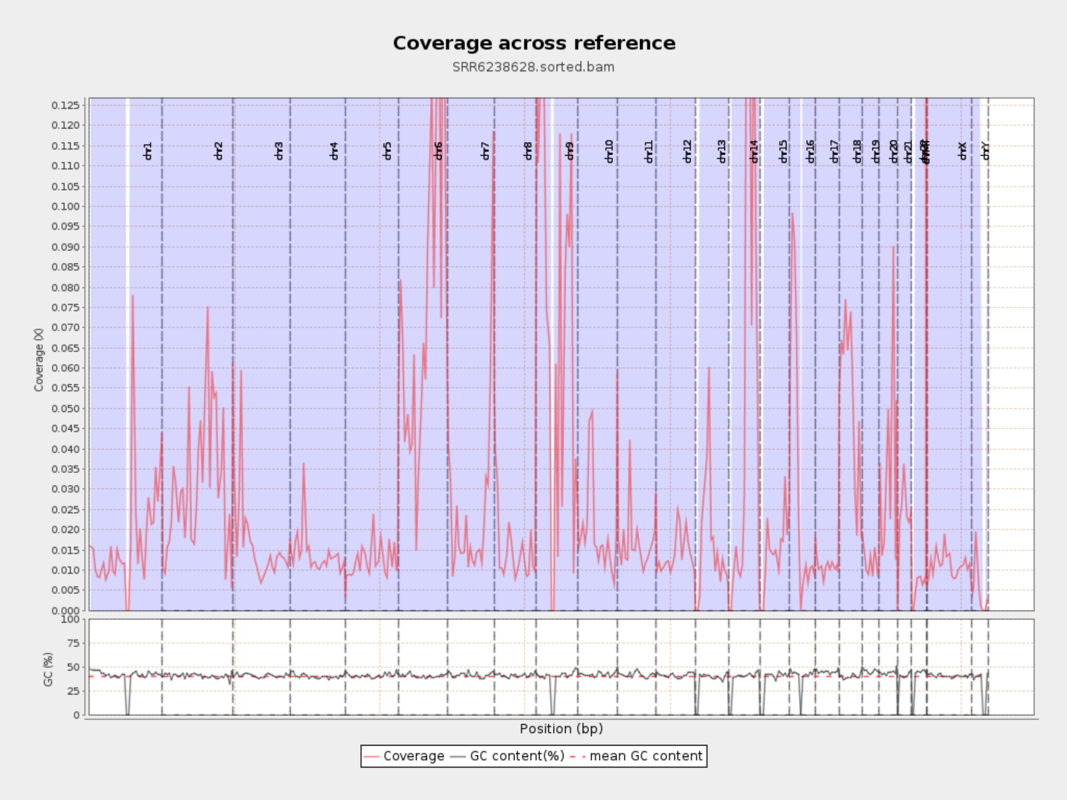
General error rate	0.65%
Mismatches	516,082
Insertions	6,223
Mapped reads with at least one insertion	0.45%
Deletions	23,017
Mapped reads with at least one deletion	1.67%
Homopolymer indels	39.34%

2.6. Chromosome stats

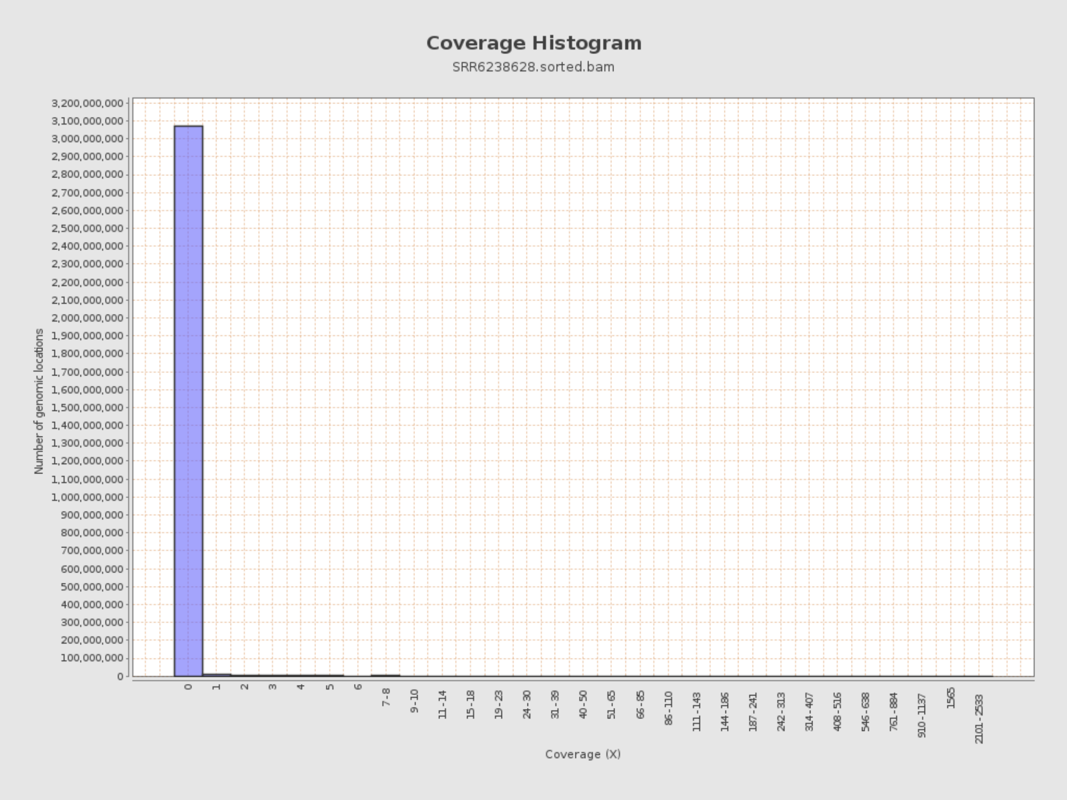
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4255279	0.0171	0.3534
chr2	243199373	7617786	0.0313	1.2431
chr3	198022430	3377213	0.0171	0.3517
chr4	191154276	2666931	0.014	0.328
chr5	180915260	2272539	0.0126	0.2989
chr6	171115067	13594402	0.0794	0.883
chr7	159138663	4001166	0.0251	0.487

chr8	146364022	2208608	0.0151	0.3906
chr9	141213431	10359525	0.0734	0.8325
chr10	135534747	2574332	0.019	0.4412
chr11	135006516	2363393	0.0175	0.3735
chr12	133851895	1894277	0.0142	0.4003
chr13	115169878	1955164	0.017	0.4415
chr14	107349540	5967246	0.0556	0.7057
chr15	102531392	1520558	0.0148	0.3868
chr16	90354753	2918742	0.0323	0.5422
chr17	81195210	882228	0.0109	0.2764
chr18	78077248	4119260	0.0528	1.4803
chr19	59128983	695837	0.0118	0.3371
chr20	63025520	2212414	0.0351	0.5403
chr21	48129895	1122929	0.0233	0.4585
chr22	51304566	286279	0.0056	0.1816
chrMT	16571	345874	20.8722	16.7161
chrX	155270560	1757639	0.0113	0.309
chrY	59373566	293887	0.0049	0.2541

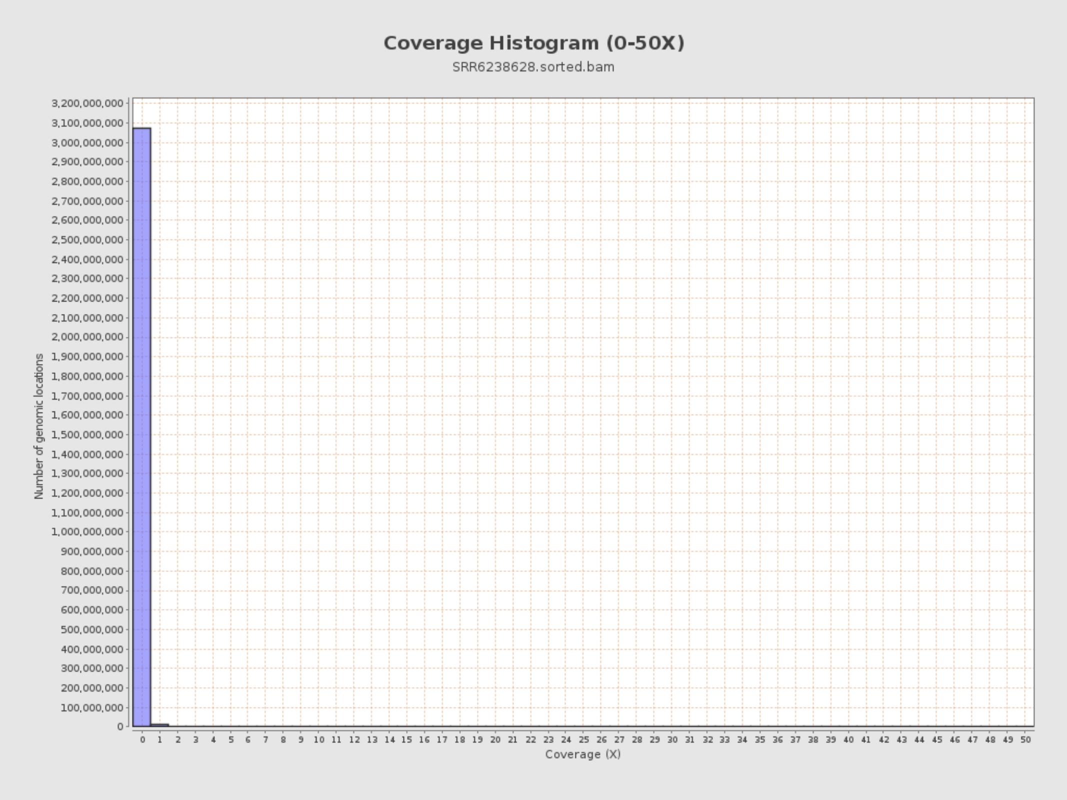
3. Results : Coverage across reference



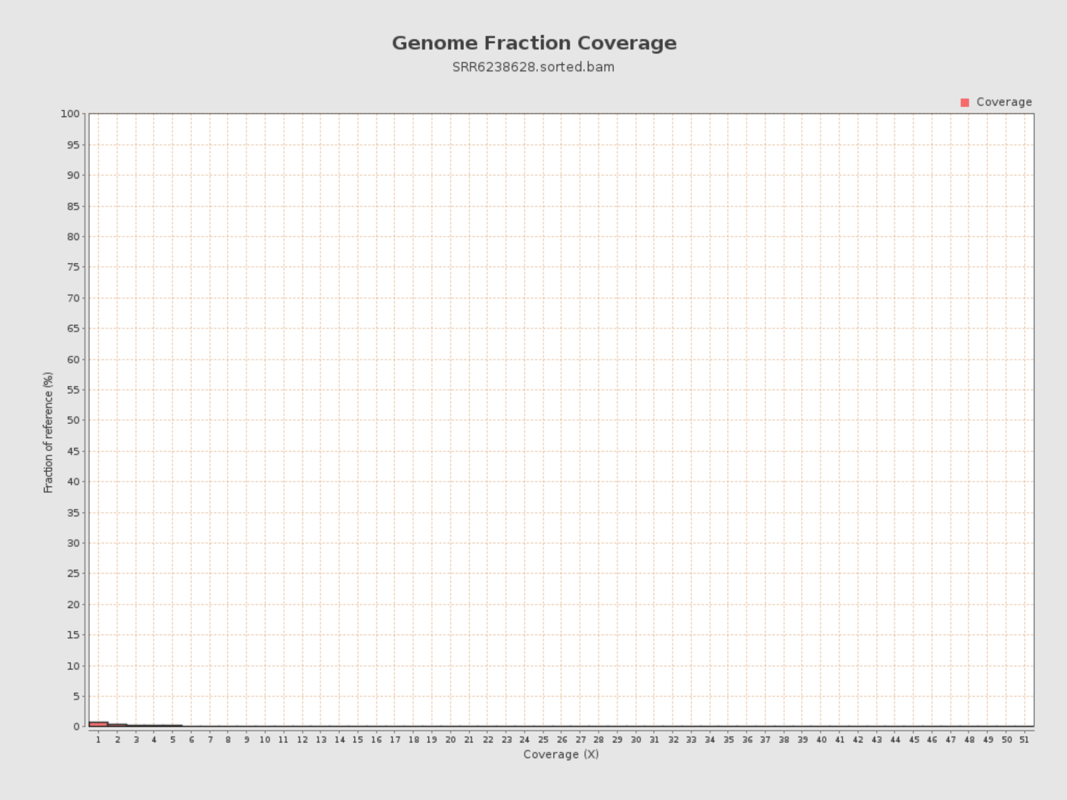
4. Results : Coverage Histogram



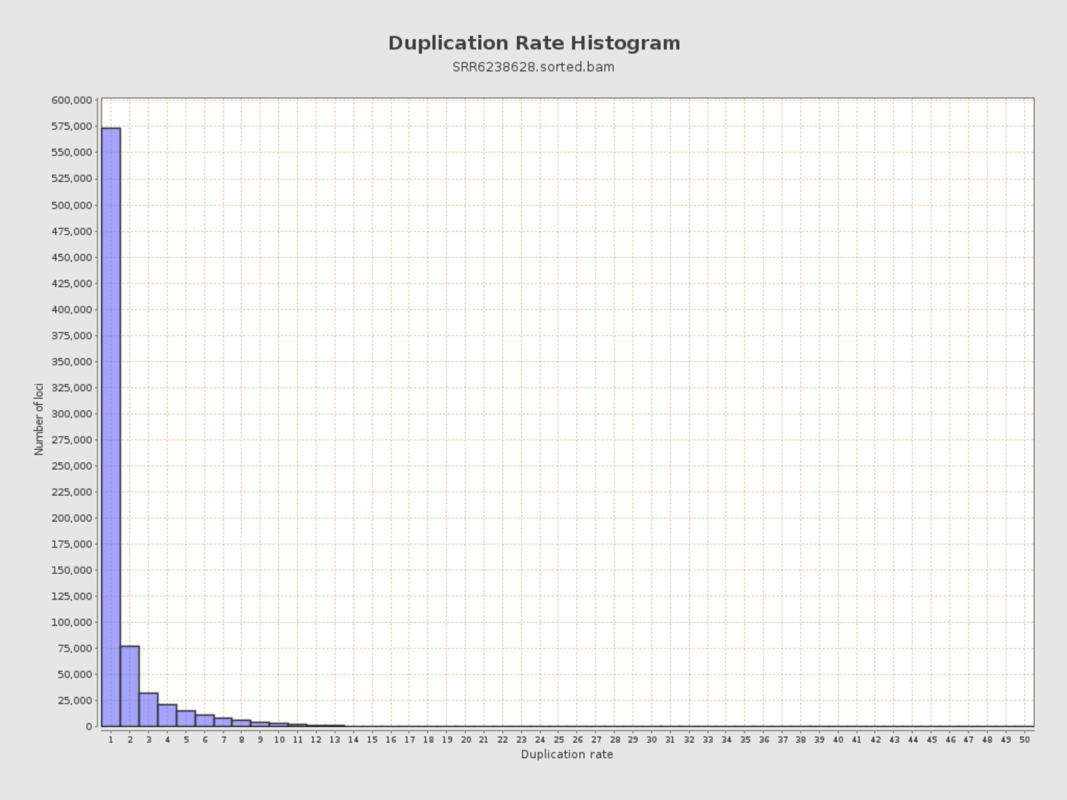
5. Results : Coverage Histogram (0-50X)



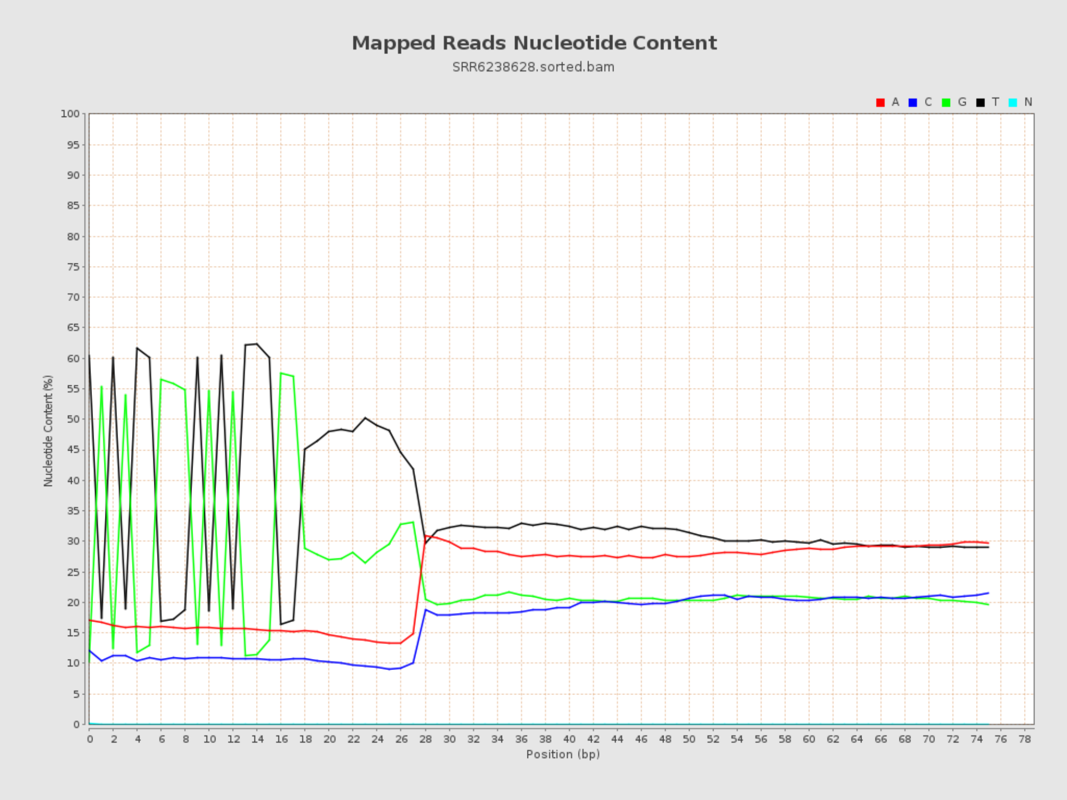
6. Results : Genome Fraction Coverage



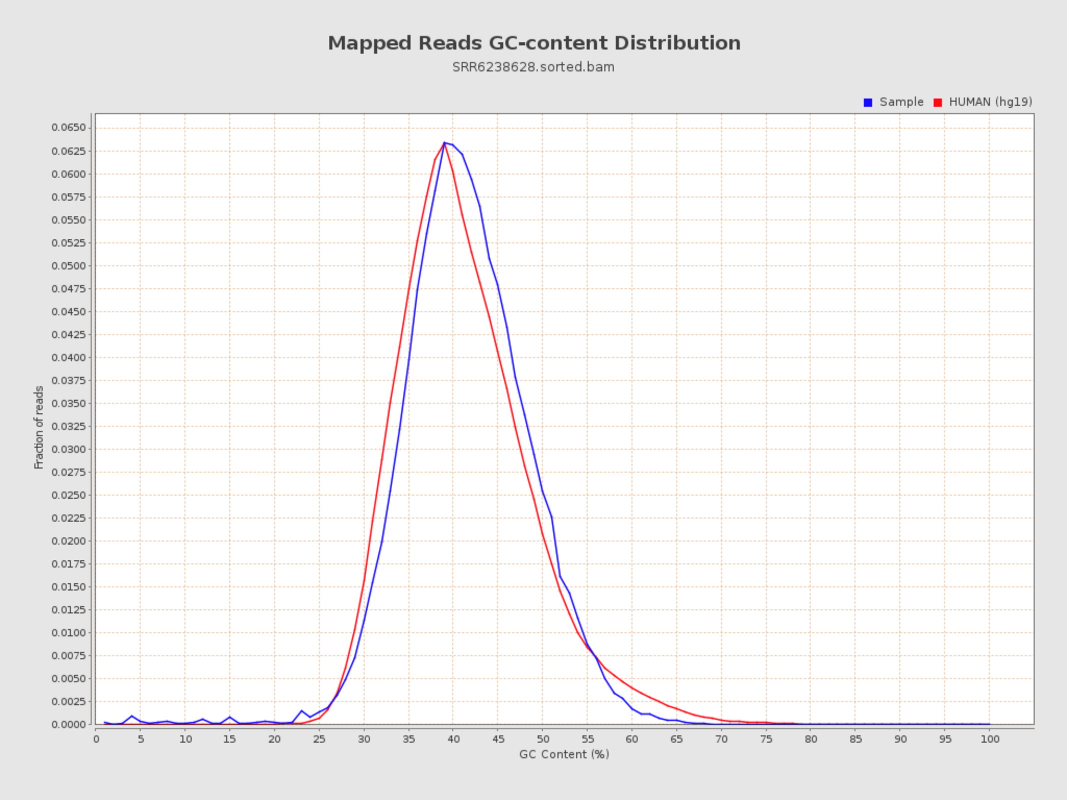
7. Results : Duplication Rate Histogram



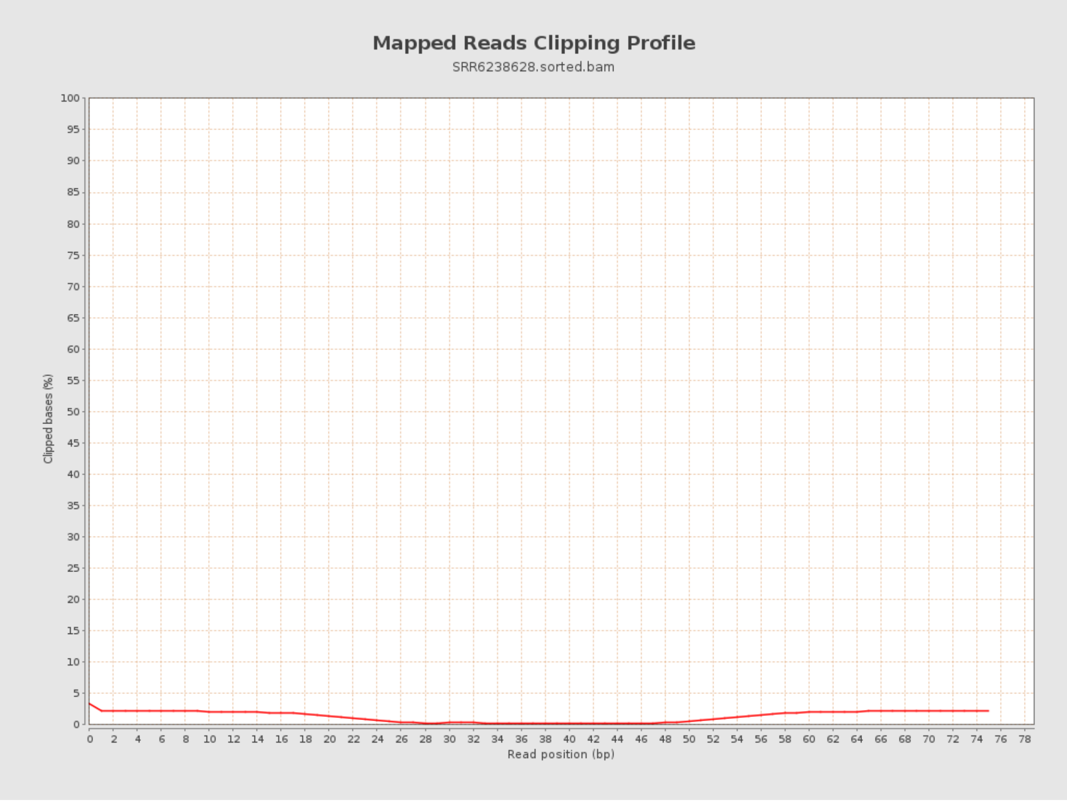
8. Results : Mapped Reads Nucleotide Content



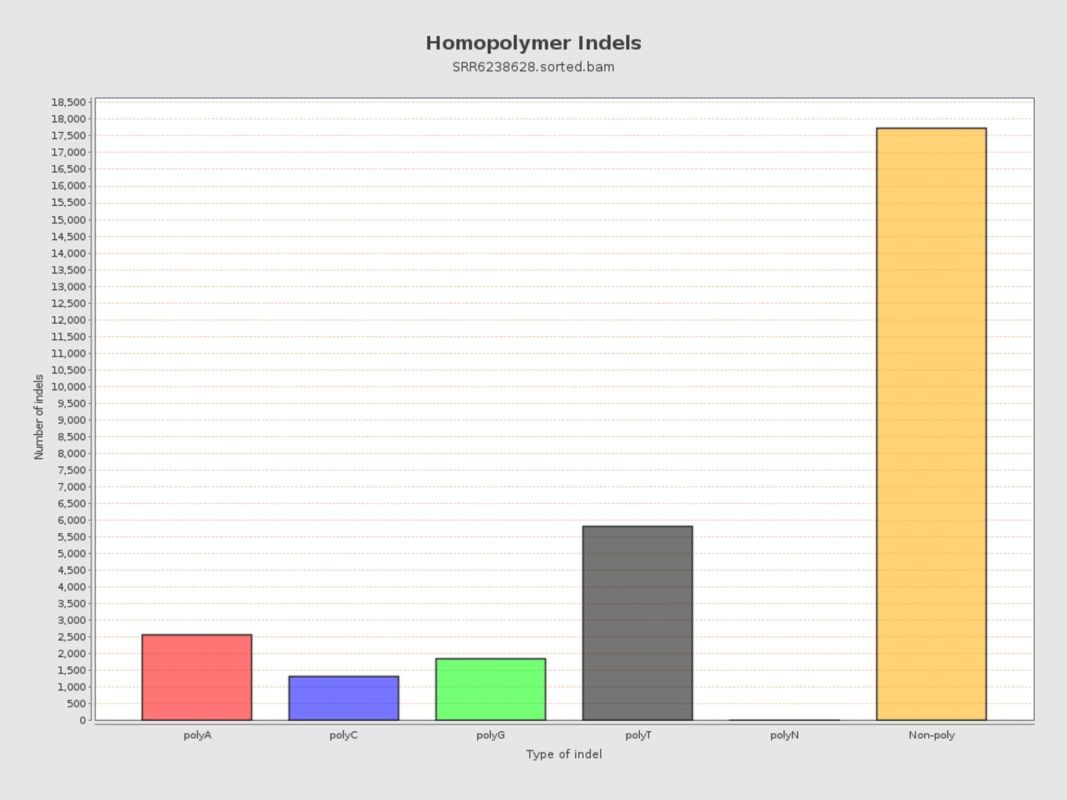
9. Results : Mapped Reads GC-content Distribution



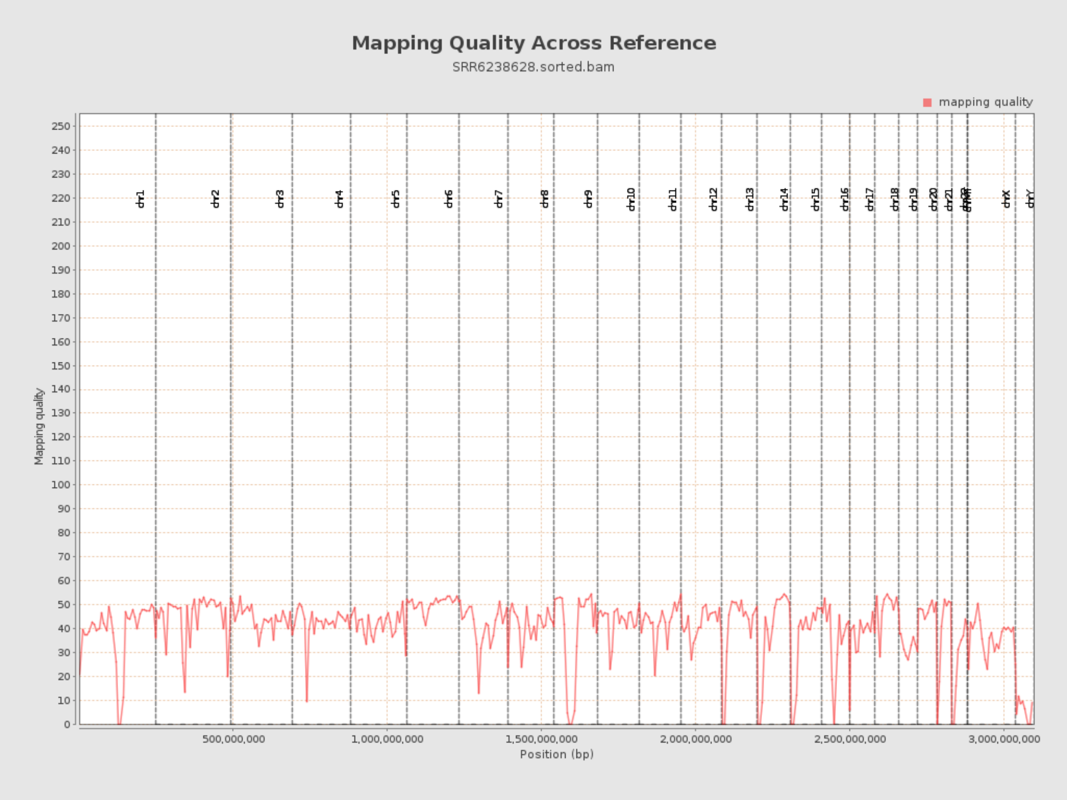
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram