Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2024/09/17 14:35:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238285.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_SRR6238285 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238285.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:35:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238285.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,322,638
Mapped reads	3,014,182 / 90.72%
Unmapped reads	308,456 / 9.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,036 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	111,584 / 3.36%
Duplication rate	2.13%
Clipped reads	1,494,387 / 44.98%

2.2. ACGT Content

Number/percentage of A's	55,190,004 / 27.84%
Number/percentage of C's	39,069,005 / 19.71%
Number/percentage of T's	58,332,013 / 29.43%
Number/percentage of G's	45,585,740 / 23%
Number/percentage of N's	54,608 / 0.03%
GC Percentage	42.71%

2.3. Coverage

Mean	0.0641

Standard Deviation	0.627

2.4. Mapping Quality

Mean Mapping Quality	42.27

2.5. Mismatches and indels

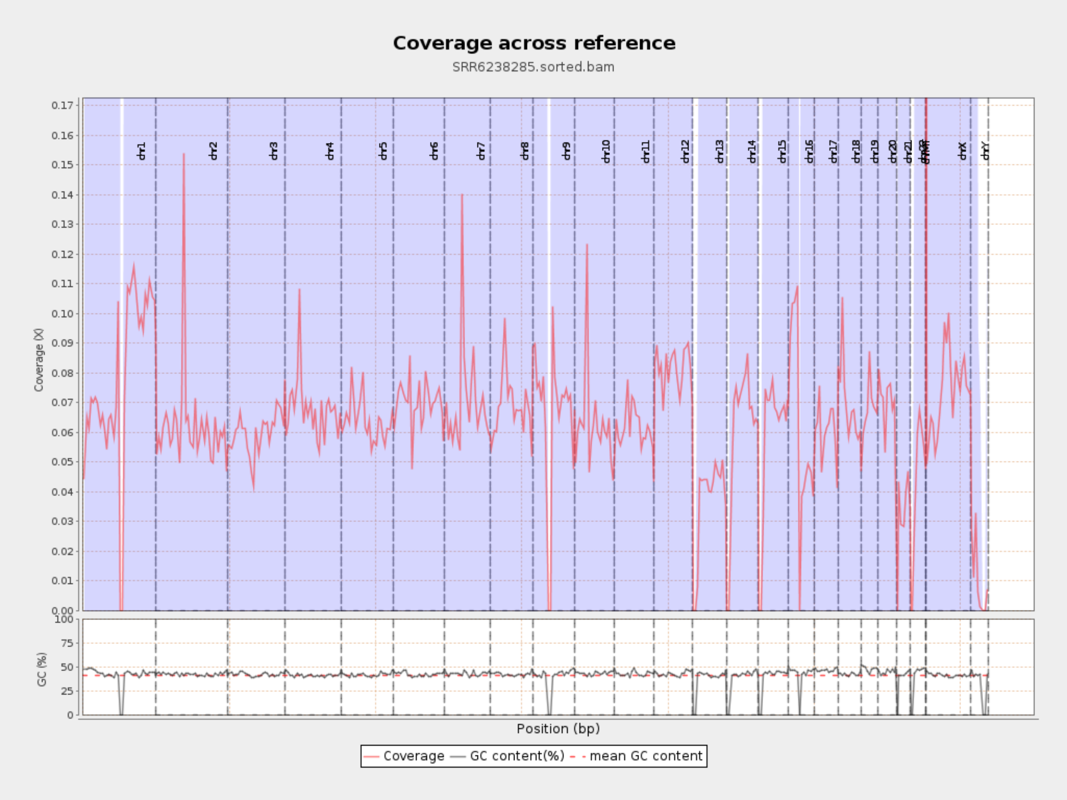
General error rate	0.89%
Mismatches	1,739,900
Insertions	17,707
Mapped reads with at least one insertion	0.58%
Deletions	55,486
Mapped reads with at least one deletion	1.82%
Homopolymer indels	44.59%

2.6. Chromosome stats

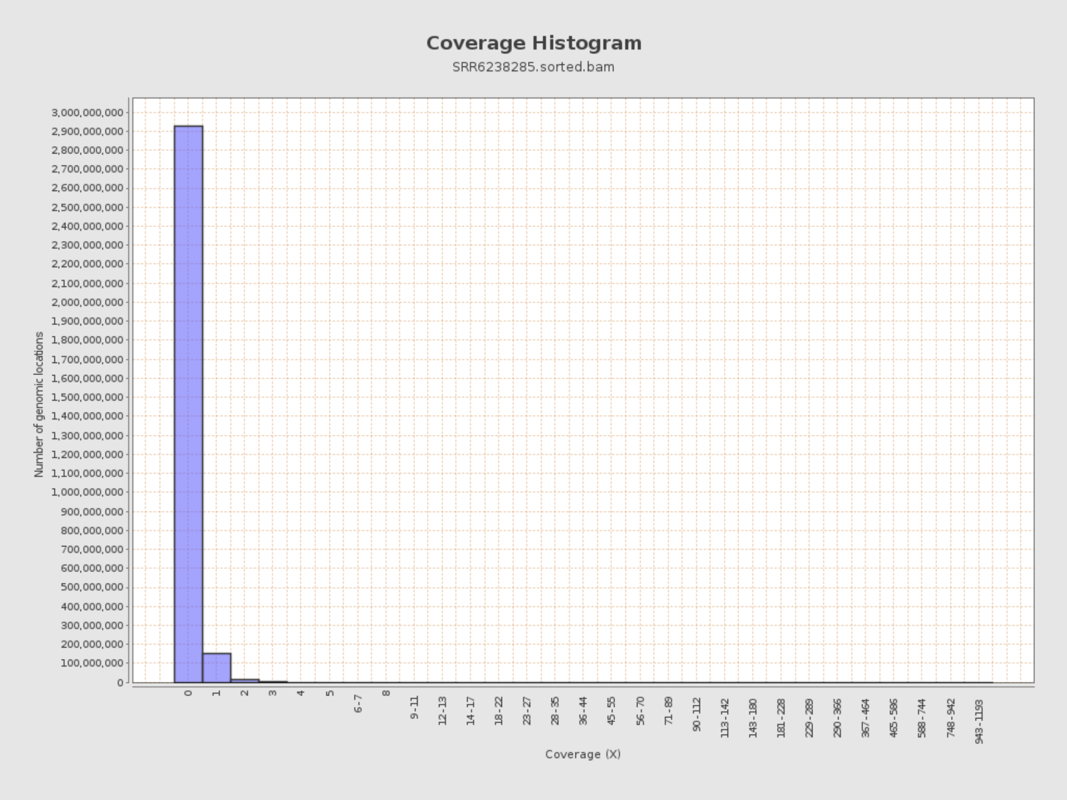
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19503133	0.0782	1.0155
chr2	243199373	15201596	0.0625	0.8578
chr3	198022430	11809542	0.0596	0.2763
chr4	191154276	13007247	0.068	0.371
chr5	180915260	11538075	0.0638	0.2932
chr6	171115067	11960202	0.0699	0.4037
chr7	159138663	11200008	0.0704	1.0024

chr8	146364022	10075500	0.0688	0.6451
chr9	141213431	9288375	0.0658	0.7473
chr10	135534747	8477604	0.0625	0.6374
chr11	135006516	8344886	0.0618	0.4931
chr12	133851895	10998226	0.0822	0.3494
chr13	115169878	4246297	0.0369	0.2154
chr14	107349540	6559844	0.0611	0.4823
chr15	102531392	5803981	0.0566	0.2874
chr16	90354753	5530135	0.0612	0.39
chr17	81195210	4978960	0.0613	0.3487
chr18	78077248	5499338	0.0704	1.3757
chr19	59128983	4031176	0.0682	0.7597
chr20	63025520	4363317	0.0692	0.3168
chr21	48129895	1623125	0.0337	0.3592
chr22	51304566	2198071	0.0428	0.2312
chrMT	16571	17197	1.0378	1.2291
chrX	155270560	11475596	0.0739	0.4184
chrY	59373566	592198	0.01	0.2901

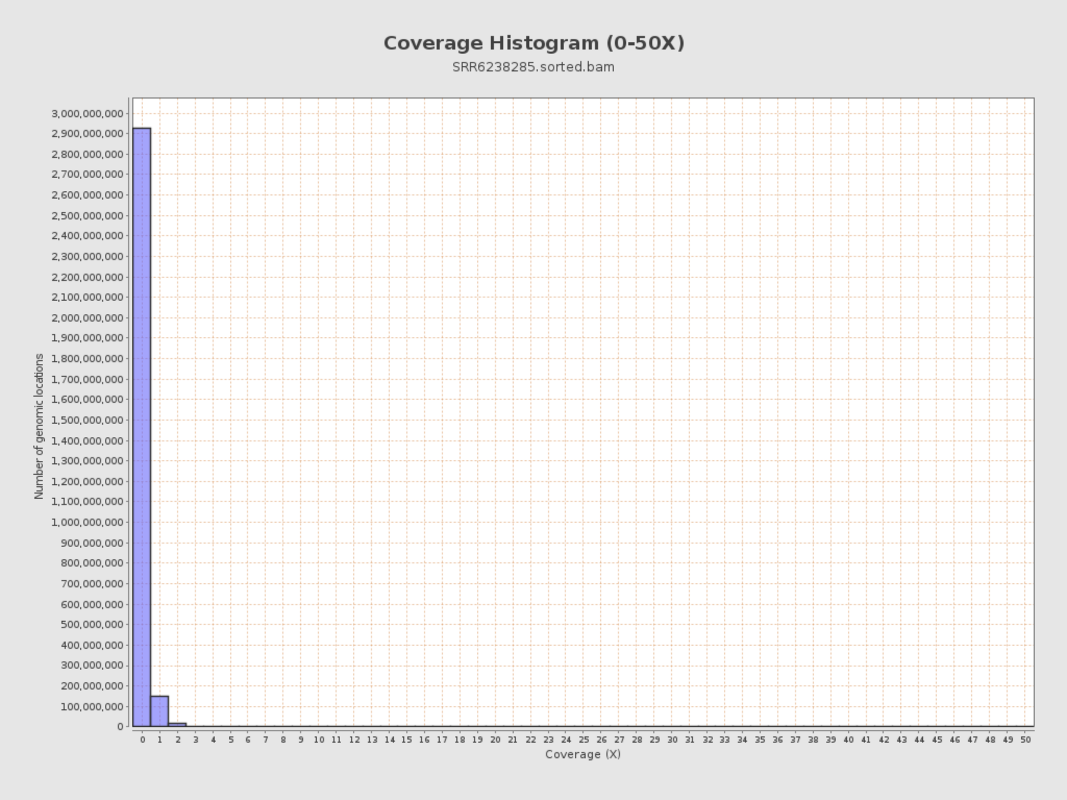
3. Results : Coverage across reference



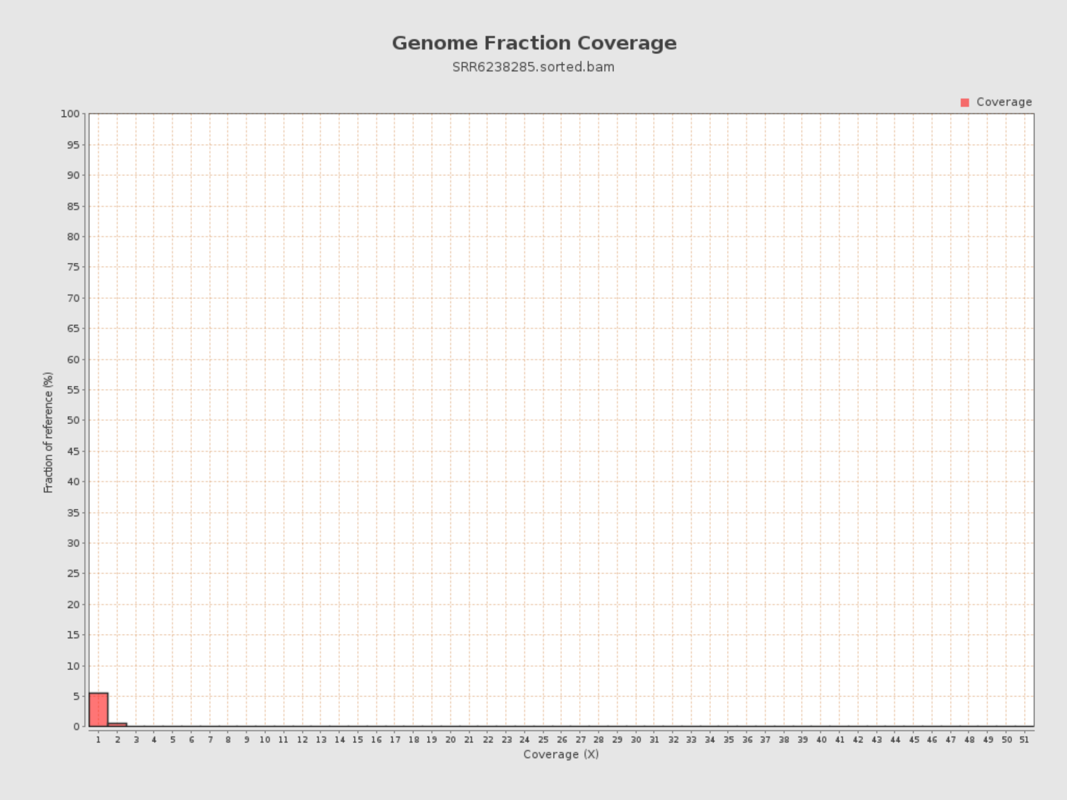
4. Results : Coverage Histogram



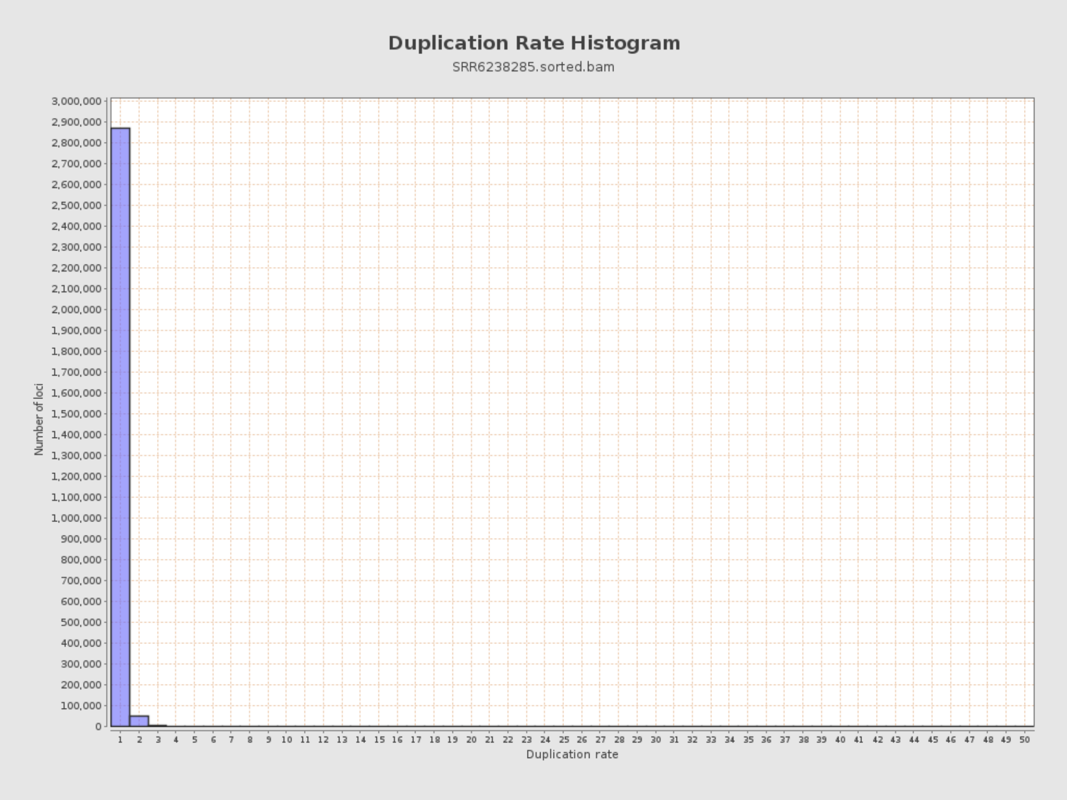
5. Results : Coverage Histogram (0-50X)



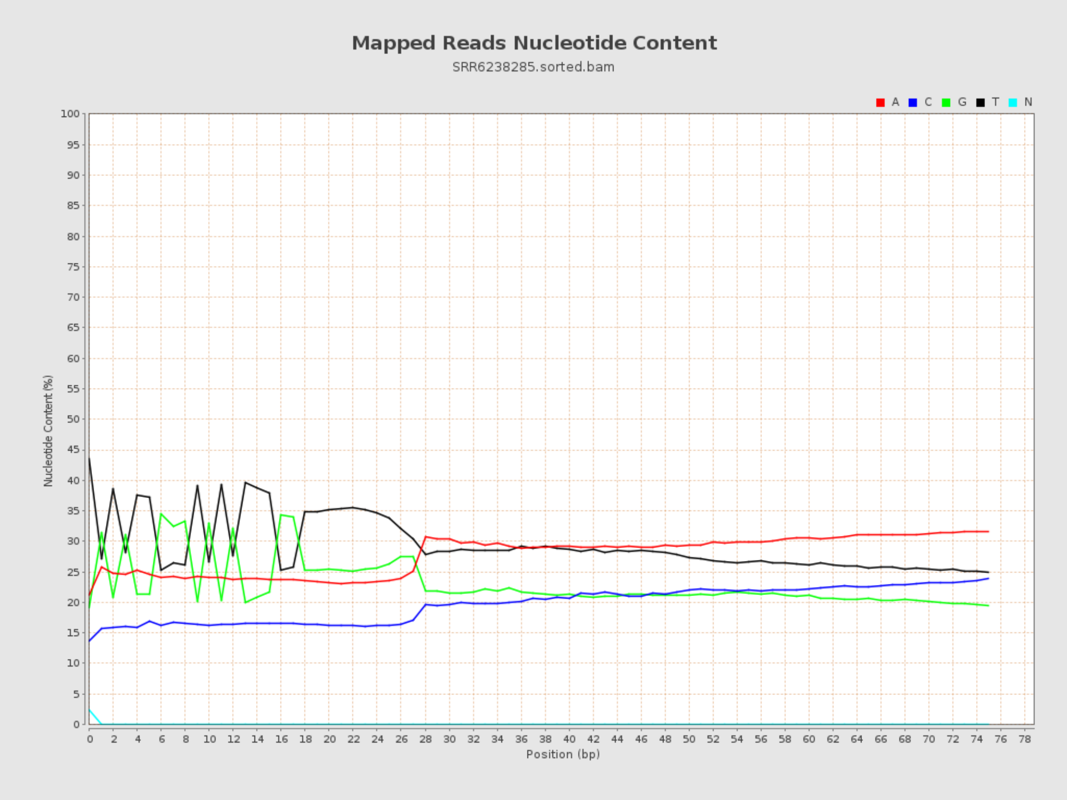
6. Results : Genome Fraction Coverage



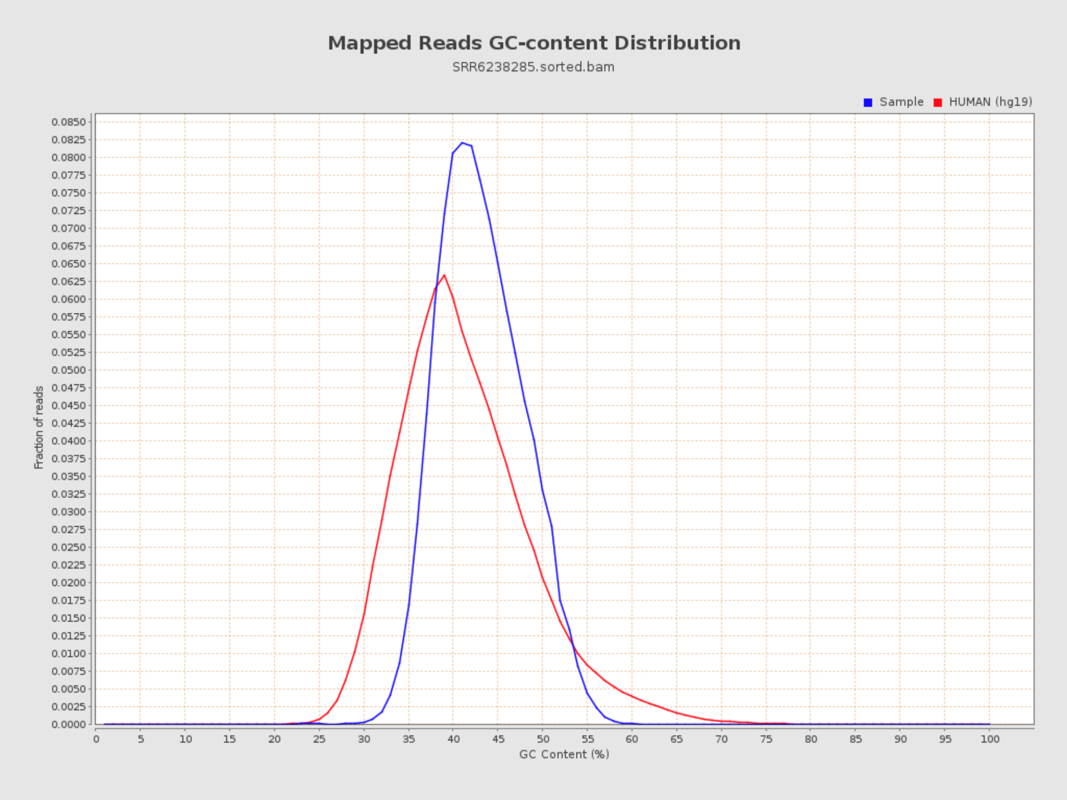
7. Results : Duplication Rate Histogram



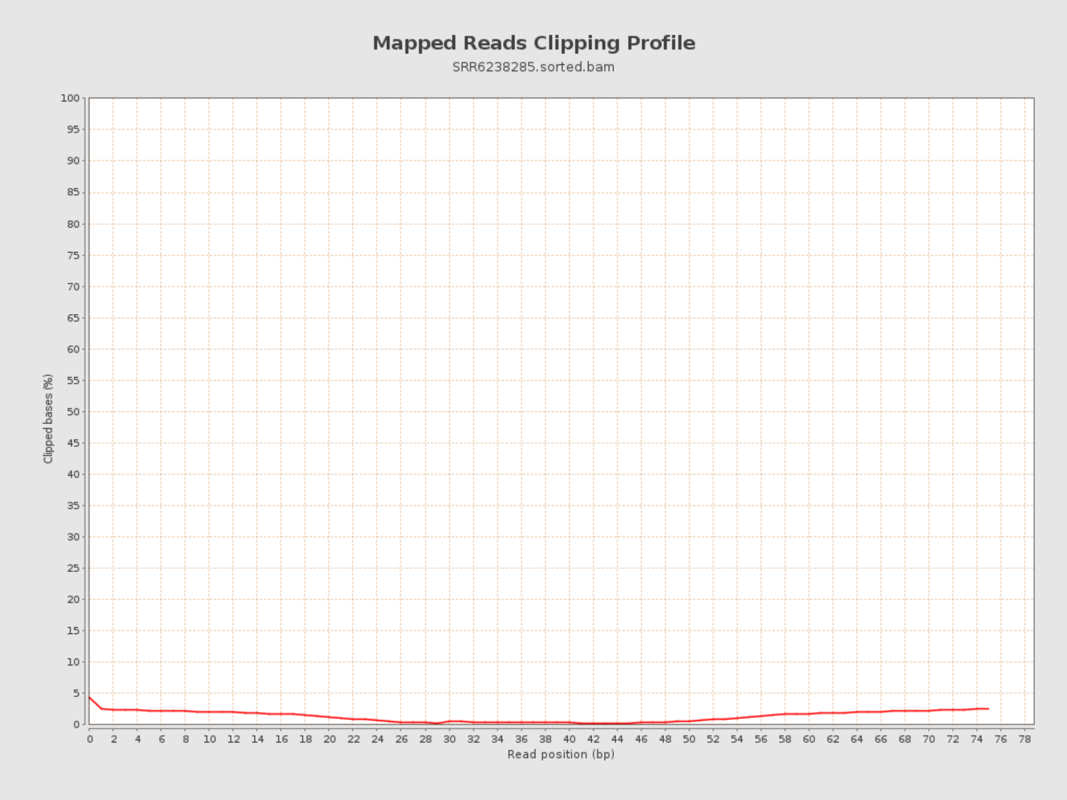
8. Results : Mapped Reads Nucleotide Content



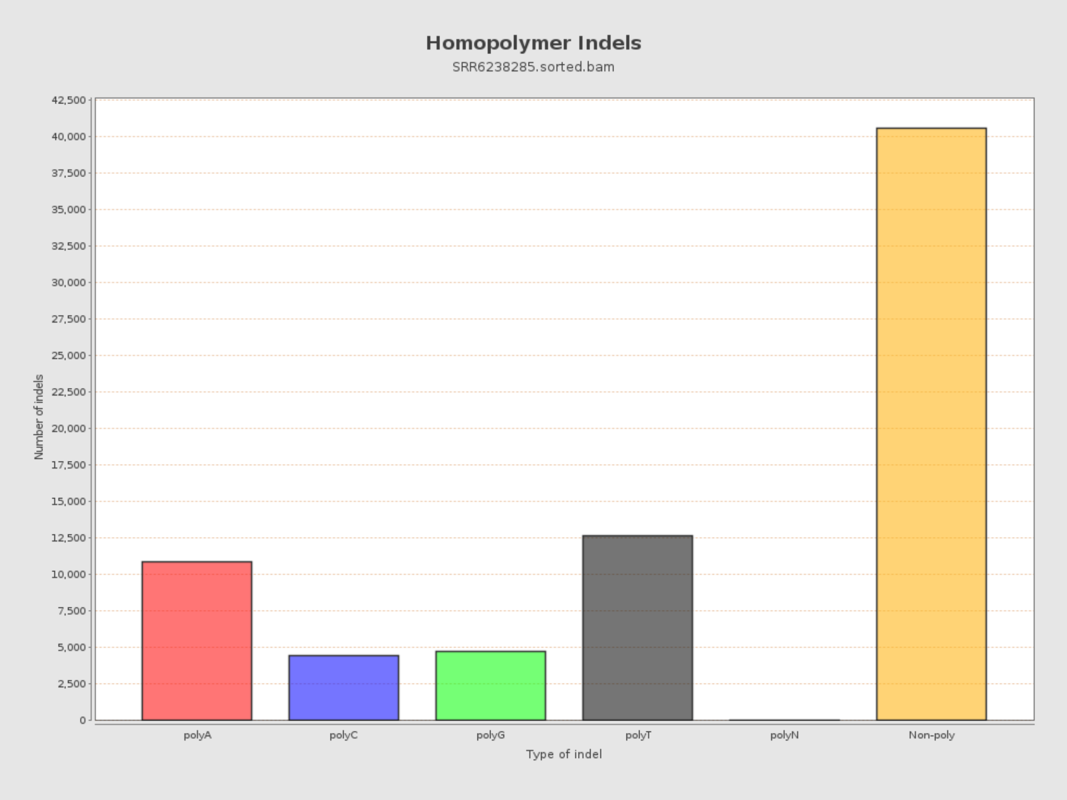
9. Results : Mapped Reads GC-content Distribution



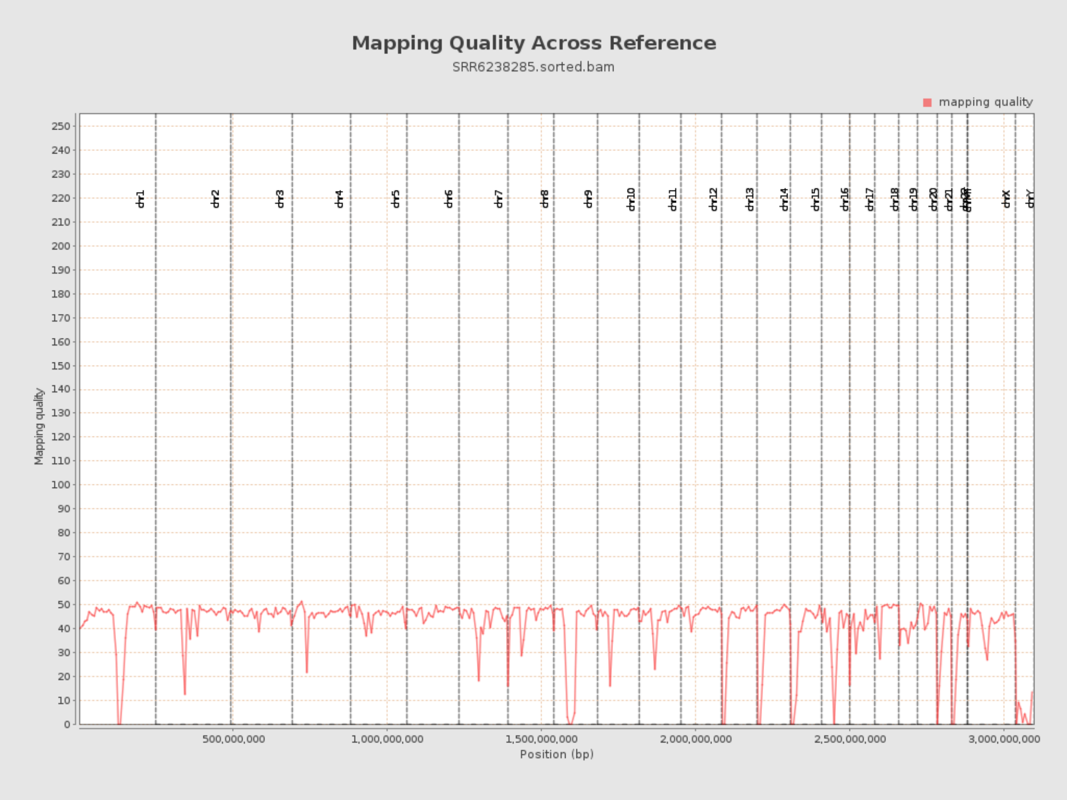
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram