Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:20:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238280.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_SRR6238280 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238280.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:20:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238280.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,753,036
Mapped reads	1,594,510 / 90.96%
Unmapped reads	158,526 / 9.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,834 / 1.07%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	82,019 / 4.68%
Duplication rate	3.78%
Clipped reads	707,826 / 40.38%

2.2. ACGT Content

Number/percentage of A's	29,484,084 / 27.81%
Number/percentage of C's	19,090,058 / 18.01%
Number/percentage of T's	34,139,948 / 32.21%
Number/percentage of G's	23,221,274 / 21.91%
Number/percentage of N's	66,137 / 0.06%
GC Percentage	39.92%

2.3. Coverage

Mean	0.0343

Standard Deviation	0.3839

2.4. Mapping Quality

Mean Mapping Quality	44.48

2.5. Mismatches and indels

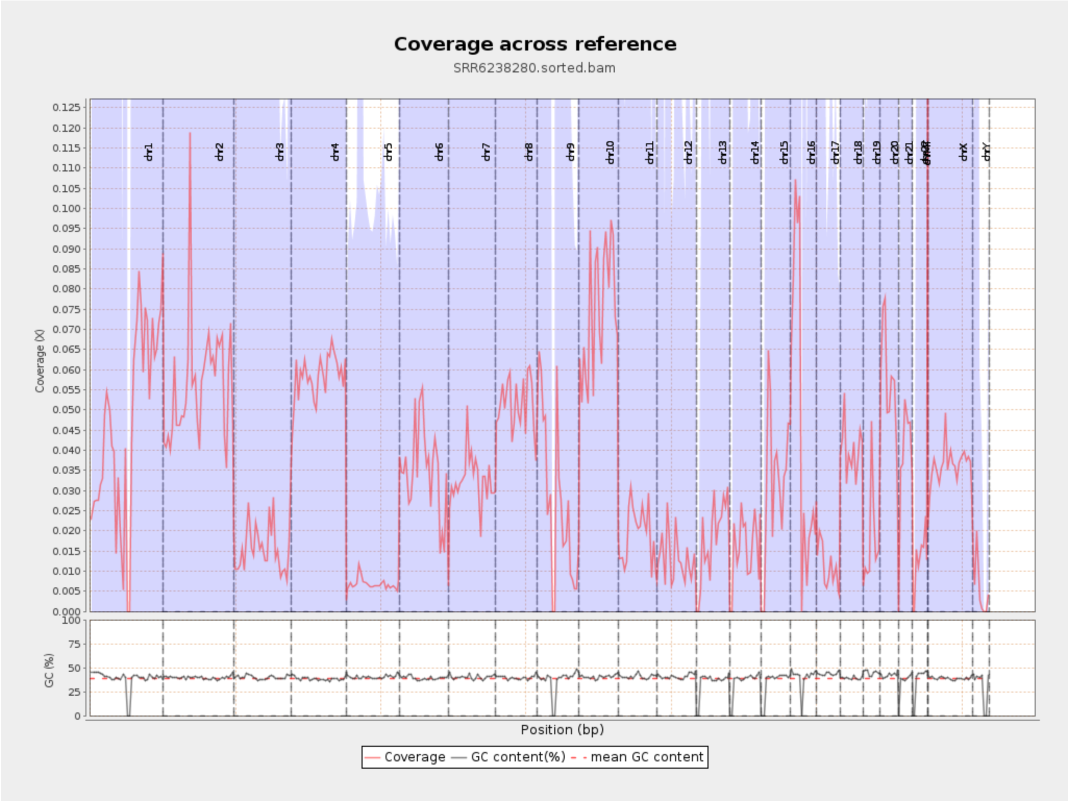
General error rate	0.89%
Mismatches	930,296
Insertions	8,687
Mapped reads with at least one insertion	0.54%
Deletions	34,199
Mapped reads with at least one deletion	2.12%
Homopolymer indels	46.24%

2.6. Chromosome stats

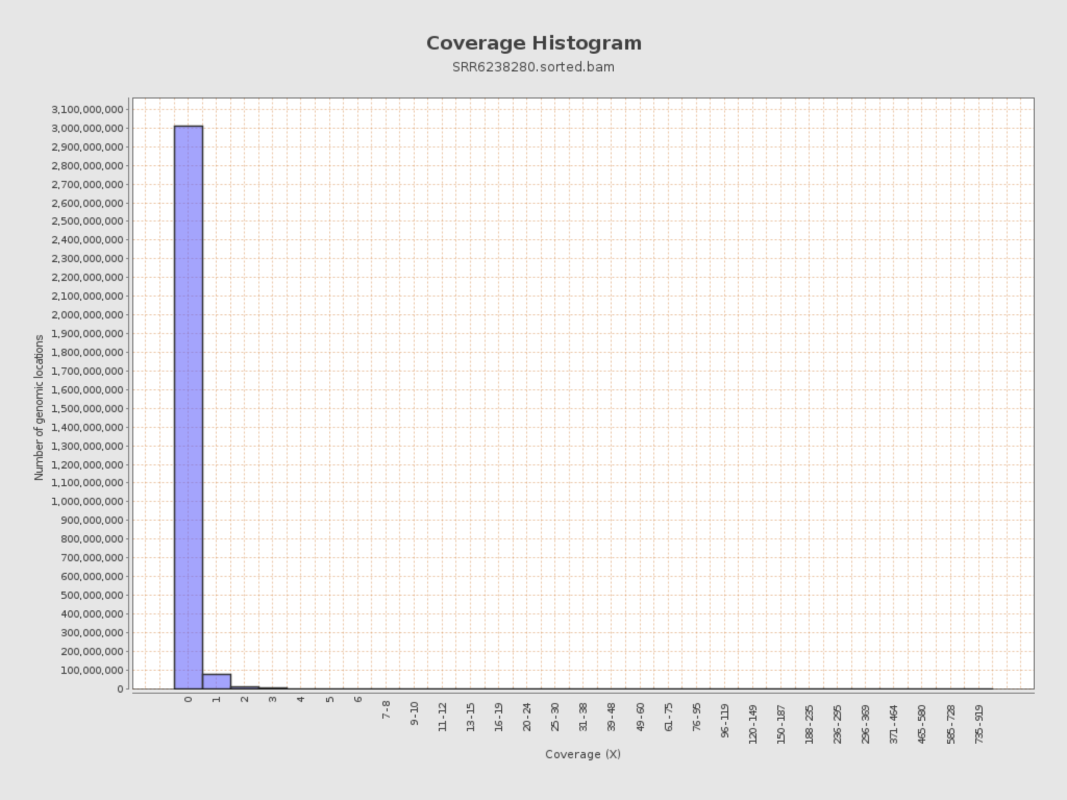
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11459713	0.046	0.6302
chr2	243199373	13682304	0.0563	0.5269
chr3	198022430	3117938	0.0157	0.1545
chr4	191154276	11165495	0.0584	0.2947
chr5	180915260	1234127	0.0068	0.1113
chr6	171115067	5928988	0.0346	0.266
chr7	159138663	5246134	0.033	0.3304

chr8	146364022	7516809	0.0514	0.4904
chr9	141213431	3826890	0.0271	0.4466
chr10	135534747	10113229	0.0746	0.4857
chr11	135006516	2603572	0.0193	0.2623
chr12	133851895	1770094	0.0132	0.1495
chr13	115169878	2085431	0.0181	0.1558
chr14	107349540	1638444	0.0153	0.1831
chr15	102531392	3298473	0.0322	0.2075
chr16	90354753	4228707	0.0468	0.3227
chr17	81195210	866592	0.0107	0.1647
chr18	78077248	3130245	0.0401	0.988
chr19	59128983	1108844	0.0188	0.3914
chr20	63025520	3592274	0.057	0.2803
chr21	48129895	1858160	0.0386	0.2537
chr22	51304566	663501	0.0129	0.1298
chrMT	16571	2570	0.1551	0.4435
chrX	155270560	5596602	0.036	0.2486
chrY	59373566	323944	0.0055	0.1682

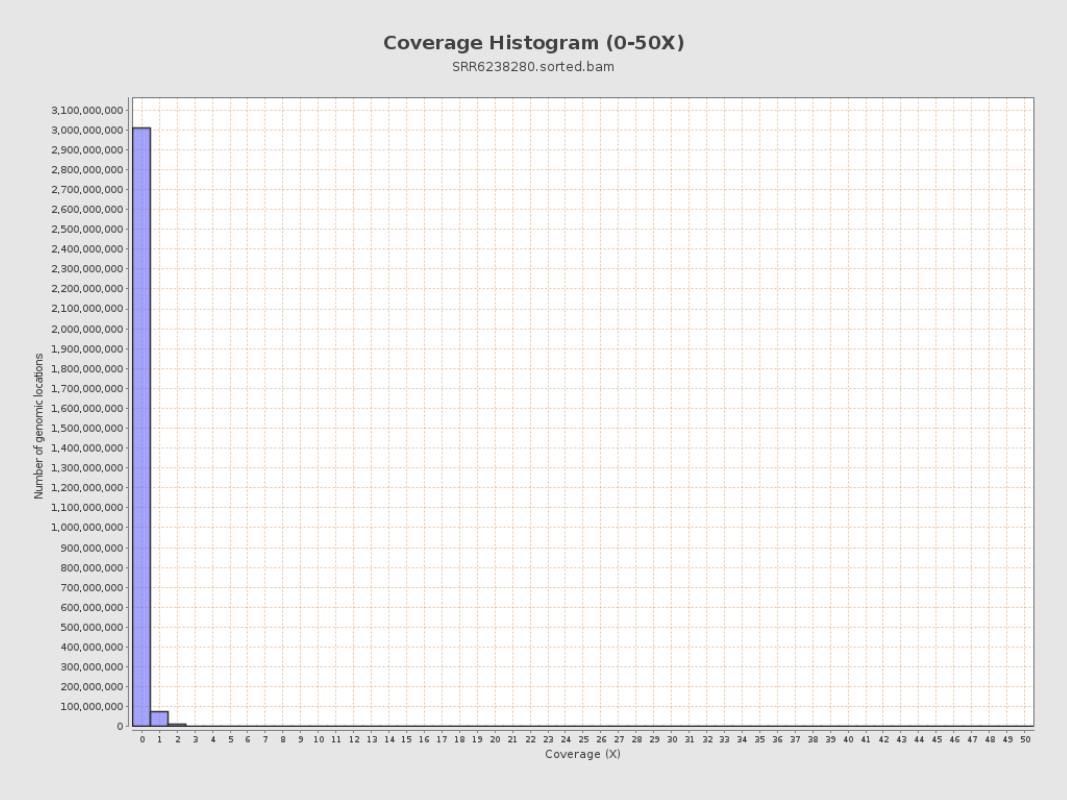
3. Results : Coverage across reference



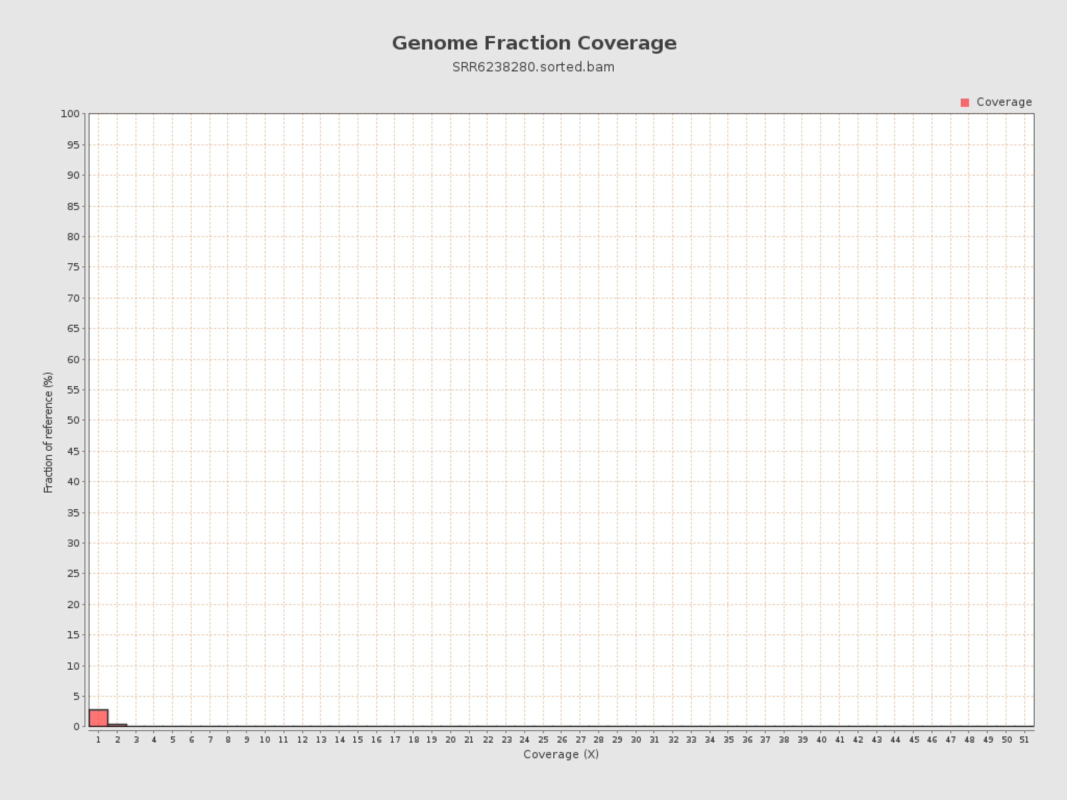
4. Results : Coverage Histogram



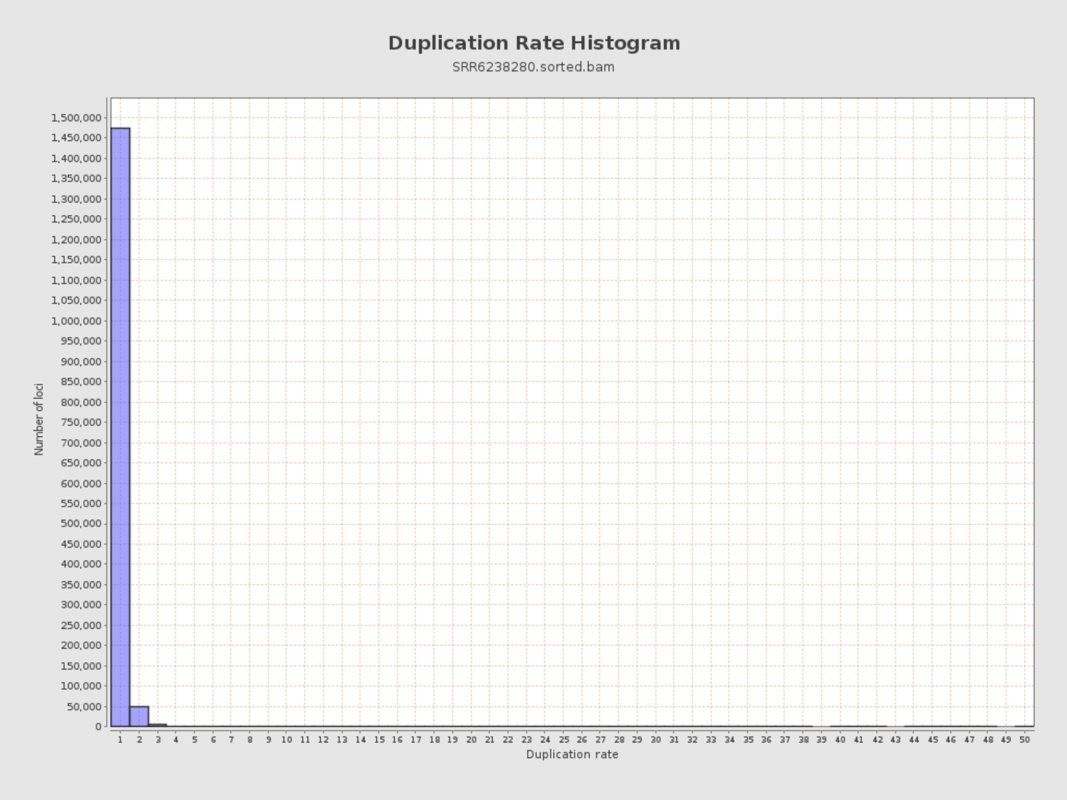
5. Results : Coverage Histogram (0-50X)



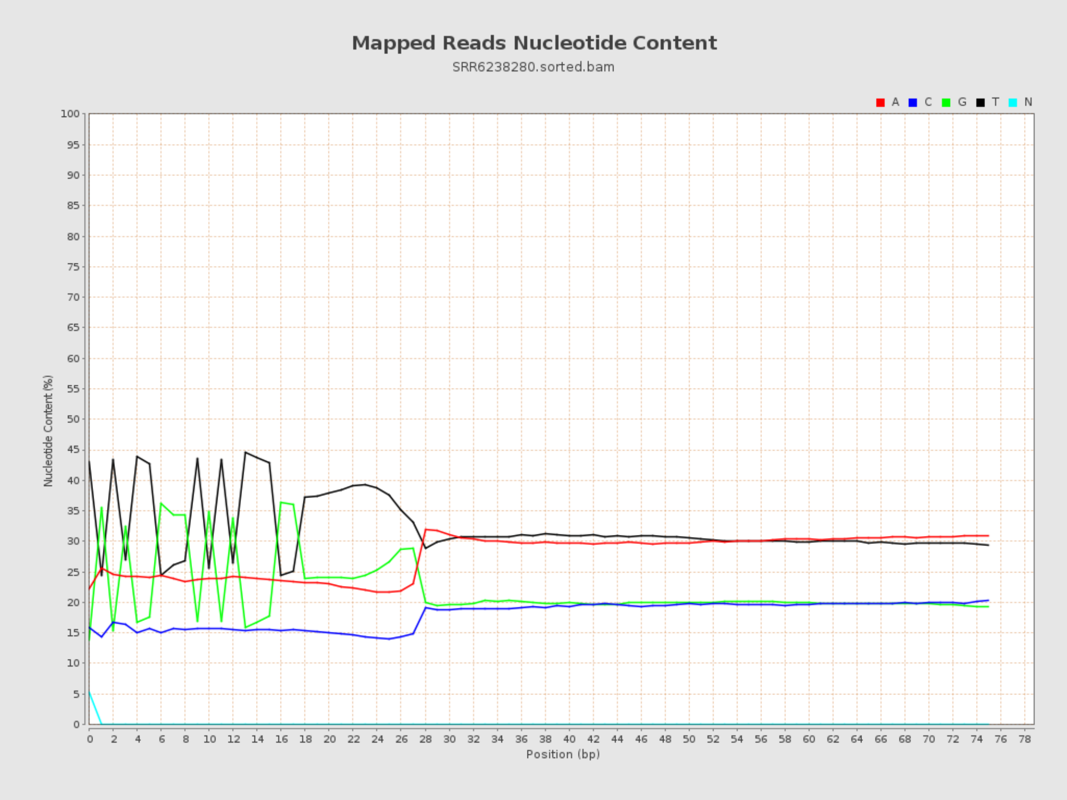
6. Results : Genome Fraction Coverage



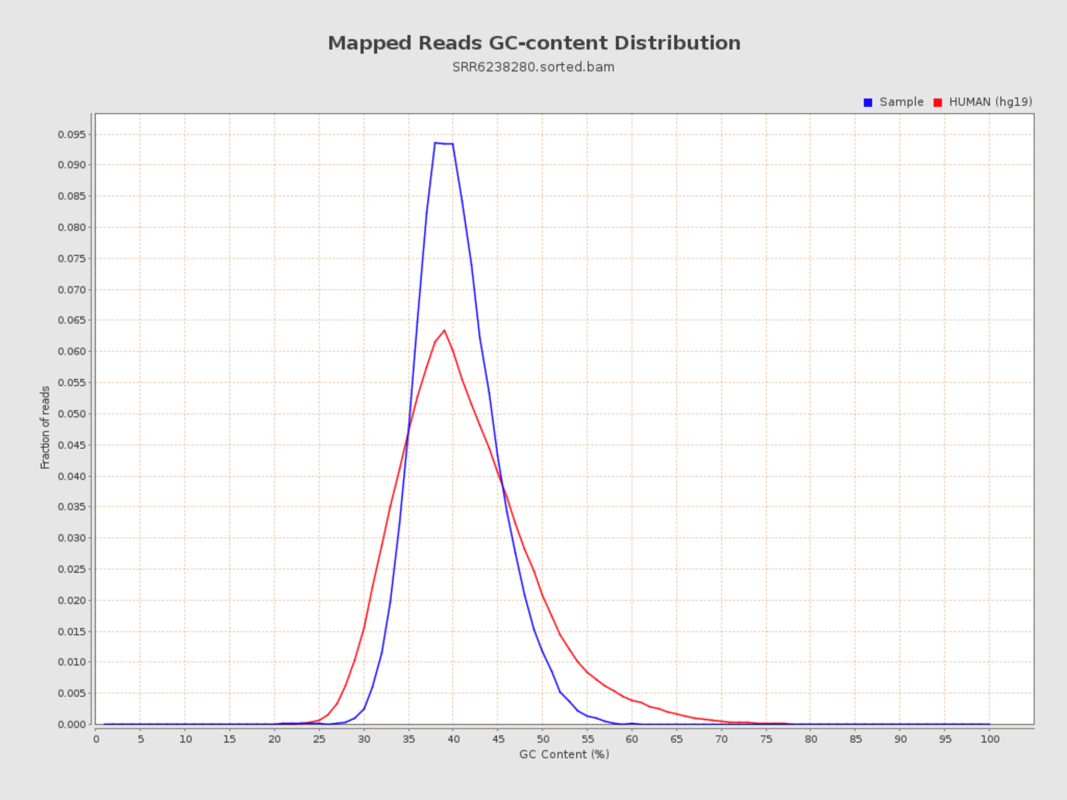
7. Results : Duplication Rate Histogram



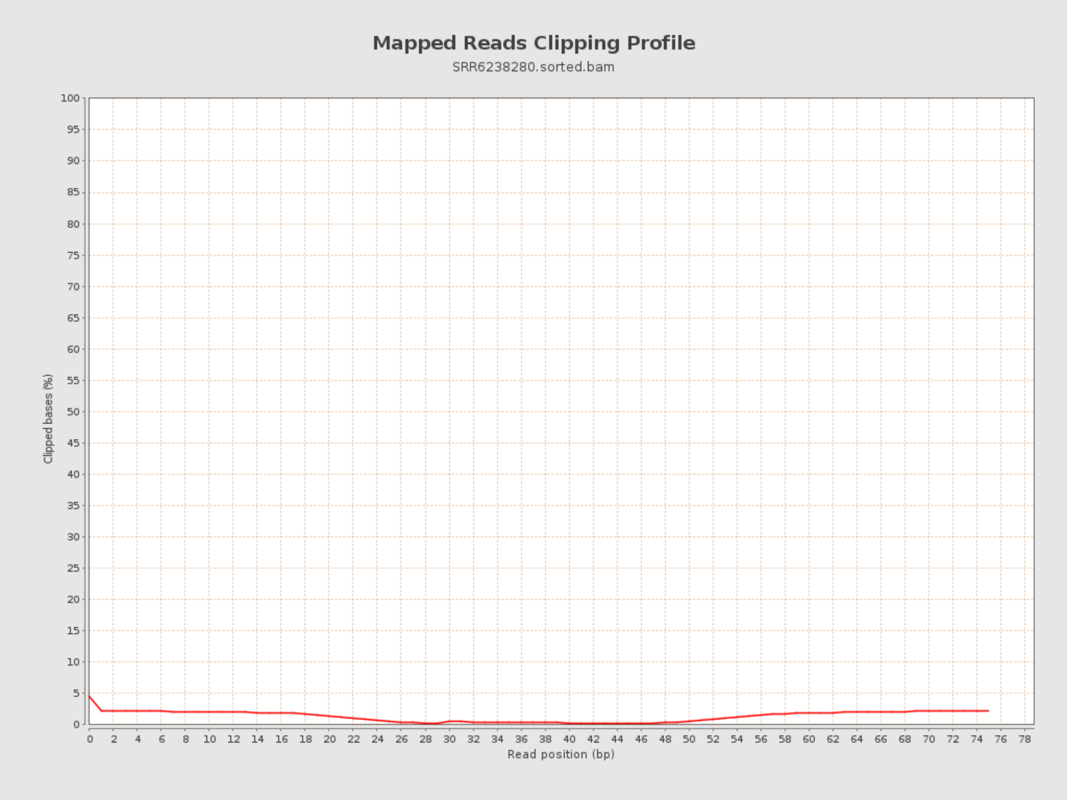
8. Results : Mapped Reads Nucleotide Content



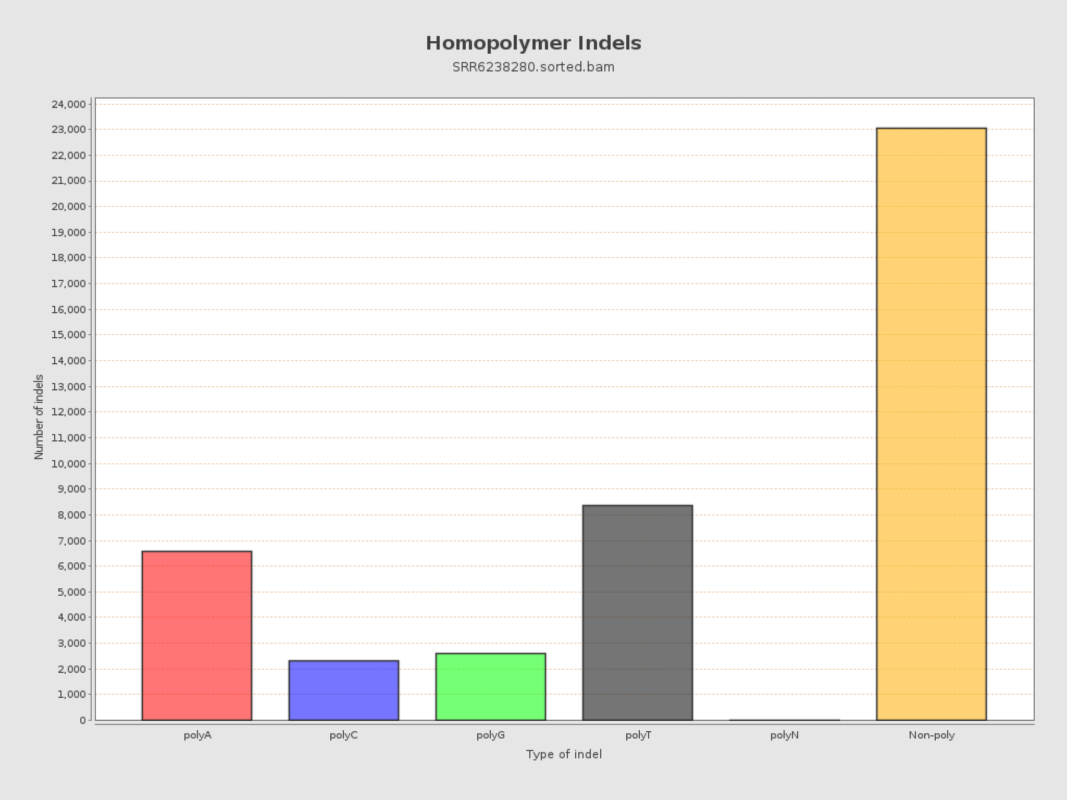
9. Results : Mapped Reads GC-content Distribution



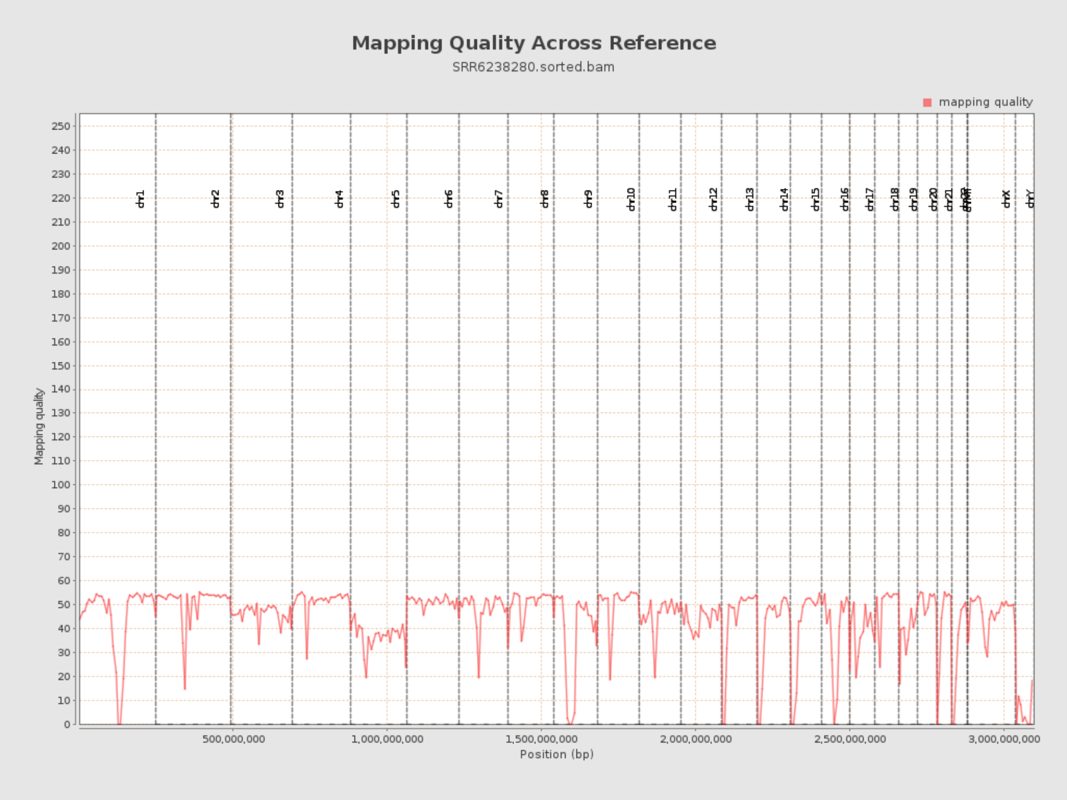
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram