Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 22:56:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238623.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_SRR6238623 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238623.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 22:56:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238623.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,622,081
Mapped reads	4,223,583 / 91.38%
Unmapped reads	398,498 / 8.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,263 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	316,548 / 6.85%
Duplication rate	5.75%
Clipped reads	2,667,162 / 57.7%

2.2. ACGT Content

Number/percentage of A's	64,284,038 / 24.72%
Number/percentage of C's	47,488,761 / 18.26%
Number/percentage of T's	83,699,371 / 32.19%
Number/percentage of G's	64,528,201 / 24.82%
Number/percentage of N's	12,829 / 0%
GC Percentage	43.08%

2.3. Coverage

Mean	0.084

Standard Deviation	0.8404

2.4. Mapping Quality

Mean Mapping Quality	41.03

2.5. Mismatches and indels

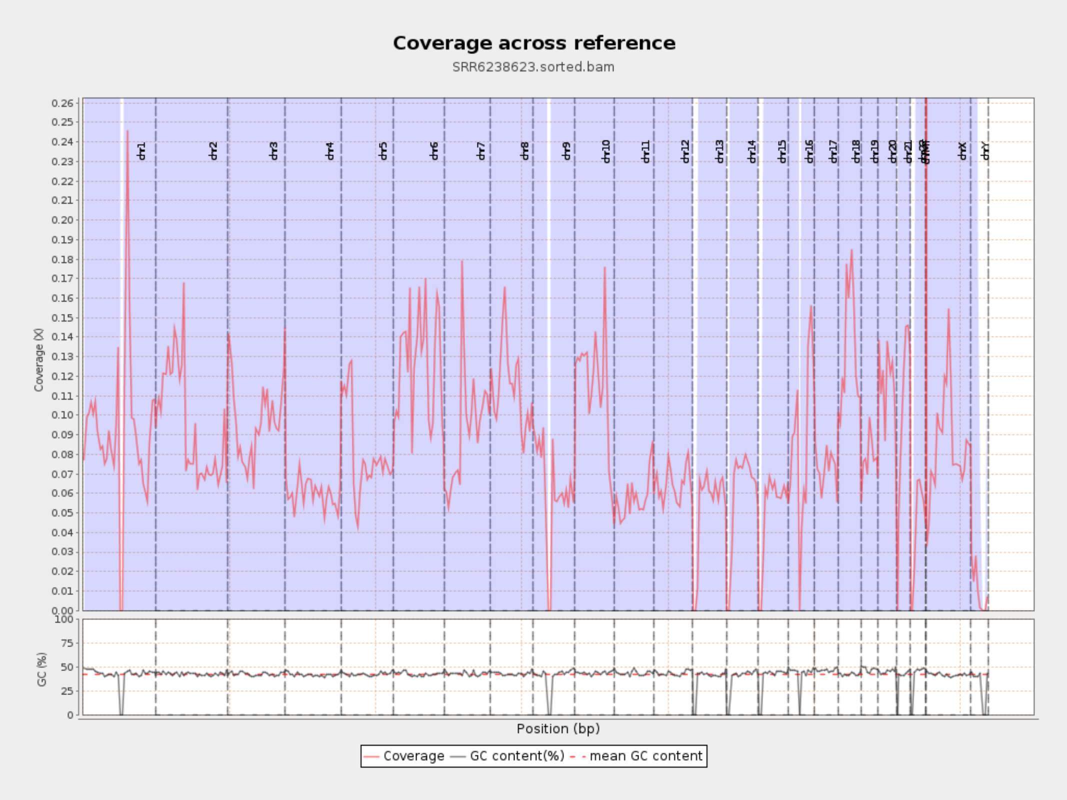
General error rate	0.56%
Mismatches	1,413,039
Insertions	18,842
Mapped reads with at least one insertion	0.44%
Deletions	61,266
Mapped reads with at least one deletion	1.44%
Homopolymer indels	41.79%

2.6. Chromosome stats

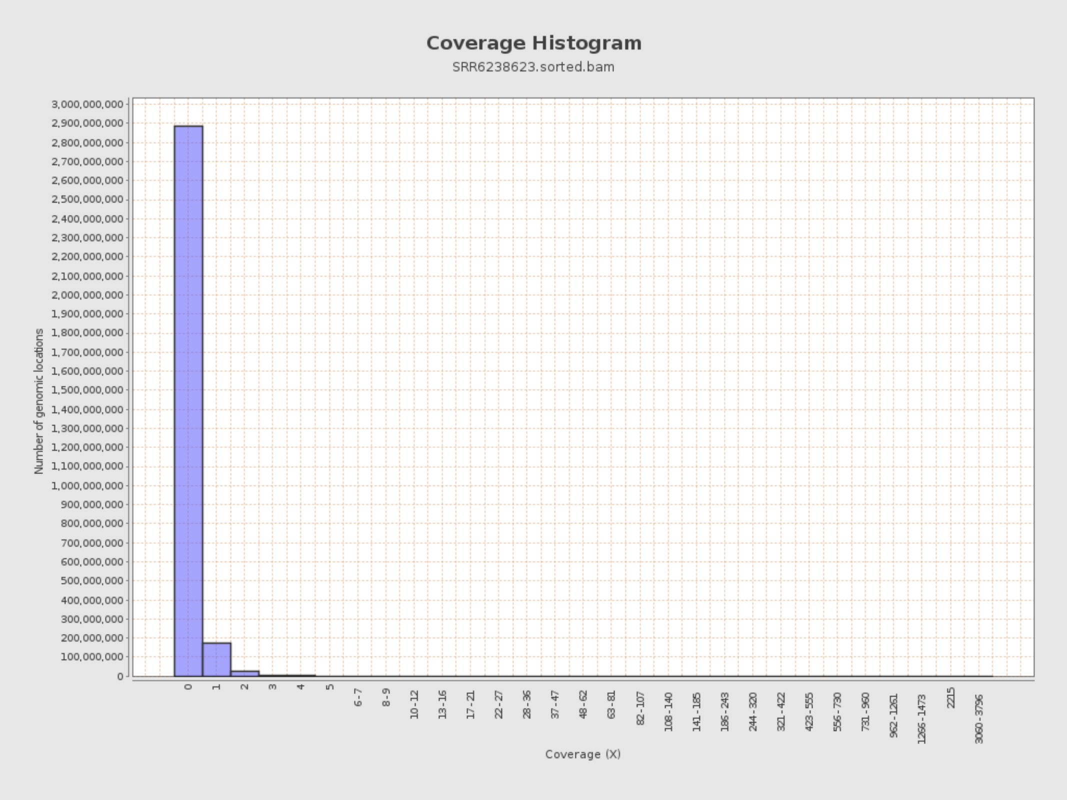
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22746504	0.0913	1.173
chr2	243199373	23103909	0.095	1.7757
chr3	198022430	19173224	0.0968	0.389
chr4	191154276	11466383	0.06	0.3315
chr5	180915260	14471687	0.08	0.3555
chr6	171115067	21698593	0.1268	0.8351
chr7	159138663	14877394	0.0935	1.3724

chr8	146364022	16707583	0.1142	0.7654
chr9	141213431	8662375	0.0613	0.6802
chr10	135534747	15822391	0.1167	0.6268
chr11	135006516	7749099	0.0574	0.4047
chr12	133851895	8739564	0.0653	0.3599
chr13	115169878	6040326	0.0524	0.3909
chr14	107349540	6467440	0.0602	0.4232
chr15	102531392	5142892	0.0502	0.4125
chr16	90354753	7558488	0.0837	0.4881
chr17	81195210	5993142	0.0738	0.341
chr18	78077248	10477632	0.1342	1.3915
chr19	59128983	4694554	0.0794	0.8002
chr20	63025520	7398173	0.1174	0.4653
chr21	48129895	4875590	0.1013	0.446
chr22	51304566	2189258	0.0427	0.2488
chrMT	16571	222693	13.4387	9.6044
chrX	155270560	13222906	0.0852	0.4274
chrY	59373566	619086	0.0104	0.2719

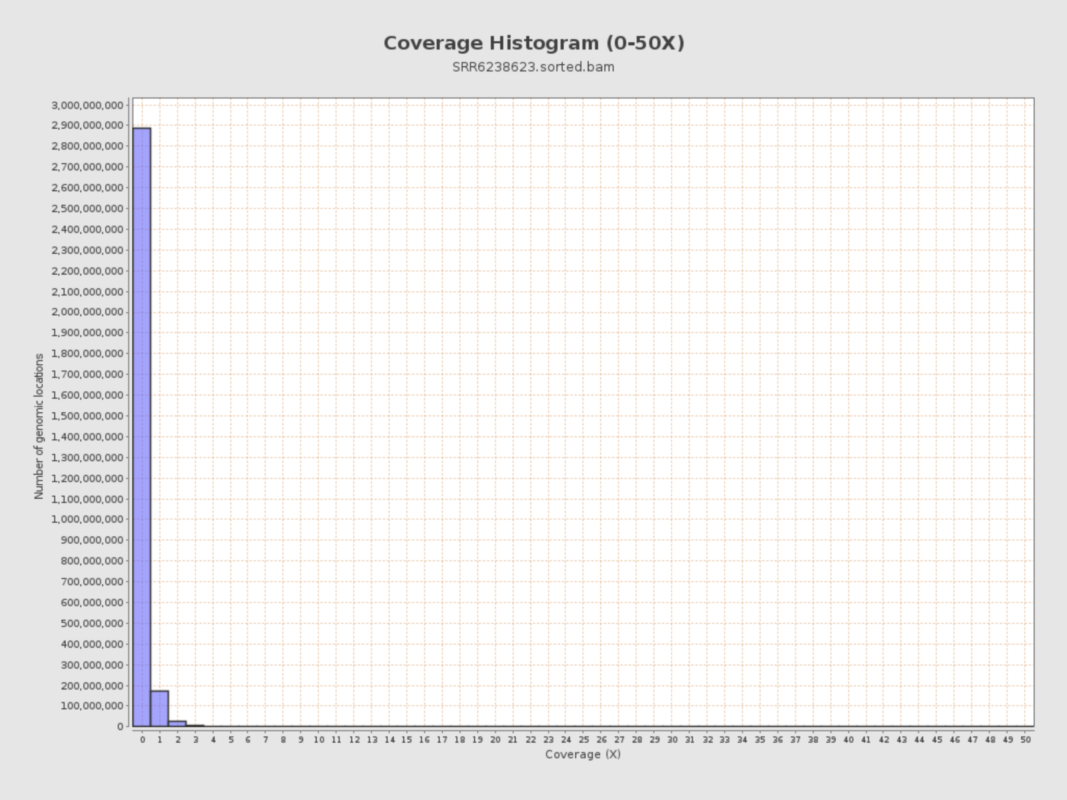
3. Results : Coverage across reference



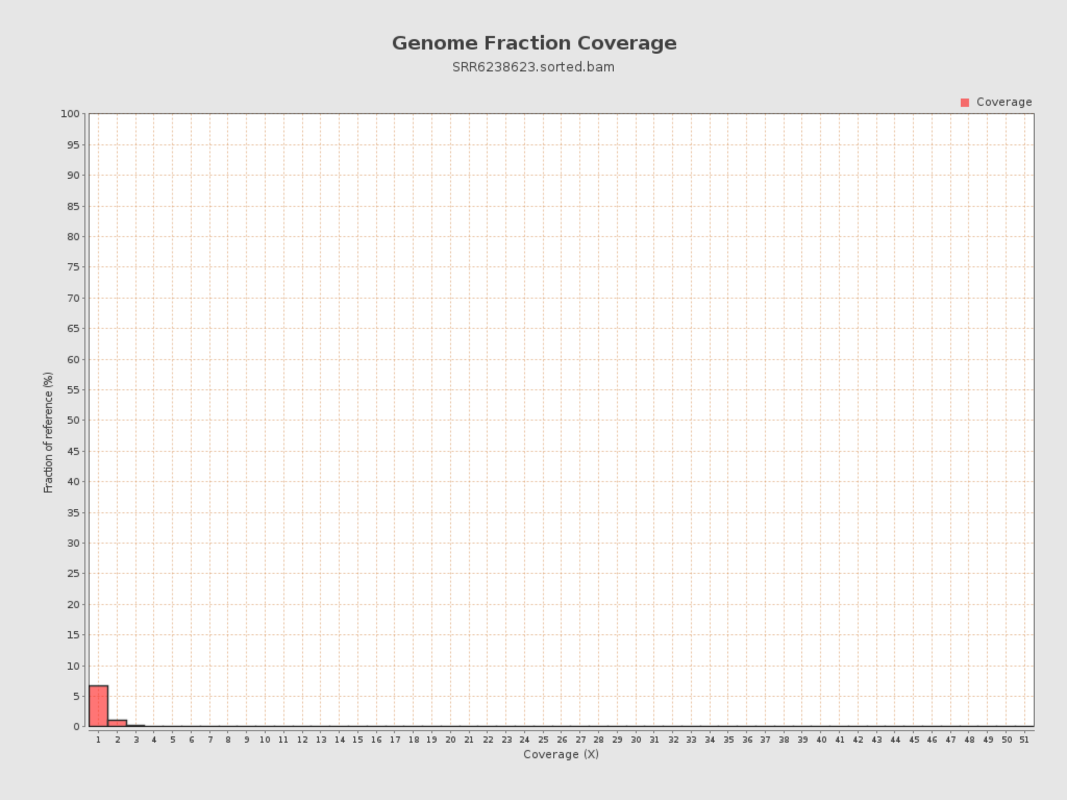
4. Results : Coverage Histogram



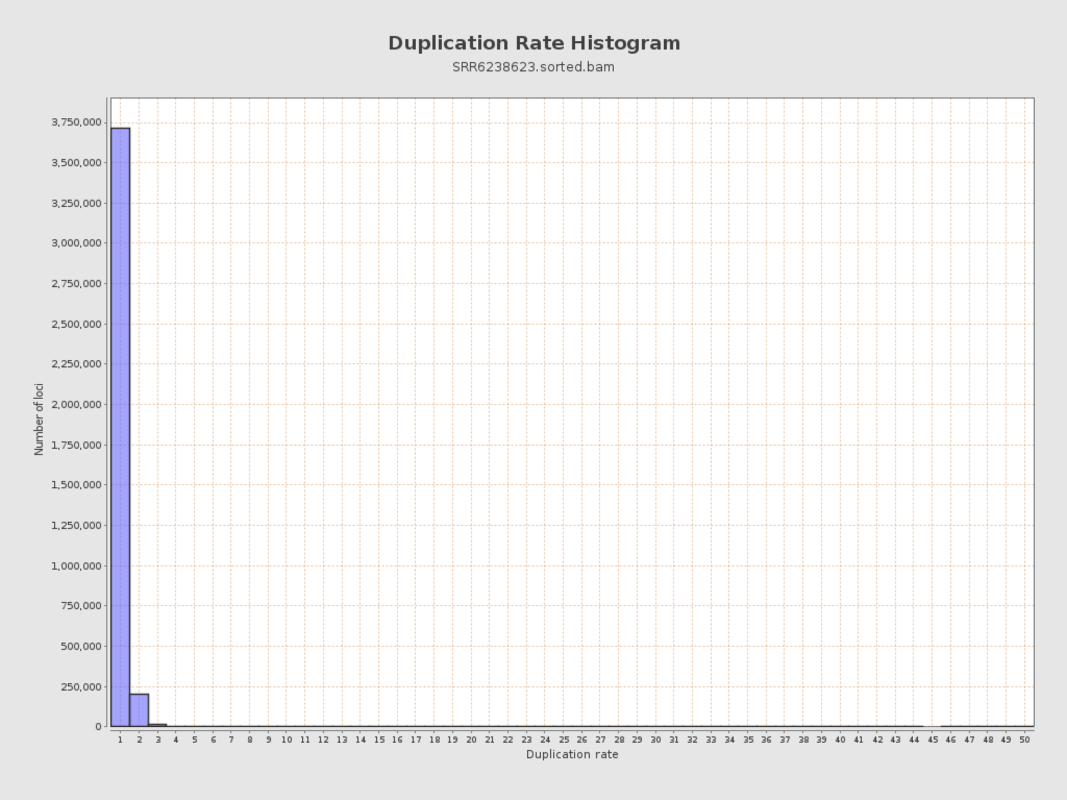
5. Results : Coverage Histogram (0-50X)



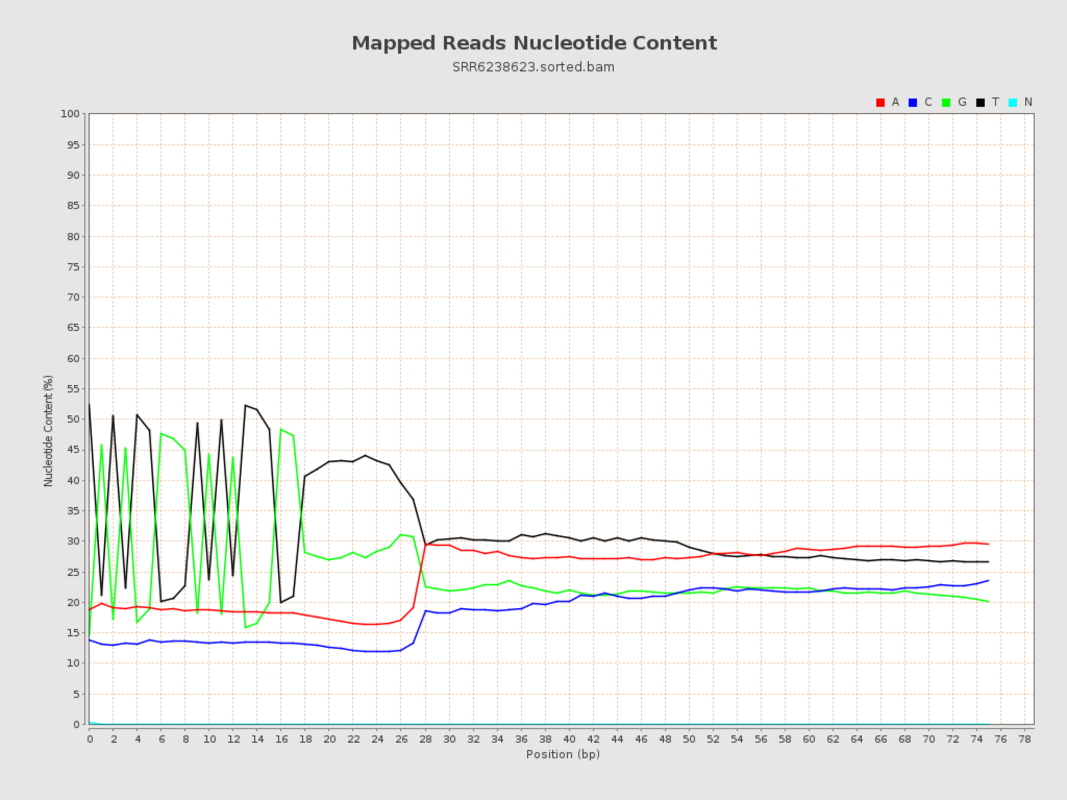
6. Results : Genome Fraction Coverage



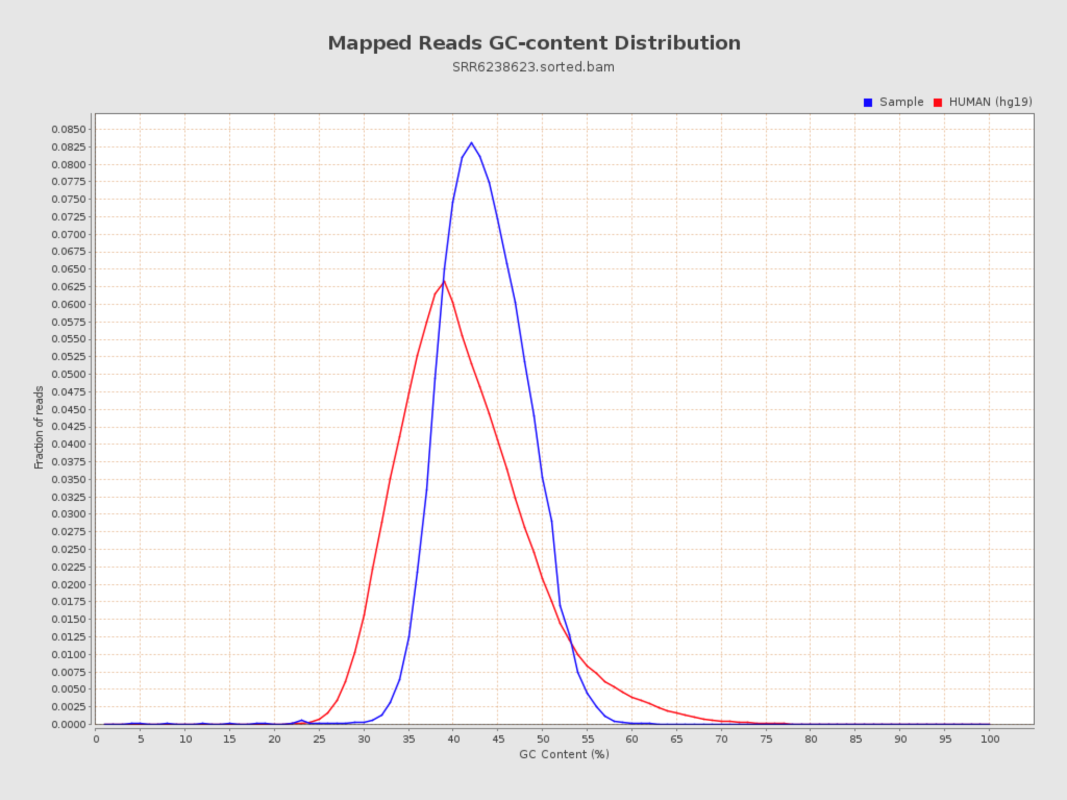
7. Results : Duplication Rate Histogram



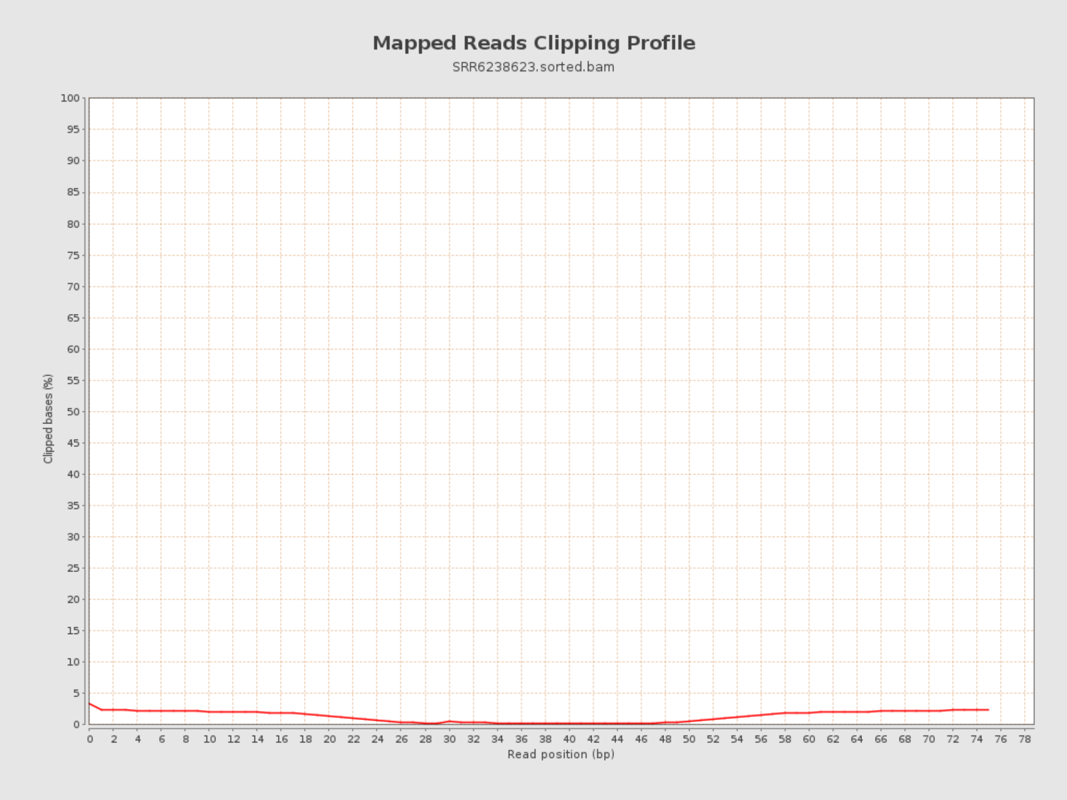
8. Results : Mapped Reads Nucleotide Content



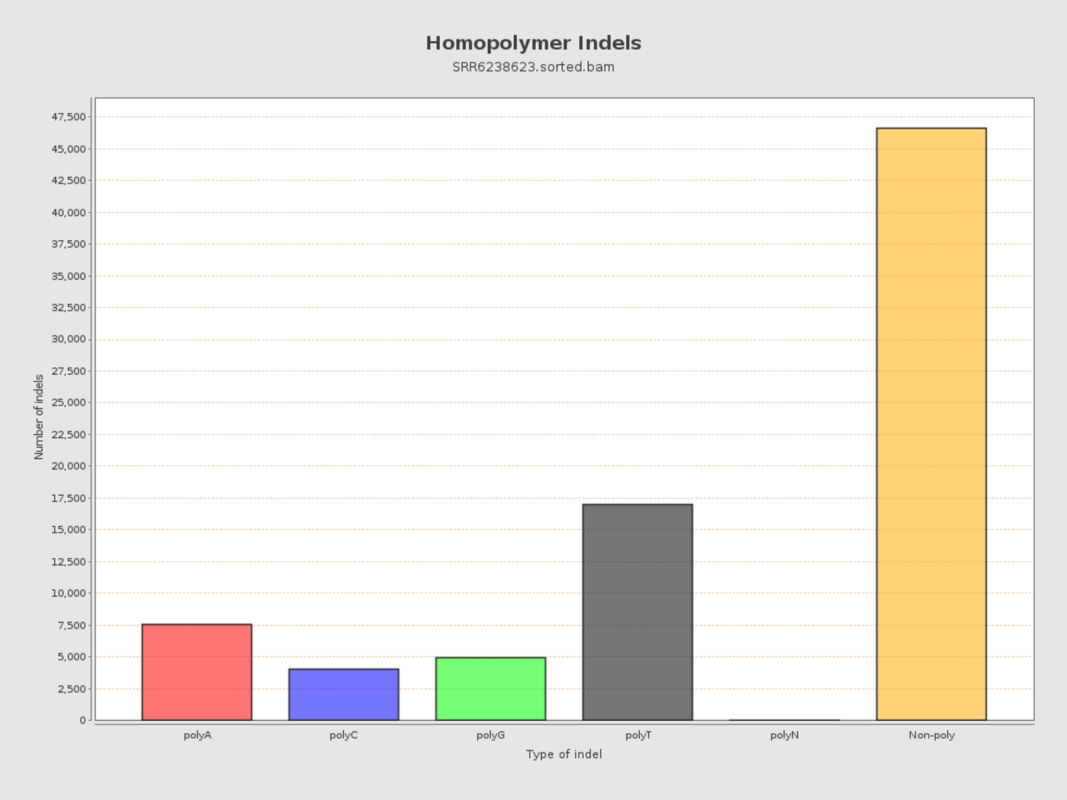
9. Results : Mapped Reads GC-content Distribution



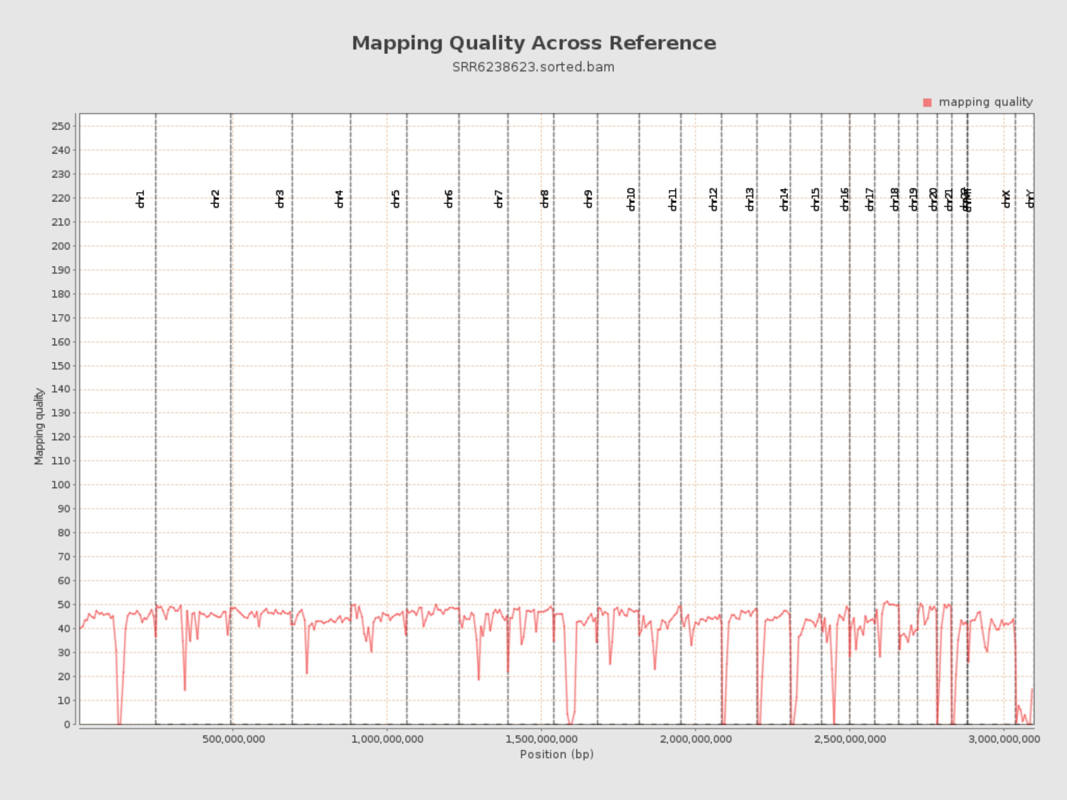
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram