Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:50:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080638.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_SRR3080638 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080638.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:50:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080638.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,211,473
Mapped reads	2,597,276 / 80.87%
Unmapped reads	614,197 / 19.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,680 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	160,972 / 5.01%
Duplication rate	5.39%
Clipped reads	1,189,363 / 37.03%

2.2. ACGT Content

Number/percentage of A's	48,243,899 / 27.81%
Number/percentage of C's	31,083,986 / 17.92%
Number/percentage of T's	56,349,402 / 32.48%
Number/percentage of G's	37,642,079 / 21.7%
Number/percentage of N's	144,374 / 0.08%
GC Percentage	39.62%

2.3. Coverage

Mean	0.0561

Standard Deviation	0.3655

2.4. Mapping Quality

Mean Mapping Quality	46.79

2.5. Mismatches and indels

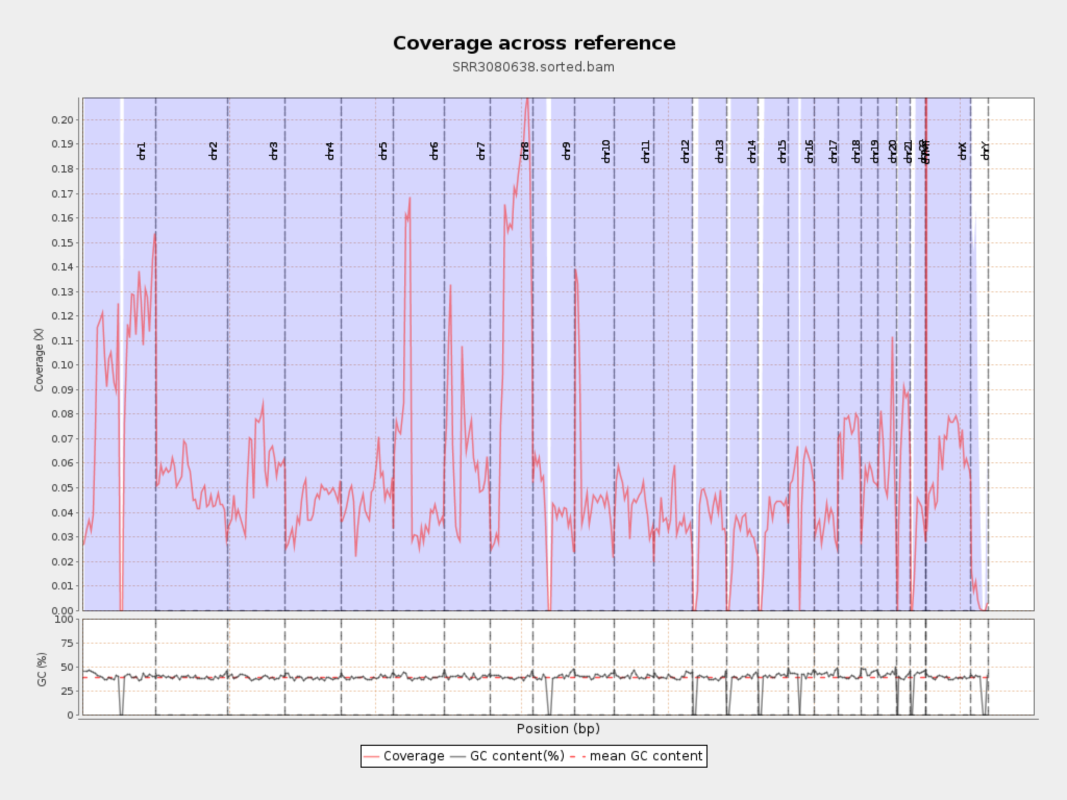
General error rate	0.91%
Mismatches	1,550,038
Insertions	13,653
Mapped reads with at least one insertion	0.52%
Deletions	39,916
Mapped reads with at least one deletion	1.52%
Homopolymer indels	49.55%

2.6. Chromosome stats

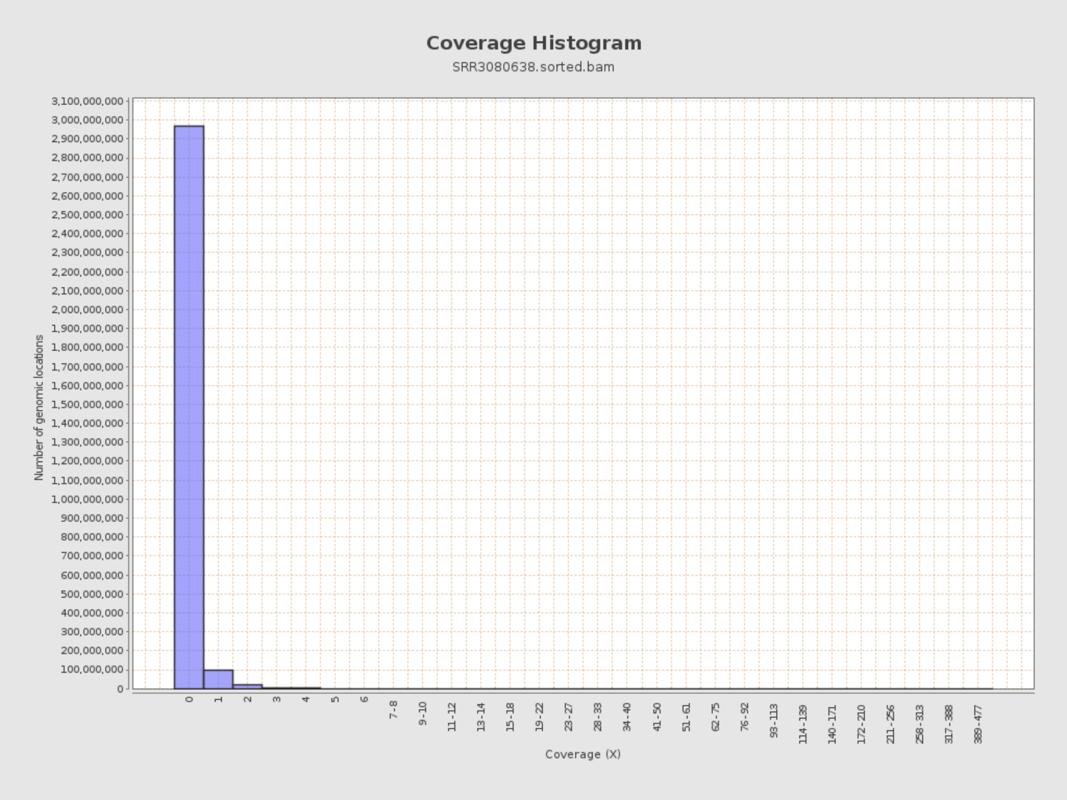
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23629614	0.0948	0.5343
chr2	243199373	12342546	0.0508	0.3546
chr3	198022430	10981861	0.0555	0.2978
chr4	191154276	8106431	0.0424	0.2616
chr5	180915260	8294349	0.0458	0.2699
chr6	171115067	10342907	0.0604	0.4072
chr7	159138663	10509785	0.066	0.5909

chr8	146364022	19551240	0.1336	0.5859
chr9	141213431	5608795	0.0397	0.2824
chr10	135534747	7431406	0.0548	0.3337
chr11	135006516	6075169	0.045	0.275
chr12	133851895	5009622	0.0374	0.2457
chr13	115169878	4068770	0.0353	0.237
chr14	107349540	2991884	0.0279	0.2169
chr15	102531392	3426573	0.0334	0.2331
chr16	90354753	4654867	0.0515	0.2953
chr17	81195210	2841661	0.035	0.2368
chr18	78077248	5698181	0.073	0.4344
chr19	59128983	3076486	0.052	0.3932
chr20	63025520	4247444	0.0674	0.3345
chr21	48129895	3149882	0.0654	0.3335
chr22	51304566	1456057	0.0284	0.2083
chrMT	16571	50368	3.0395	5.8206
chrX	155270560	9686886	0.0624	0.34
chrY	59373566	295425	0.005	0.0932

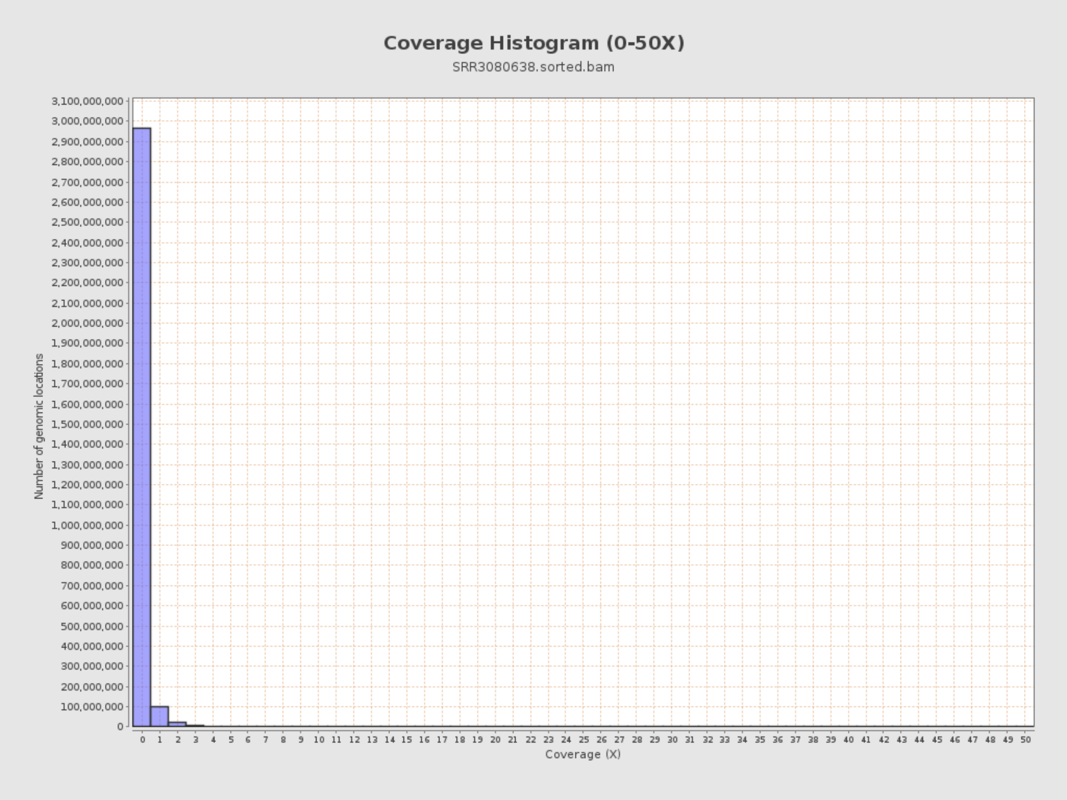
3. Results : Coverage across reference



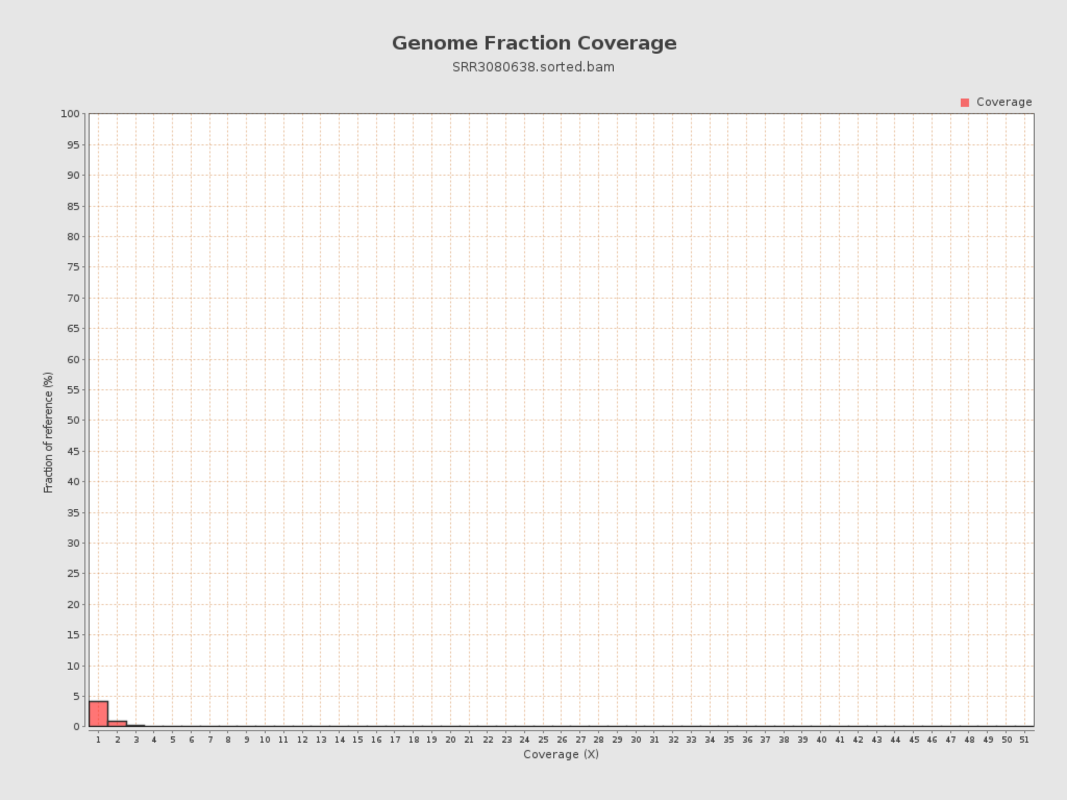
4. Results : Coverage Histogram



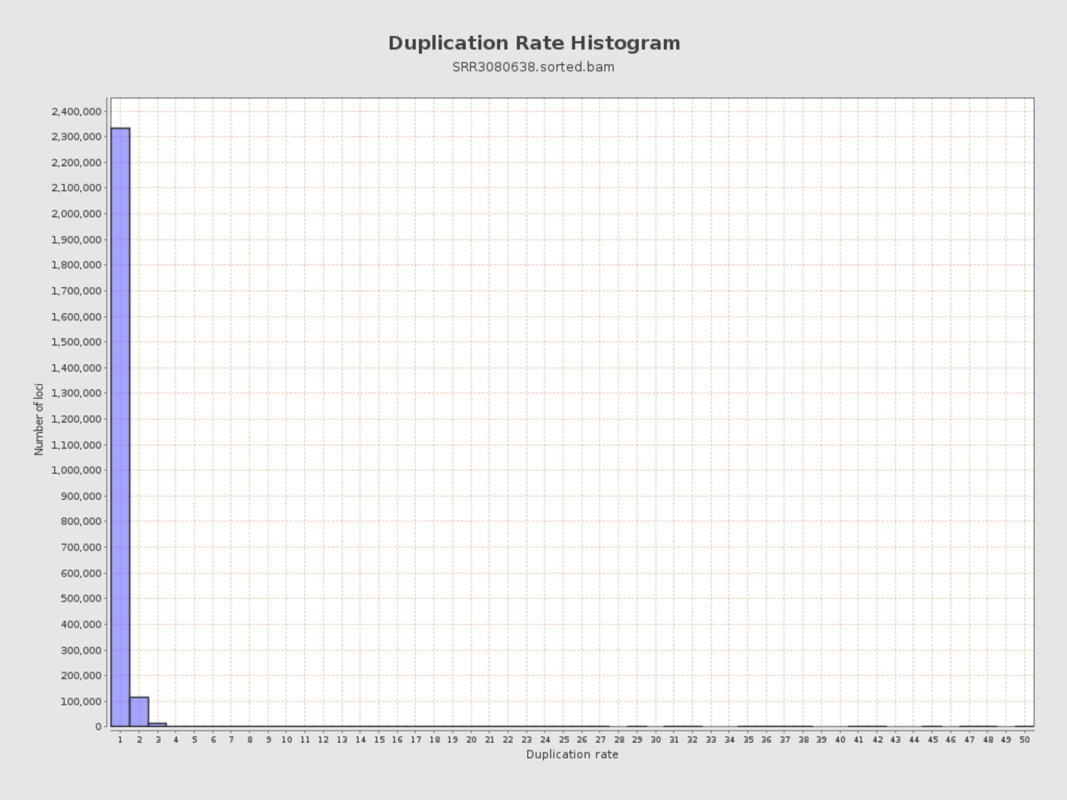
5. Results : Coverage Histogram (0-50X)



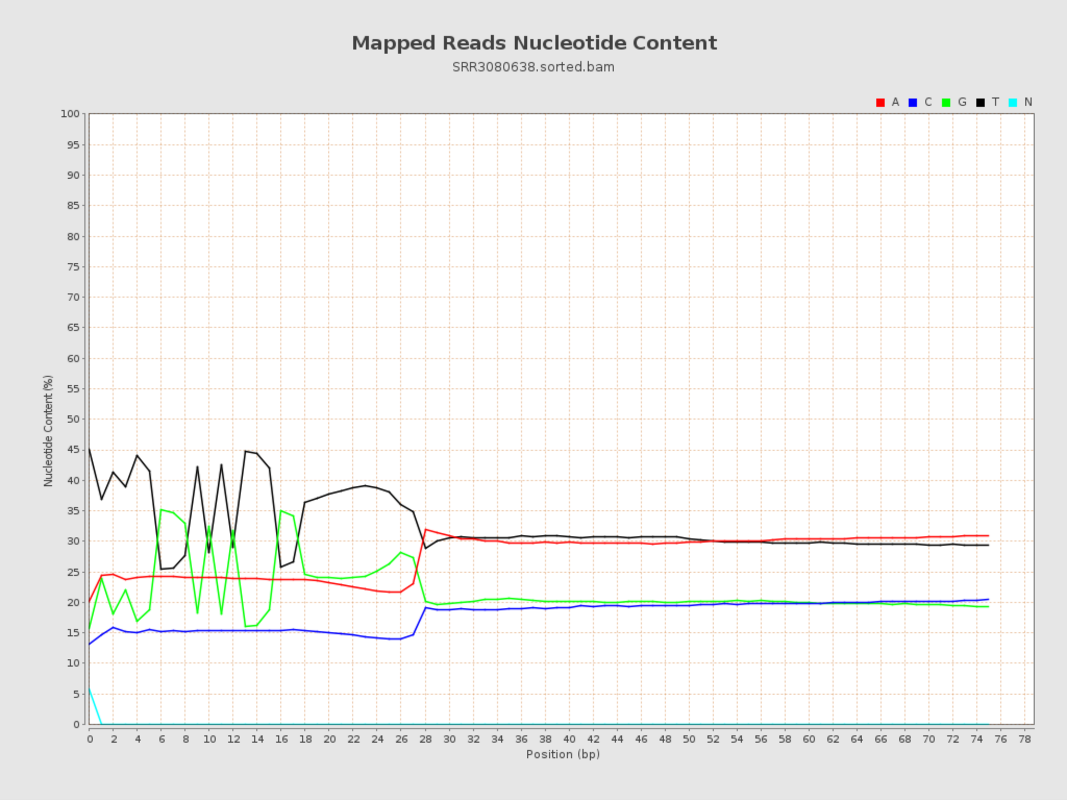
6. Results : Genome Fraction Coverage



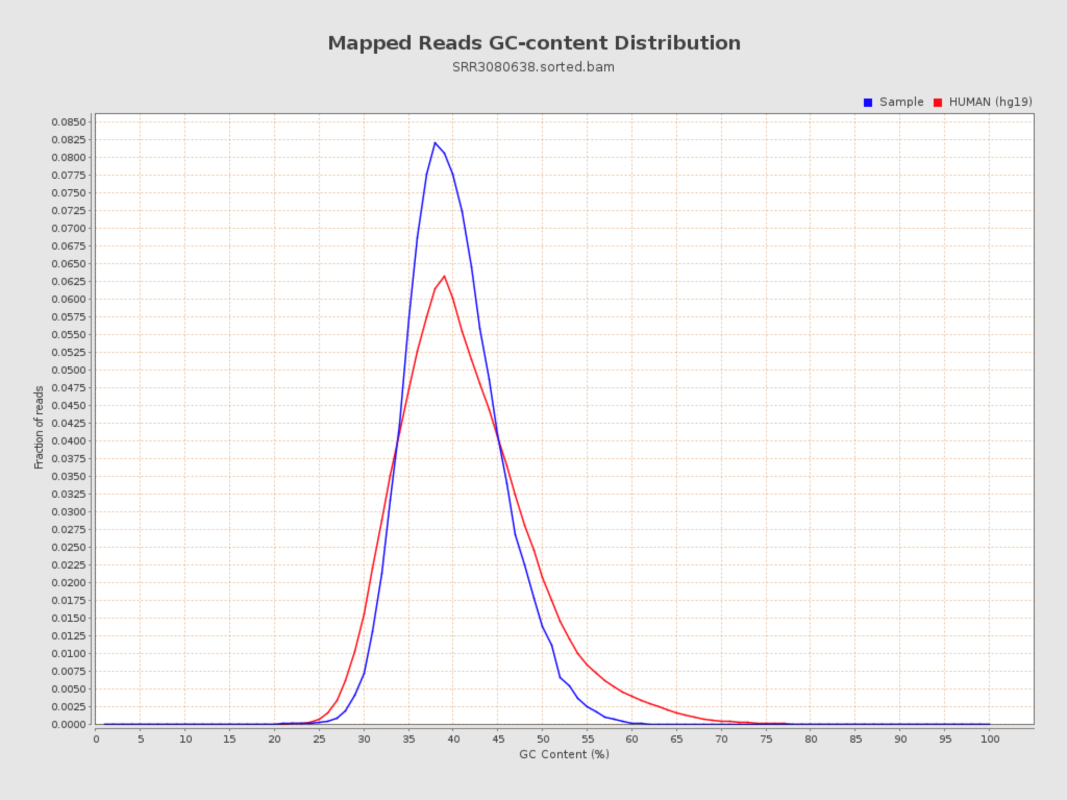
7. Results : Duplication Rate Histogram



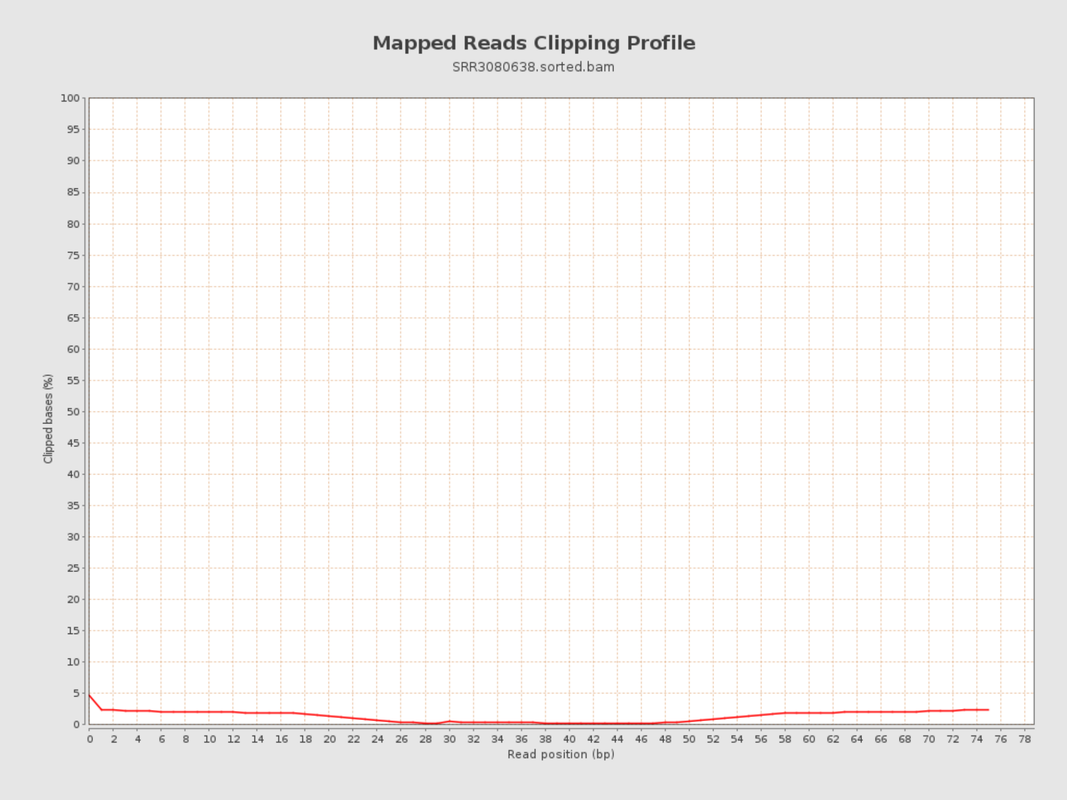
8. Results : Mapped Reads Nucleotide Content



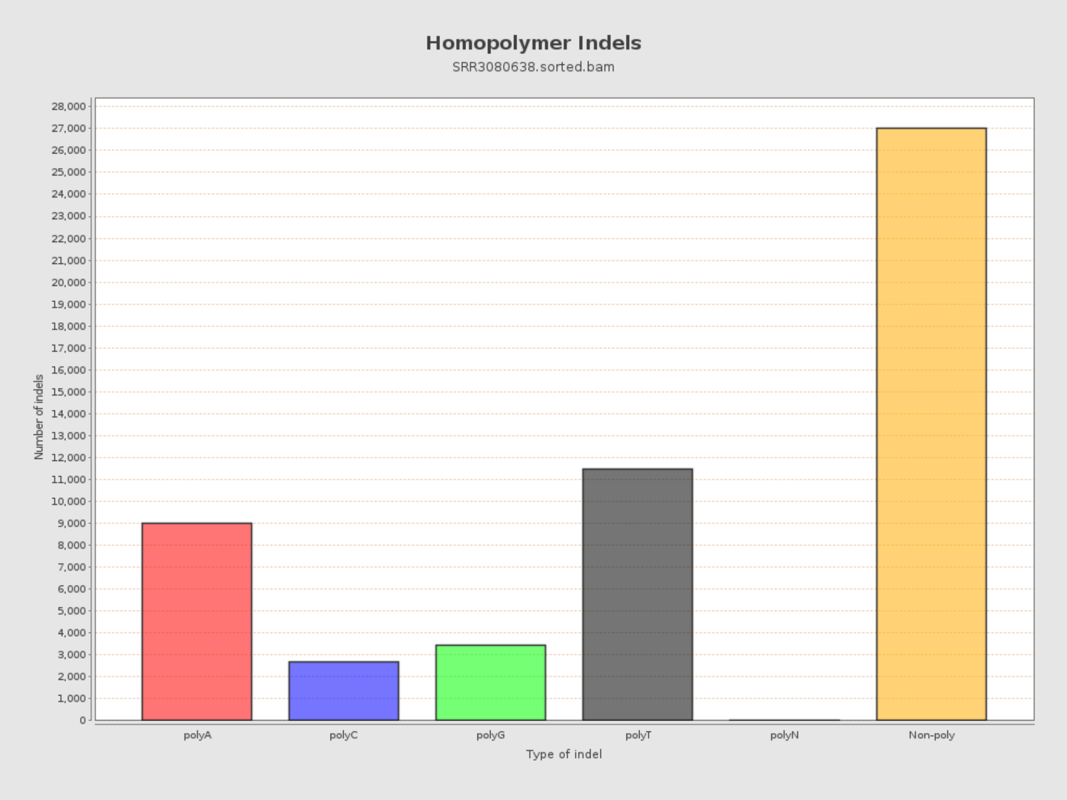
9. Results : Mapped Reads GC-content Distribution



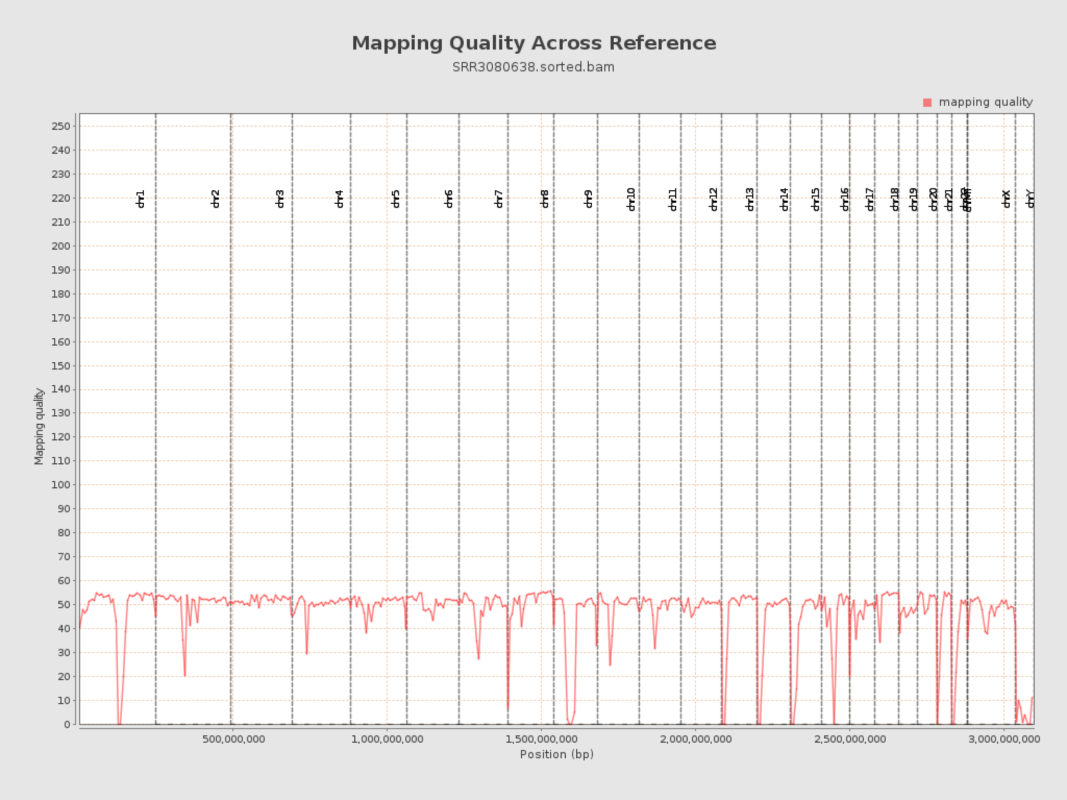
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram