Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:47:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013308.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_SRR6013308 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013308.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:47:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013308.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,753,875
Mapped reads	2,485,484 / 90.25%
Unmapped reads	268,391 / 9.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,331 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	83,477 / 3.03%
Duplication rate	2.29%
Clipped reads	1,281,024 / 46.52%

2.2. ACGT Content

Number/percentage of A's	44,507,520 / 27.56%
Number/percentage of C's	30,822,767 / 19.09%
Number/percentage of T's	49,222,408 / 30.48%
Number/percentage of G's	36,882,440 / 22.84%
Number/percentage of N's	38,611 / 0.02%
GC Percentage	41.93%

2.3. Coverage

Mean	0.0522

Standard Deviation	0.4809

2.4. Mapping Quality

Mean Mapping Quality	44.04

2.5. Mismatches and indels

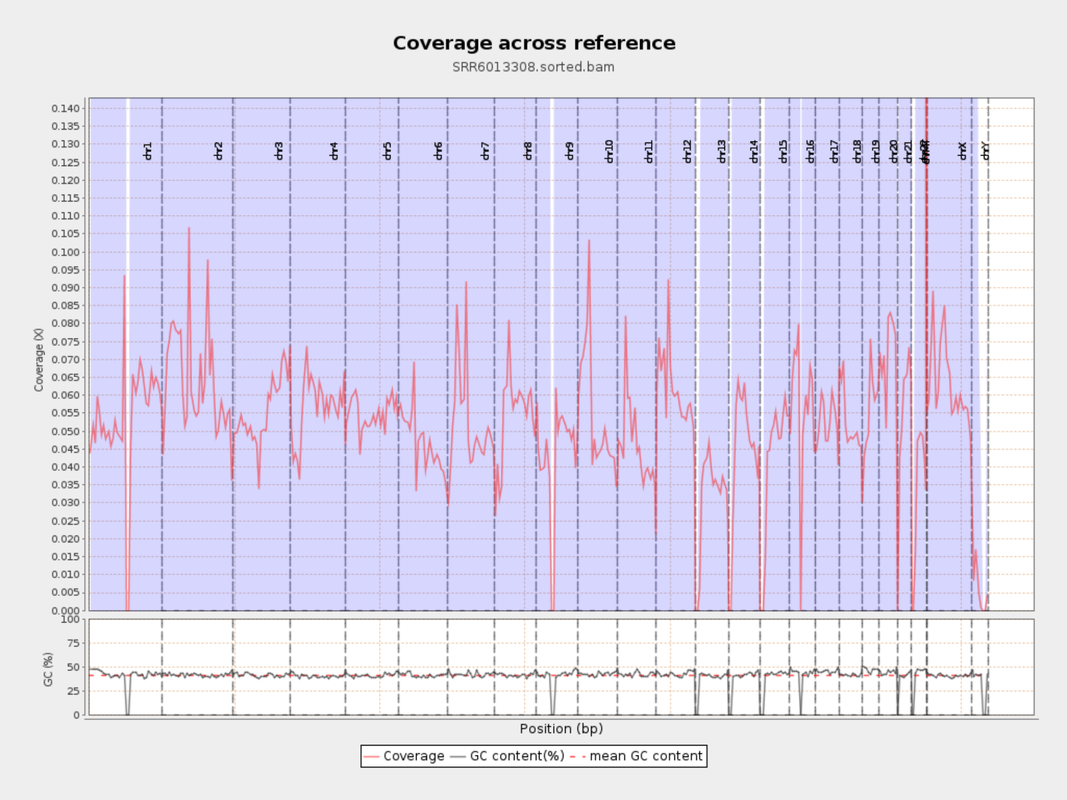
General error rate	0.81%
Mismatches	1,285,744
Insertions	11,428
Mapped reads with at least one insertion	0.45%
Deletions	39,913
Mapped reads with at least one deletion	1.59%
Homopolymer indels	44.81%

2.6. Chromosome stats

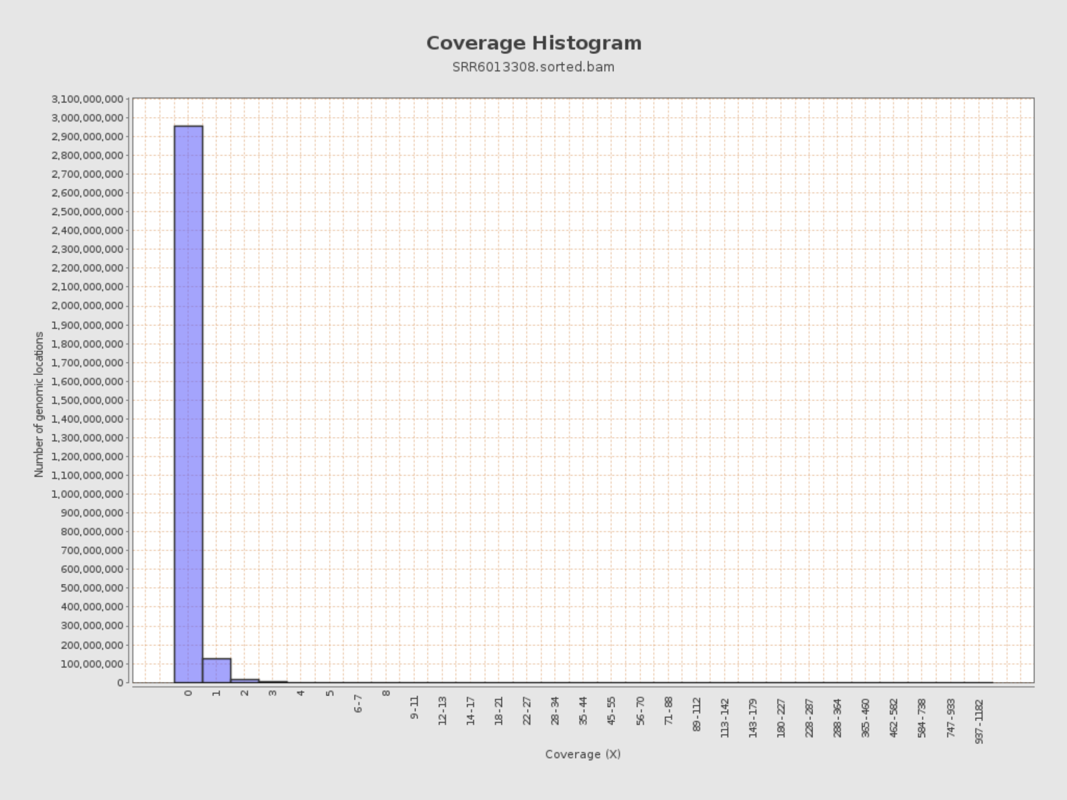
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13327813	0.0535	1.0073
chr2	243199373	15638061	0.0643	0.5667
chr3	198022430	10943887	0.0553	0.2628
chr4	191154276	10833675	0.0567	0.2755
chr5	180915260	9925316	0.0549	0.2612
chr6	171115067	8040535	0.047	0.3255
chr7	159138663	8407446	0.0528	0.6682

chr8	146364022	7938229	0.0542	0.4741
chr9	141213431	5979443	0.0423	0.3974
chr10	135534747	7457052	0.055	0.5264
chr11	135006516	6254741	0.0463	0.3276
chr12	133851895	8265701	0.0618	0.2823
chr13	115169878	3592340	0.0312	0.1972
chr14	107349540	4706903	0.0438	0.2619
chr15	102531392	4212289	0.0411	0.2279
chr16	90354753	5125835	0.0567	0.2992
chr17	81195210	4230898	0.0521	0.2885
chr18	78077248	4128693	0.0529	0.6864
chr19	59128983	3306468	0.0559	0.7804
chr20	63025520	4510020	0.0716	0.3068
chr21	48129895	2619479	0.0544	0.2804
chr22	51304566	1637204	0.0319	0.196
chrMT	16571	180551	10.8956	7.2954
chrX	155270560	9886969	0.0637	0.3273
chrY	59373566	393262	0.0066	0.1344

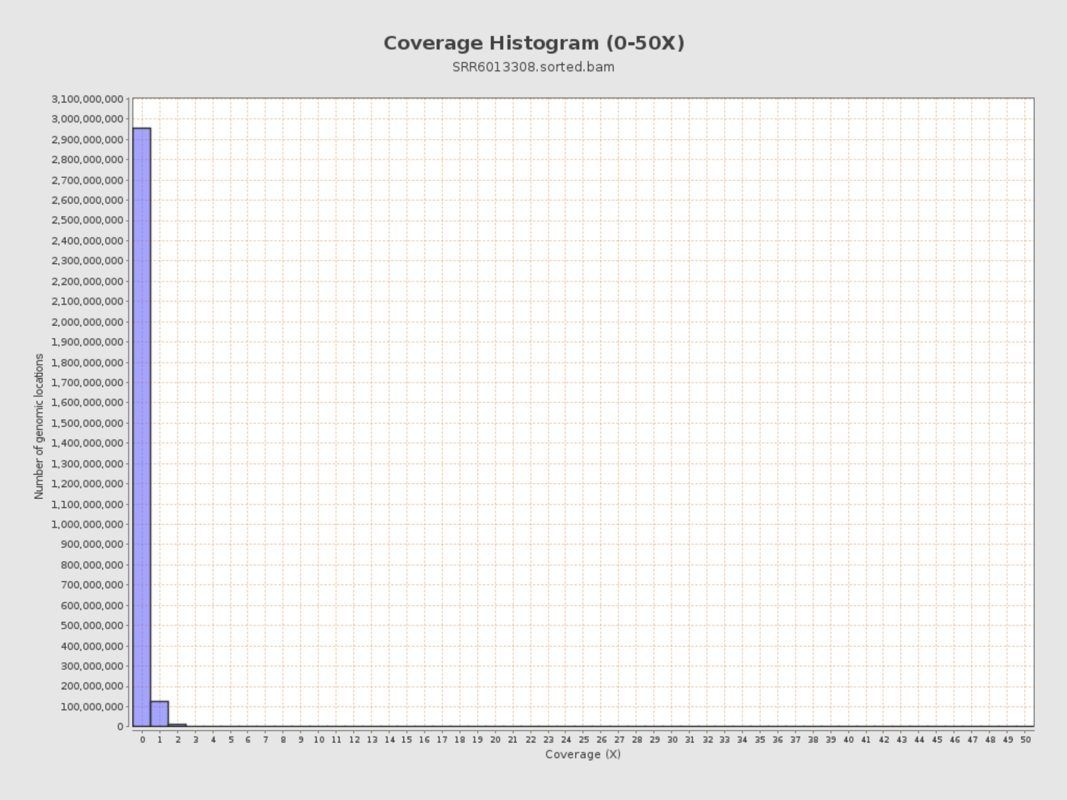
3. Results : Coverage across reference



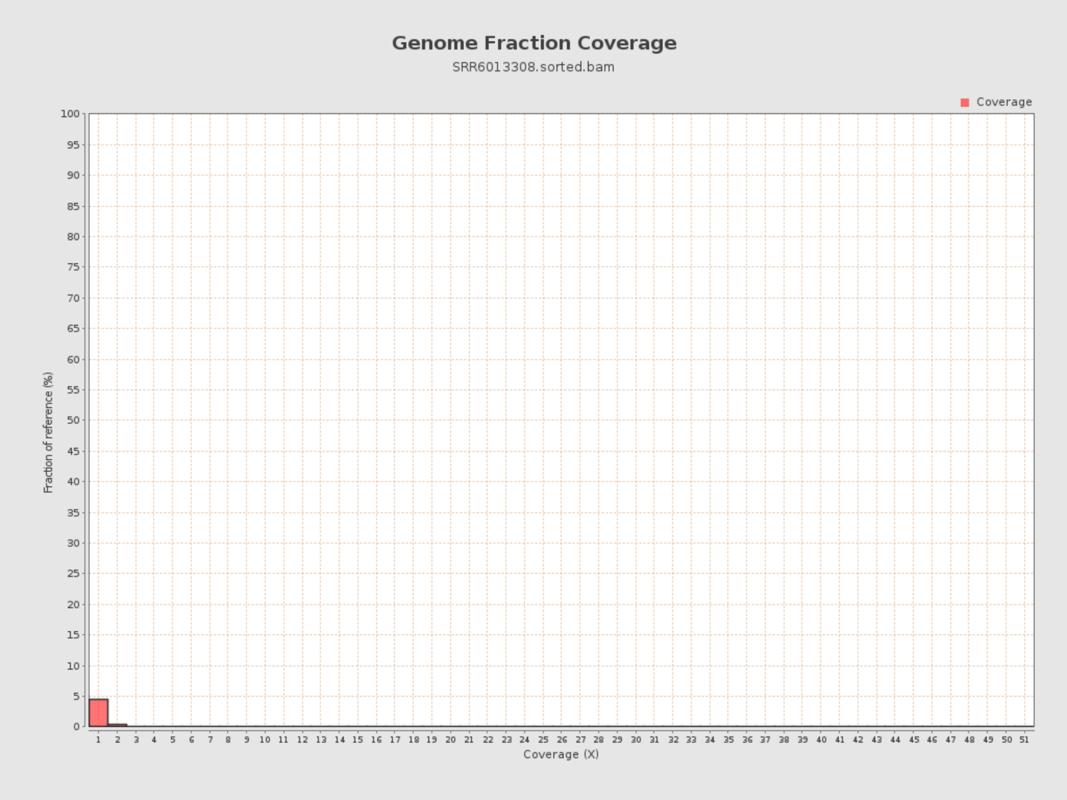
4. Results : Coverage Histogram



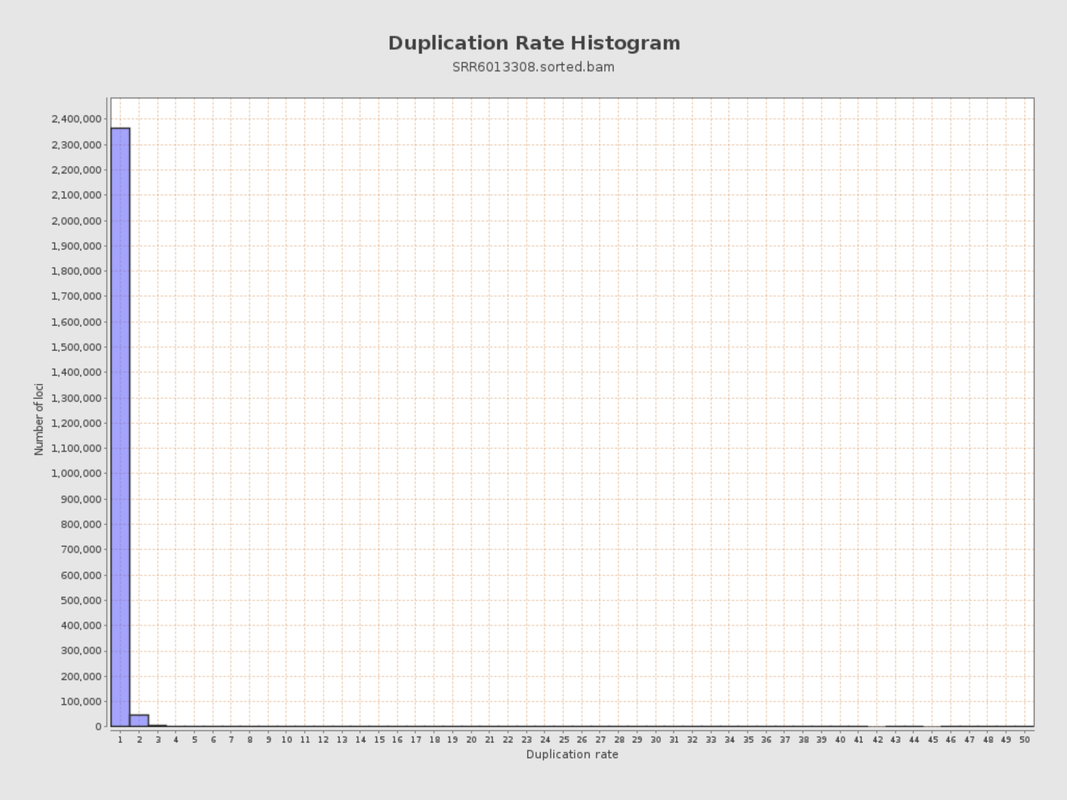
5. Results : Coverage Histogram (0-50X)



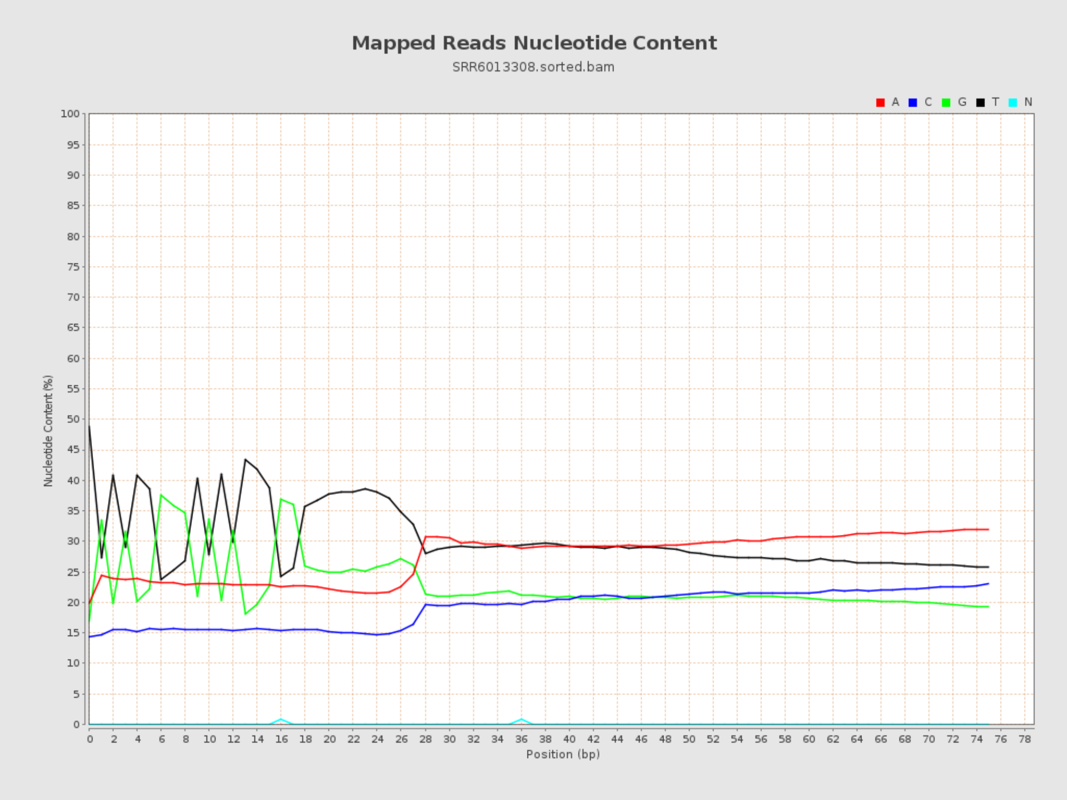
6. Results : Genome Fraction Coverage



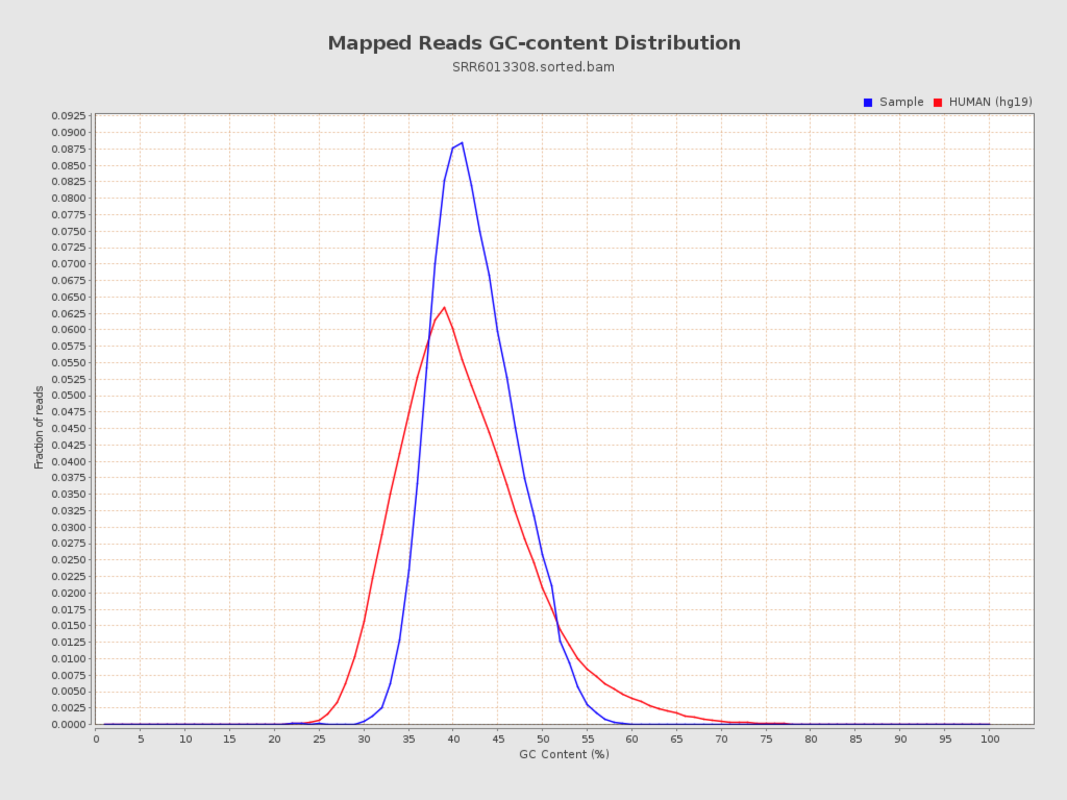
7. Results : Duplication Rate Histogram



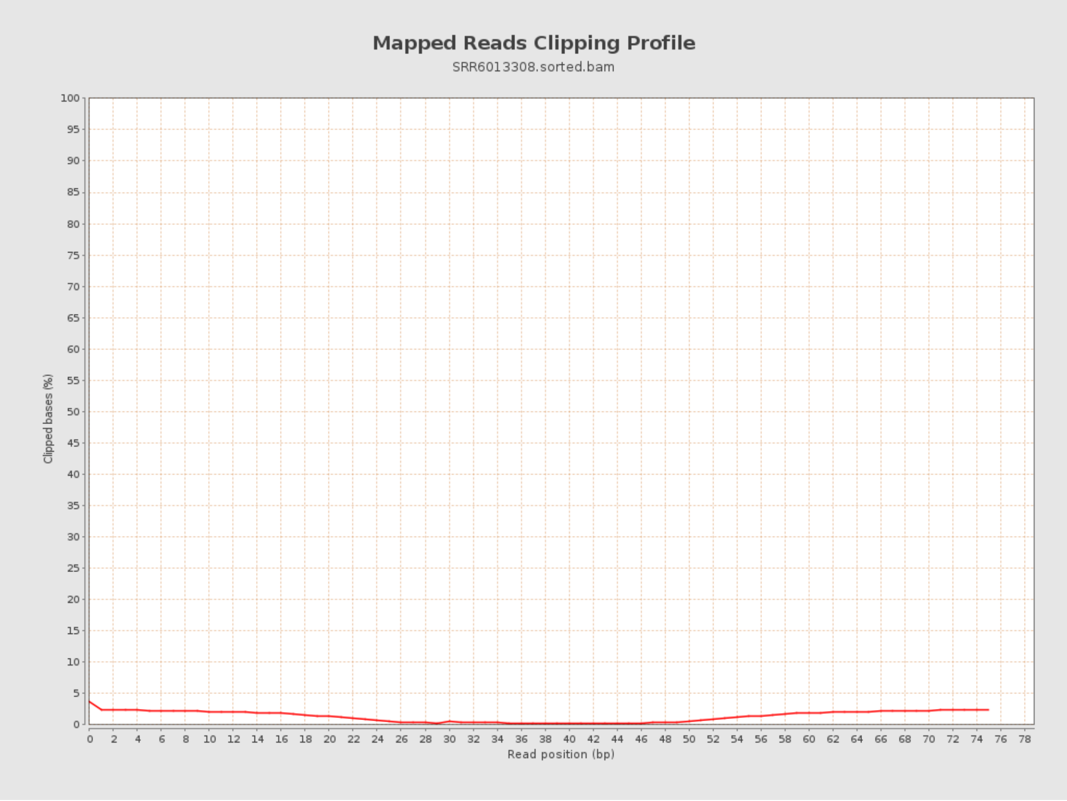
8. Results : Mapped Reads Nucleotide Content



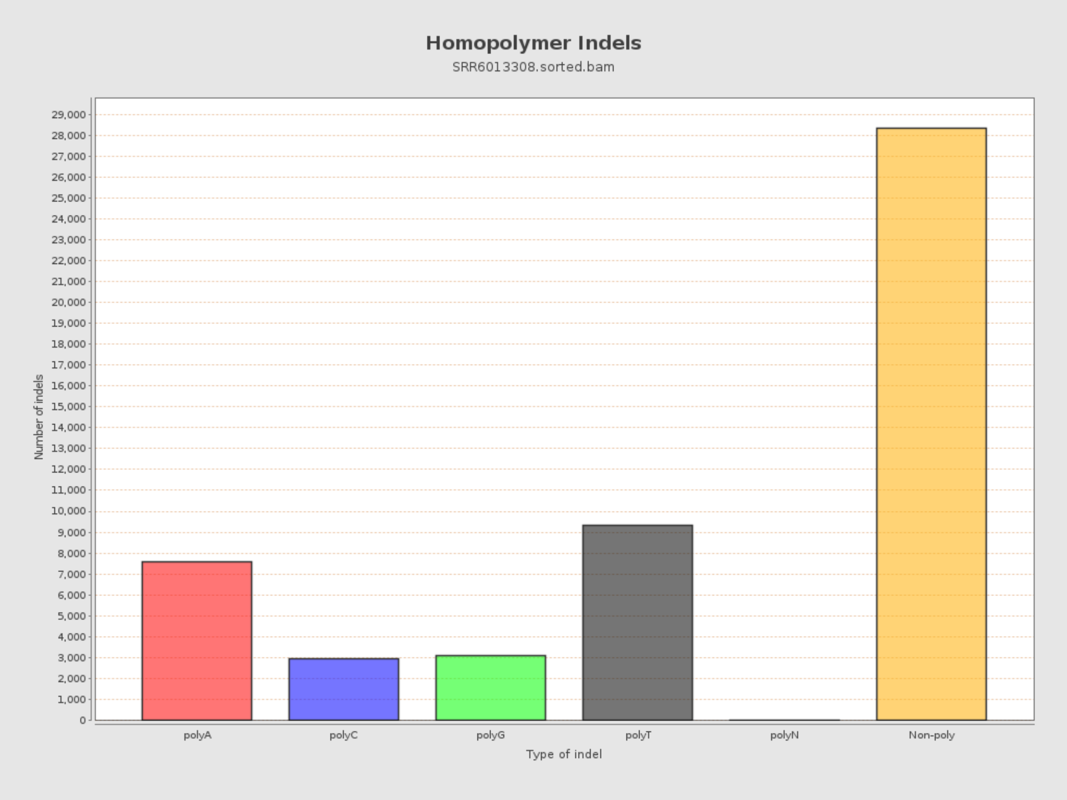
9. Results : Mapped Reads GC-content Distribution



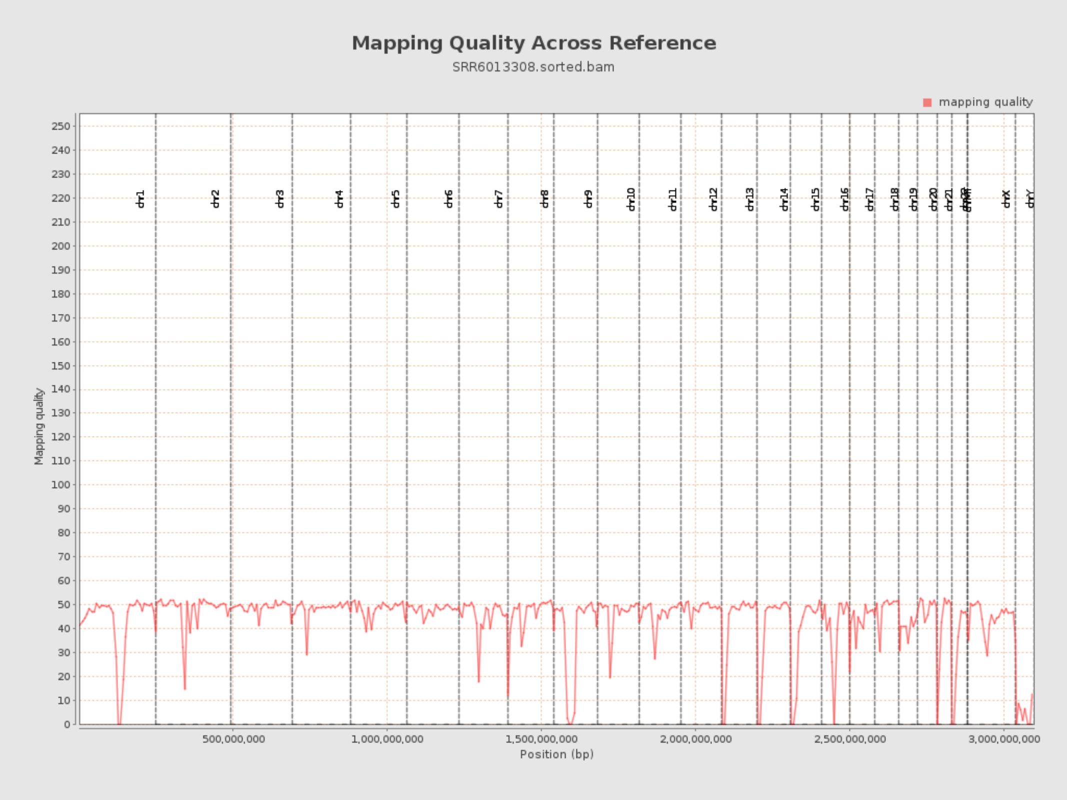
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram