Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 02:44:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231788.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_SRR6231788 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231788.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 02:44:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231788.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,656,610
Mapped reads	1,677,184 / 29.65%
Unmapped reads	3,979,426 / 70.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,264 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	305,119 / 5.39%
Duplication rate	10.75%
Clipped reads	1,107,643 / 19.58%

2.2. ACGT Content

Number/percentage of A's	29,417,022 / 28.78%
Number/percentage of C's	20,482,941 / 20.04%
Number/percentage of T's	28,464,824 / 27.85%
Number/percentage of G's	23,835,576 / 23.32%
Number/percentage of N's	7,990 / 0.01%
GC Percentage	43.36%

2.3. Coverage

Mean	0.033

Standard Deviation	5.4566

2.4. Mapping Quality

Mean Mapping Quality	43.43

2.5. Mismatches and indels

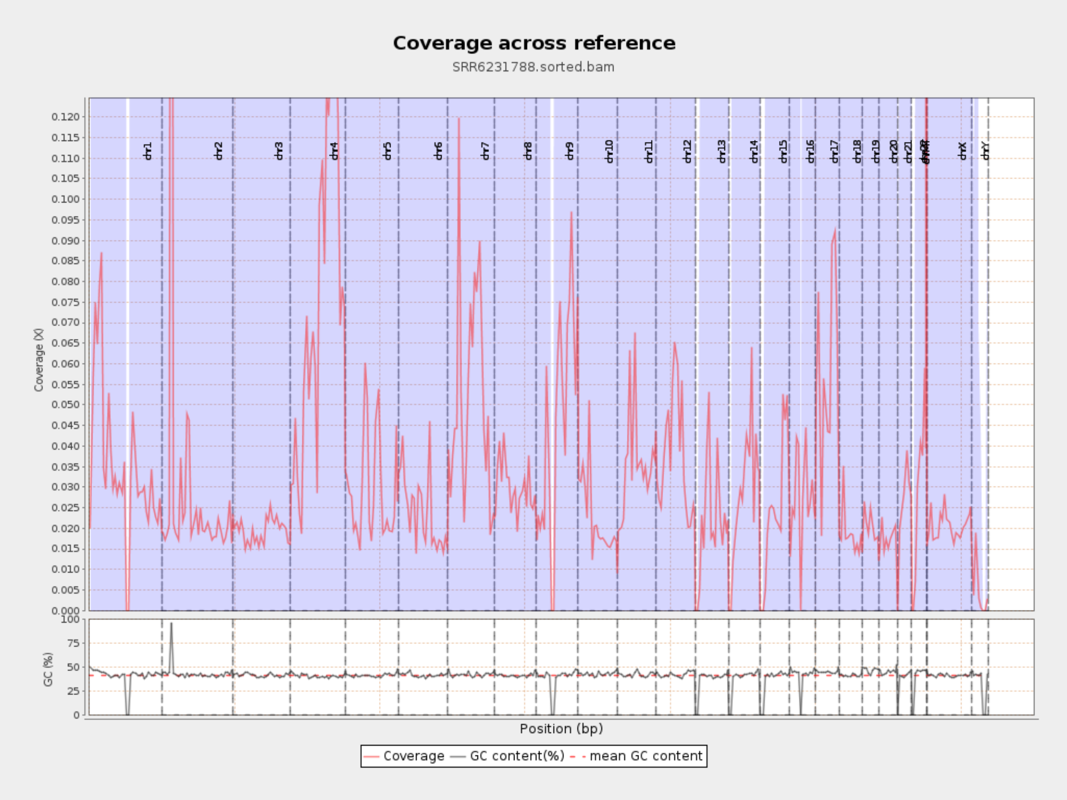
General error rate	0.65%
Mismatches	642,869
Insertions	7,967
Mapped reads with at least one insertion	0.47%
Deletions	22,034
Mapped reads with at least one deletion	1.3%
Homopolymer indels	44.68%

2.6. Chromosome stats

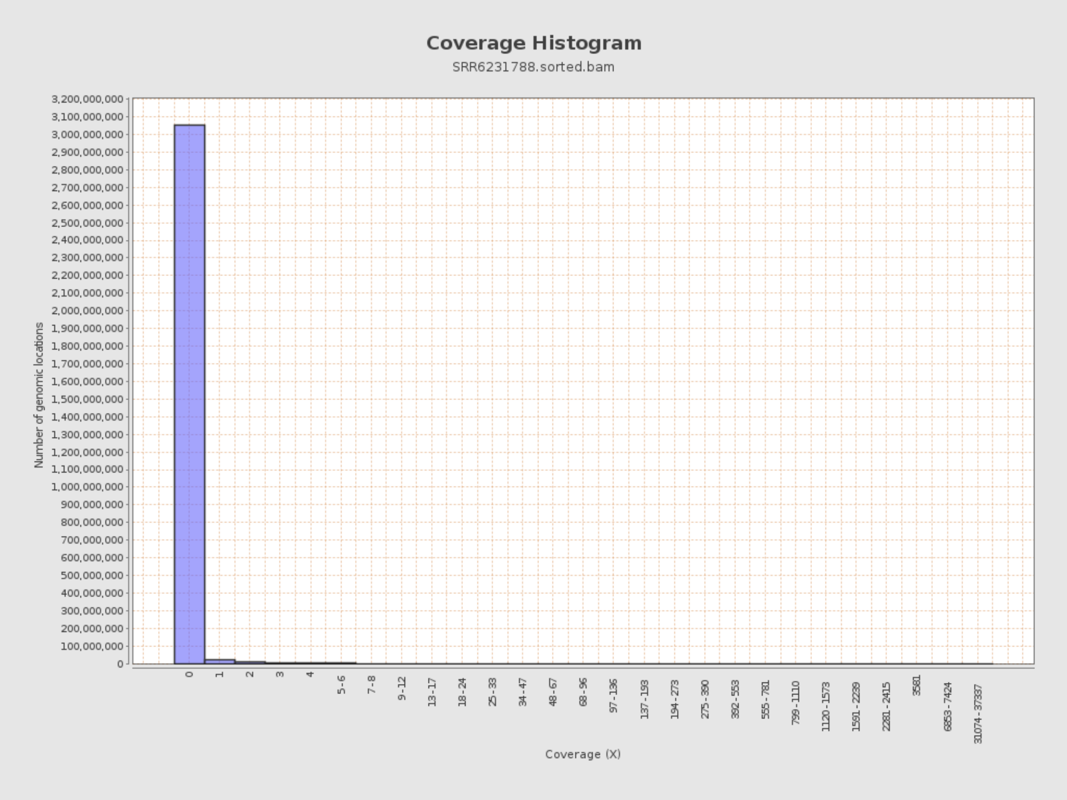
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8792828	0.0353	0.4618
chr2	243199373	8410651	0.0346	19.4163
chr3	198022430	3872940	0.0196	0.2696
chr4	191154276	14436859	0.0755	0.563
chr5	180915260	5259744	0.0291	0.3315
chr6	171115067	4128830	0.0241	0.3175
chr7	159138663	8394156	0.0527	0.5201

chr8	146364022	4385234	0.03	0.377
chr9	141213431	6453025	0.0457	0.5392
chr10	135534747	3086377	0.0228	0.4328
chr11	135006516	4789443	0.0355	0.4048
chr12	133851895	5064985	0.0378	0.3949
chr13	115169878	2446681	0.0212	0.298
chr14	107349540	3074741	0.0286	0.443
chr15	102531392	2498931	0.0244	0.307
chr16	90354753	2448390	0.0271	0.3631
chr17	81195210	4743863	0.0584	0.478
chr18	78077248	1460227	0.0187	0.6732
chr19	59128983	1209428	0.0205	0.3689
chr20	63025520	1109186	0.0176	0.2765
chr21	48129895	1239530	0.0258	0.3756
chr22	51304566	1431910	0.0279	0.3196
chrMT	16571	51781	3.1248	3.484
chrX	155270560	3185446	0.0205	0.3151
chrY	59373566	268207	0.0045	0.2028

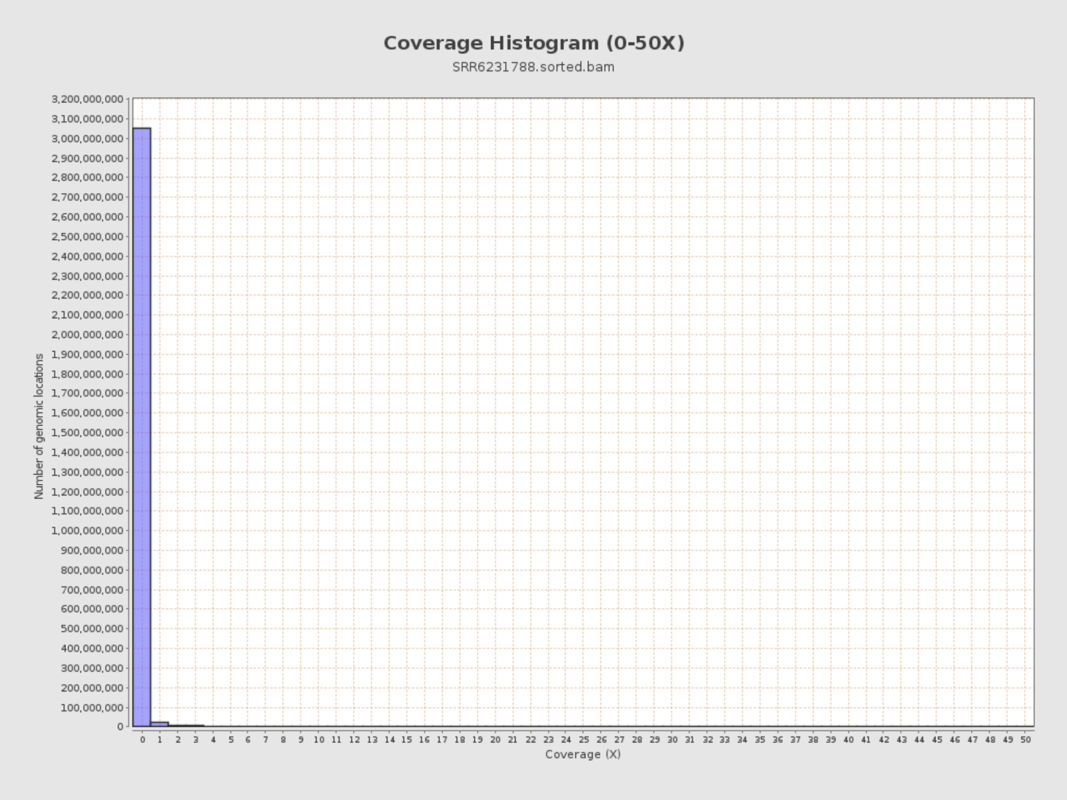
3. Results : Coverage across reference



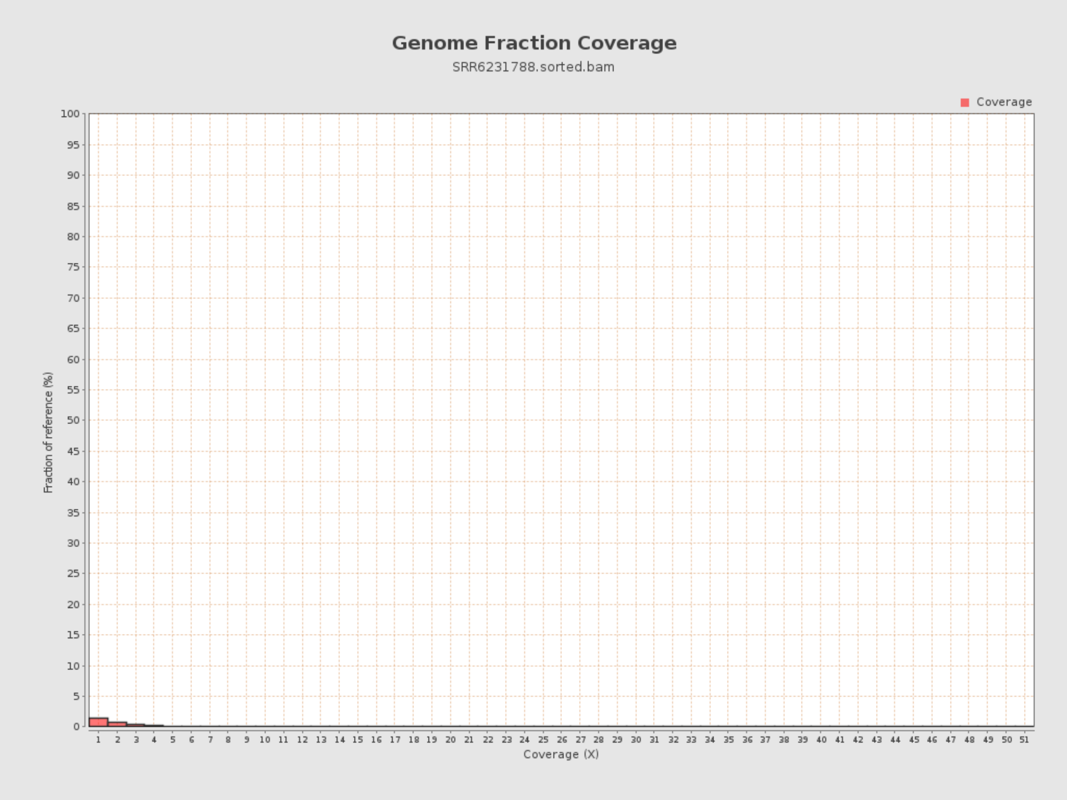
4. Results : Coverage Histogram



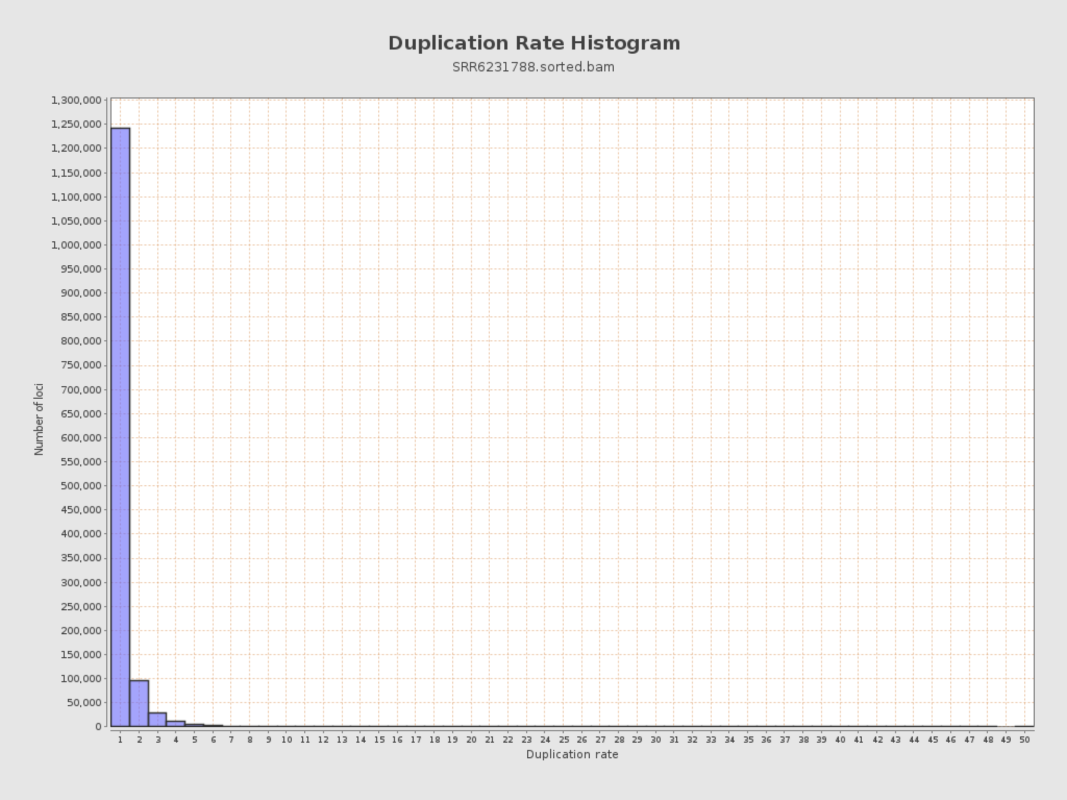
5. Results : Coverage Histogram (0-50X)



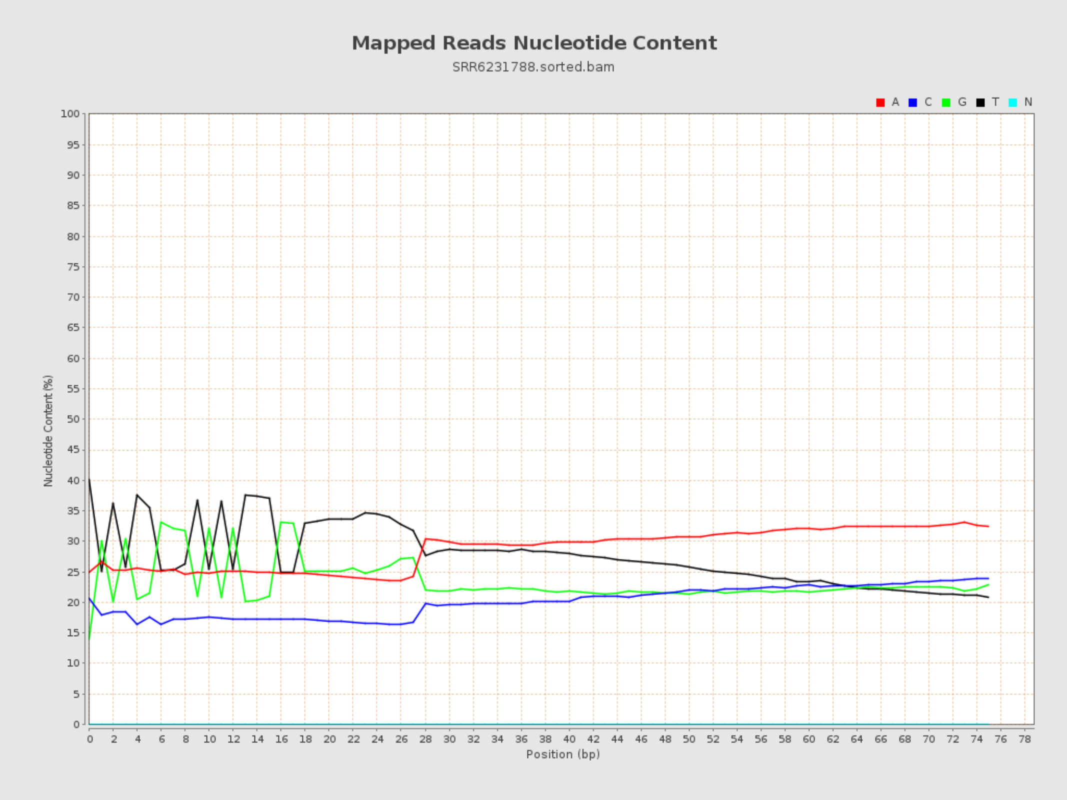
6. Results : Genome Fraction Coverage



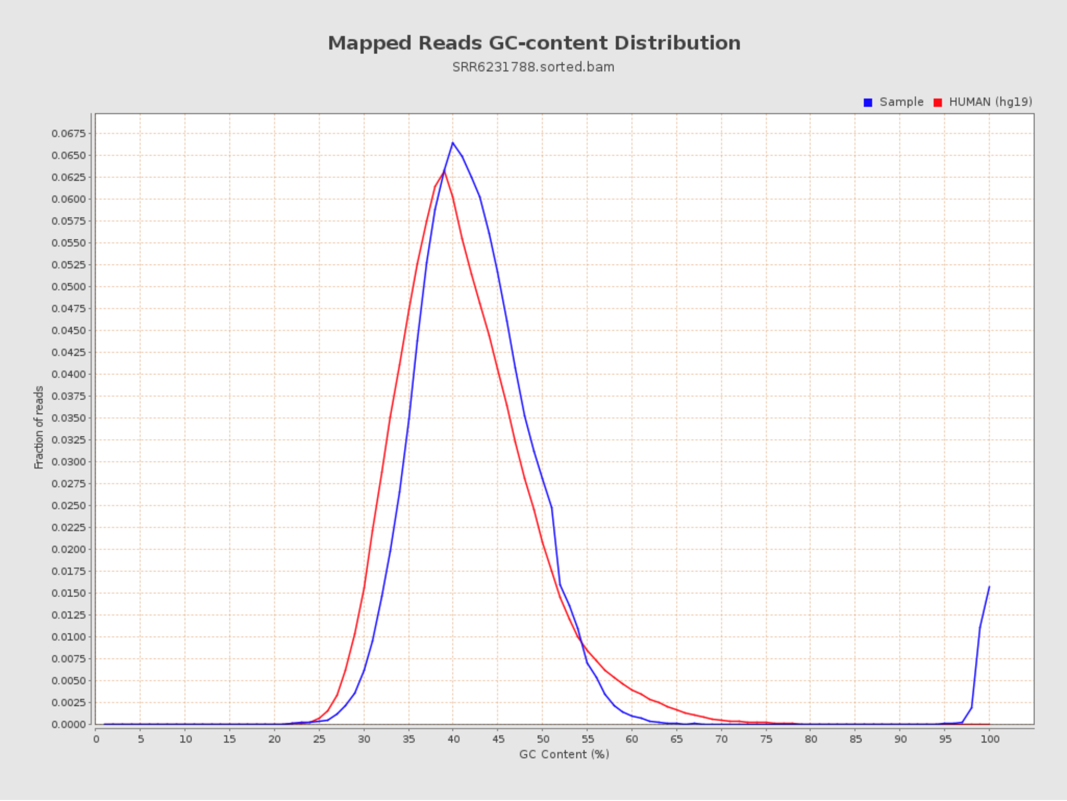
7. Results : Duplication Rate Histogram



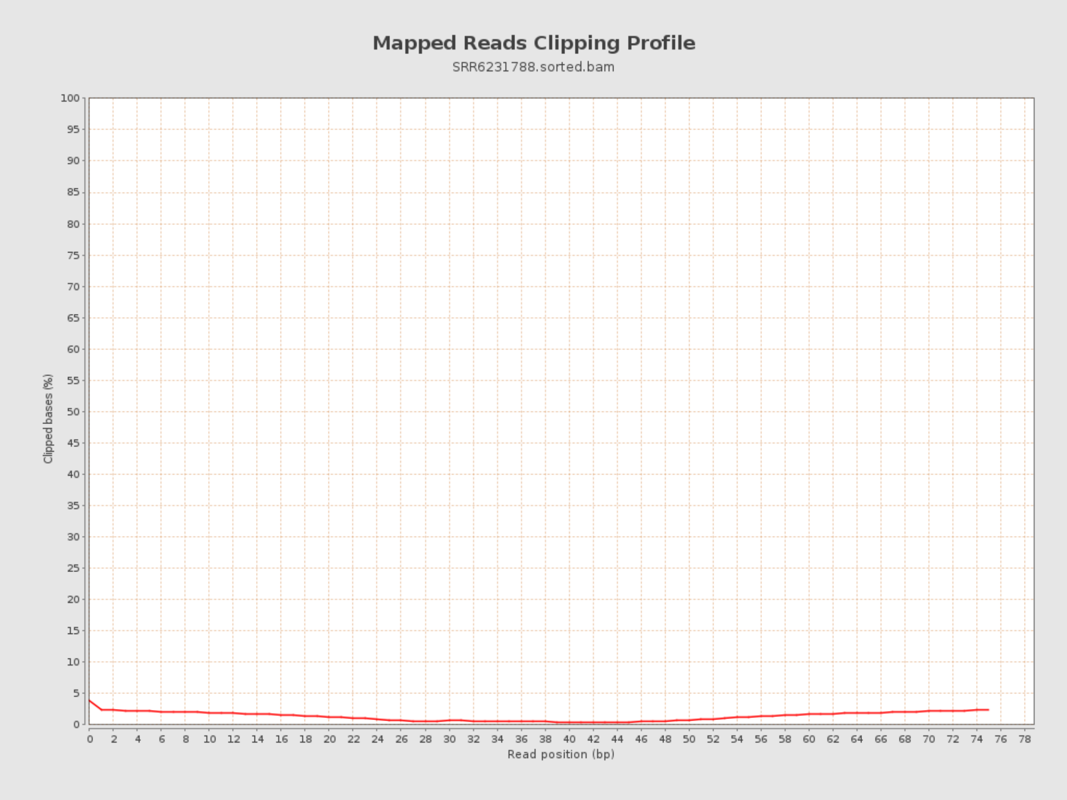
8. Results : Mapped Reads Nucleotide Content



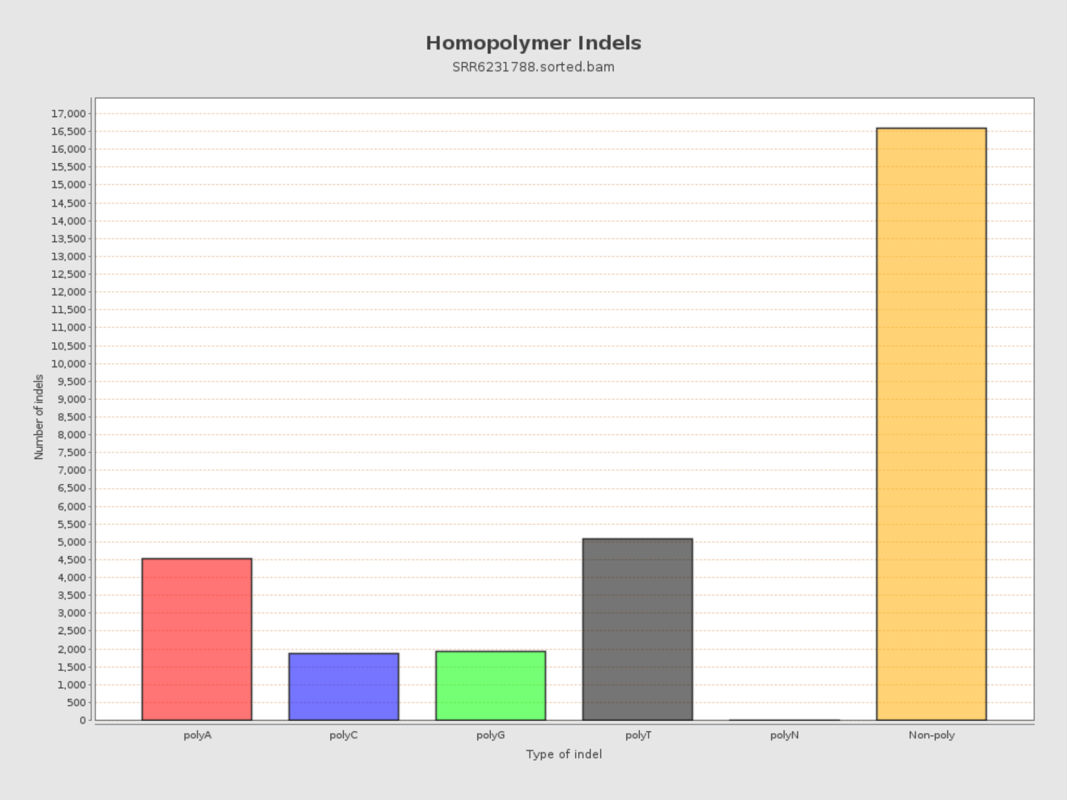
9. Results : Mapped Reads GC-content Distribution



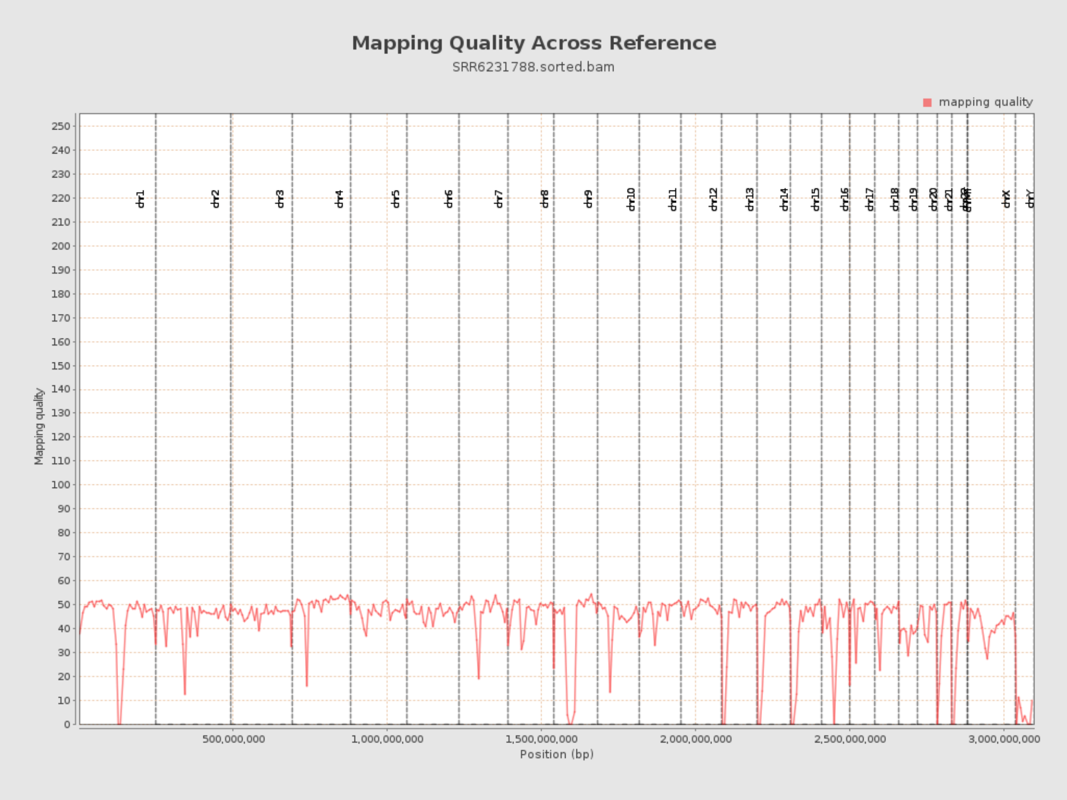
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram