Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:30:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231744.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_SRR6231744 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231744.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:30:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231744.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	869,466
Mapped reads	671,563 / 77.24%
Unmapped reads	197,903 / 22.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,928 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	36,810 / 4.23%
Duplication rate	4.24%
Clipped reads	322,684 / 37.11%

2.2. ACGT Content

Number/percentage of A's	12,632,698 / 28.68%
Number/percentage of C's	7,440,355 / 16.89%
Number/percentage of T's	14,749,248 / 33.49%
Number/percentage of G's	9,221,027 / 20.94%
Number/percentage of N's	1,954 / 0%
GC Percentage	37.83%

2.3. Coverage

Mean	0.0142

Standard Deviation	0.3595

2.4. Mapping Quality

Mean Mapping Quality	46.11

2.5. Mismatches and indels

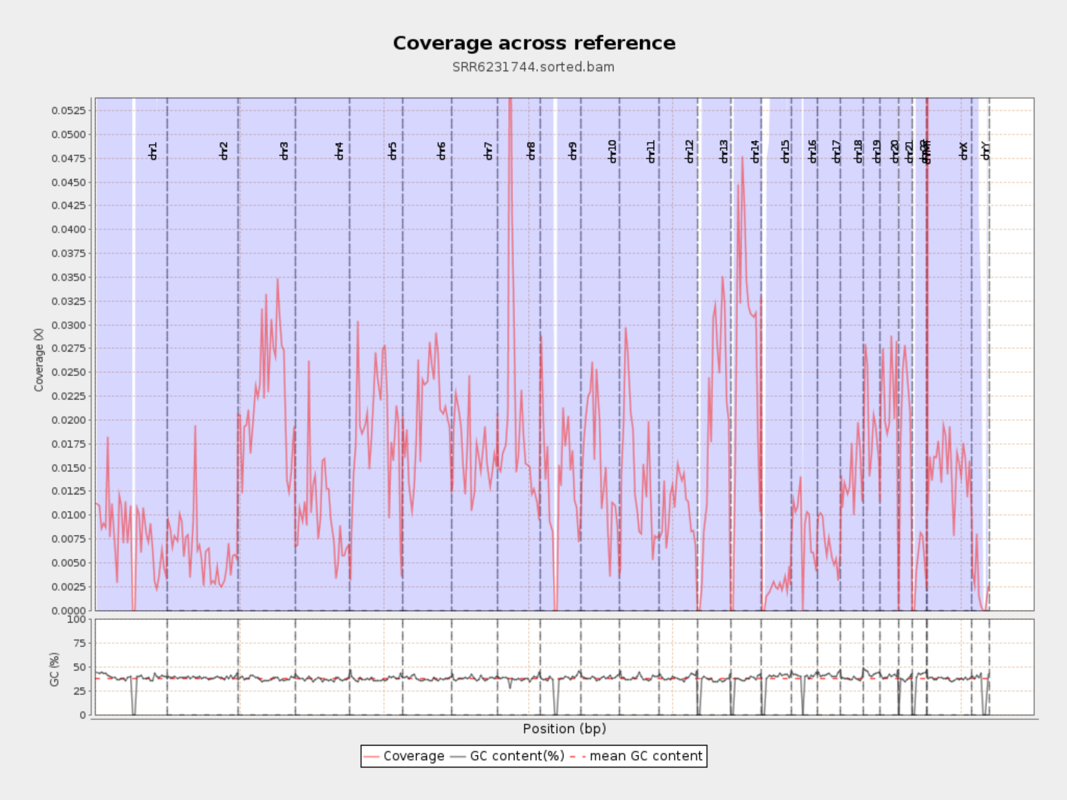
General error rate	0.92%
Mismatches	398,896
Insertions	3,974
Mapped reads with at least one insertion	0.59%
Deletions	15,526
Mapped reads with at least one deletion	2.27%
Homopolymer indels	44.41%

2.6. Chromosome stats

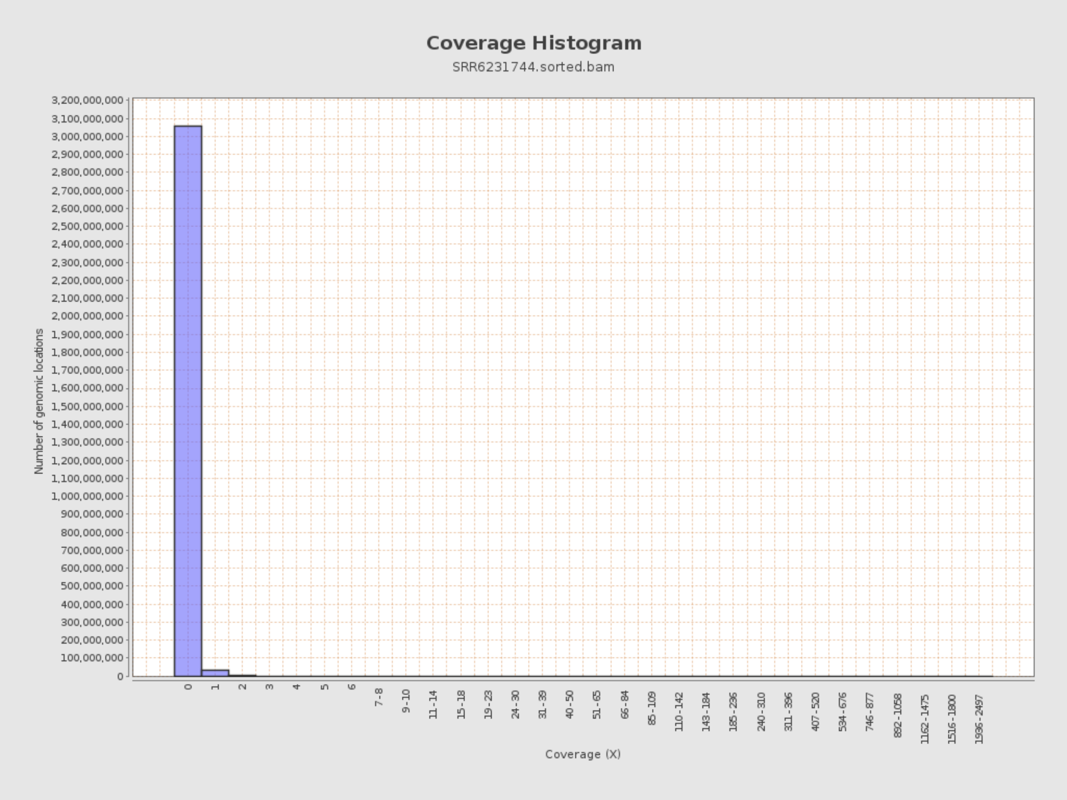
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1926307	0.0077	0.1665
chr2	243199373	1526313	0.0063	0.1359
chr3	198022430	4523836	0.0228	0.1727
chr4	191154276	1929880	0.0101	0.1262
chr5	180915260	3462610	0.0191	0.1599
chr6	171115067	3559393	0.0208	0.1689
chr7	159138663	2640639	0.0166	0.188

chr8	146364022	2995319	0.0205	1.5037
chr9	141213431	1938257	0.0137	0.1472
chr10	135534747	2070937	0.0153	0.1743
chr11	135006516	1951704	0.0145	0.143
chr12	133851895	1440229	0.0108	0.1203
chr13	115169878	2245880	0.0195	0.1621
chr14	107349540	2891052	0.0269	0.1912
chr15	102531392	233443	0.0023	0.0534
chr16	90354753	758327	0.0084	0.109
chr17	81195210	562206	0.0069	0.0957
chr18	78077248	1103413	0.0141	0.2123
chr19	59128983	1148332	0.0194	0.1796
chr20	63025520	1416256	0.0225	0.1748
chr21	48129895	971964	0.0202	0.1684
chr22	51304566	236551	0.0046	0.0746
chrMT	16571	41256	2.4897	2.1669
chrX	155270560	2359350	0.0152	0.1436
chrY	59373566	139172	0.0023	0.0709

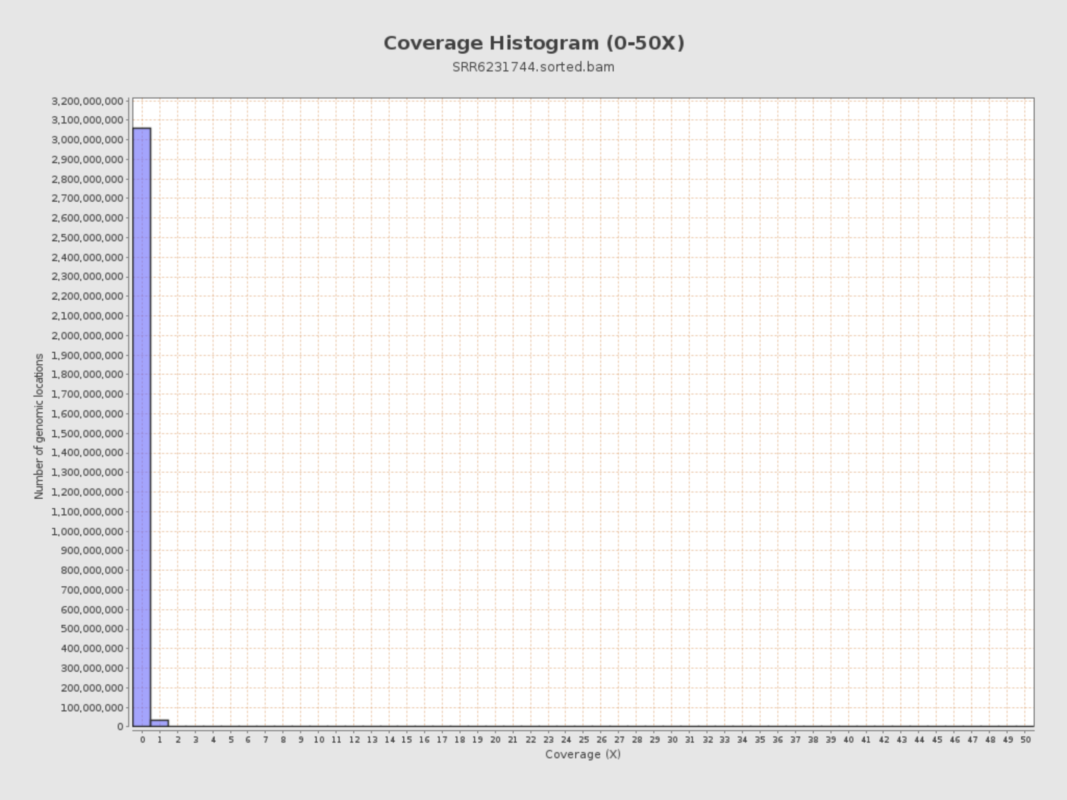
3. Results : Coverage across reference



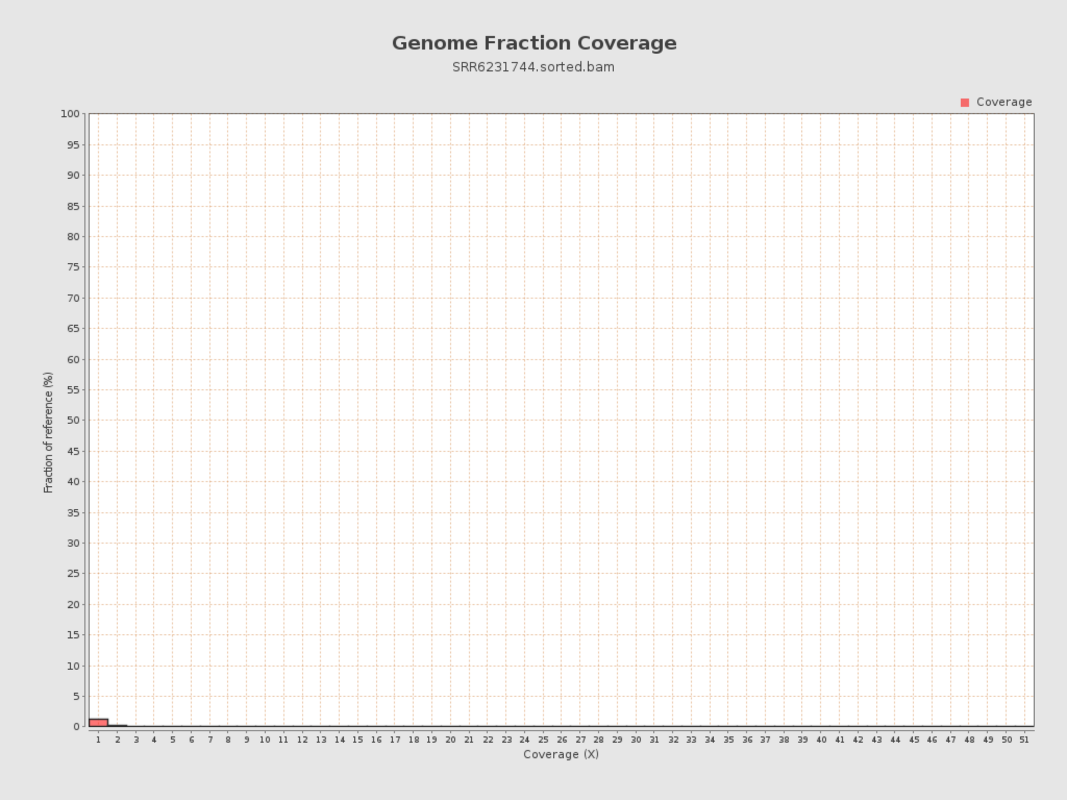
4. Results : Coverage Histogram



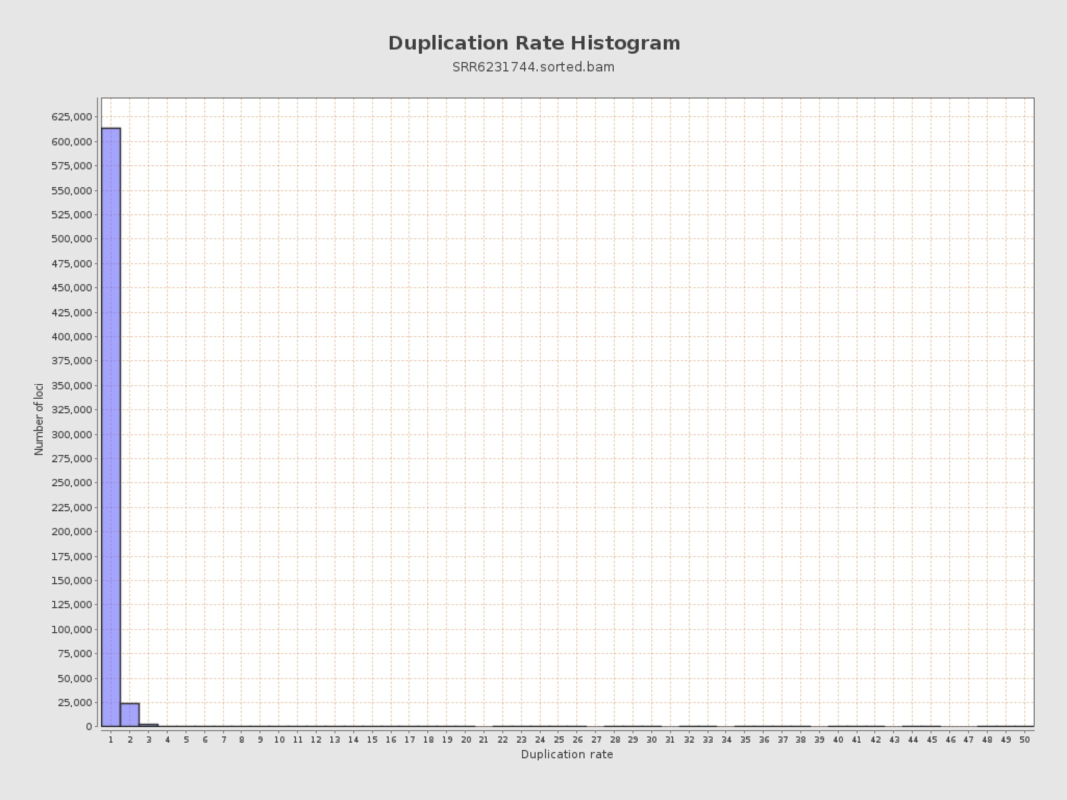
5. Results : Coverage Histogram (0-50X)



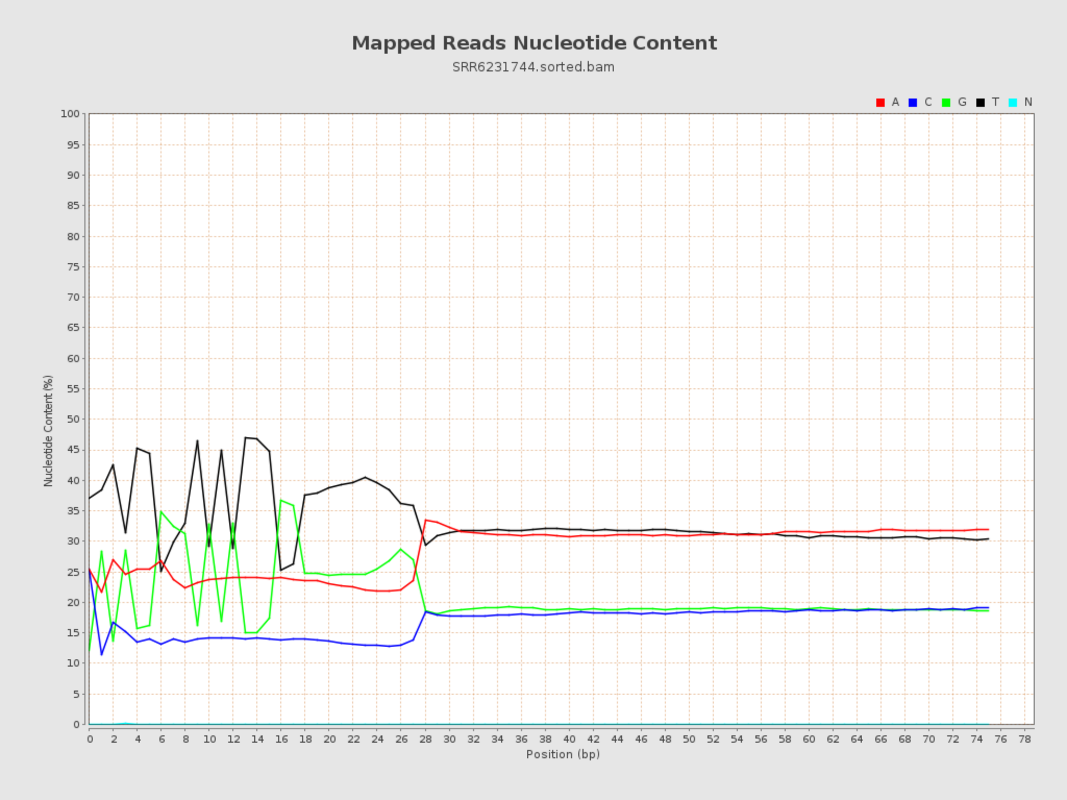
6. Results : Genome Fraction Coverage



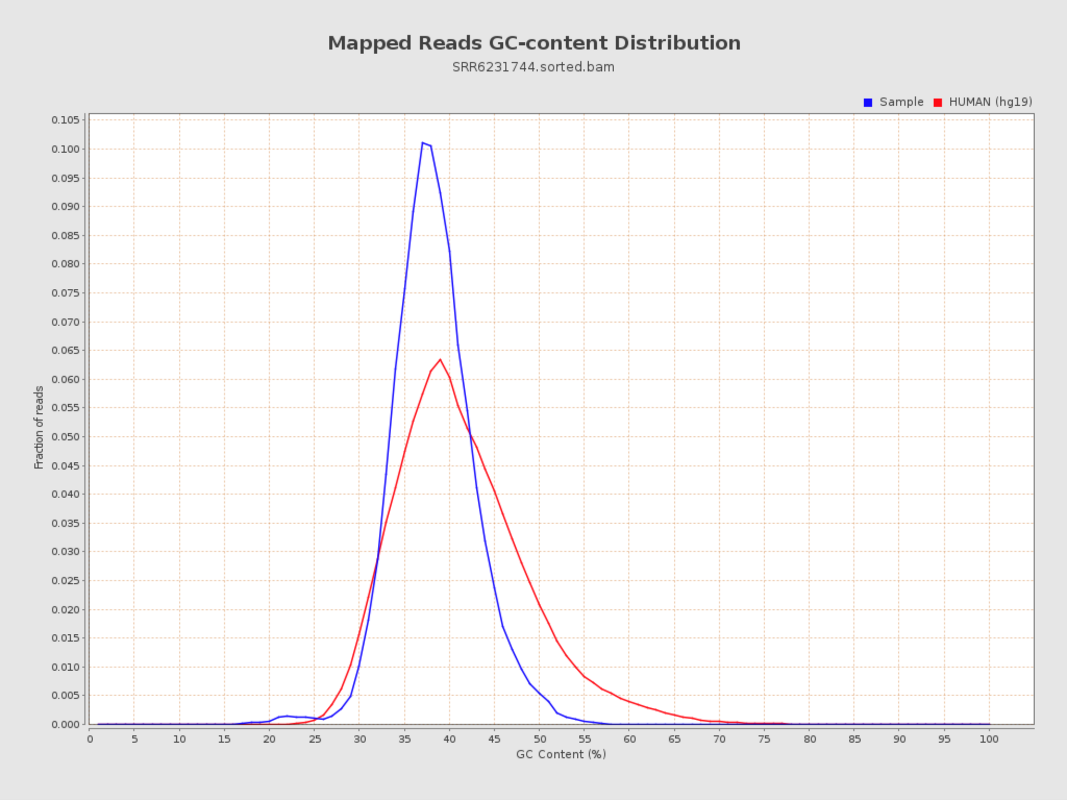
7. Results : Duplication Rate Histogram



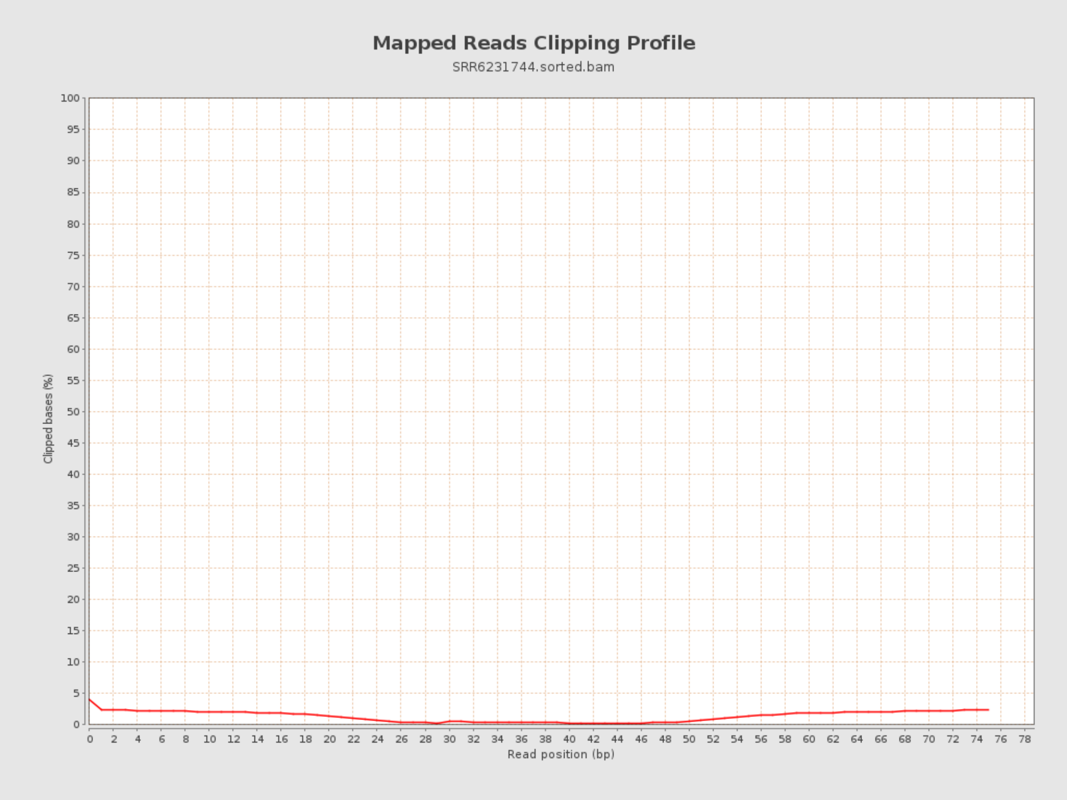
8. Results : Mapped Reads Nucleotide Content



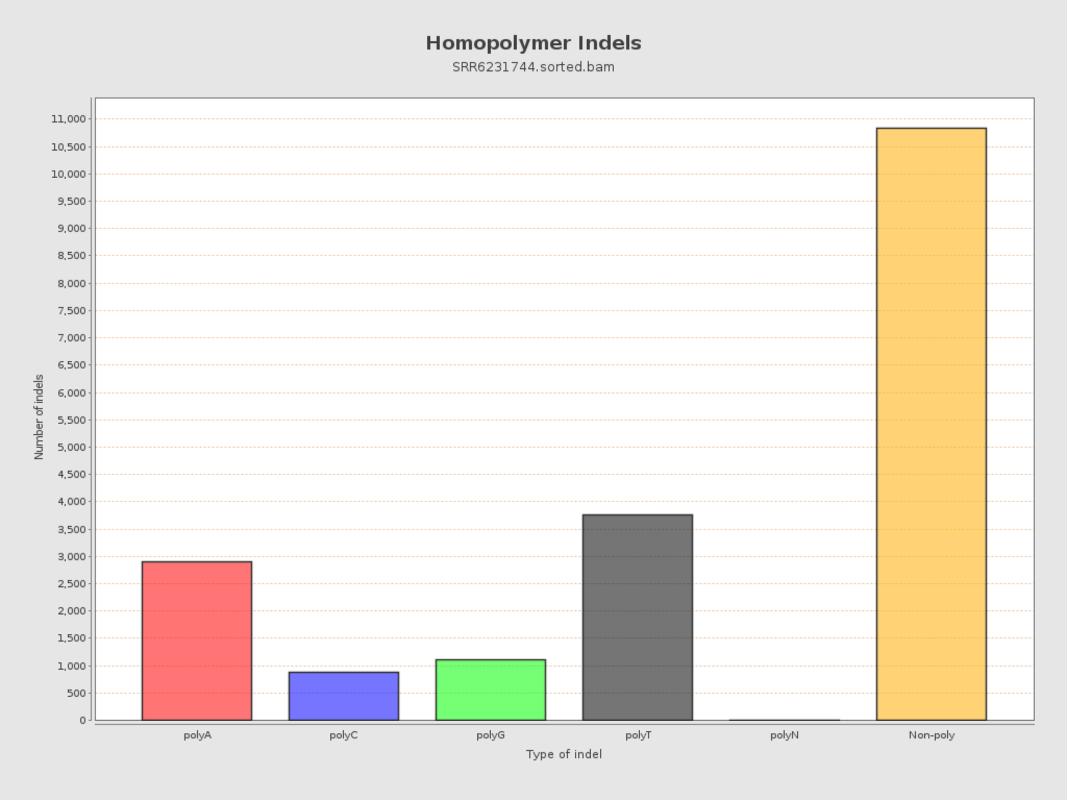
9. Results : Mapped Reads GC-content Distribution



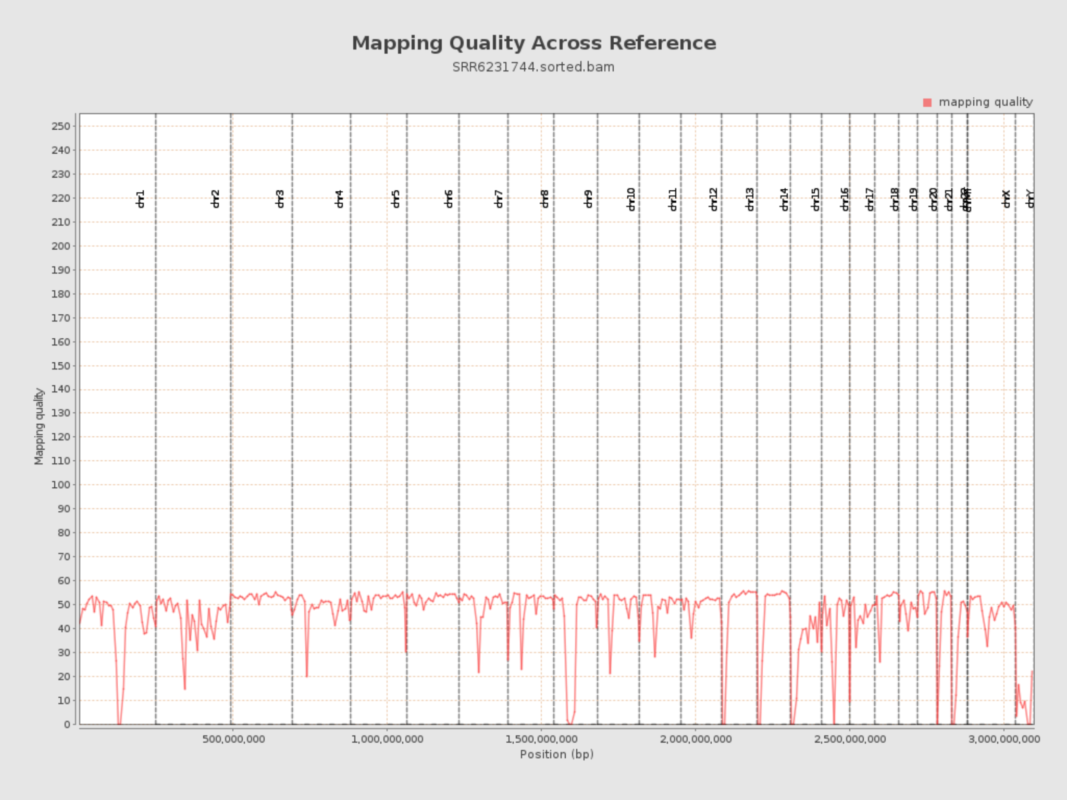
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram