Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:18:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231739.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_SRR6231739 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231739.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:18:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231739.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,041,067
Mapped reads	1,237,606 / 60.64%
Unmapped reads	803,461 / 39.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,978 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	204,567 / 10.02%
Duplication rate	11.21%
Clipped reads	569,836 / 27.92%

2.2. ACGT Content

Number/percentage of A's	23,315,139 / 28.62%
Number/percentage of C's	14,063,534 / 17.26%
Number/percentage of T's	27,059,287 / 33.22%
Number/percentage of G's	17,025,073 / 20.9%
Number/percentage of N's	2,209 / 0%
GC Percentage	38.16%

2.3. Coverage

Mean	0.0263

Standard Deviation	0.6543

2.4. Mapping Quality

Mean Mapping Quality	44.9

2.5. Mismatches and indels

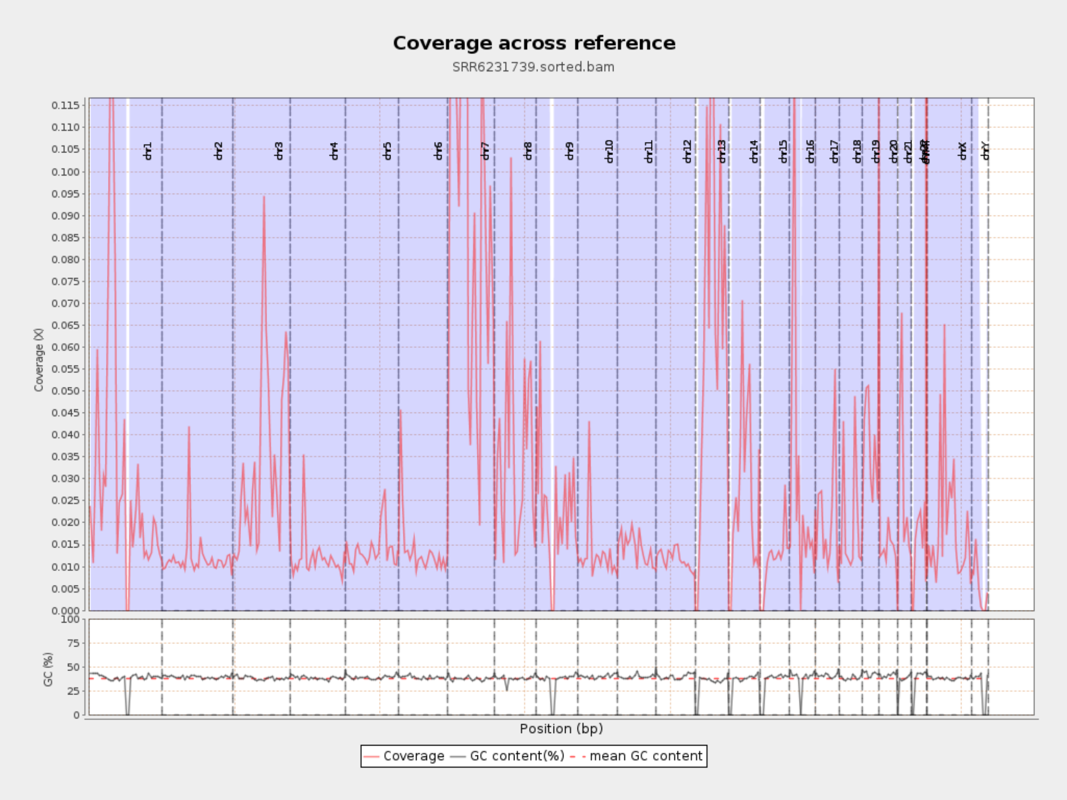
General error rate	0.93%
Mismatches	738,747
Insertions	7,696
Mapped reads with at least one insertion	0.61%
Deletions	31,409
Mapped reads with at least one deletion	2.49%
Homopolymer indels	44.52%

2.6. Chromosome stats

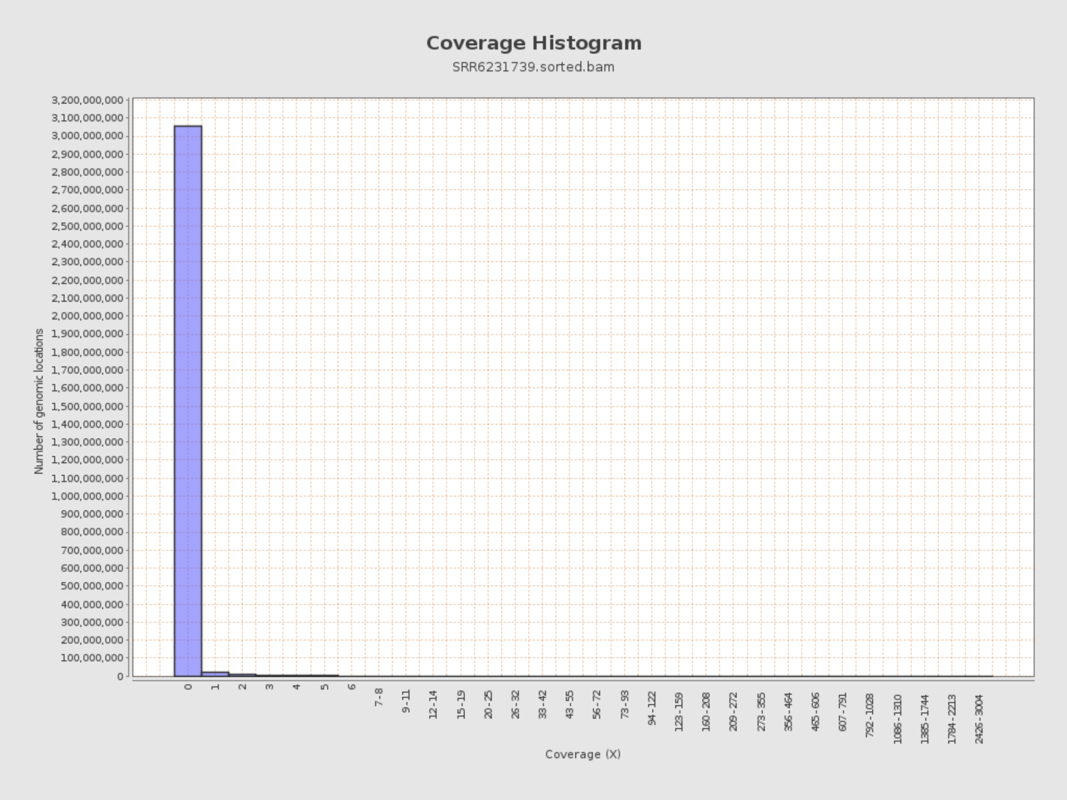
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7960796	0.0319	0.5168
chr2	243199373	2948618	0.0121	0.3116
chr3	198022430	6756384	0.0341	0.3395
chr4	191154276	2279146	0.0119	0.1985
chr5	180915260	2550184	0.0141	0.2139
chr6	171115067	2399018	0.014	0.2227
chr7	159138663	15751635	0.099	1.6724

chr8	146364022	5317886	0.0363	1.8371
chr9	141213431	3139294	0.0222	0.3517
chr10	135534747	1748856	0.0129	0.2939
chr11	135006516	1878398	0.0139	0.2886
chr12	133851895	1571097	0.0117	0.1907
chr13	115169878	7837311	0.0681	0.4967
chr14	107349540	2776101	0.0259	0.3306
chr15	102531392	1199422	0.0117	0.1991
chr16	90354753	2747553	0.0304	0.3439
chr17	81195210	1602761	0.0197	0.2492
chr18	78077248	1568852	0.0201	0.8921
chr19	59128983	2358213	0.0399	0.3939
chr20	63025520	893738	0.0142	0.212
chr21	48129895	1322117	0.0275	0.306
chr22	51304566	777387	0.0152	0.1986
chrMT	16571	786603	47.4687	27.1119
chrX	155270560	3035116	0.0195	0.2704
chrY	59373566	313604	0.0053	0.1244

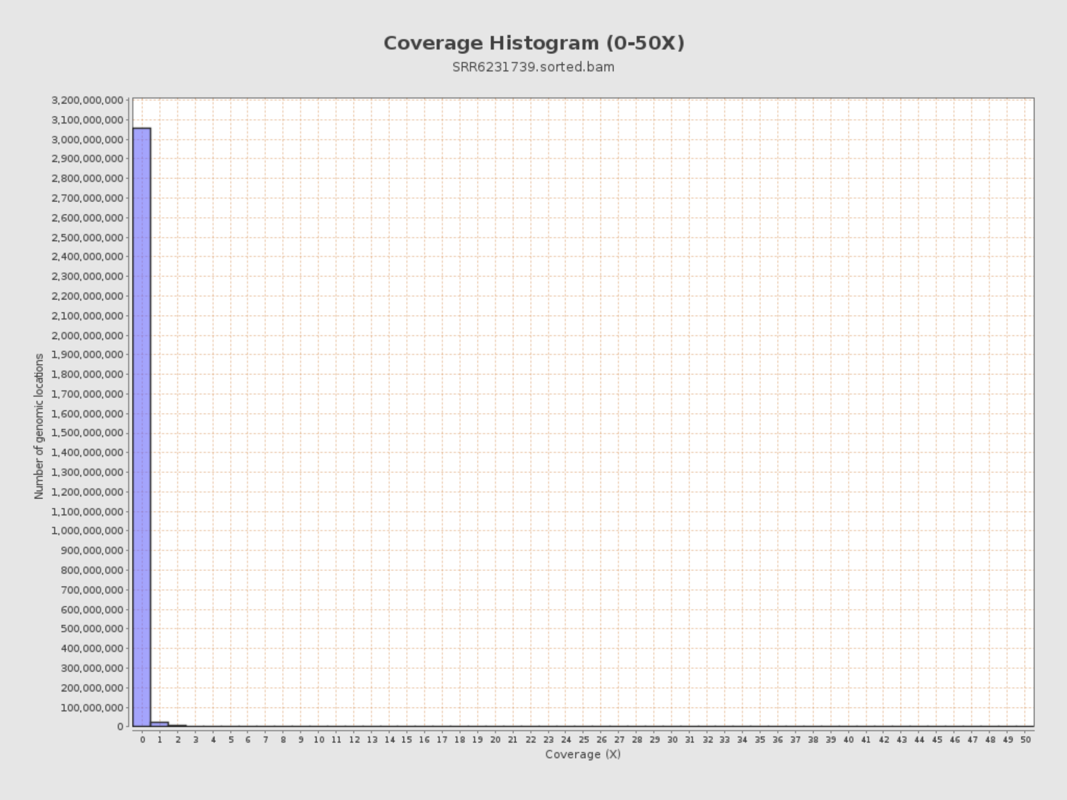
3. Results : Coverage across reference



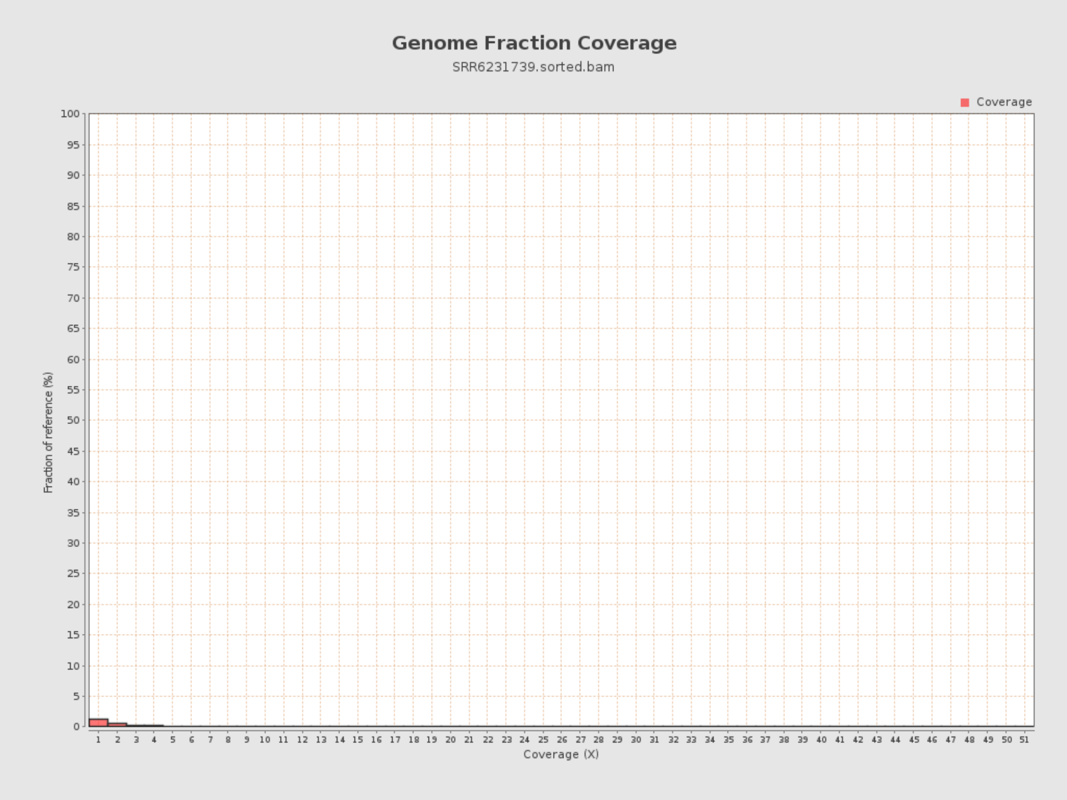
4. Results : Coverage Histogram



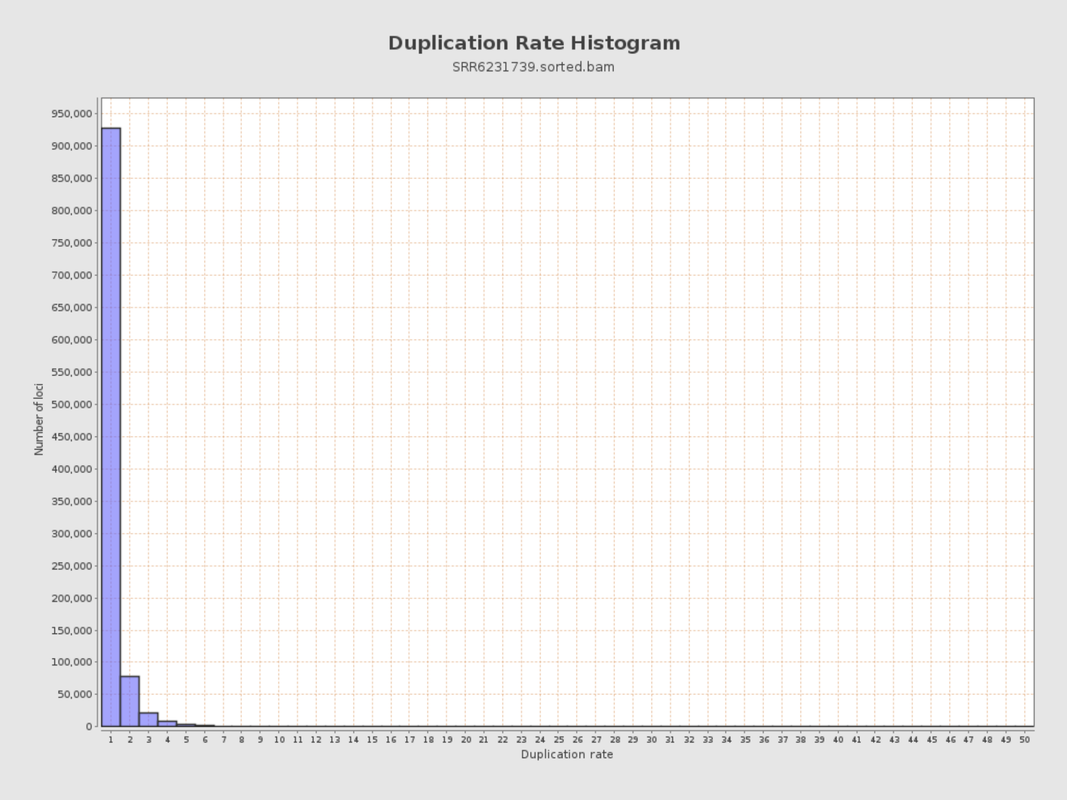
5. Results : Coverage Histogram (0-50X)



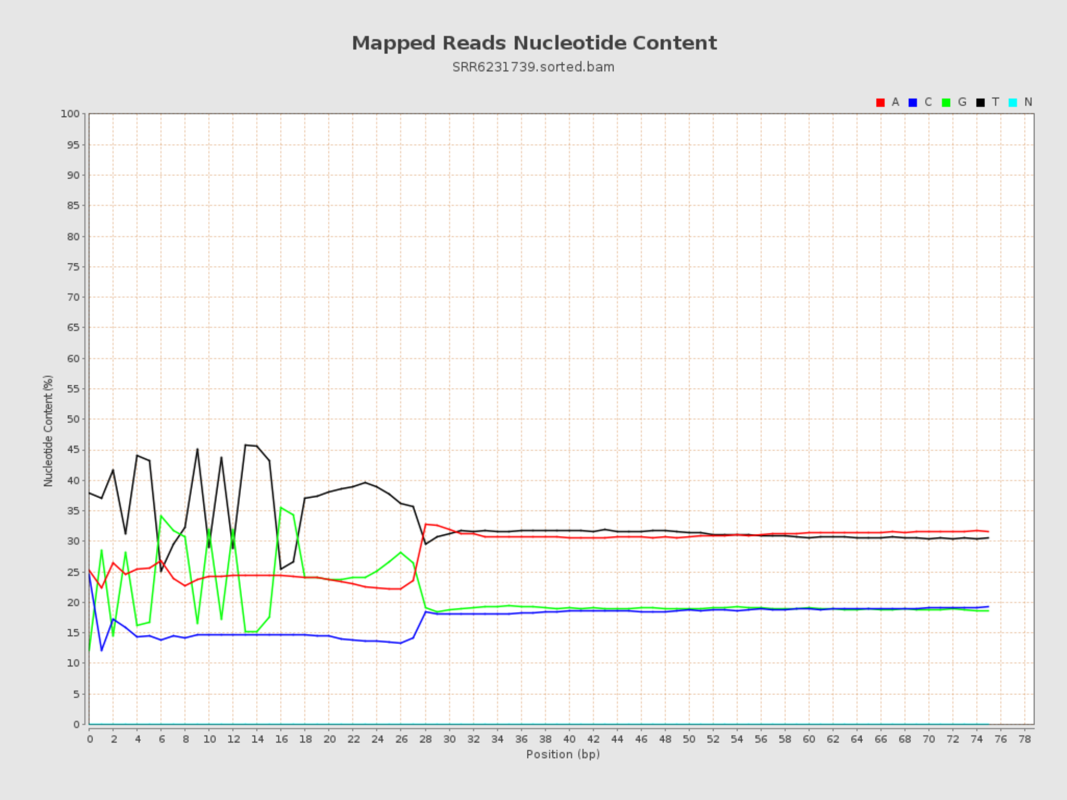
6. Results : Genome Fraction Coverage



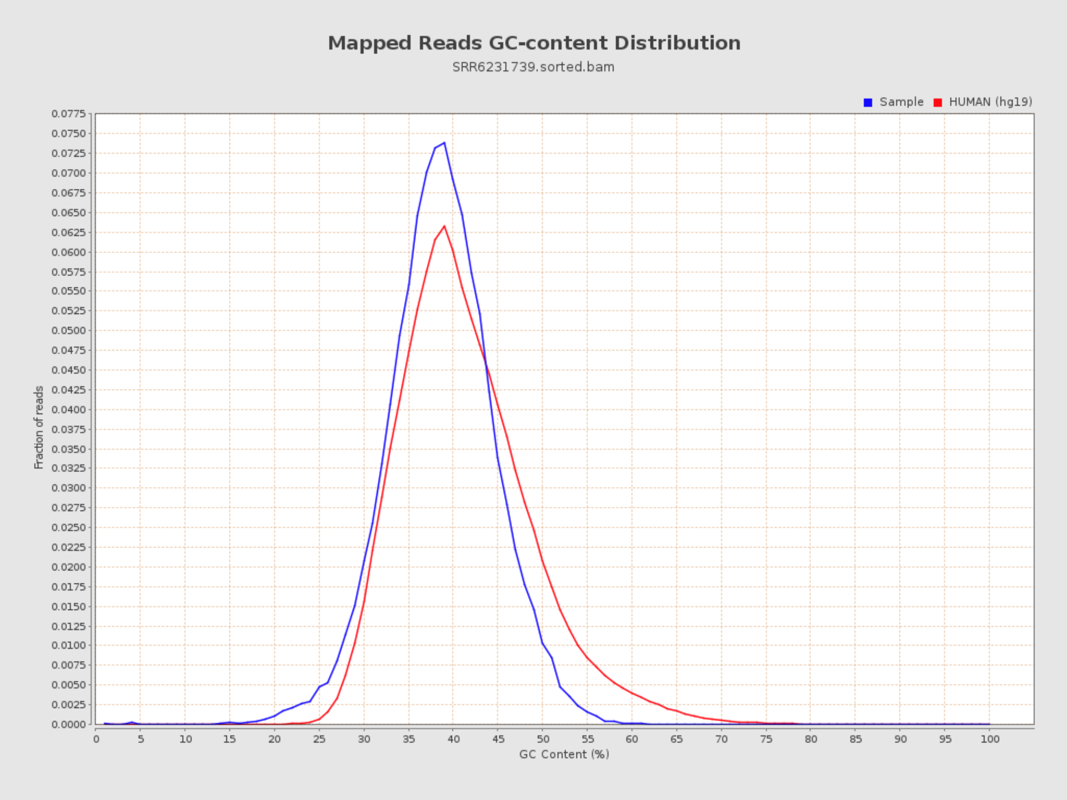
7. Results : Duplication Rate Histogram



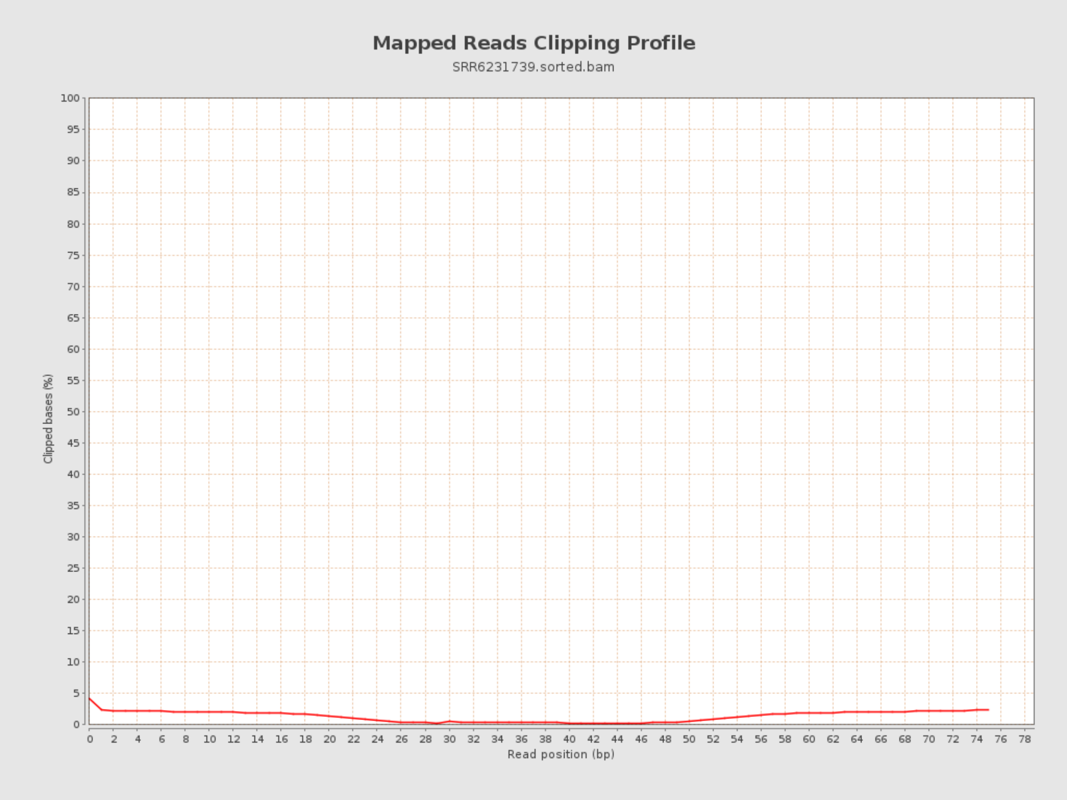
8. Results : Mapped Reads Nucleotide Content



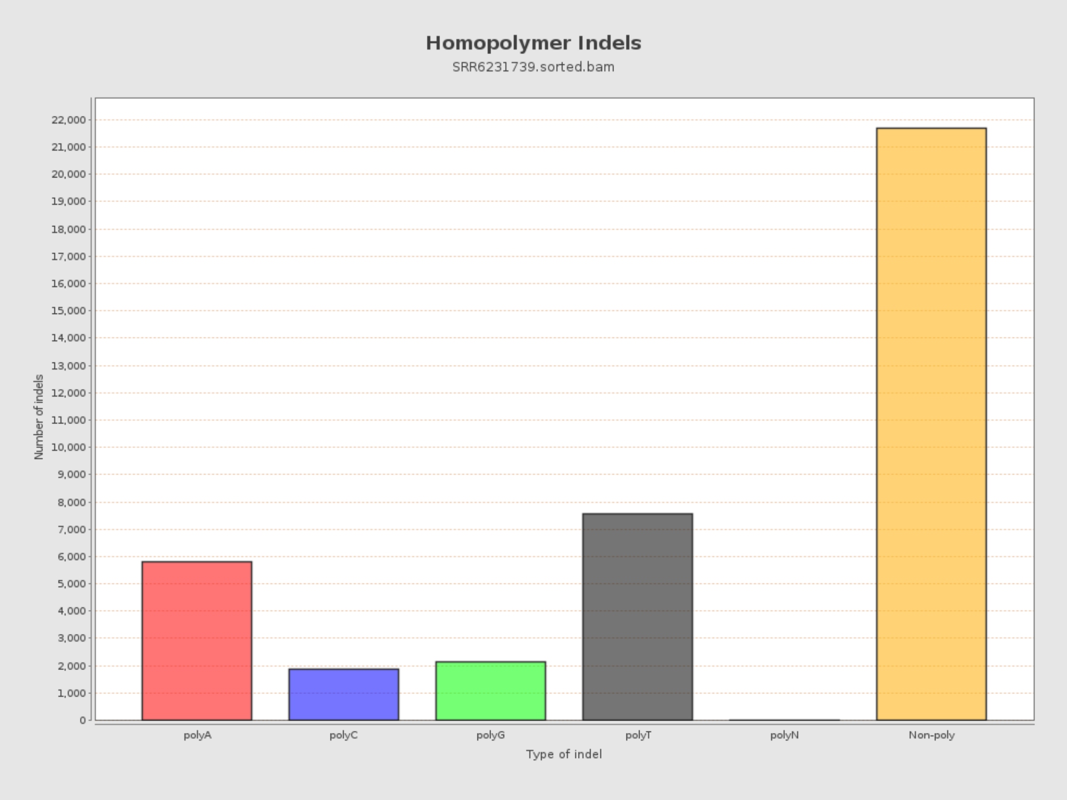
9. Results : Mapped Reads GC-content Distribution



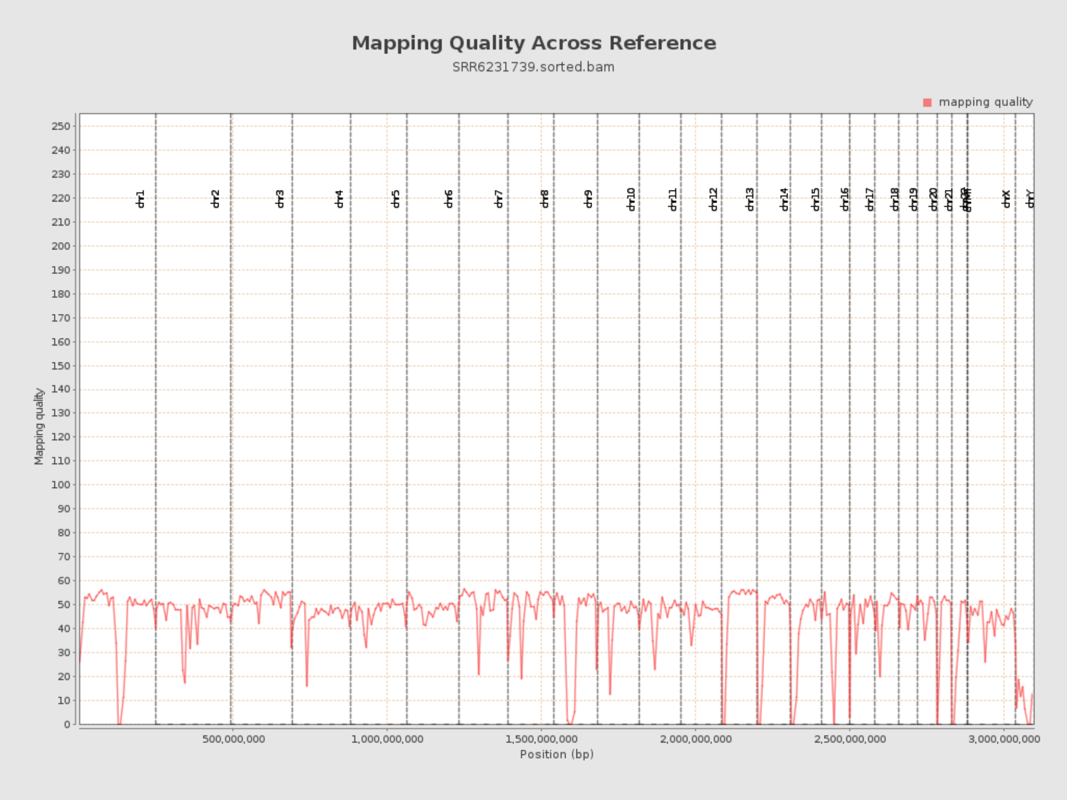
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram