Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:57:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234089.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_SRR6234089 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234089.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:57:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234089.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,957,946
Mapped reads	2,406,965 / 81.37%
Unmapped reads	550,981 / 18.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,238 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	120,686 / 4.08%
Duplication rate	3.86%
Clipped reads	1,432,255 / 48.42%

2.2. ACGT Content

Number/percentage of A's	40,859,555 / 26.92%
Number/percentage of C's	27,890,736 / 18.38%
Number/percentage of T's	47,666,284 / 31.41%
Number/percentage of G's	35,337,616 / 23.28%
Number/percentage of N's	21,036 / 0.01%
GC Percentage	41.66%

2.3. Coverage

Mean	0.0491

Standard Deviation	0.4553

2.4. Mapping Quality

Mean Mapping Quality	43.21

2.5. Mismatches and indels

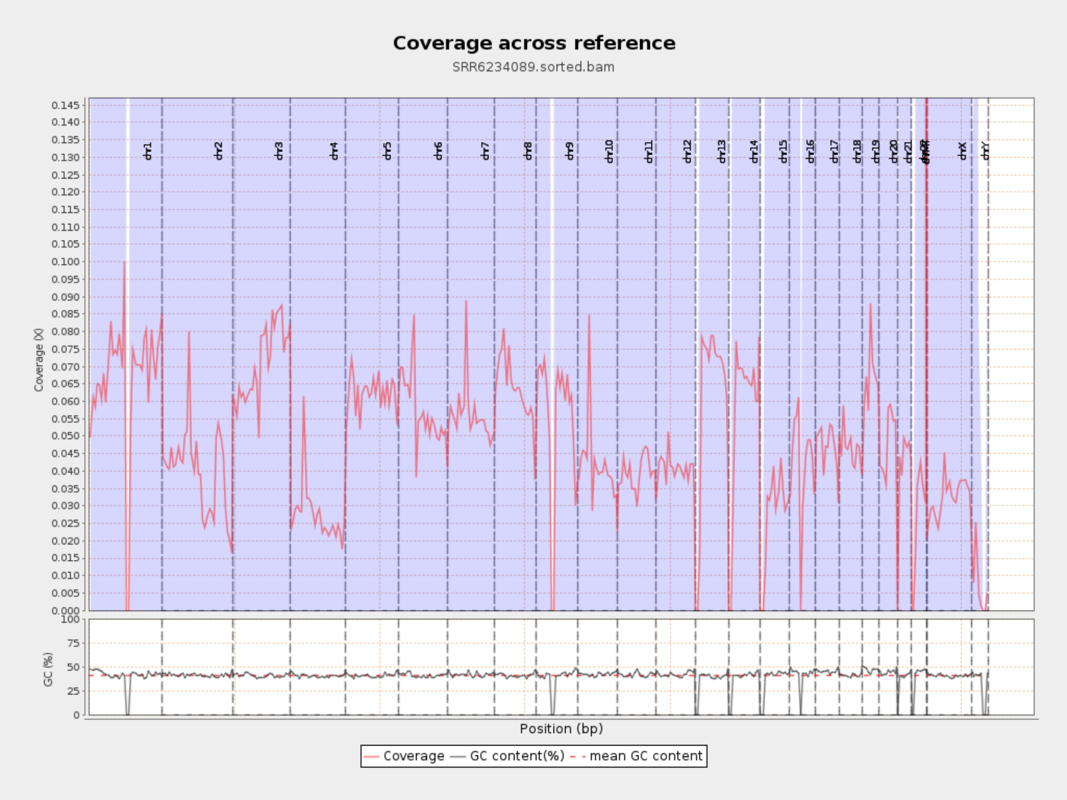
General error rate	0.86%
Mismatches	1,287,156
Insertions	11,070
Mapped reads with at least one insertion	0.46%
Deletions	54,088
Mapped reads with at least one deletion	2.21%
Homopolymer indels	42.49%

2.6. Chromosome stats

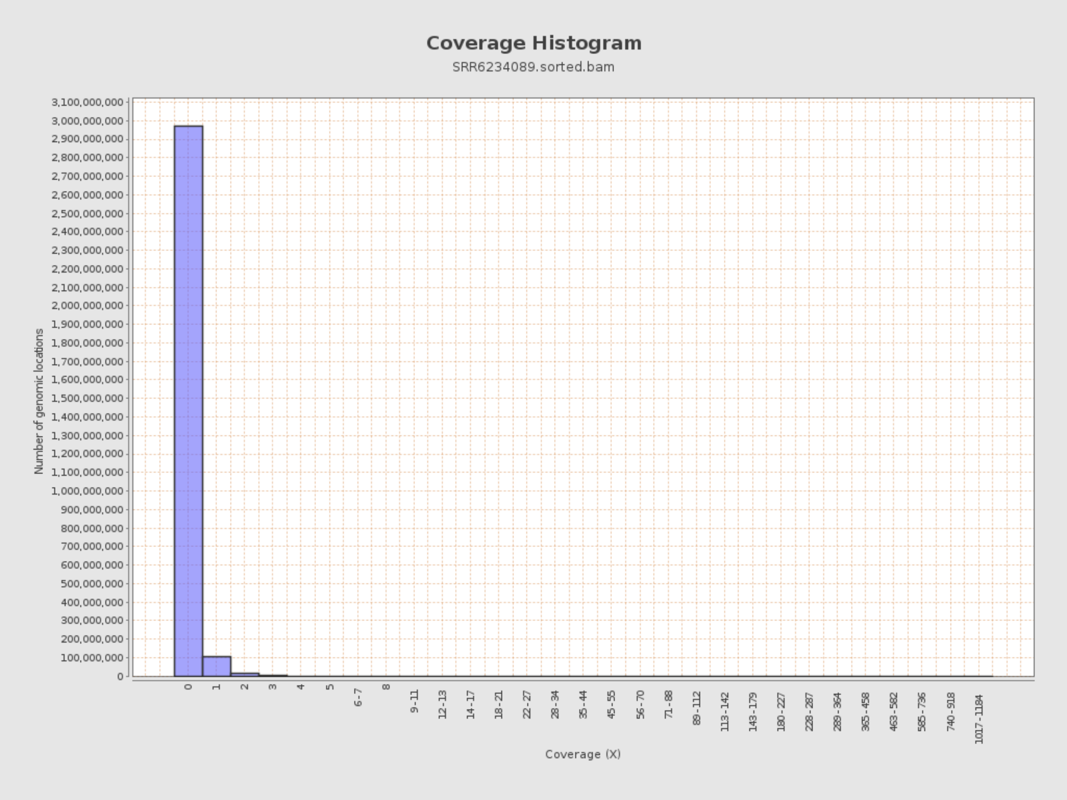
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16512730	0.0662	0.9213
chr2	243199373	9700433	0.0399	0.5706
chr3	198022430	14061660	0.071	0.3179
chr4	191154276	5218852	0.0273	0.2264
chr5	180915260	11256316	0.0622	0.2979
chr6	171115067	9858322	0.0576	0.3755
chr7	159138663	8979411	0.0564	0.5522

chr8	146364022	9296876	0.0635	0.613
chr9	141213431	7734860	0.0548	0.3728
chr10	135534747	5721586	0.0422	0.4195
chr11	135006516	5310158	0.0393	0.2952
chr12	133851895	5456556	0.0408	0.2425
chr13	115169878	7010704	0.0609	0.2932
chr14	107349540	6015138	0.056	0.3031
chr15	102531392	2822794	0.0275	0.2047
chr16	90354753	3801562	0.0421	0.2784
chr17	81195210	3815636	0.047	0.2738
chr18	78077248	3648188	0.0467	0.6469
chr19	59128983	3915634	0.0662	0.6262
chr20	63025520	2990448	0.0474	0.2745
chr21	48129895	1975610	0.041	0.259
chr22	51304566	1318408	0.0257	0.1868
chrMT	16571	23183	1.399	1.5786
chrX	155270560	5025009	0.0324	0.2453
chrY	59373566	399110	0.0067	0.1642

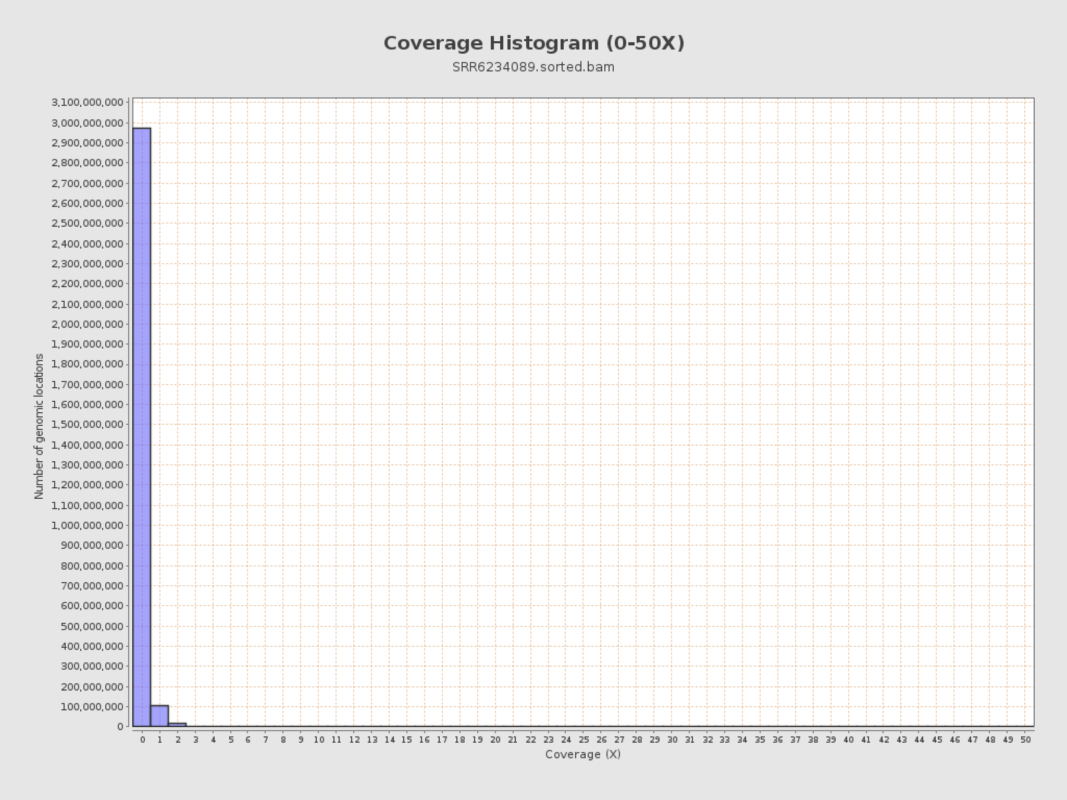
3. Results : Coverage across reference



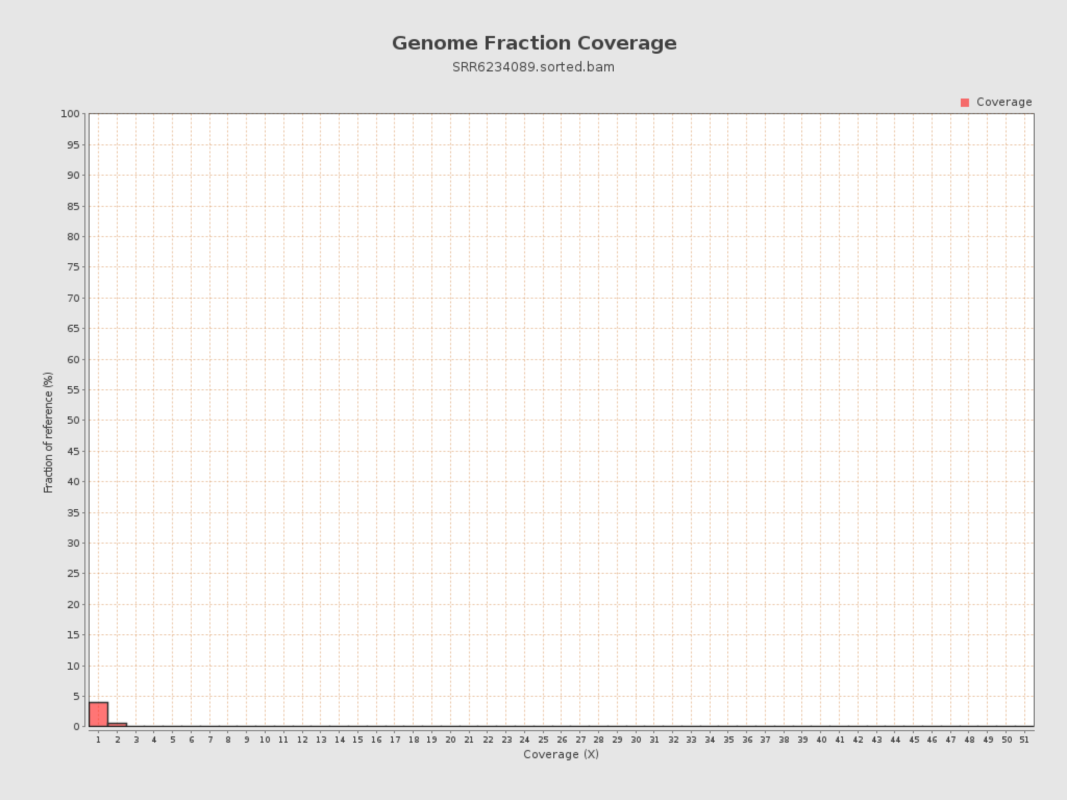
4. Results : Coverage Histogram



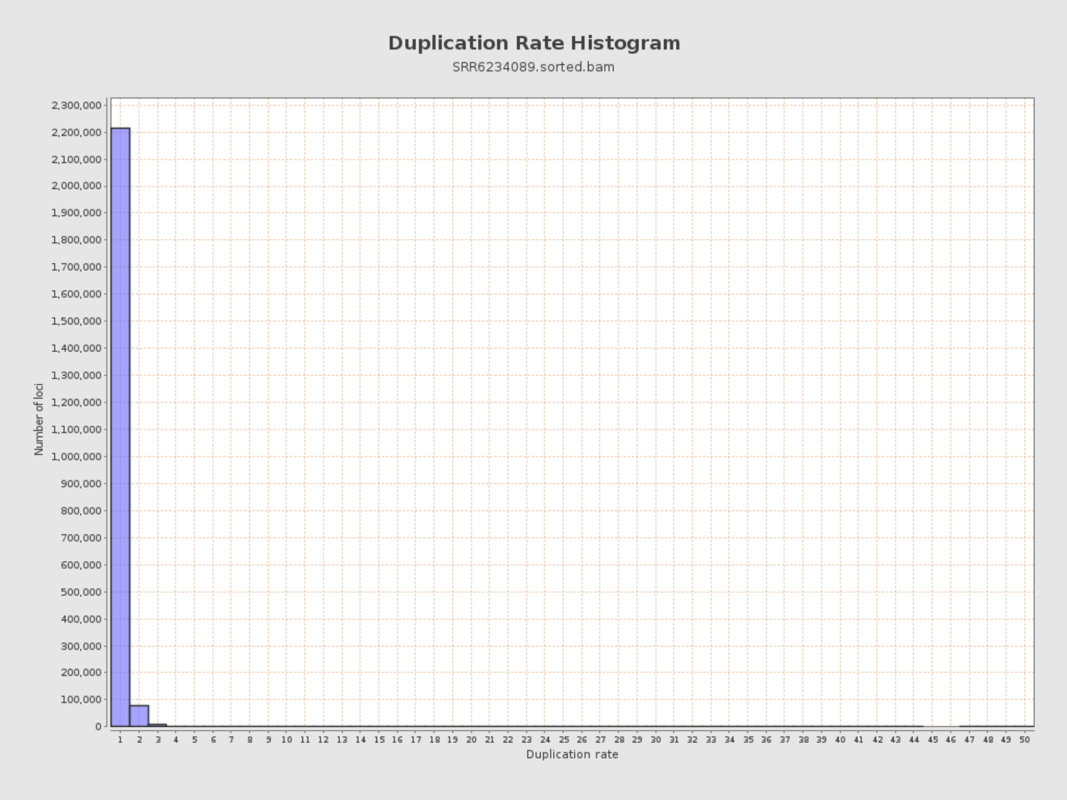
5. Results : Coverage Histogram (0-50X)



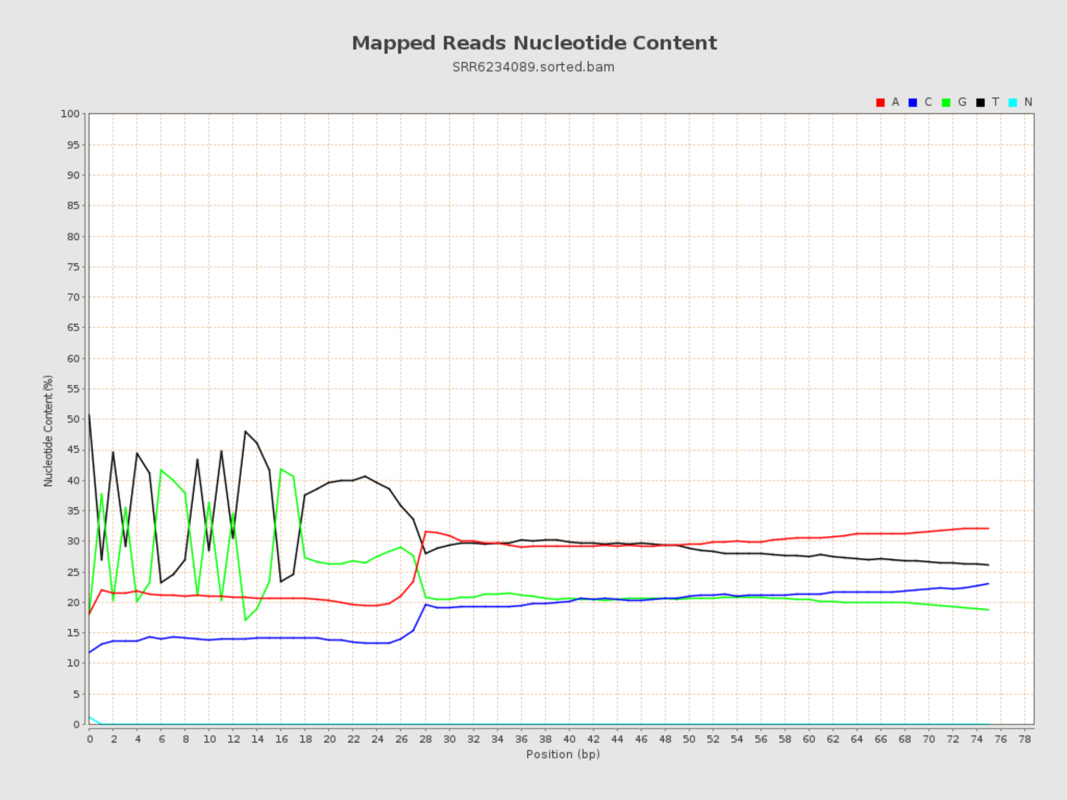
6. Results : Genome Fraction Coverage



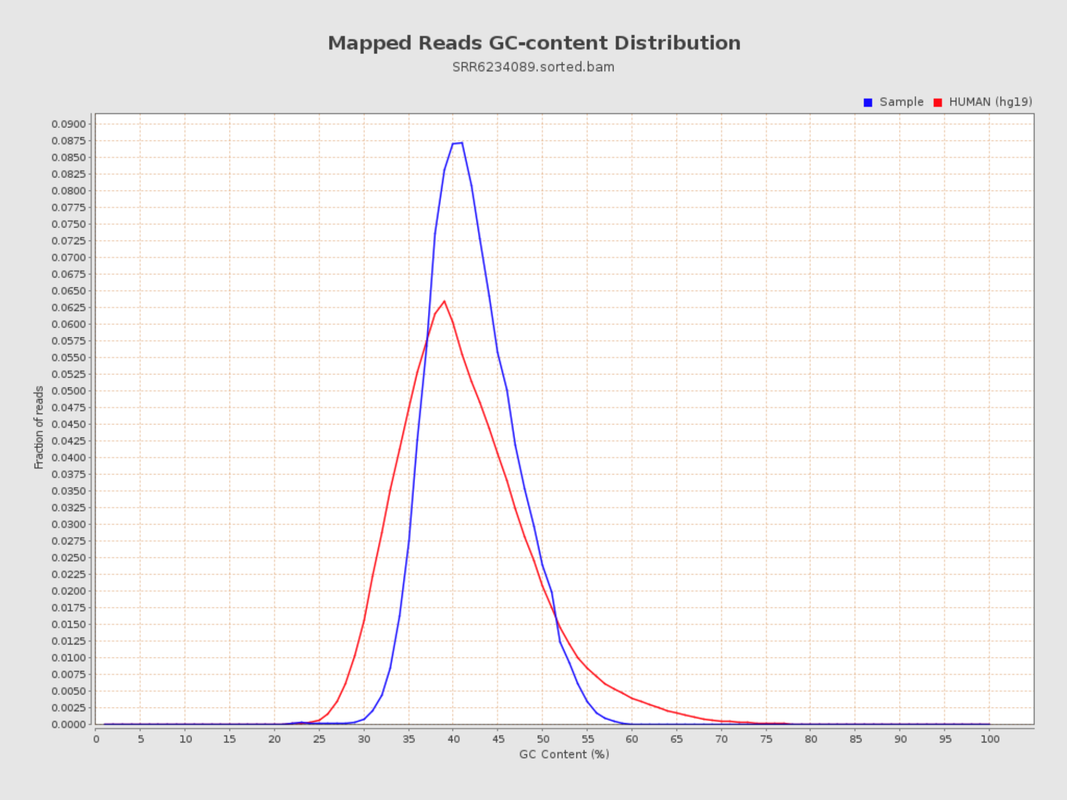
7. Results : Duplication Rate Histogram



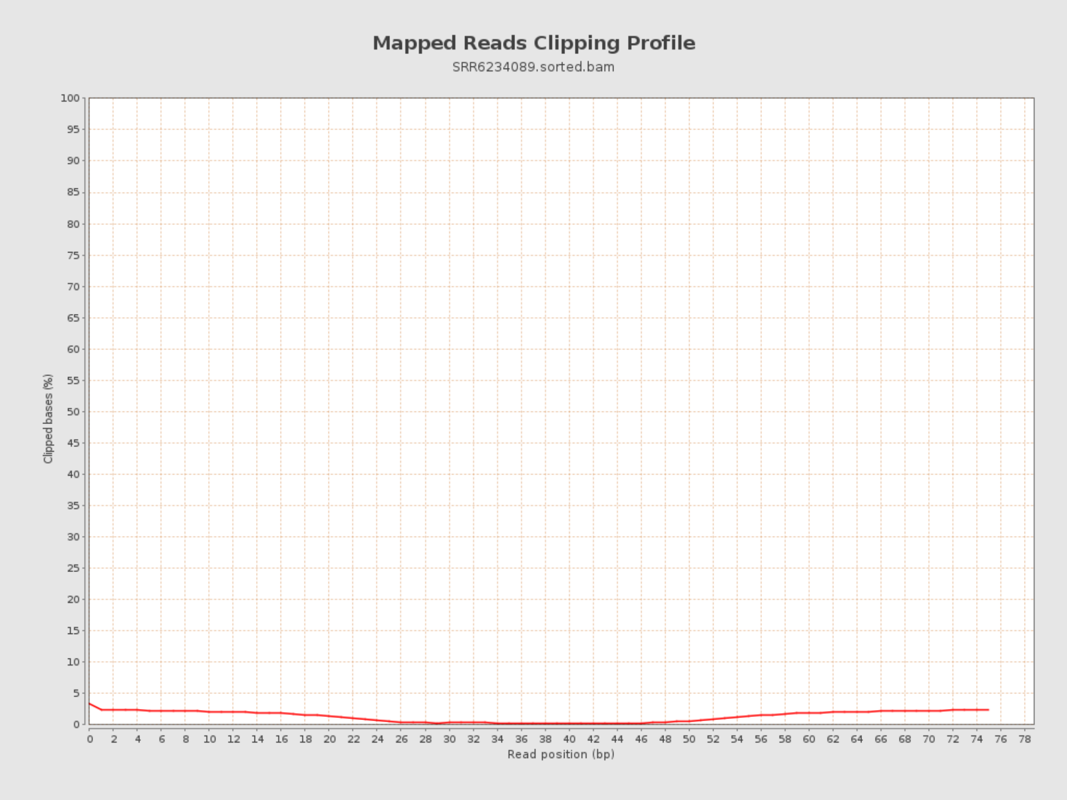
8. Results : Mapped Reads Nucleotide Content



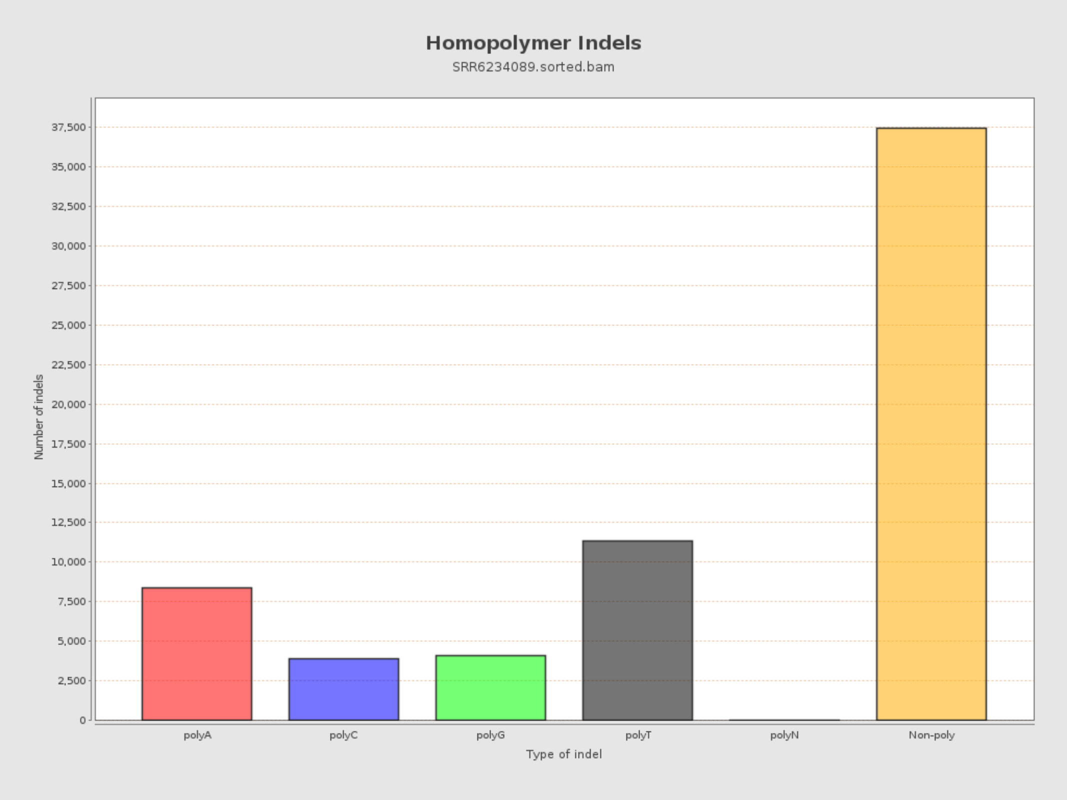
9. Results : Mapped Reads GC-content Distribution



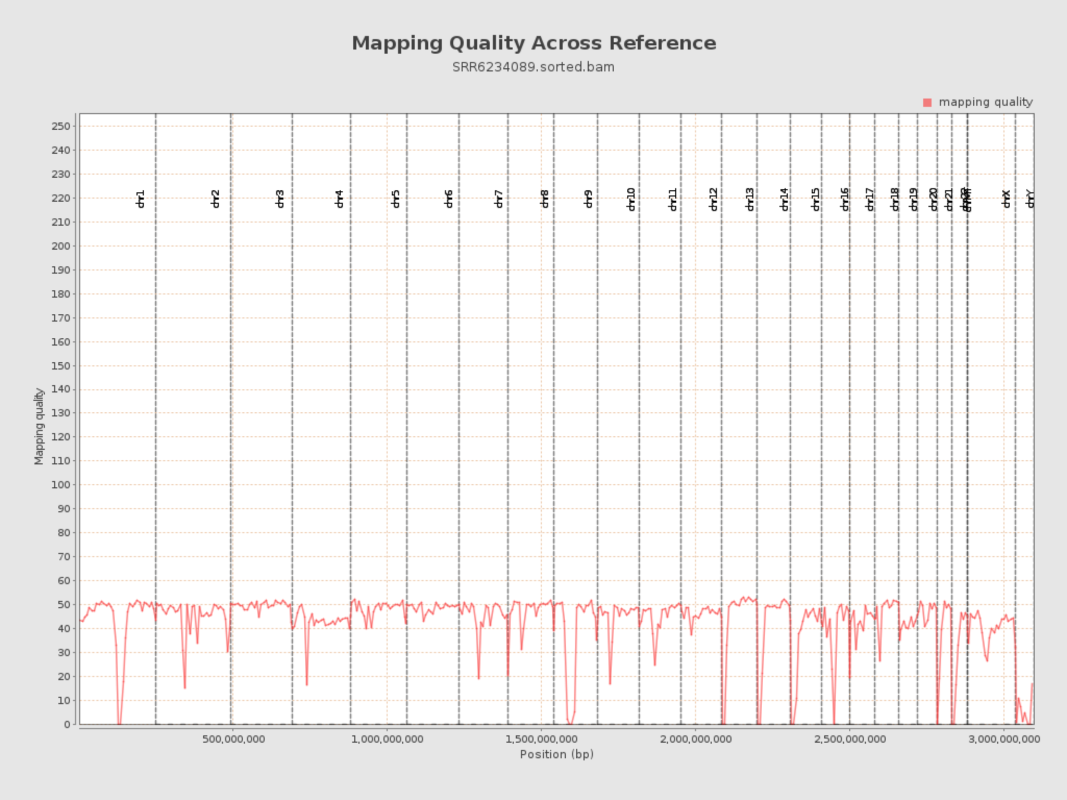
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram