Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:12:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081123.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_SRR3081123 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081123.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:12:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081123.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,284,892
Mapped reads	2,134,043 / 93.4%
Unmapped reads	150,849 / 6.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,783 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	90,390 / 3.96%
Duplication rate	3.15%
Clipped reads	820,065 / 35.89%

2.2. ACGT Content

Number/percentage of A's	40,869,392 / 28.06%
Number/percentage of C's	28,159,075 / 19.33%
Number/percentage of T's	44,840,831 / 30.79%
Number/percentage of G's	31,784,885 / 21.82%
Number/percentage of N's	1,628 / 0%
GC Percentage	41.15%

2.3. Coverage

Mean	0.0471

Standard Deviation	0.4198

2.4. Mapping Quality

Mean Mapping Quality	46.14

2.5. Mismatches and indels

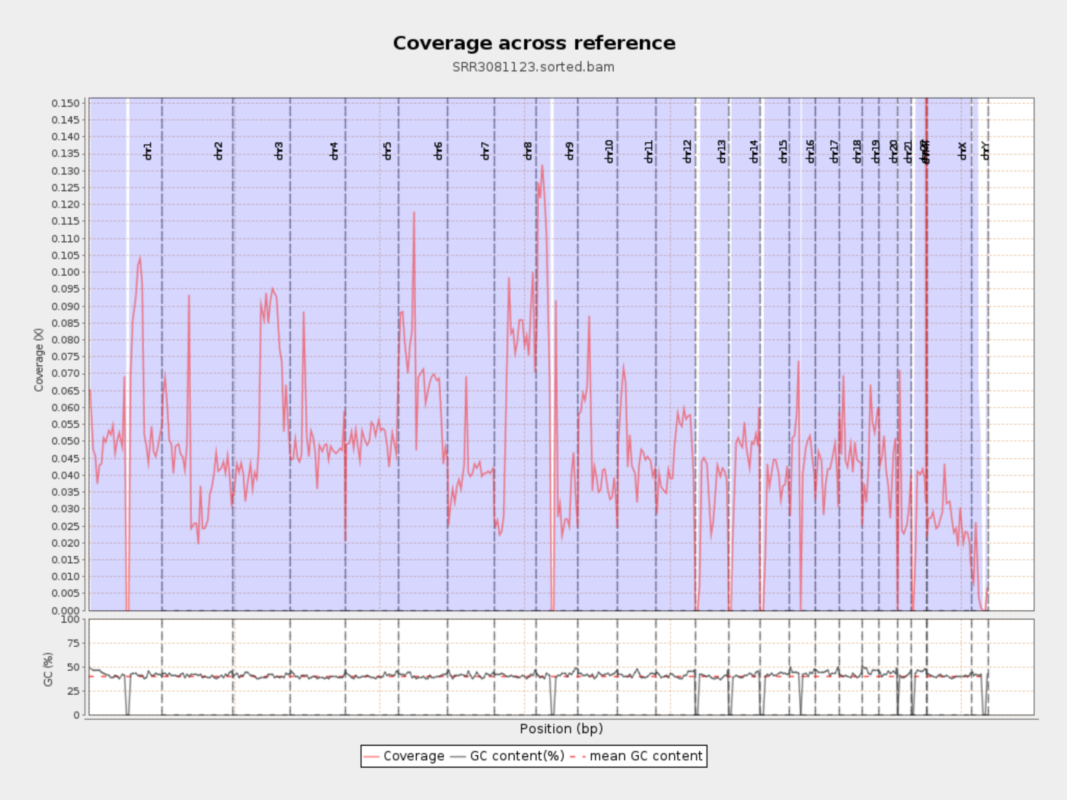
General error rate	0.89%
Mismatches	1,279,930
Insertions	11,153
Mapped reads with at least one insertion	0.52%
Deletions	31,580
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.12%

2.6. Chromosome stats

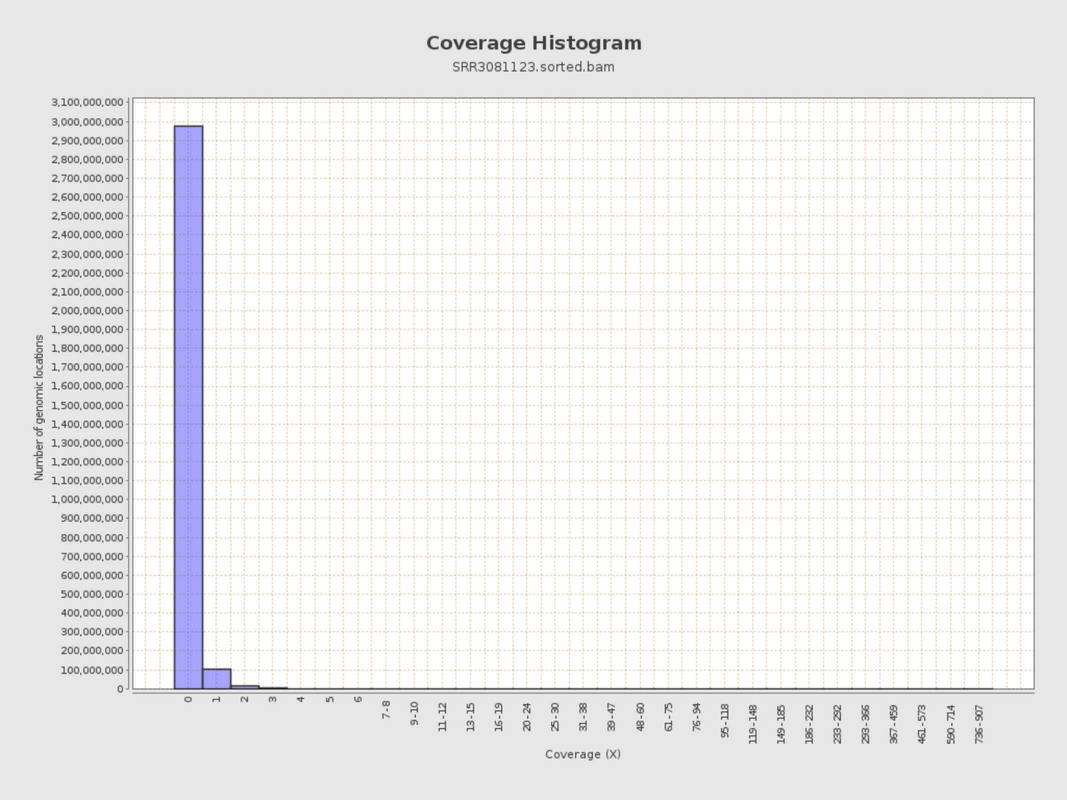
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13656879	0.0548	0.5661
chr2	243199373	10309761	0.0424	0.4818
chr3	198022430	12045093	0.0608	0.2884
chr4	191154276	9411713	0.0492	0.2984
chr5	180915260	9175625	0.0507	0.2621
chr6	171115067	11997458	0.0701	0.4631
chr7	159138663	6437011	0.0404	0.4325

chr8	146364022	9861154	0.0674	0.4369
chr9	141213431	8290129	0.0587	0.6339
chr10	135534747	6362514	0.0469	0.4351
chr11	135006516	6408152	0.0475	0.3449
chr12	133851895	6128055	0.0458	0.2792
chr13	115169878	3616847	0.0314	0.2004
chr14	107349540	4449501	0.0414	0.3564
chr15	102531392	3310826	0.0323	0.2134
chr16	90354753	4103668	0.0454	0.3704
chr17	81195210	3310170	0.0408	0.2452
chr18	78077248	3752191	0.0481	1.0256
chr19	59128983	2867515	0.0485	0.4803
chr20	63025520	2665042	0.0423	0.2573
chr21	48129895	1544556	0.0321	0.361
chr22	51304566	1440235	0.0281	0.1894
chrMT	16571	83886	5.0622	3.6844
chrX	155270560	4084302	0.0263	0.2329
chrY	59373566	400577	0.0067	0.1976

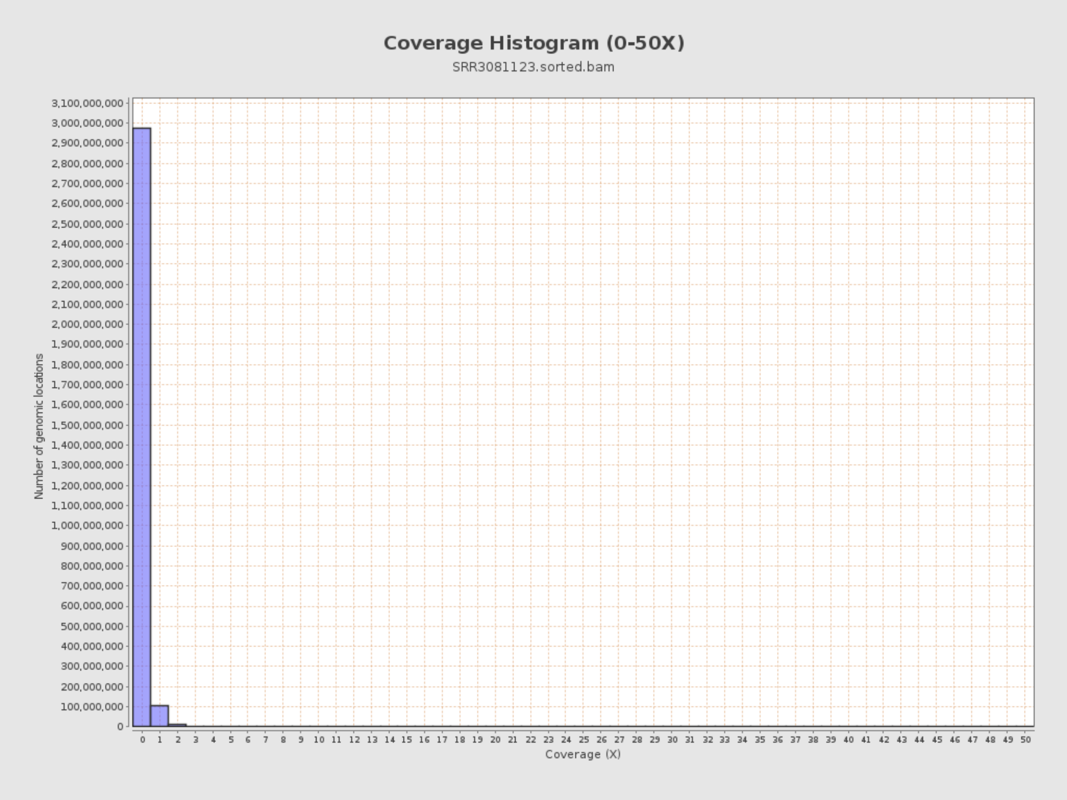
3. Results : Coverage across reference



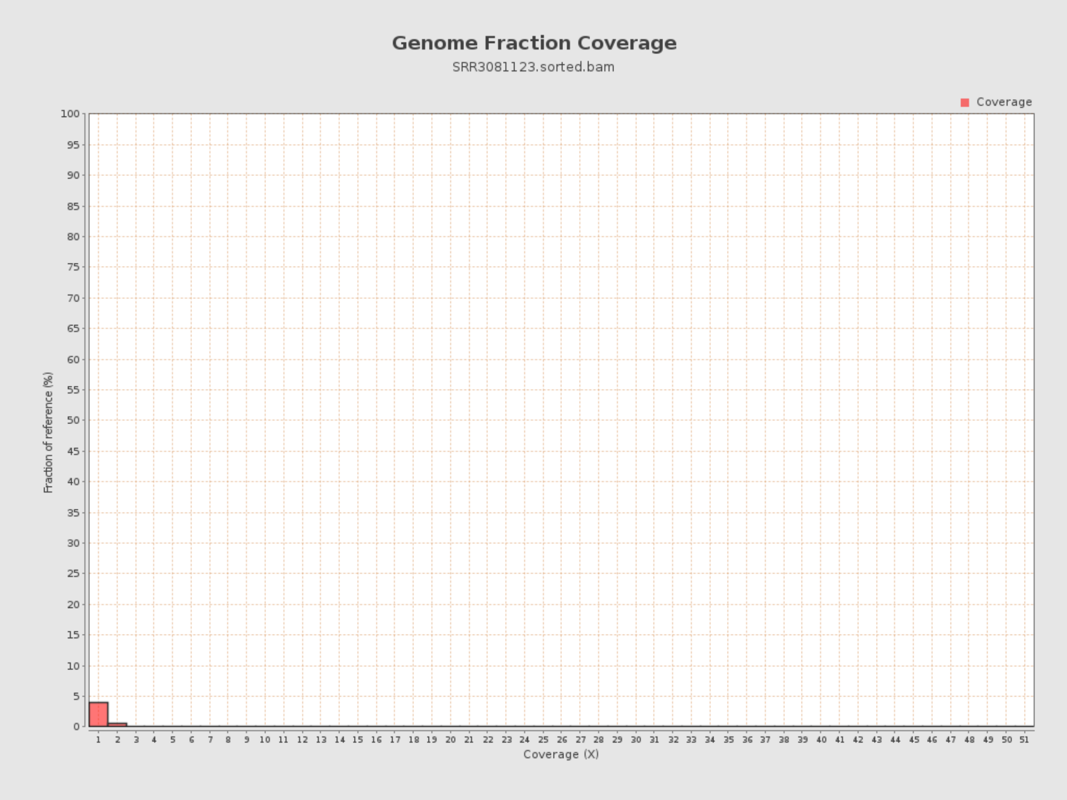
4. Results : Coverage Histogram



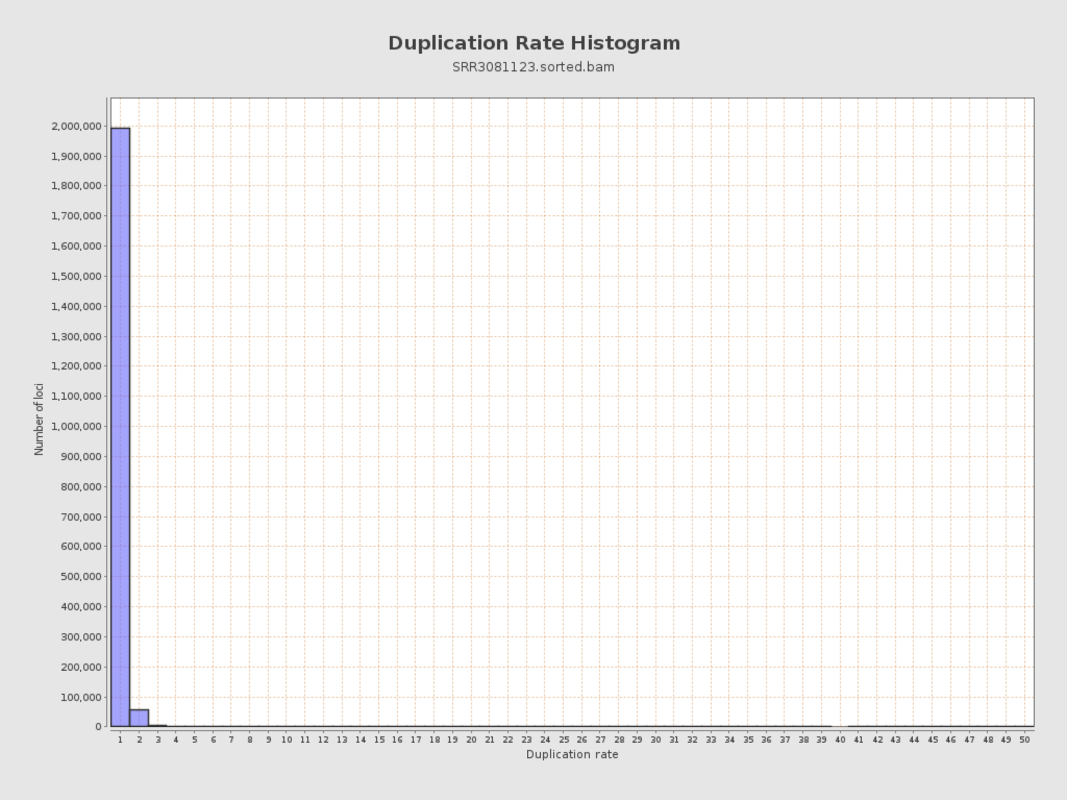
5. Results : Coverage Histogram (0-50X)



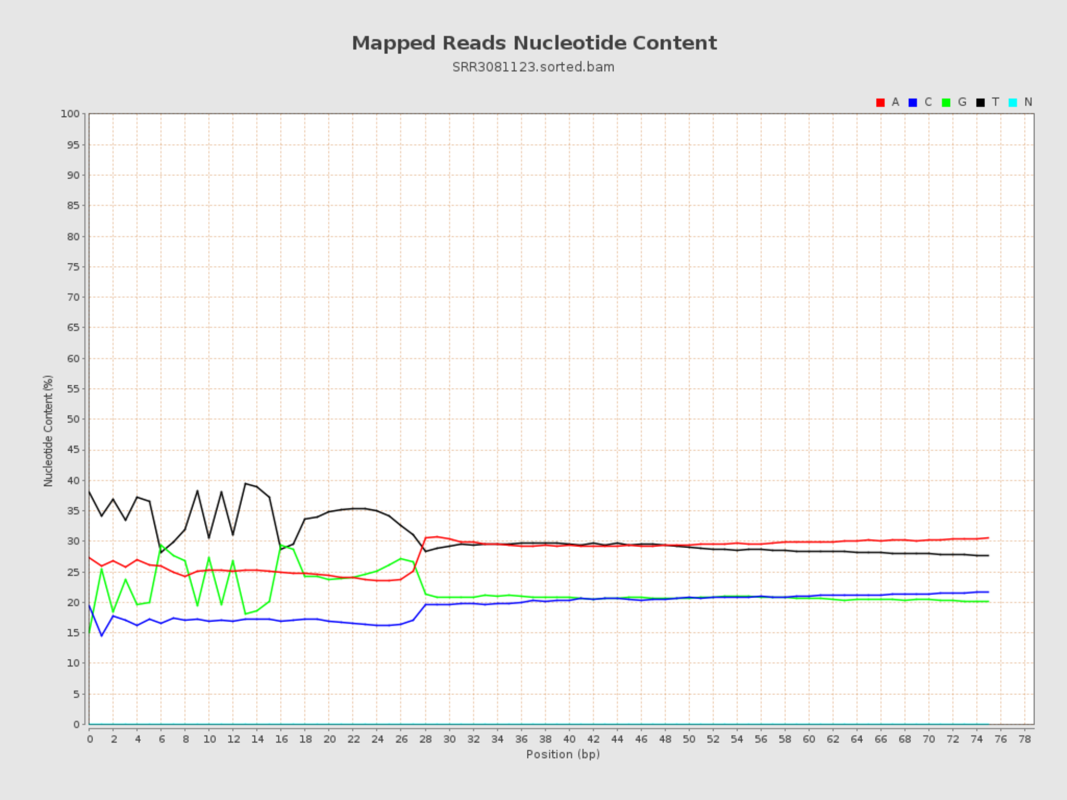
6. Results : Genome Fraction Coverage



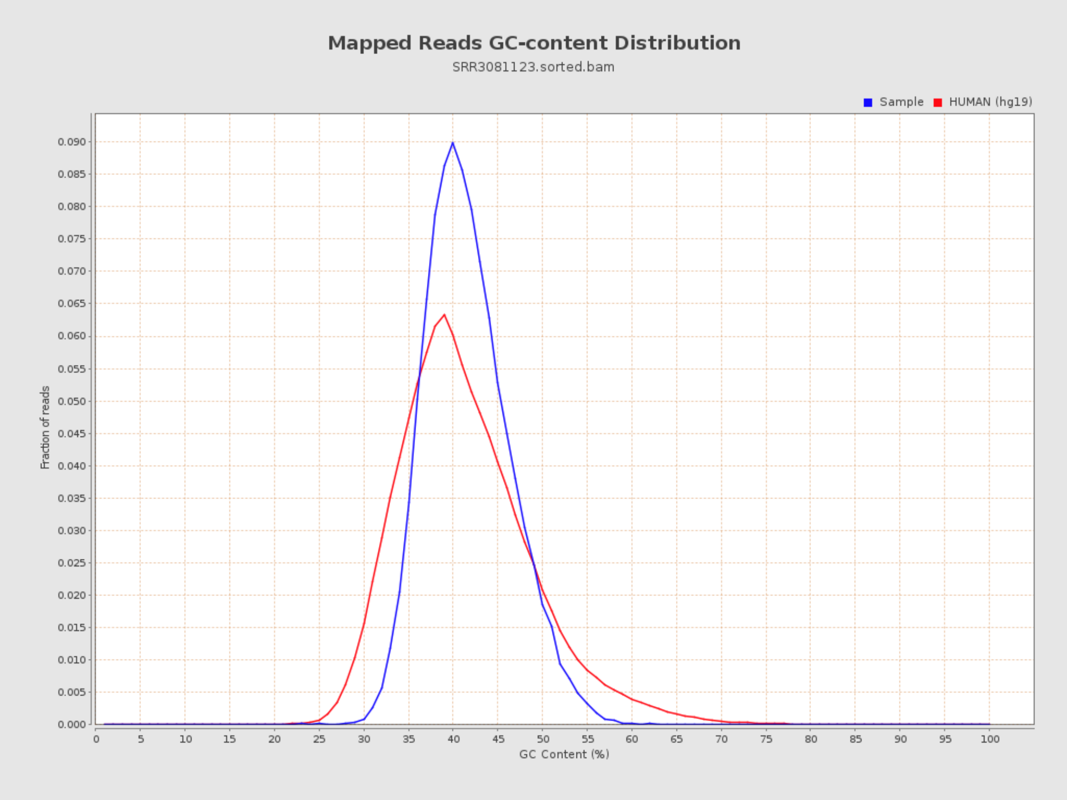
7. Results : Duplication Rate Histogram



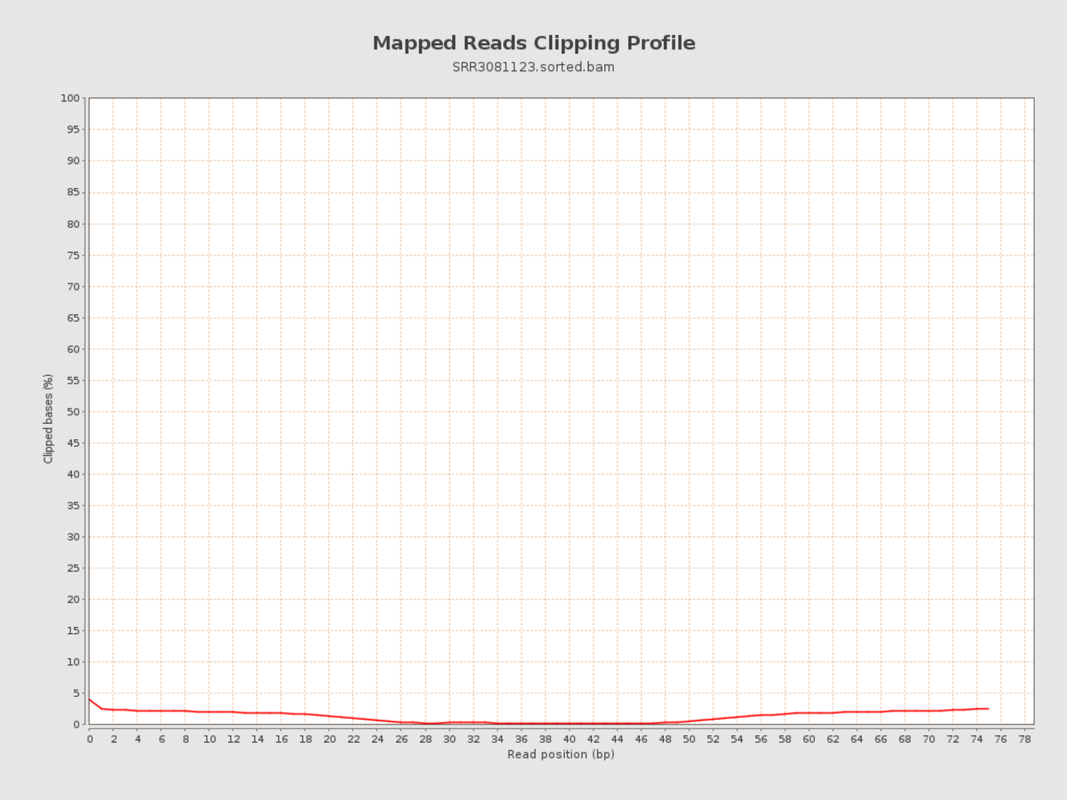
8. Results : Mapped Reads Nucleotide Content



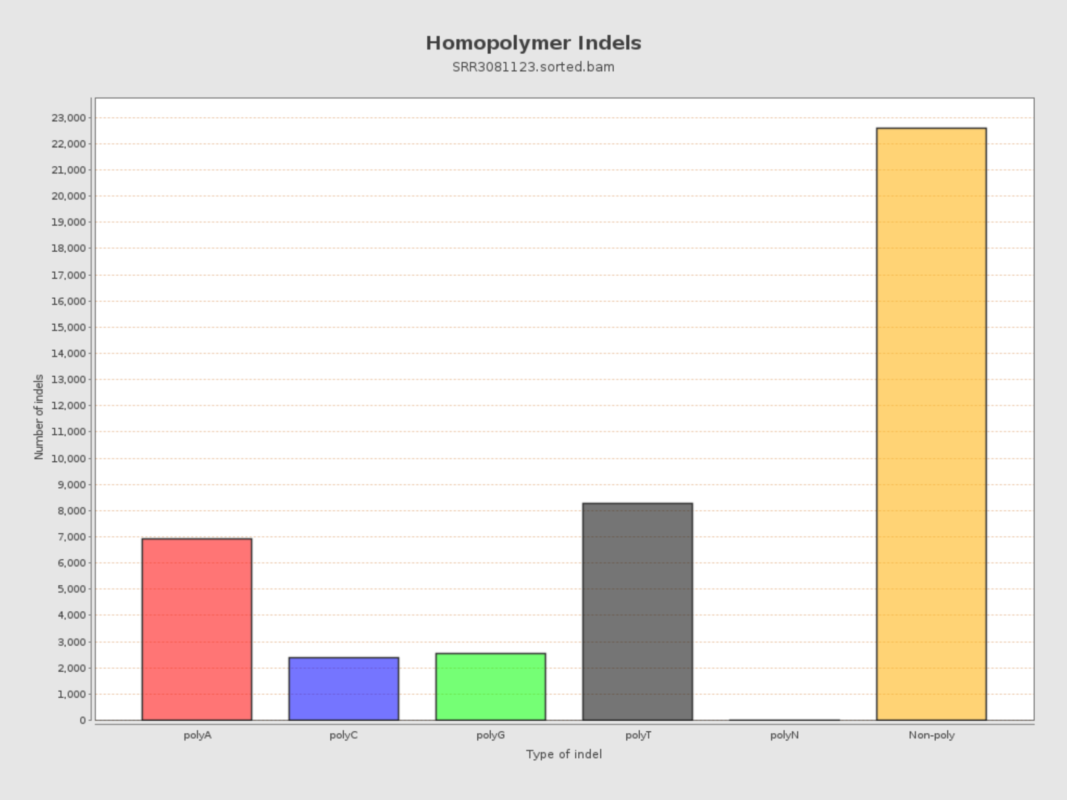
9. Results : Mapped Reads GC-content Distribution



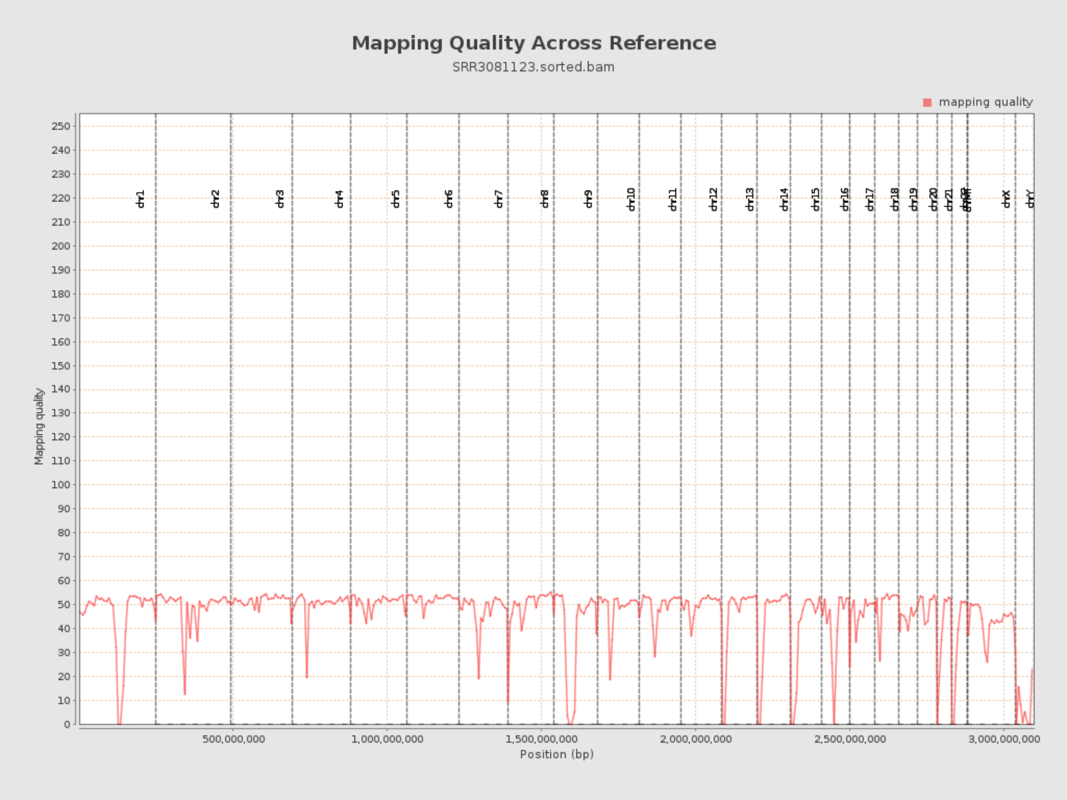
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram