Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:32:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR23117301.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_SRR23117301 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR23117301.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:32:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR23117301.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	165,182
Mapped reads	157,841 / 95.56%
Unmapped reads	7,341 / 4.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	654 / 0.4%
Read min/max/mean length	25 / 548 / 261.25
Duplicated reads (estimated)	19,467 / 11.79%
Duplication rate	10.97%
Clipped reads	158,495 / 95.95%

2.2. ACGT Content

Number/percentage of A's	10,804,004 / 29.42%
Number/percentage of C's	7,565,748 / 20.6%
Number/percentage of T's	10,717,701 / 29.19%
Number/percentage of G's	7,634,964 / 20.79%
Number/percentage of N's	0 / 0%
GC Percentage	41.39%

2.3. Coverage

Mean	0.0119

Standard Deviation	0.2457

2.4. Mapping Quality

Mean Mapping Quality	53.59

2.5. Mismatches and indels

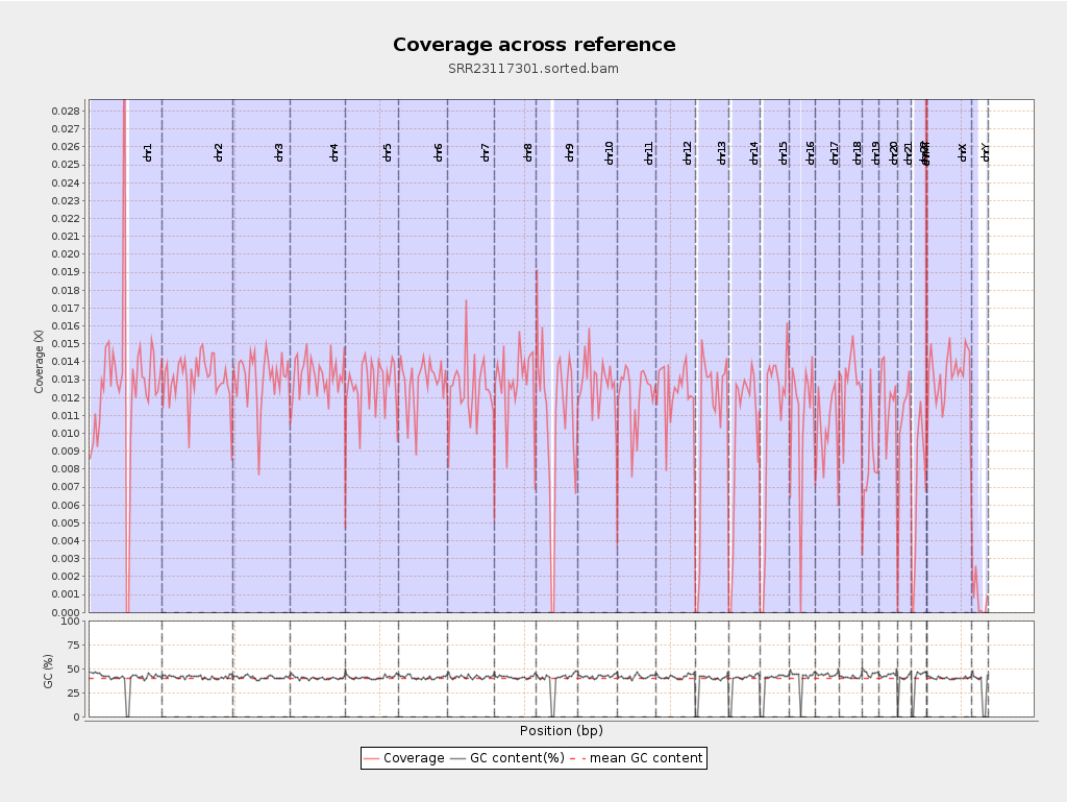
General error rate	1.03%
Mismatches	185,546
Insertions	172,474
Mapped reads with at least one insertion	48.21%
Deletions	58,574
Mapped reads with at least one deletion	25.65%
Homopolymer indels	30.78%

2.6. Chromosome stats

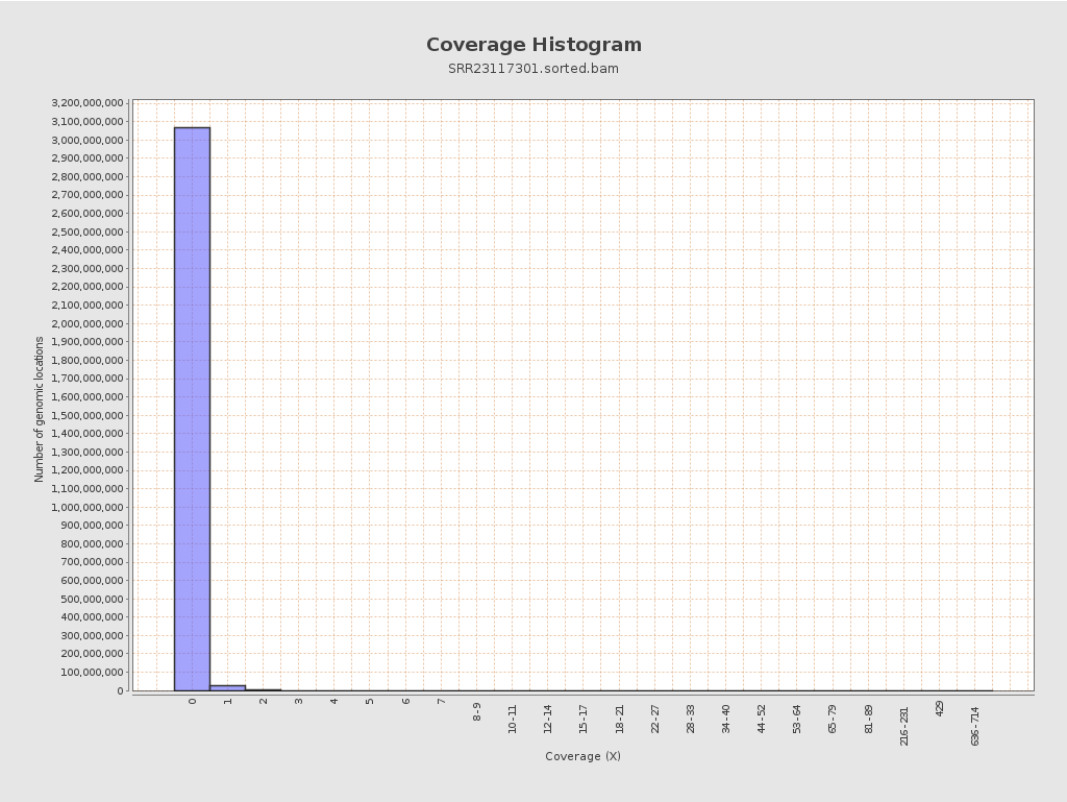
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3145600	0.0126	0.7082
chr2	243199373	3177725	0.0131	0.1323
chr3	198022430	2602532	0.0131	0.1315
chr4	191154276	2528768	0.0132	0.1345
chr5	180915260	2301631	0.0127	0.1284
chr6	171115067	2200693	0.0129	0.1294
chr7	159138663	1999714	0.0126	0.3091

chr8	146364022	1879977	0.0128	0.1302
chr9	141213431	1517838	0.0107	0.1213
chr10	135534747	1744656	0.0129	0.1671
chr11	135006516	1628518	0.0121	0.1268
chr12	133851895	1647684	0.0123	0.1279
chr13	115169878	1243418	0.0108	0.1184
chr14	107349540	1069199	0.01	0.1139
chr15	102531392	1085521	0.0106	0.1176
chr16	90354753	977379	0.0108	0.1326
chr17	81195210	816660	0.0101	0.1169
chr18	78077248	1018758	0.013	0.137
chr19	59128983	494428	0.0084	0.2125
chr20	63025520	741952	0.0118	0.1284
chr21	48129895	491220	0.0102	0.1201
chr22	51304566	344761	0.0067	0.0939
chrMT	16571	40570	2.4483	5.6883
chrX	155270560	2051015	0.0132	0.1314
chrY	59373566	43816	0.0007	0.0481

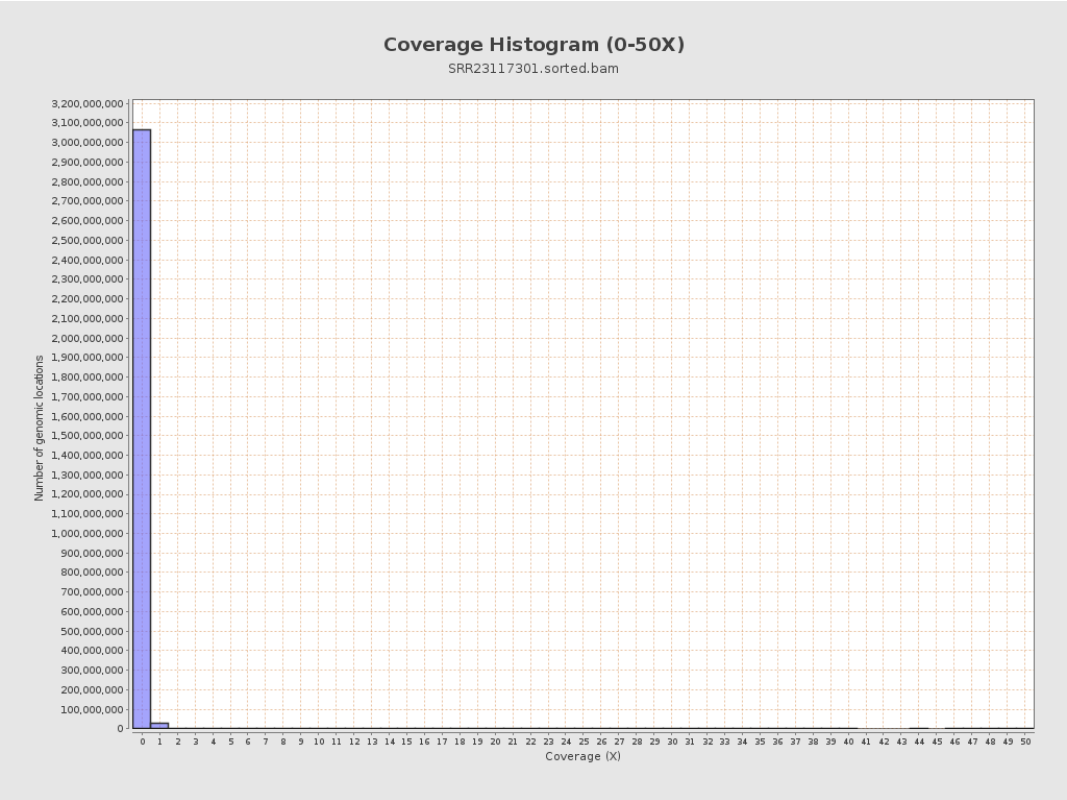
3. Results : Coverage across reference



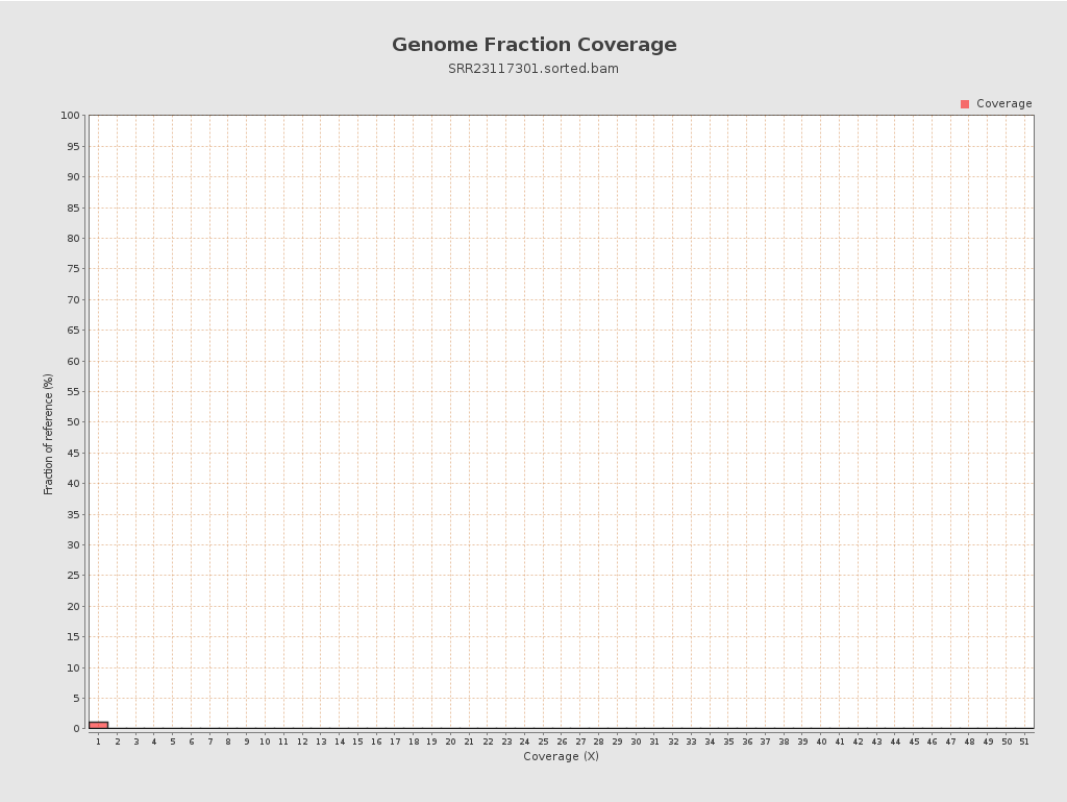
4. Results : Coverage Histogram



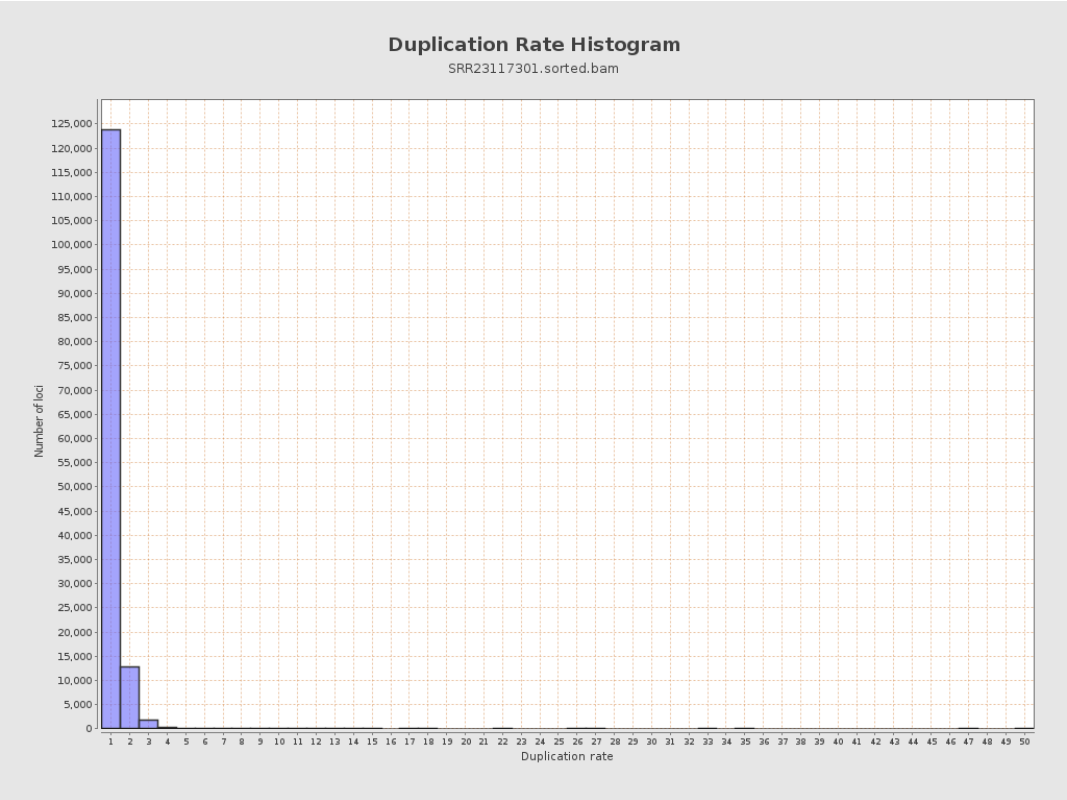
5. Results : Coverage Histogram (0-50X)



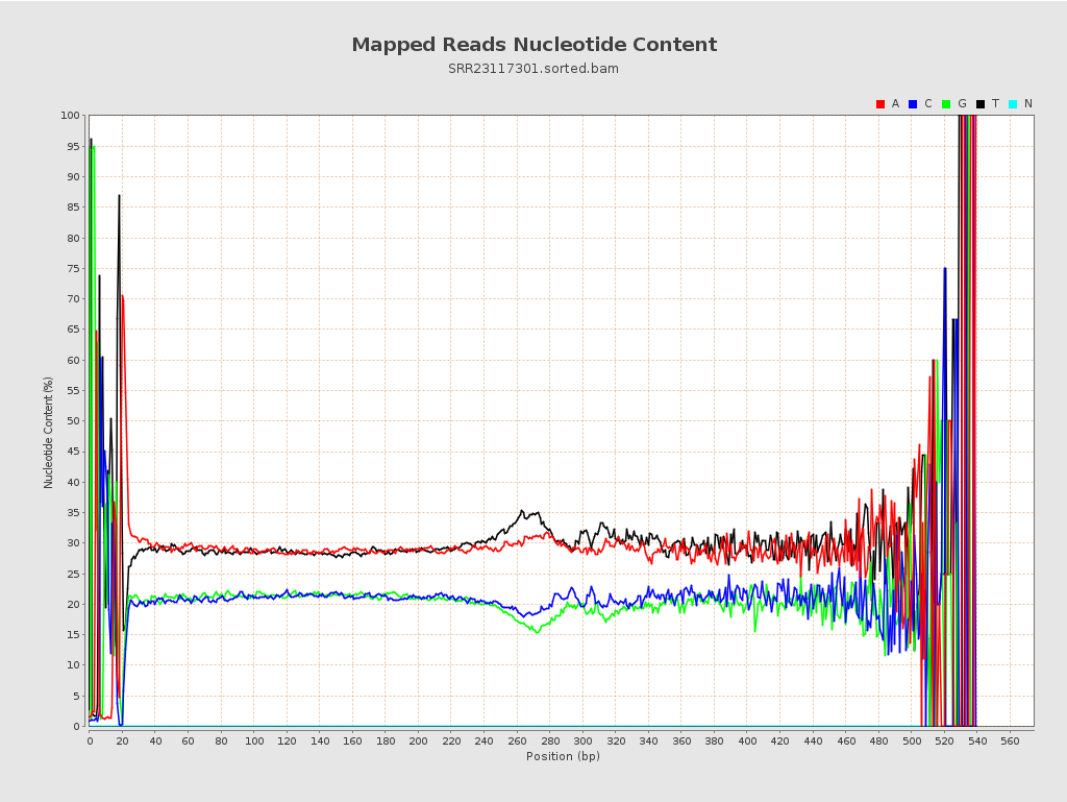
6. Results : Genome Fraction Coverage



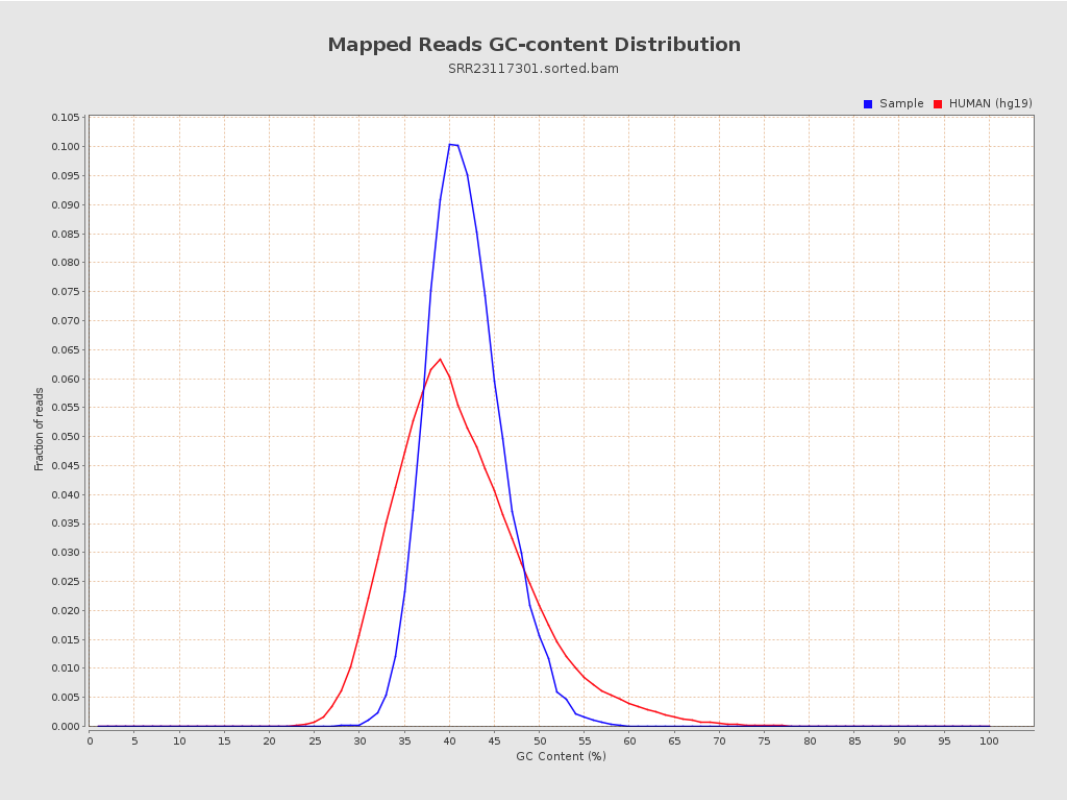
7. Results : Duplication Rate Histogram



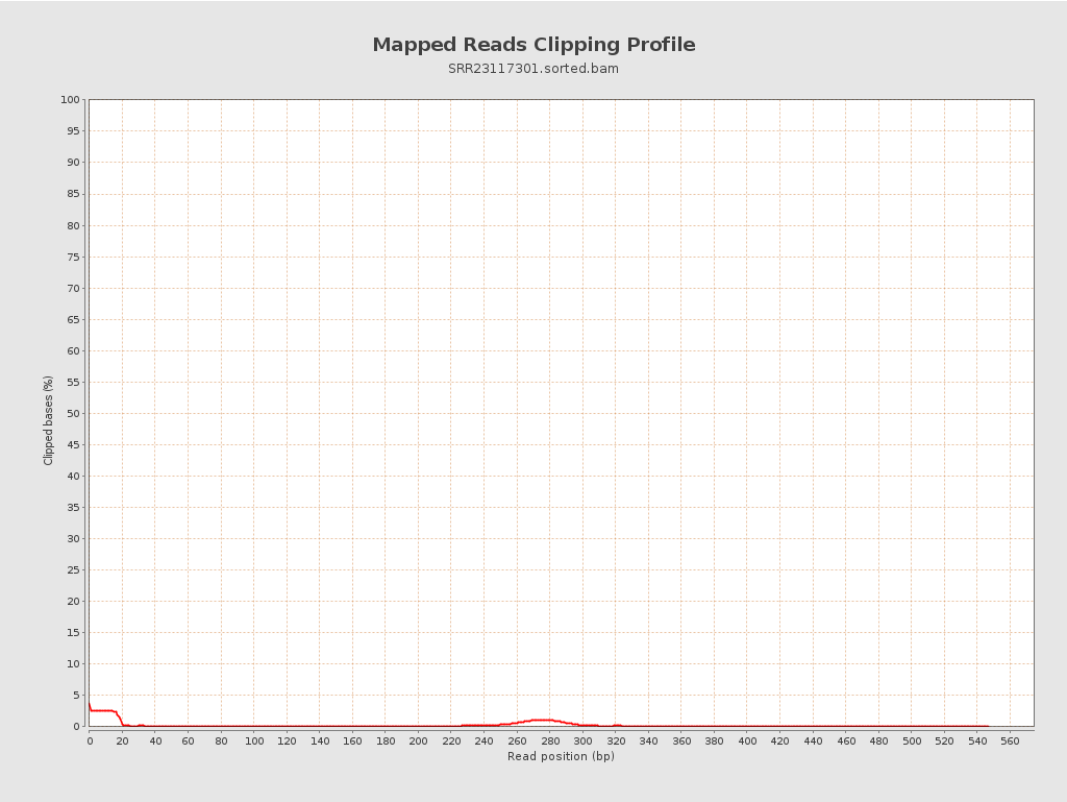
8. Results : Mapped Reads Nucleotide Content



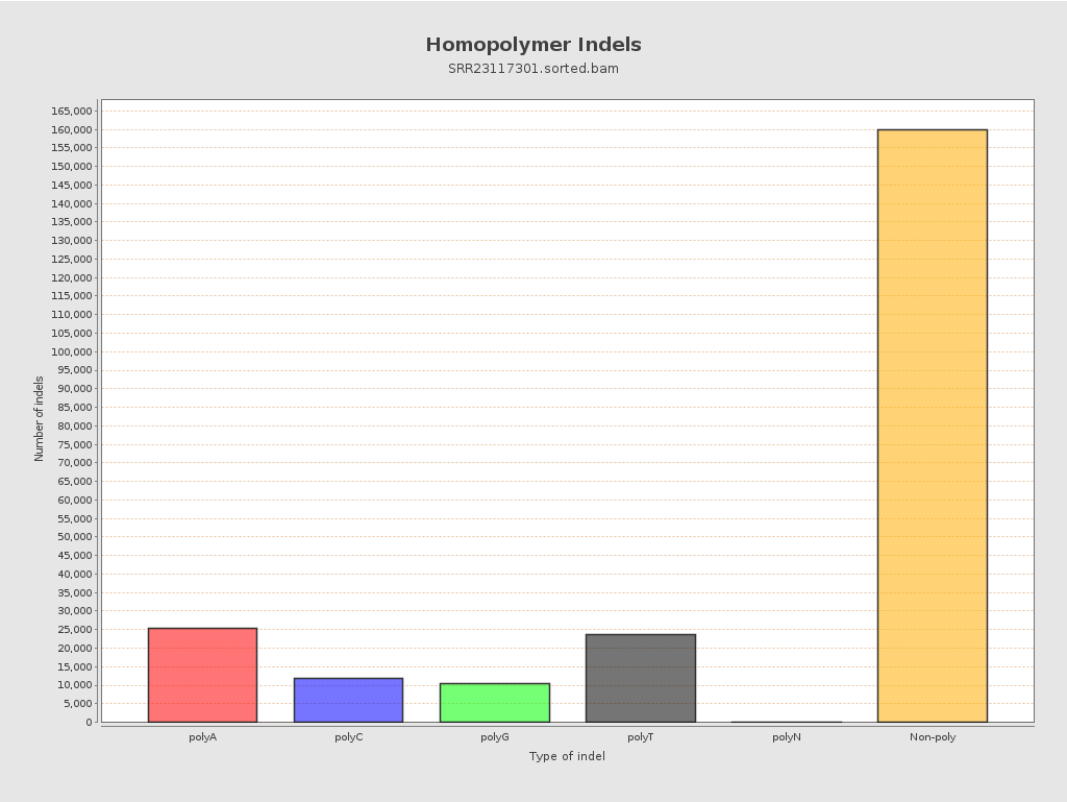
9. Results : Mapped Reads GC-content Distribution



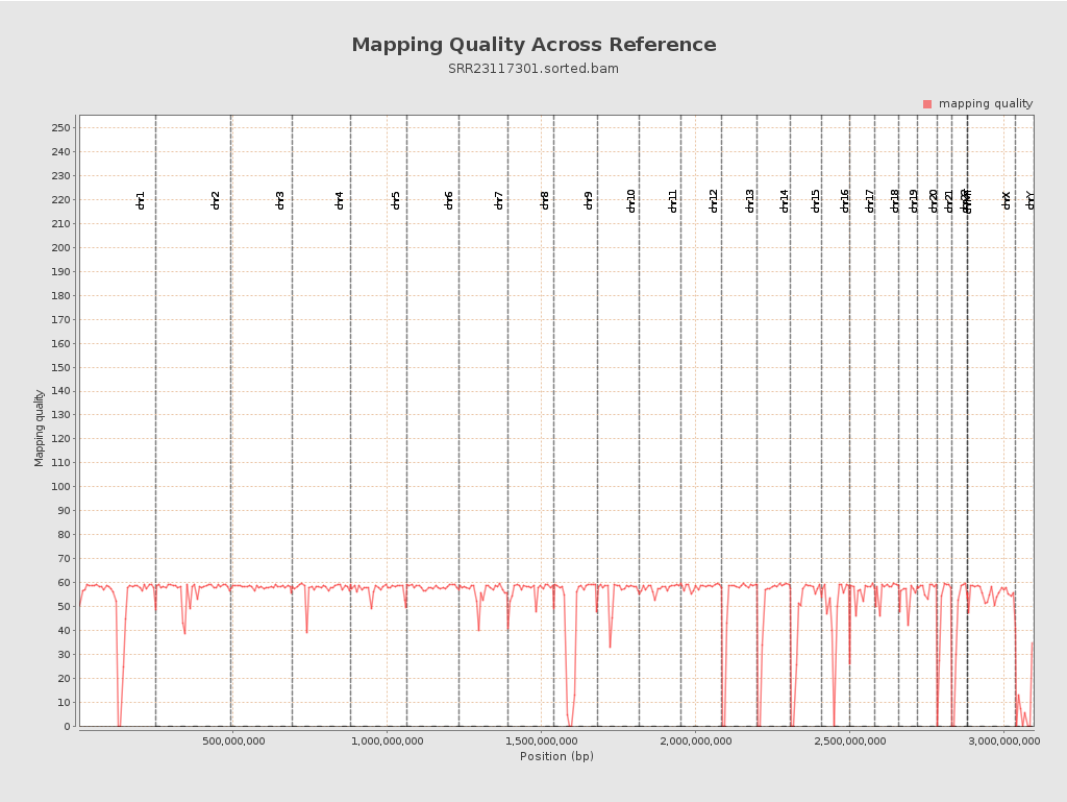
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram