Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:10:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525230.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_SRR10525230 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525230.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:10:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525230.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	489,157
Mapped reads	454,874 / 92.99%
Unmapped reads	34,283 / 7.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,538 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	8,238 / 1.68%
Duplication rate	1.38%
Clipped reads	456,291 / 93.28%

2.2. ACGT Content

Number/percentage of A's	6,687,397 / 24.62%
Number/percentage of C's	5,430,458 / 19.99%
Number/percentage of T's	8,294,082 / 30.54%
Number/percentage of G's	6,747,506 / 24.84%
Number/percentage of N's	554 / 0%
GC Percentage	44.84%

2.3. Coverage

Mean	0.0088

Standard Deviation	0.1126

2.4. Mapping Quality

Mean Mapping Quality	46.19

2.5. Mismatches and indels

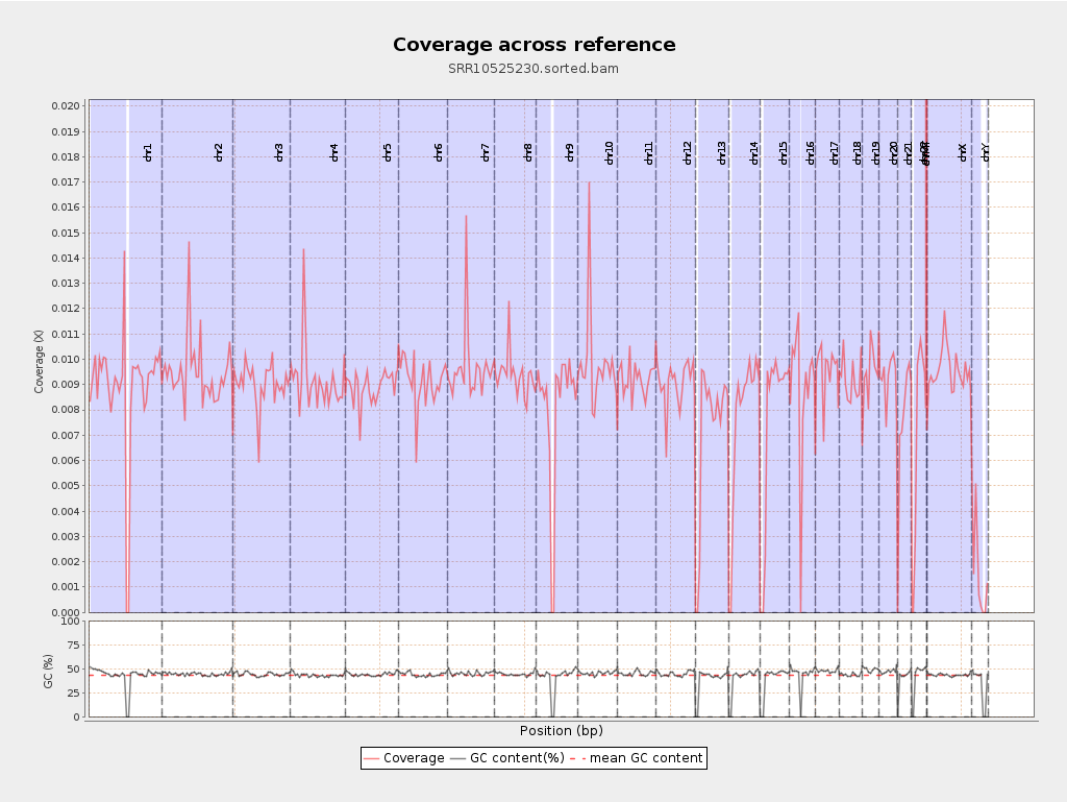
General error rate	0.51%
Mismatches	134,878
Insertions	1,562
Mapped reads with at least one insertion	0.34%
Deletions	5,487
Mapped reads with at least one deletion	1.2%
Homopolymer indels	44.33%

2.6. Chromosome stats

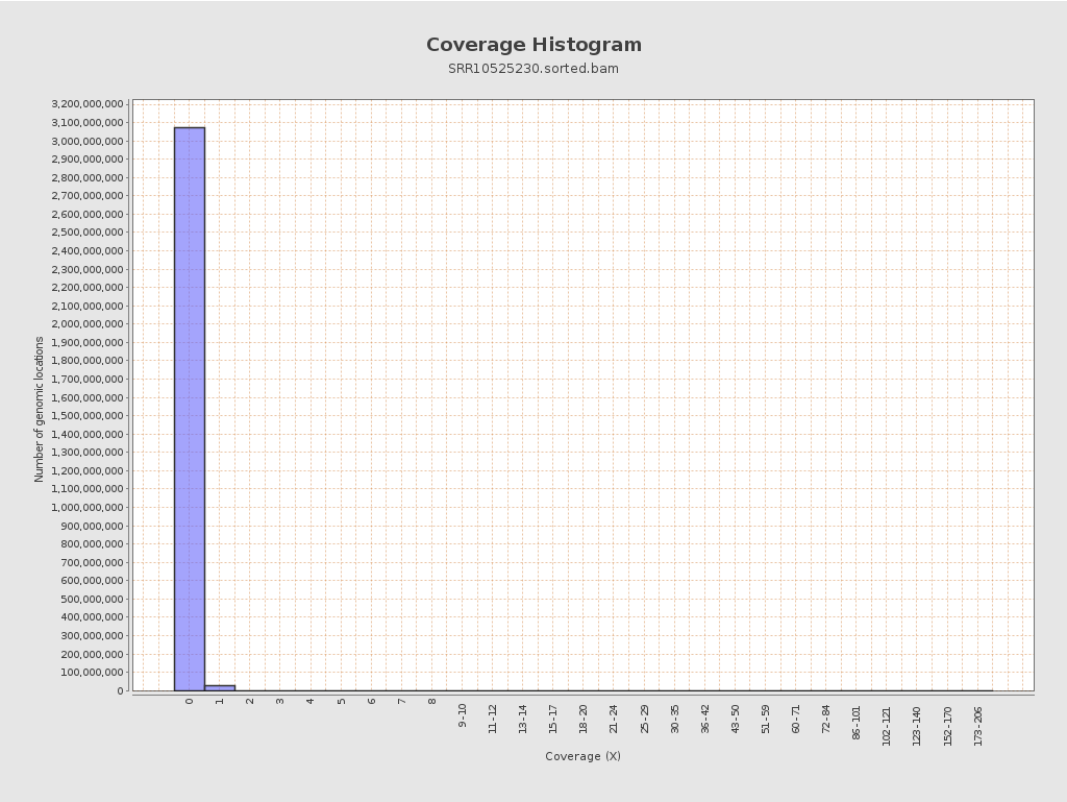
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2205358	0.0088	0.164
chr2	243199373	2307598	0.0095	0.1254
chr3	198022430	1783753	0.009	0.0982
chr4	191154276	1743343	0.0091	0.1019
chr5	180915260	1610495	0.0089	0.097
chr6	171115067	1572087	0.0092	0.1021
chr7	159138663	1537450	0.0097	0.1373

chr8	146364022	1369899	0.0094	0.1088
chr9	141213431	1126145	0.008	0.1021
chr10	135534747	1323914	0.0098	0.1191
chr11	135006516	1239176	0.0092	0.1071
chr12	133851895	1212429	0.0091	0.0985
chr13	115169878	821522	0.0071	0.0871
chr14	107349540	814180	0.0076	0.0905
chr15	102531392	772318	0.0075	0.0896
chr16	90354753	801219	0.0089	0.1007
chr17	81195210	775068	0.0095	0.1031
chr18	78077248	717199	0.0092	0.1482
chr19	59128983	564785	0.0096	0.1311
chr20	63025520	583175	0.0093	0.0999
chr21	48129895	365591	0.0076	0.0939
chr22	51304566	349598	0.0068	0.0853
chrMT	16571	3195	0.1928	0.526
chrX	155270560	1483178	0.0096	0.1035
chrY	59373566	86403	0.0015	0.0528

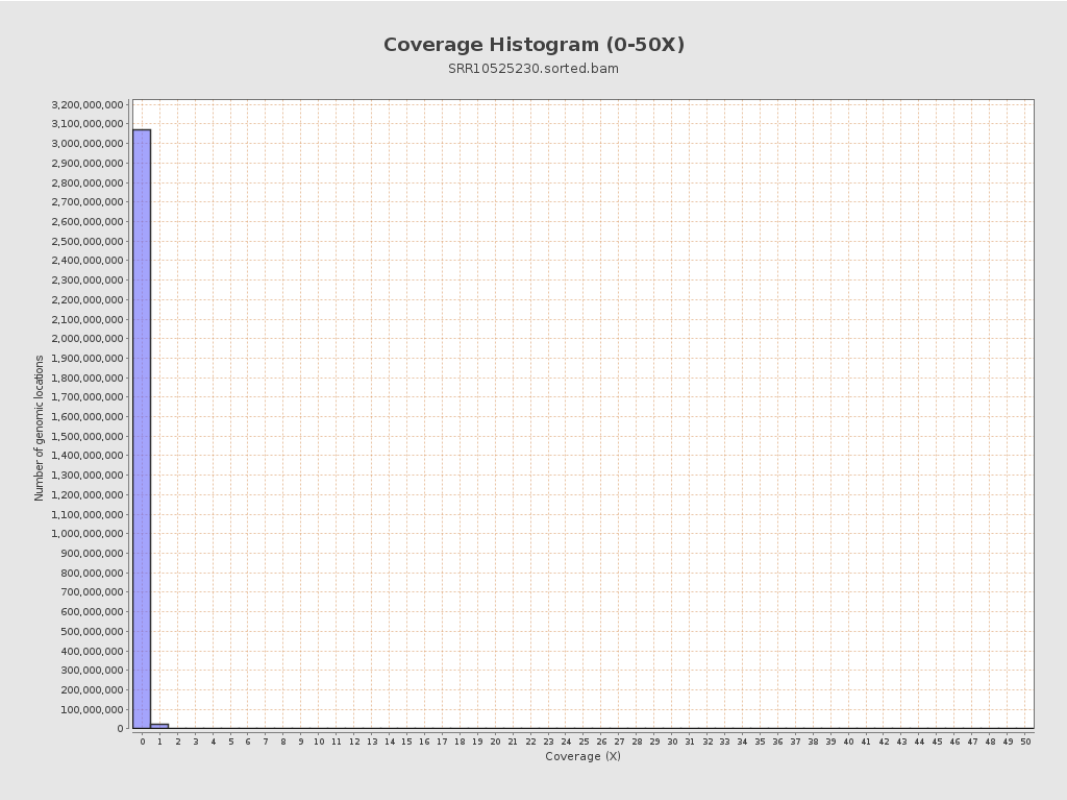
3. Results : Coverage across reference



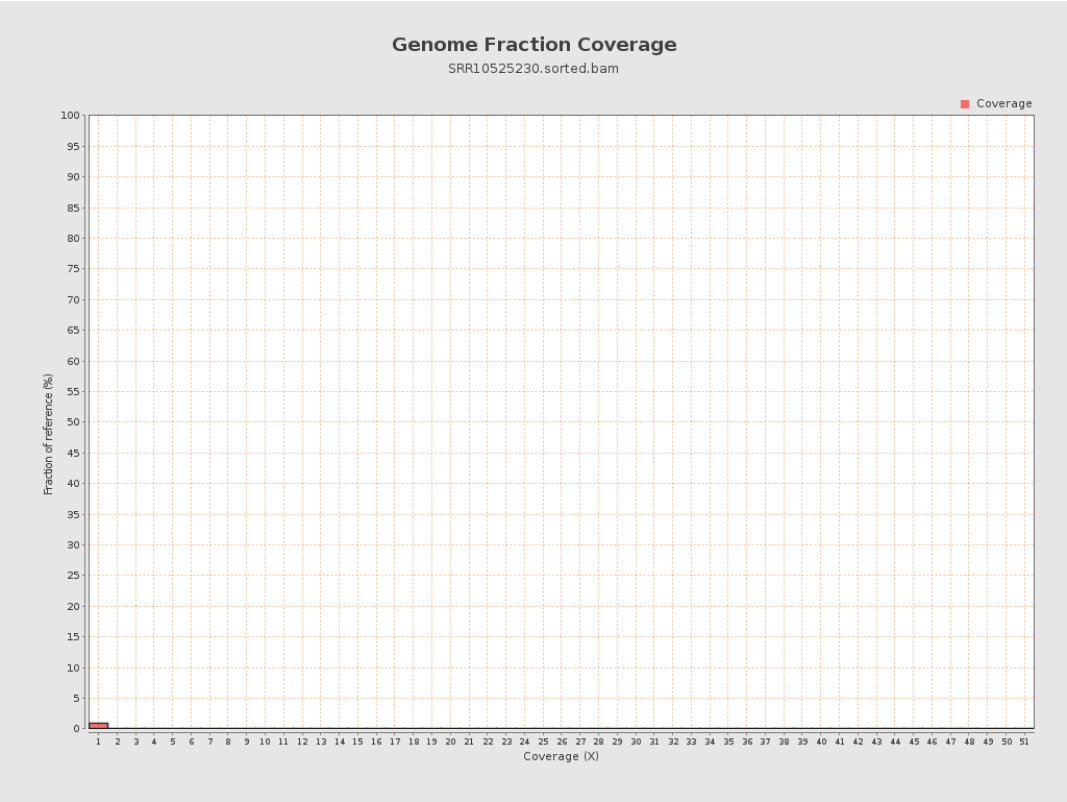
4. Results : Coverage Histogram



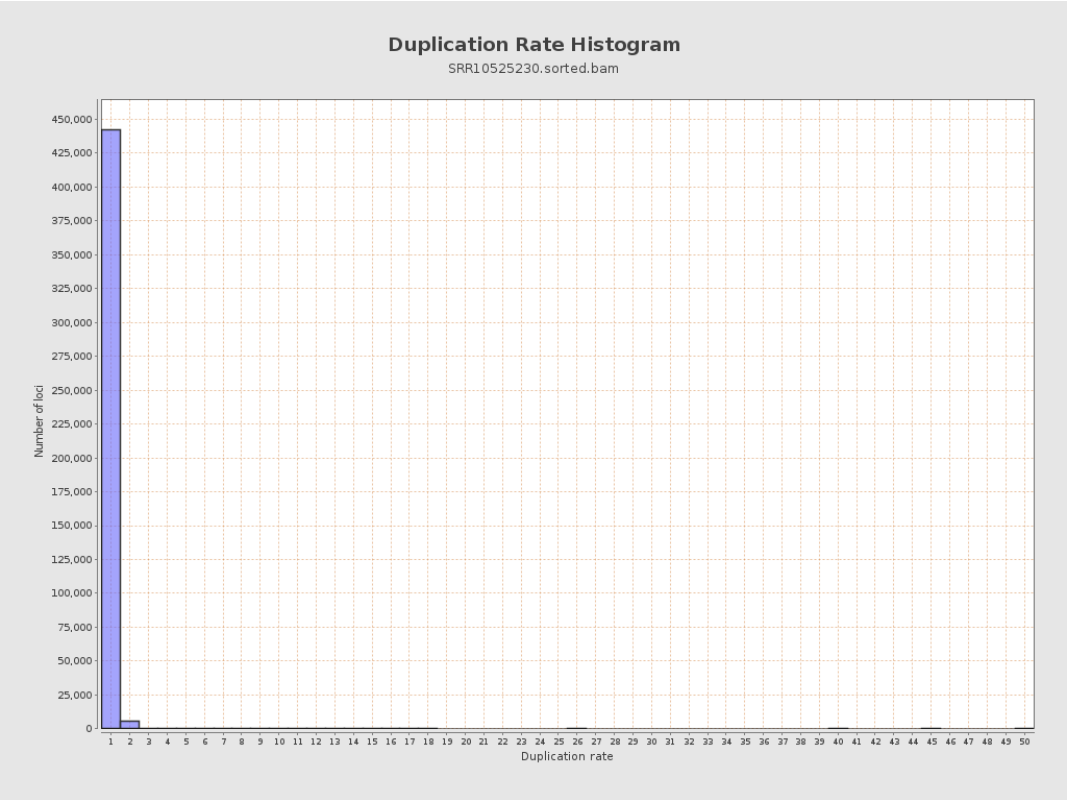
5. Results : Coverage Histogram (0-50X)



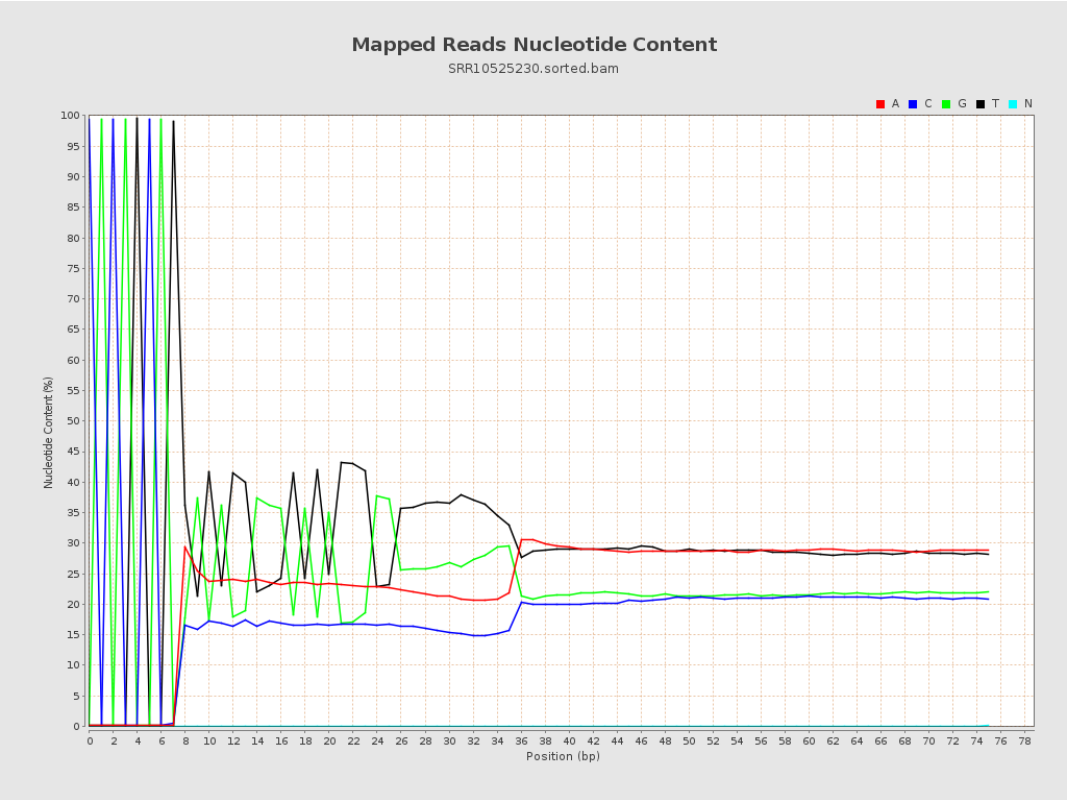
6. Results : Genome Fraction Coverage



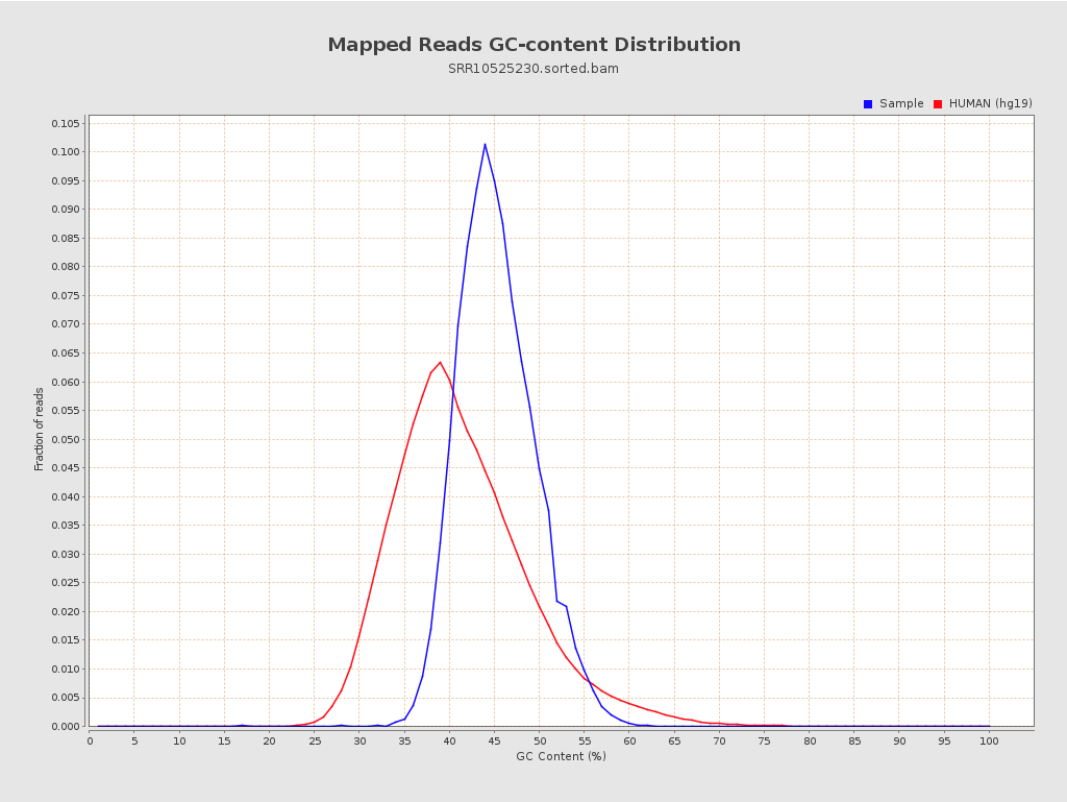
7. Results : Duplication Rate Histogram



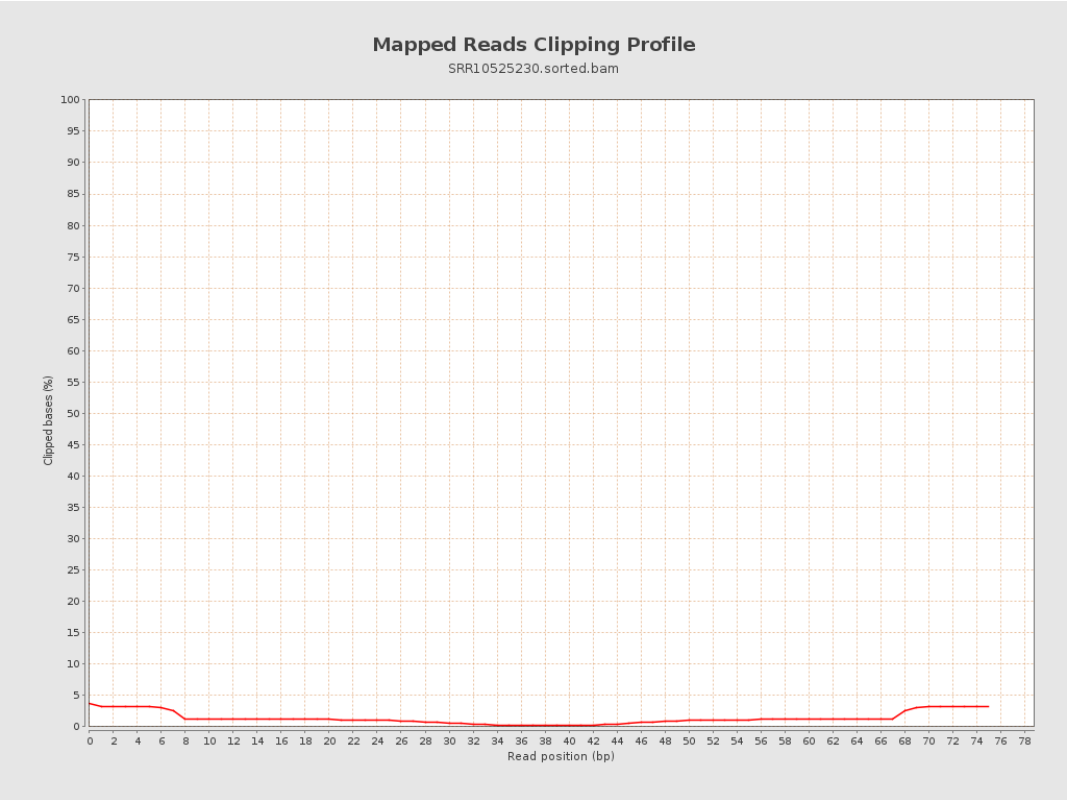
8. Results : Mapped Reads Nucleotide Content



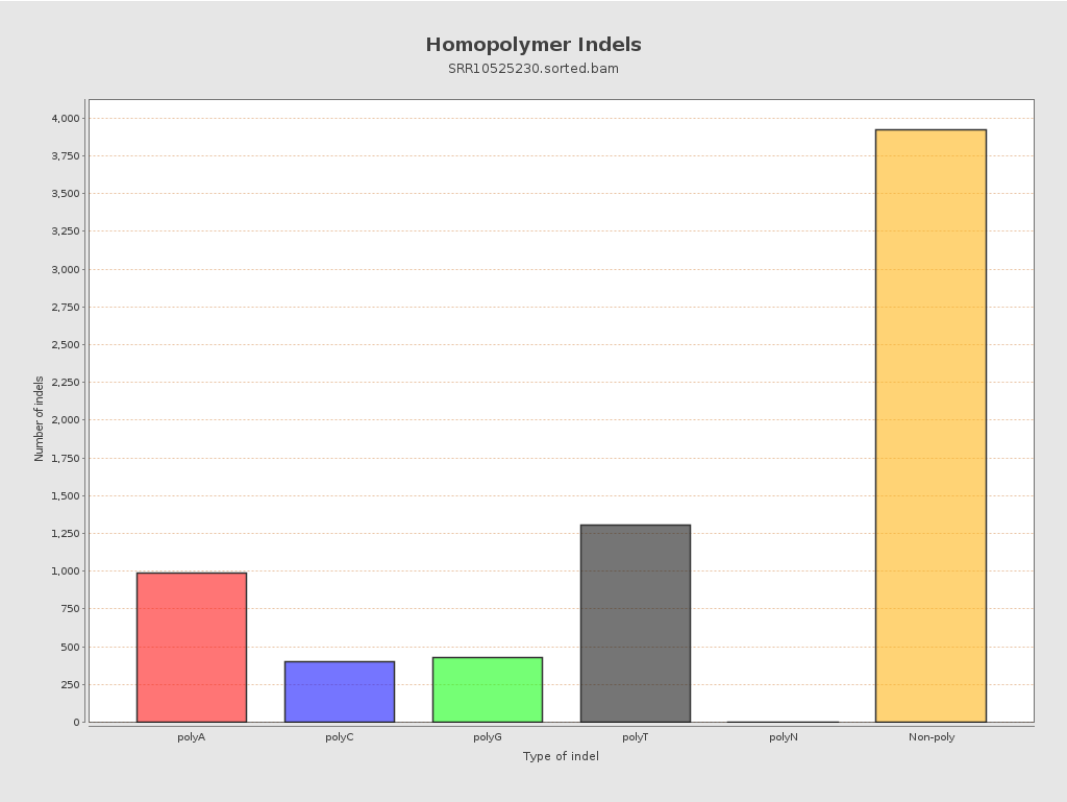
9. Results : Mapped Reads GC-content Distribution



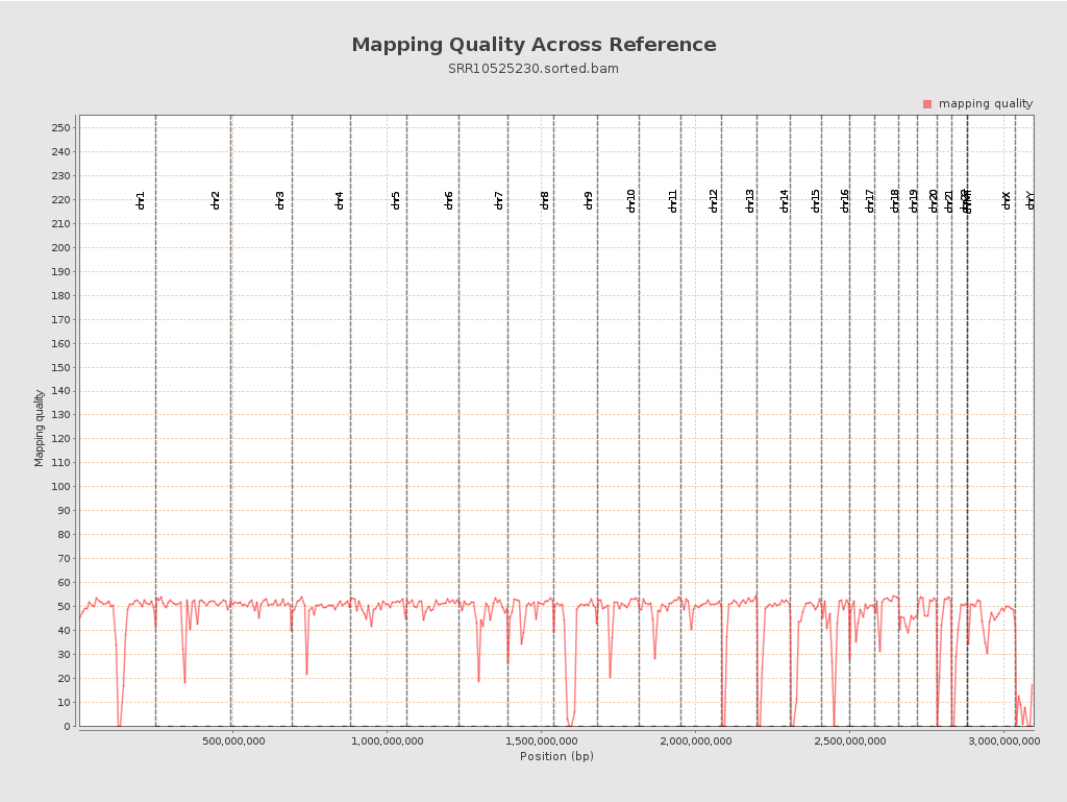
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram