Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:56:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524602.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_SRR10524602 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524602.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:56:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524602.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,384,440
Mapped reads	1,285,790 / 92.87%
Unmapped reads	98,650 / 7.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,608 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	50,002 / 3.61%
Duplication rate	3%
Clipped reads	1,283,889 / 92.74%

2.2. ACGT Content

Number/percentage of A's	19,093,438 / 25.62%
Number/percentage of C's	13,605,480 / 18.26%
Number/percentage of T's	24,180,147 / 32.45%
Number/percentage of G's	17,635,463 / 23.67%
Number/percentage of N's	464 / 0%
GC Percentage	41.93%

2.3. Coverage

Mean	0.0241

Standard Deviation	0.2276

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

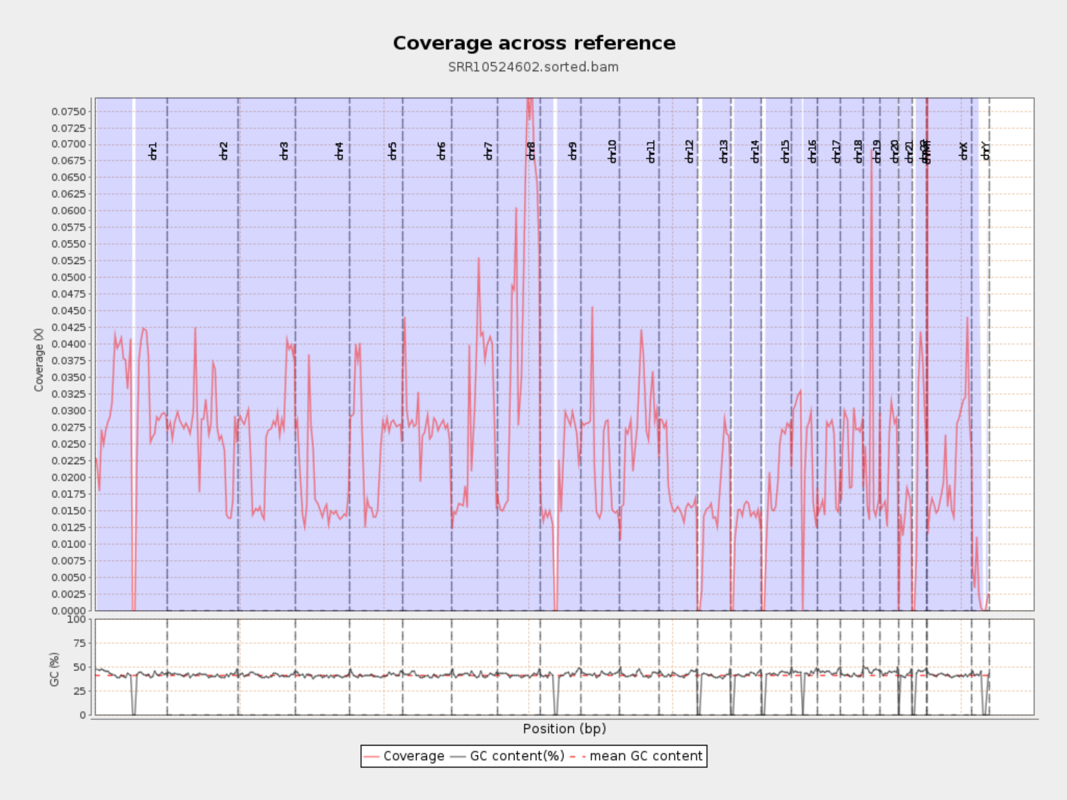
General error rate	0.49%
Mismatches	353,324
Insertions	5,214
Mapped reads with at least one insertion	0.4%
Deletions	14,202
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.4%

2.6. Chromosome stats

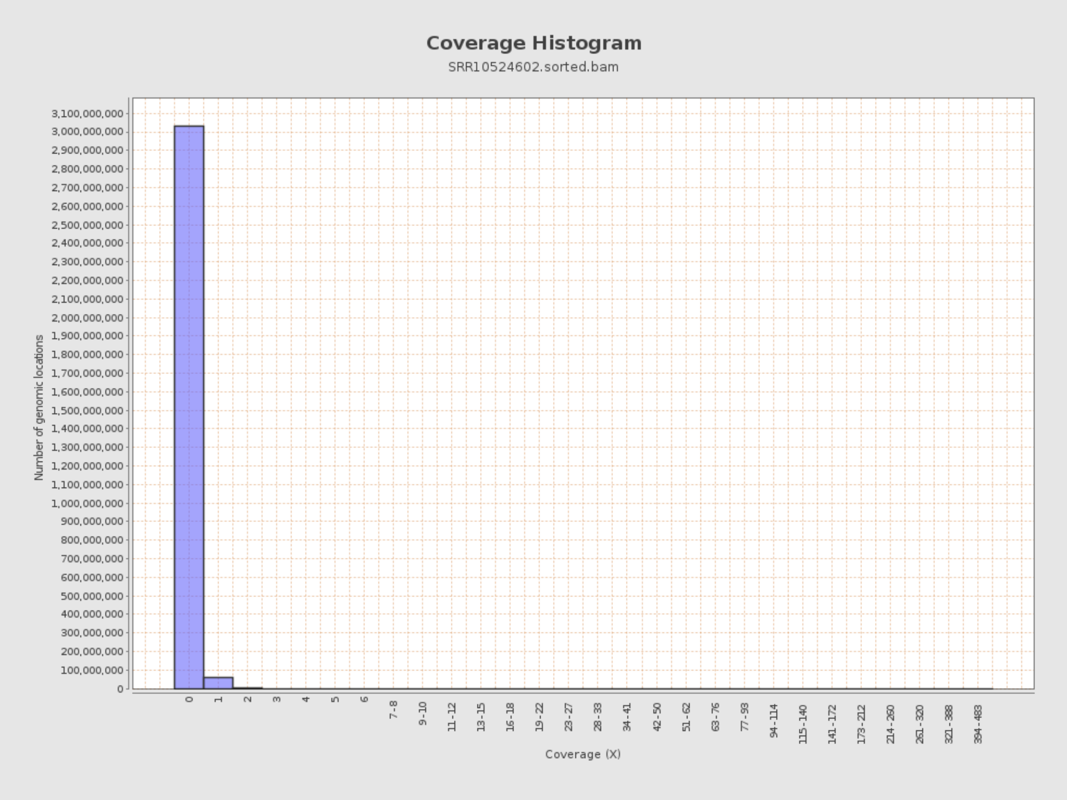
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7535579	0.0302	0.3831
chr2	243199373	6524806	0.0268	0.2639
chr3	198022430	5281491	0.0267	0.1789
chr4	191154276	3427192	0.0179	0.1713
chr5	180915260	4588912	0.0254	0.1739
chr6	171115067	4840771	0.0283	0.1965
chr7	159138663	4548942	0.0286	0.2844

chr8	146364022	6650398	0.0454	0.3077
chr9	141213431	2666279	0.0189	0.2079
chr10	135534747	3146153	0.0232	0.2265
chr11	135006516	3764512	0.0279	0.2263
chr12	133851895	2473878	0.0185	0.153
chr13	115169878	1802285	0.0156	0.1372
chr14	107349540	1369388	0.0128	0.1272
chr15	102531392	1867548	0.0182	0.1573
chr16	90354753	2135434	0.0236	0.176
chr17	81195210	1647210	0.0203	0.1584
chr18	78077248	1989914	0.0255	0.3065
chr19	59128983	1426579	0.0241	0.2753
chr20	63025520	1385995	0.022	0.1642
chr21	48129895	647799	0.0135	0.1383
chr22	51304566	1191463	0.0232	0.1662
chrMT	16571	4141	0.2499	0.5871
chrX	155270560	3438527	0.0221	0.1808
chrY	59373566	183984	0.0031	0.0963

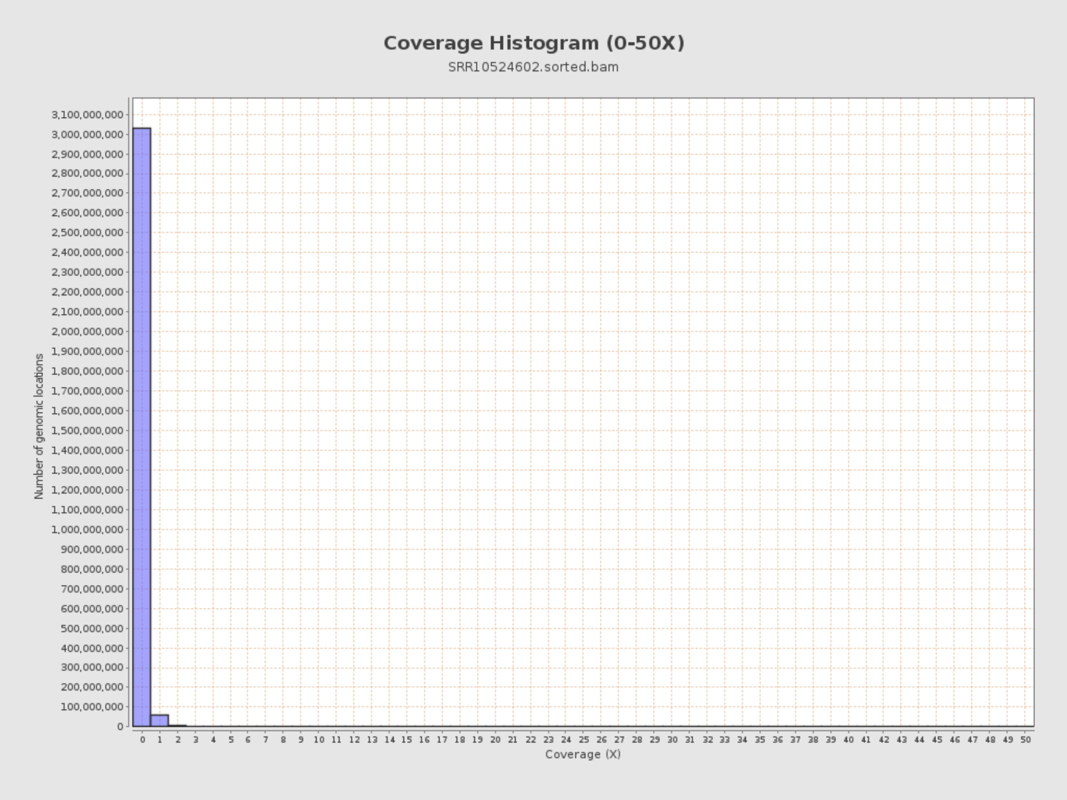
3. Results : Coverage across reference



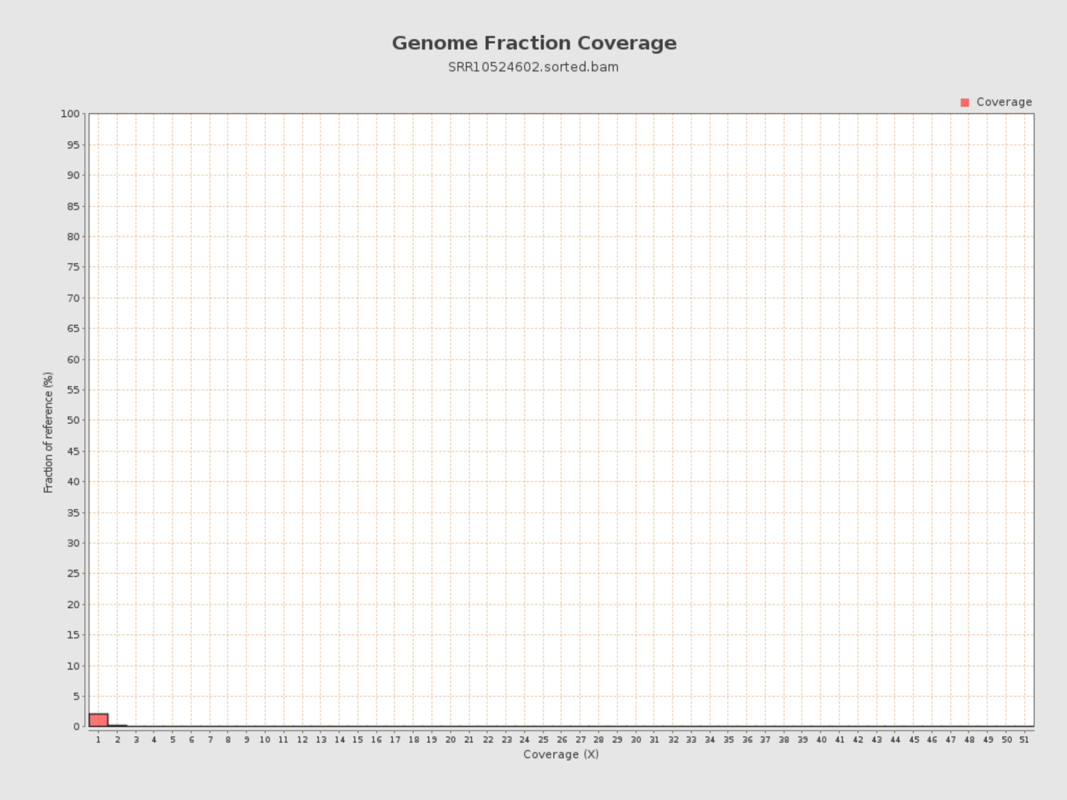
4. Results : Coverage Histogram



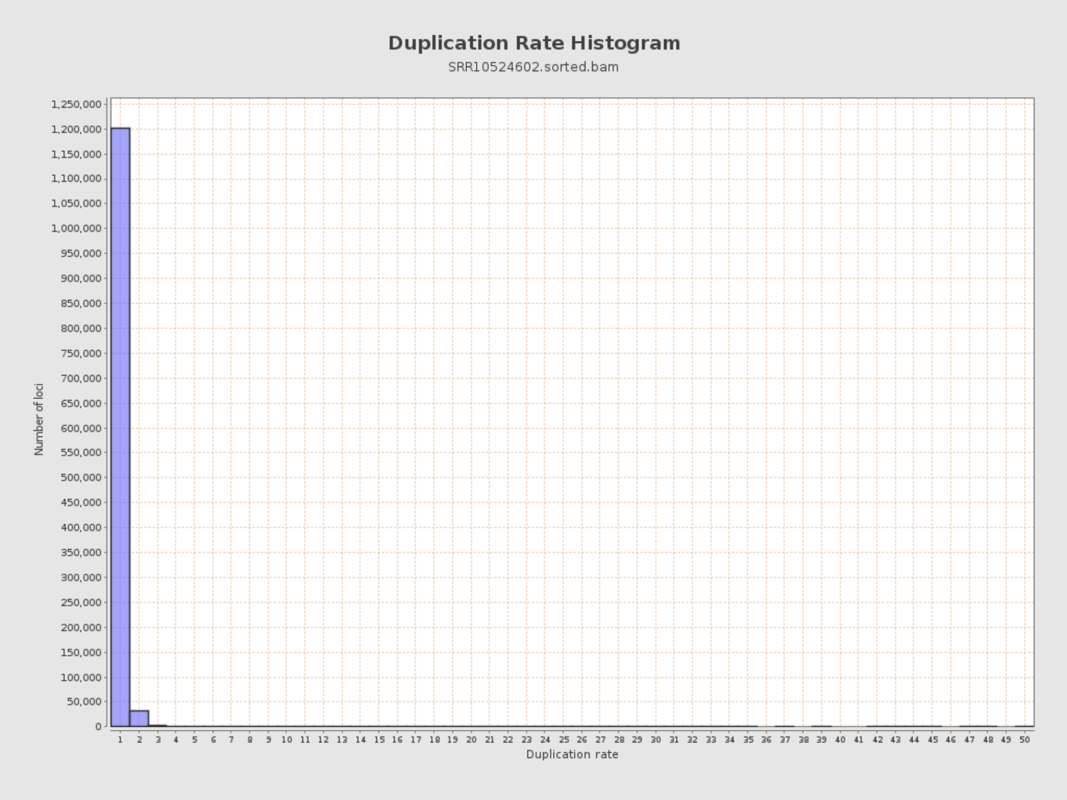
5. Results : Coverage Histogram (0-50X)



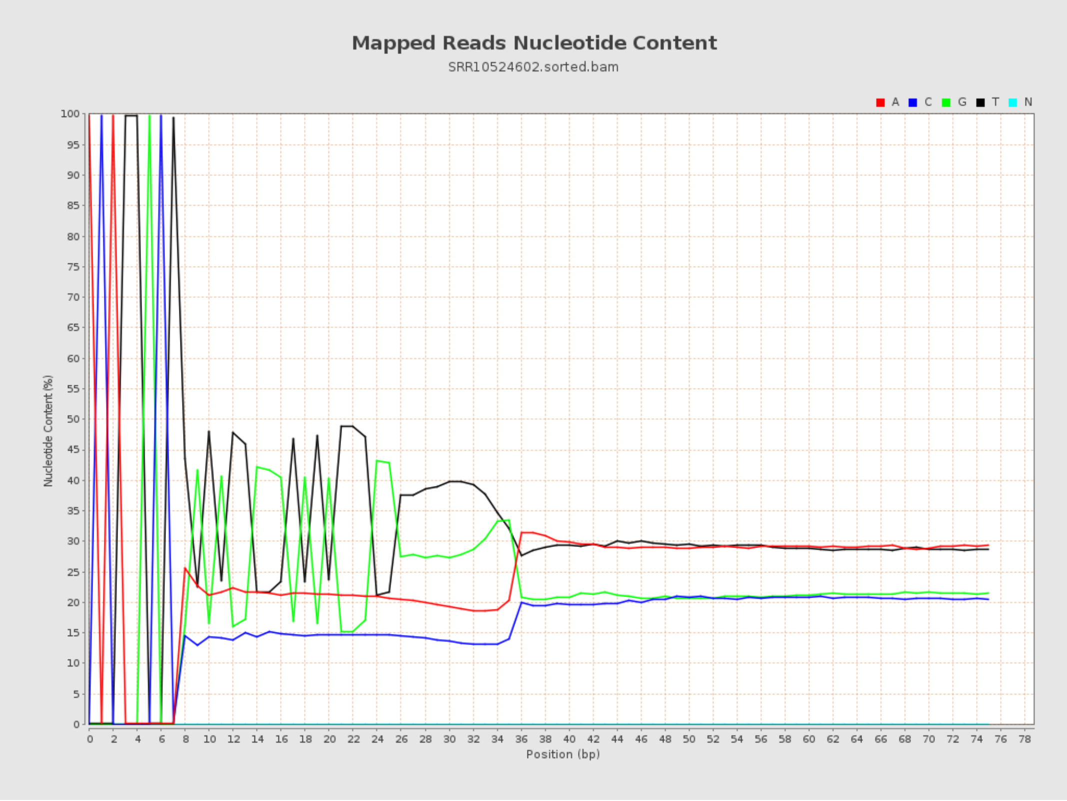
6. Results : Genome Fraction Coverage



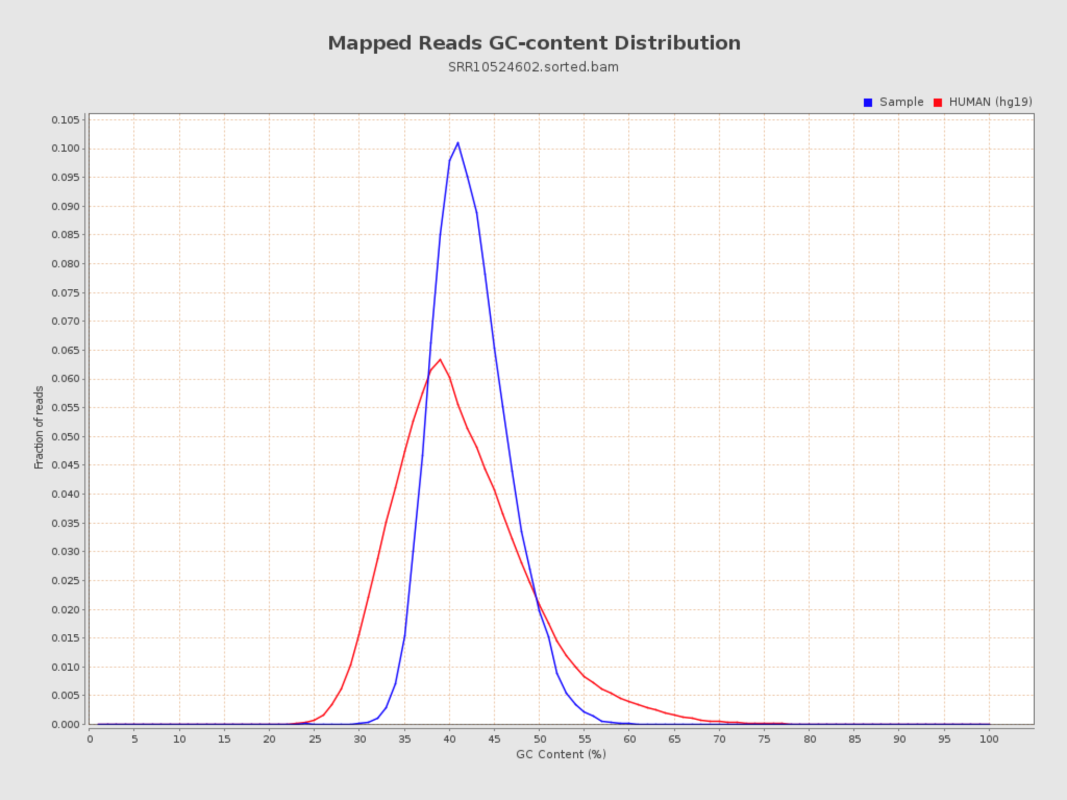
7. Results : Duplication Rate Histogram



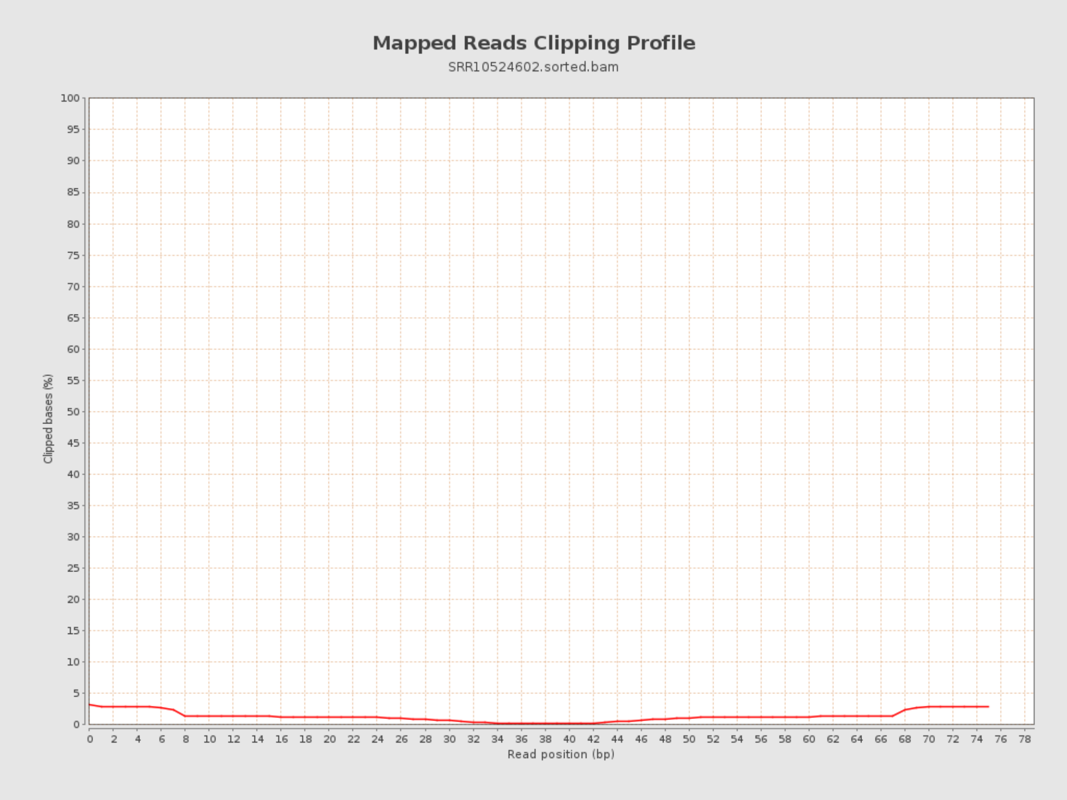
8. Results : Mapped Reads Nucleotide Content



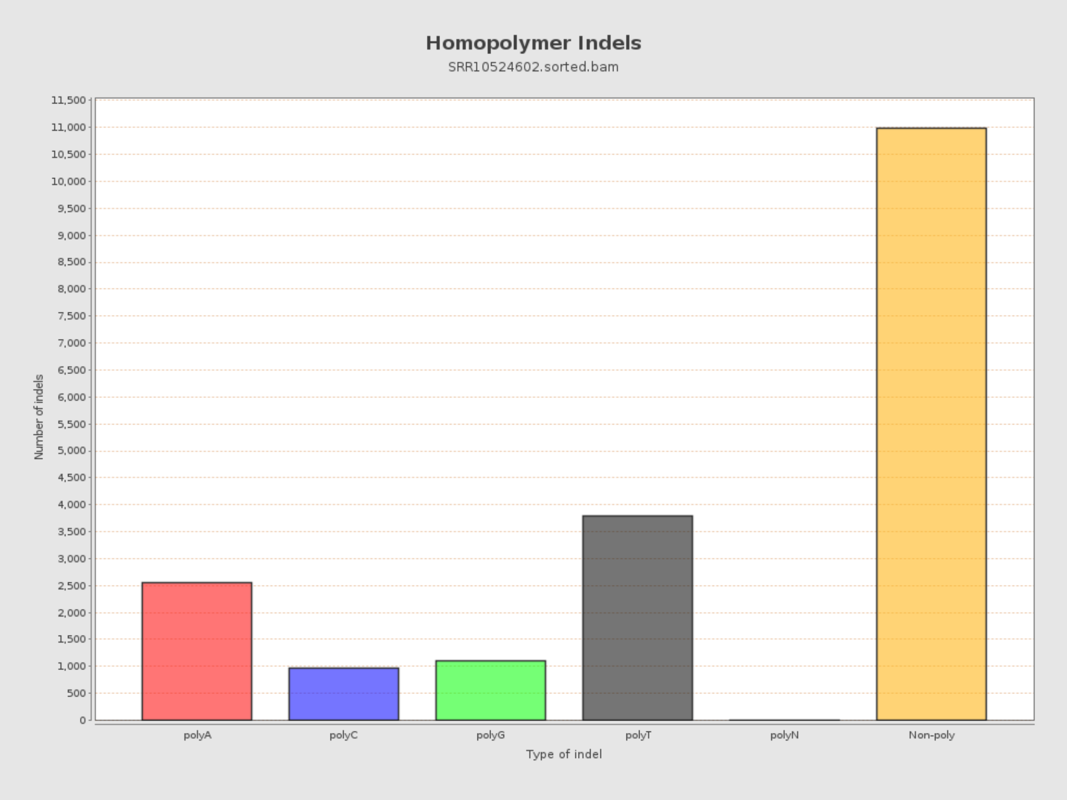
9. Results : Mapped Reads GC-content Distribution



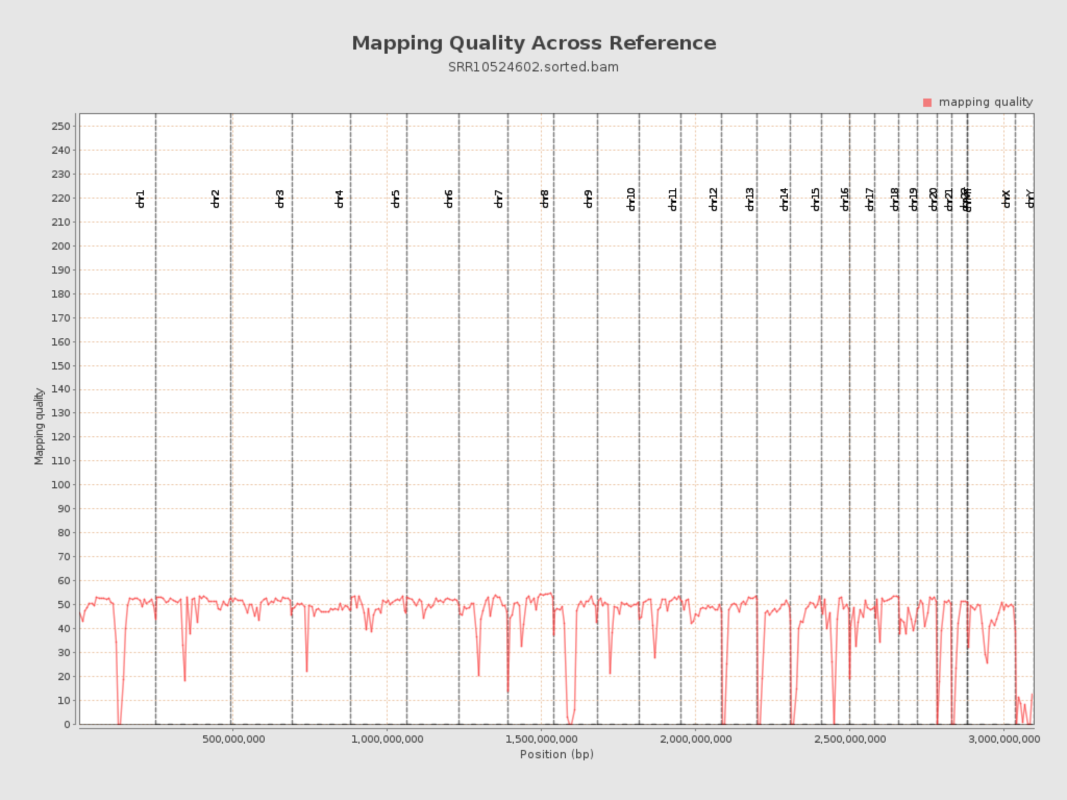
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram