Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:26:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549048.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_SRR1549048 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549048.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:26:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549048.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,594,787
Mapped reads	3,869,558 / 84.22%
Unmapped reads	725,229 / 15.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	128,155 / 2.79%
Duplication rate	2.59%
Clipped reads	332,753 / 7.24%

2.2. ACGT Content

Number/percentage of A's	41,984,241 / 27.46%
Number/percentage of C's	33,810,074 / 22.11%
Number/percentage of T's	43,177,111 / 28.24%
Number/percentage of G's	33,920,539 / 22.19%
Number/percentage of N's	1,169 / 0%
GC Percentage	44.3%

2.3. Coverage

Mean	0.0494
Standard Deviation	0.3685

2.4. Mapping Quality

Mean Mapping Quality	36.59

2.5. Mismatches and indels

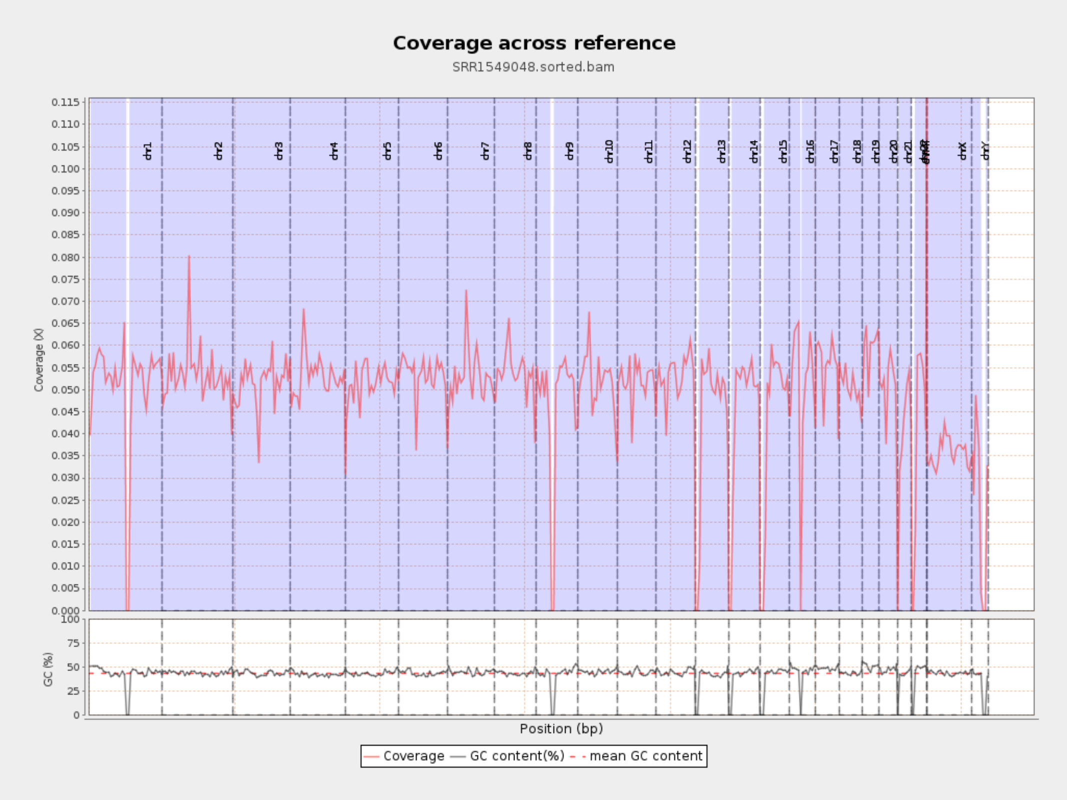
General error rate	0.29%
Mismatches	444,044
Insertions	4,944
Mapped reads with at least one insertion	0.13%
Deletions	10,626
Mapped reads with at least one deletion	0.27%
Homopolymer indels	38.79%

2.6. Chromosome stats

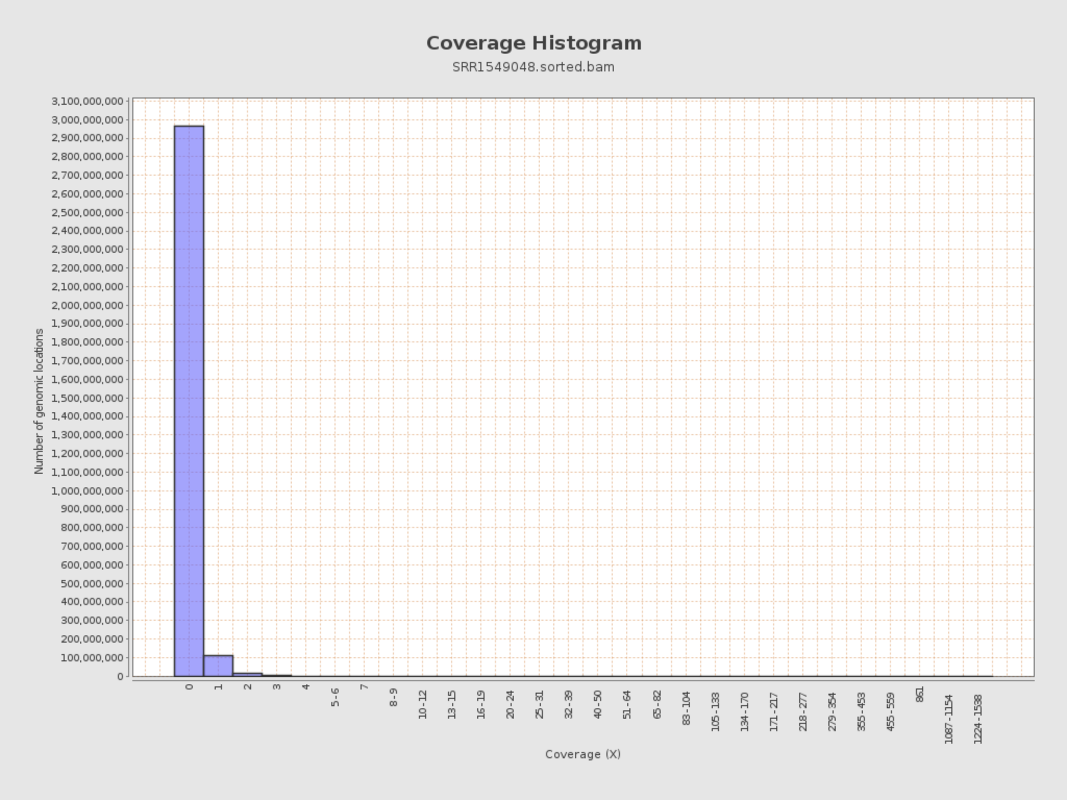
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12578113	0.0505	0.4775
chr2	243199373	13010400	0.0535	0.3753
chr3	198022430	10167705	0.0513	0.2605
chr4	191154276	10129743	0.053	0.2774
chr5	180915260	9335190	0.0516	0.2622
chr6	171115067	9110284	0.0532	0.2718
chr7	159138663	8468167	0.0532	0.404
chr8	146364022	7840158	0.0536	0.8036

chr9	141213431	6451645	0.0457	0.3669
chr10	135534747	7081606	0.0522	0.3192
chr11	135006516	6982440	0.0517	0.2902
chr12	133851895	7107294	0.0531	0.2665
chr13	115169878	4987792	0.0433	0.2384
chr14	107349540	4774541	0.0445	0.275
chr15	102531392	4396758	0.0429	0.2375
chr16	90354753	4619067	0.0511	0.2799
chr17	81195210	4493206	0.0553	0.2765
chr18	78077248	3971596	0.0509	0.5962
chr19	59128983	3500366	0.0592	0.5037
chr20	63025520	3187524	0.0506	0.2626
chr21	48129895	1887384	0.0392	0.2703
chr22	51304566	1935862	0.0377	0.2937
chrMT	16571	2229	0.1345	0.4244
chrX	155270560	5553822	0.0358	0.2534
chrY	59373566	1333803	0.0225	0.2275

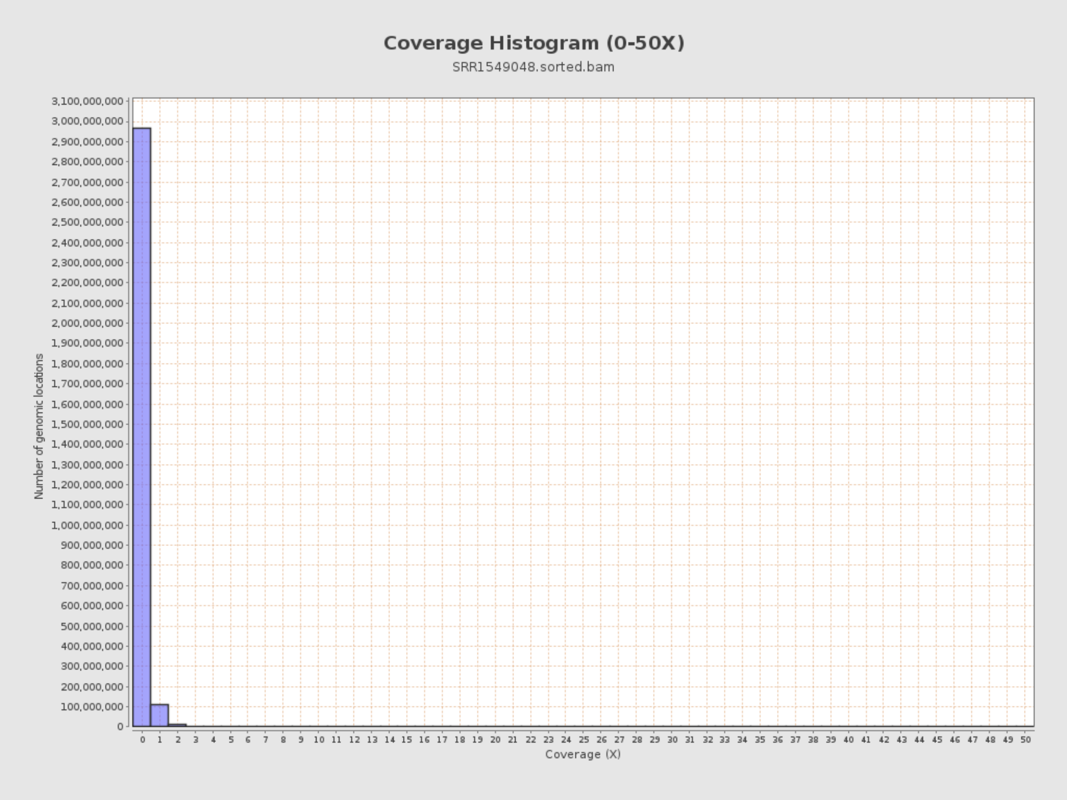
3. Results : Coverage across reference



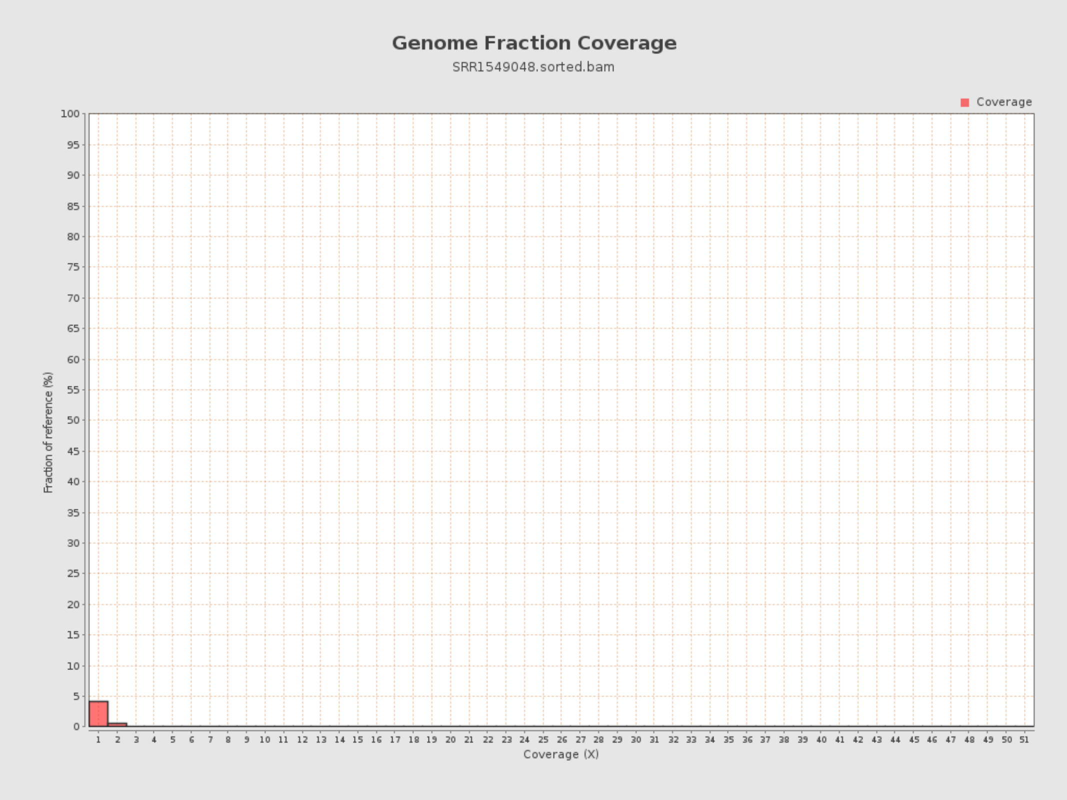
4. Results : Coverage Histogram



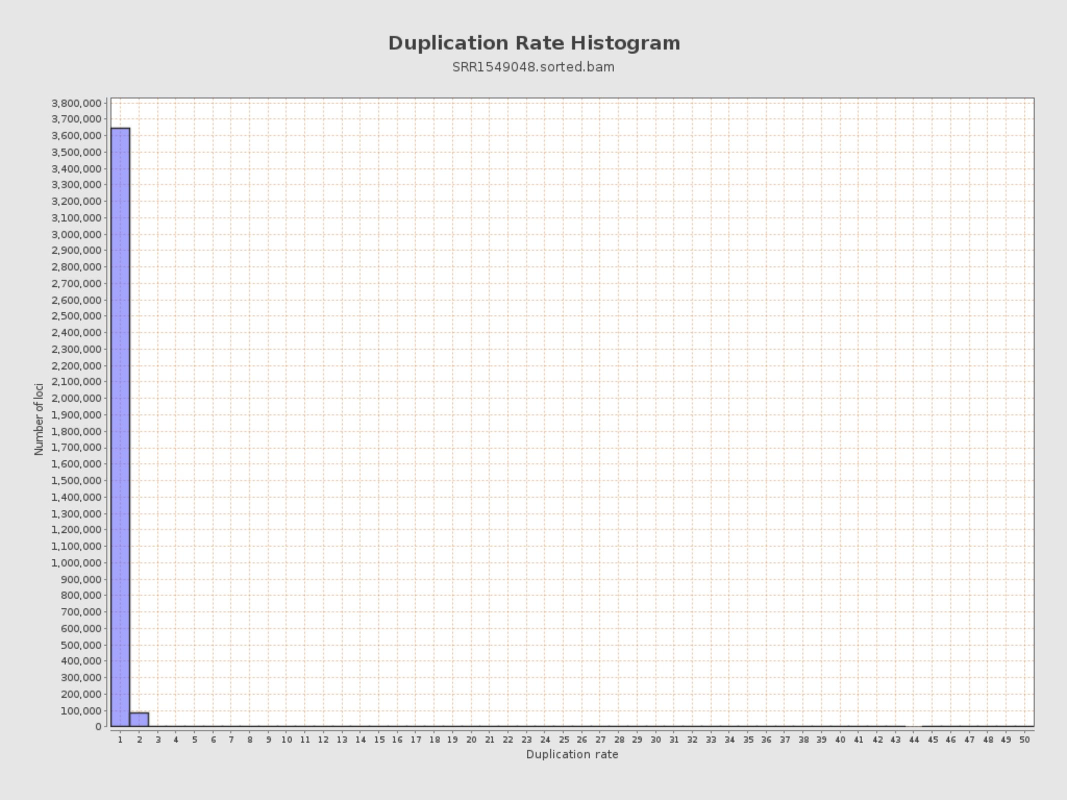
5. Results : Coverage Histogram (0-50X)



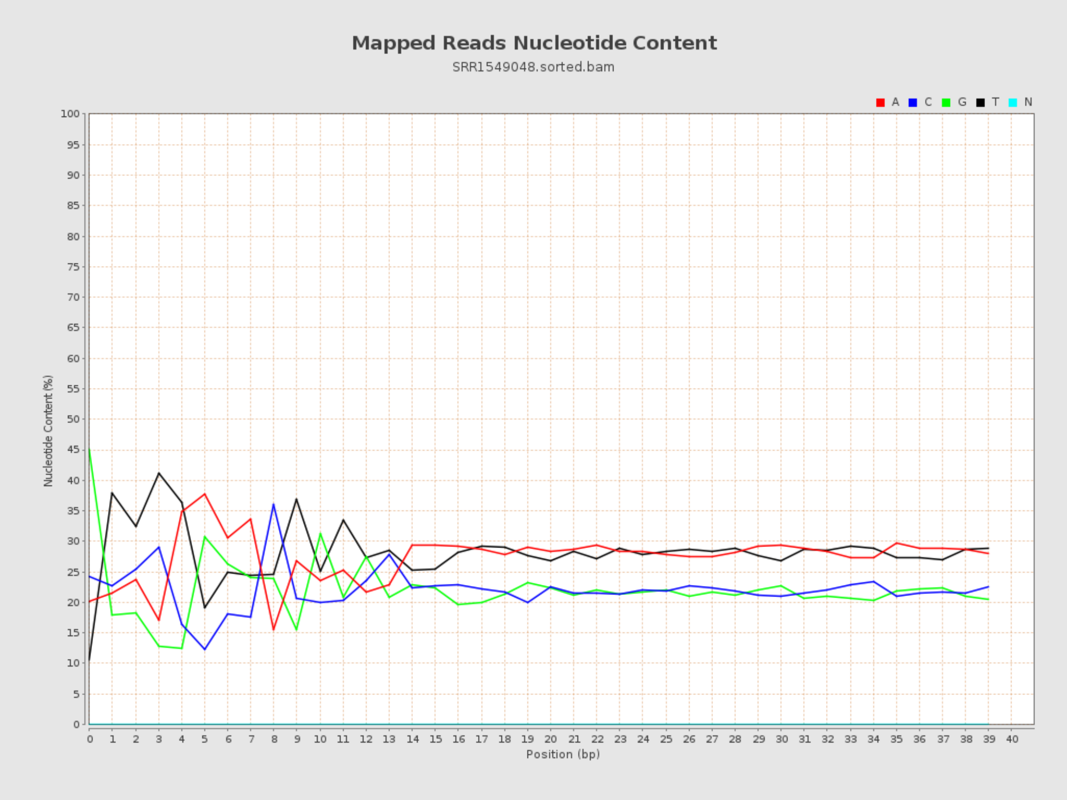
6. Results : Genome Fraction Coverage



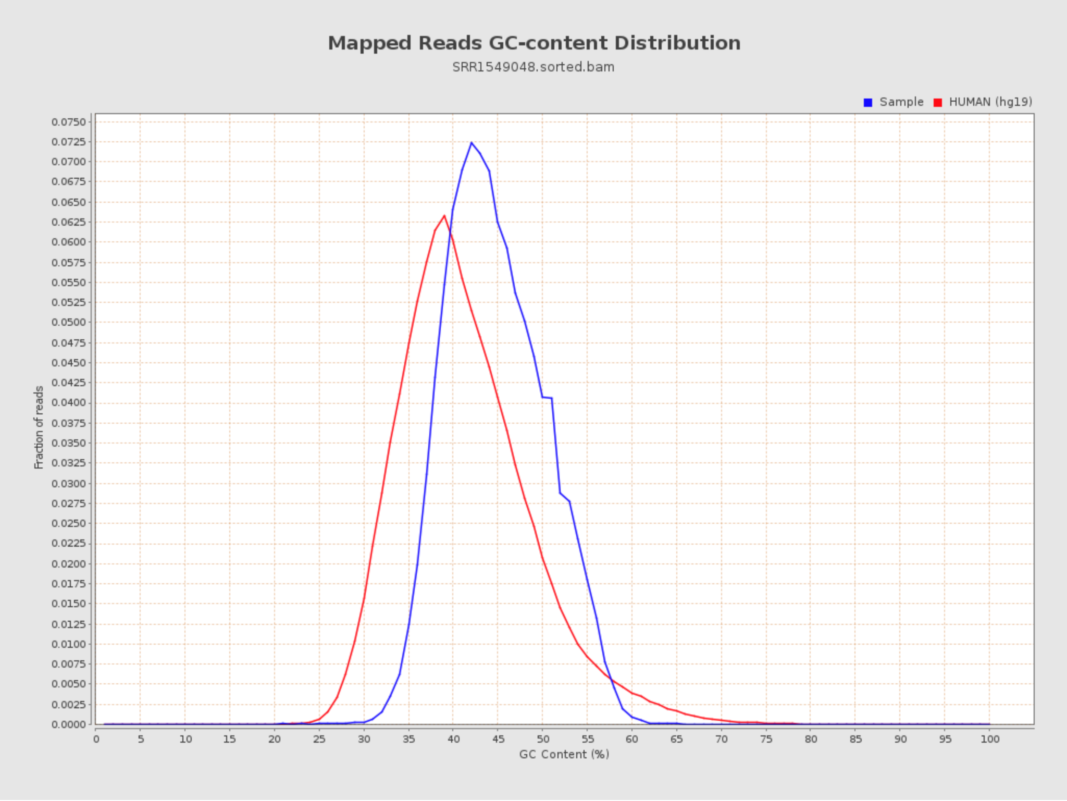
7. Results : Duplication Rate Histogram



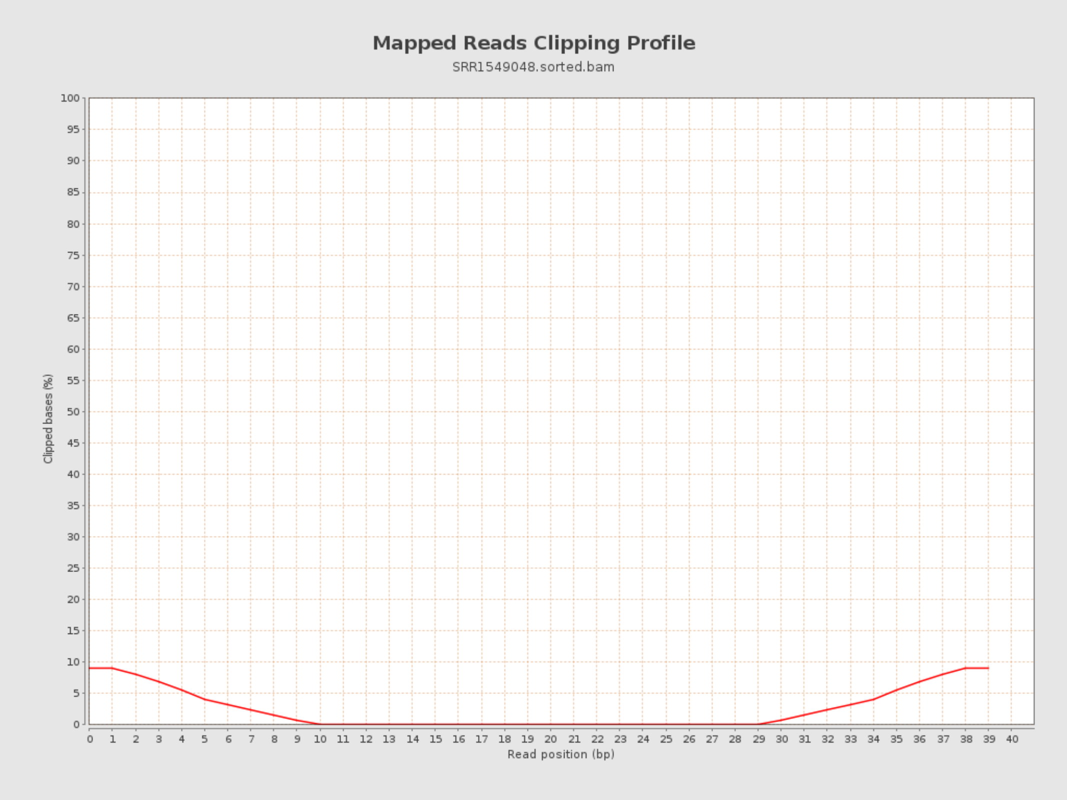
8. Results : Mapped Reads Nucleotide Content



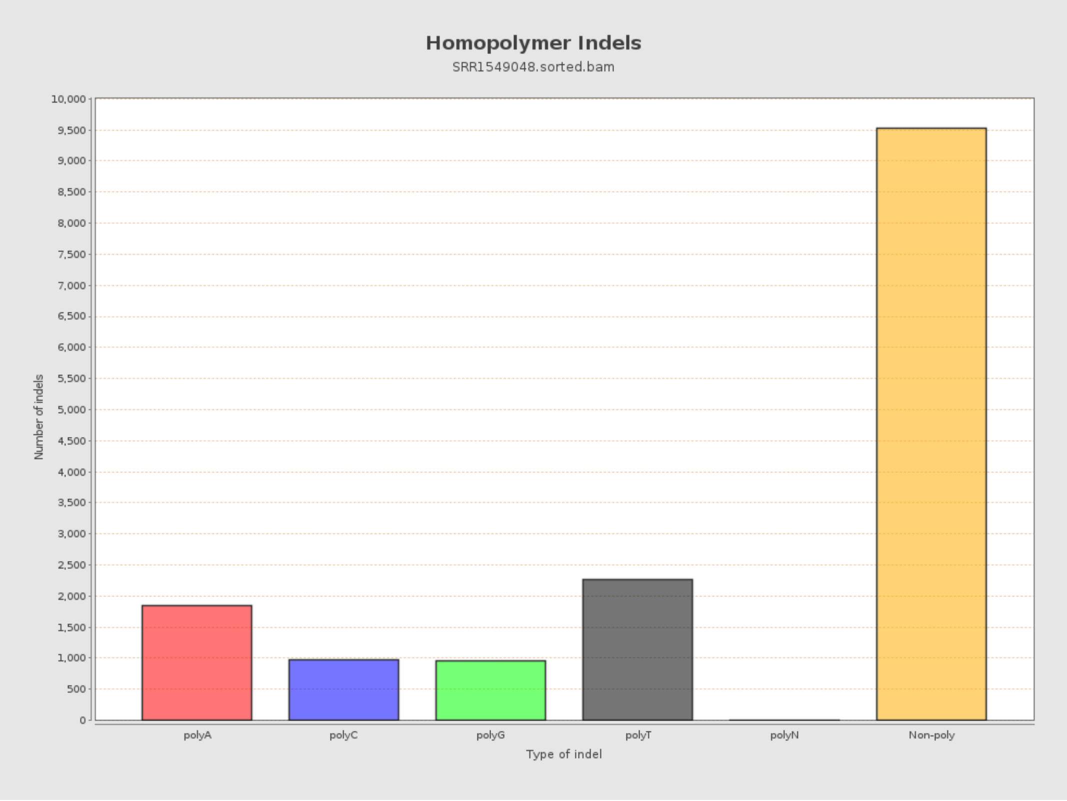
9. Results : Mapped Reads GC-content Distribution



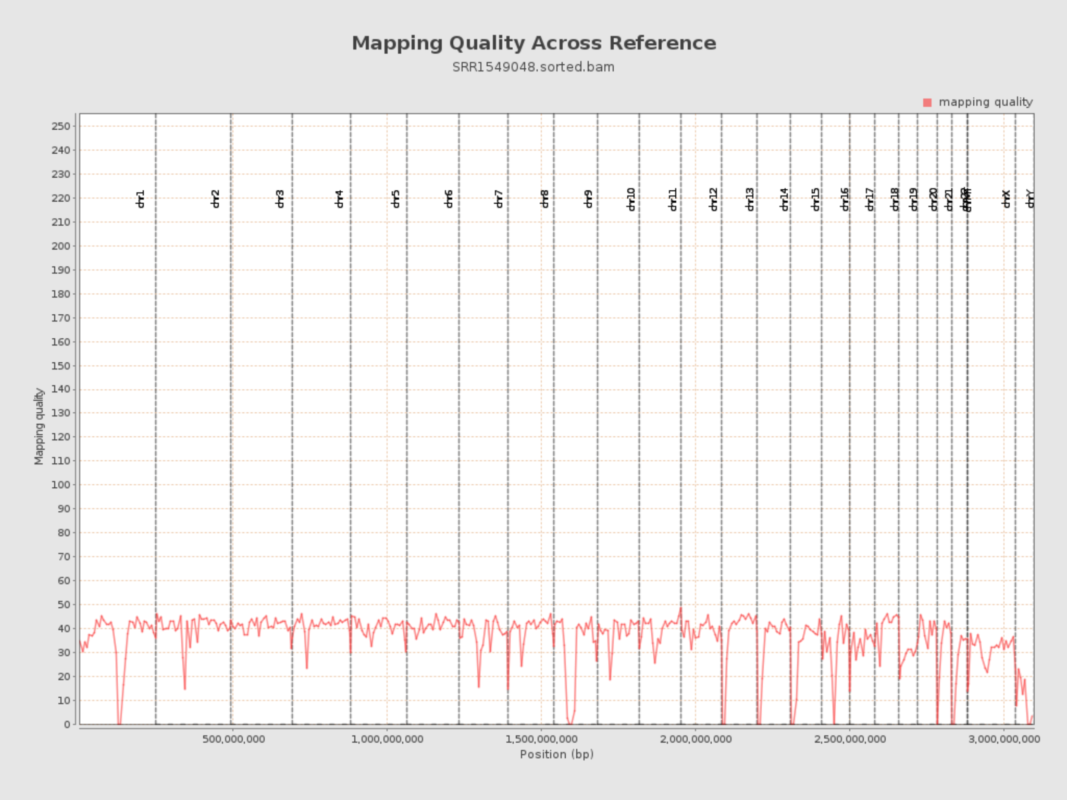
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram