Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:19:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548947.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_SRR1548947 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548947.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:19:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548947.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,455,876
Mapped reads	4,764,872 / 87.33%
Unmapped reads	691,004 / 12.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	192,150 / 3.52%
Duplication rate	2.58%
Clipped reads	394,688 / 7.23%

2.2. ACGT Content

Number/percentage of A's	53,002,344 / 28.14%
Number/percentage of C's	40,599,053 / 21.56%
Number/percentage of T's	54,172,146 / 28.76%
Number/percentage of G's	40,568,109 / 21.54%
Number/percentage of N's	1,549 / 0%
GC Percentage	43.1%

2.3. Coverage

Mean	0.0608
Standard Deviation	0.6489

2.4. Mapping Quality

Mean Mapping Quality	37.48

2.5. Mismatches and indels

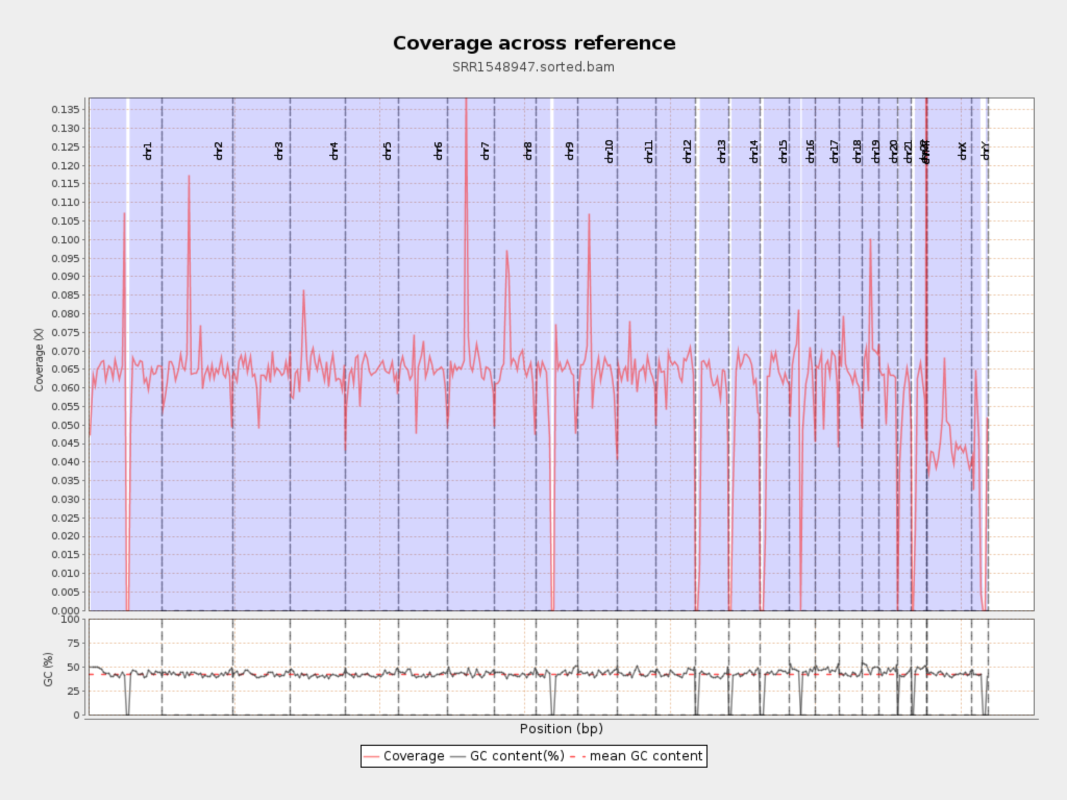
General error rate	0.31%
Mismatches	574,480
Insertions	6,424
Mapped reads with at least one insertion	0.13%
Deletions	14,670
Mapped reads with at least one deletion	0.31%
Homopolymer indels	39.32%

2.6. Chromosome stats

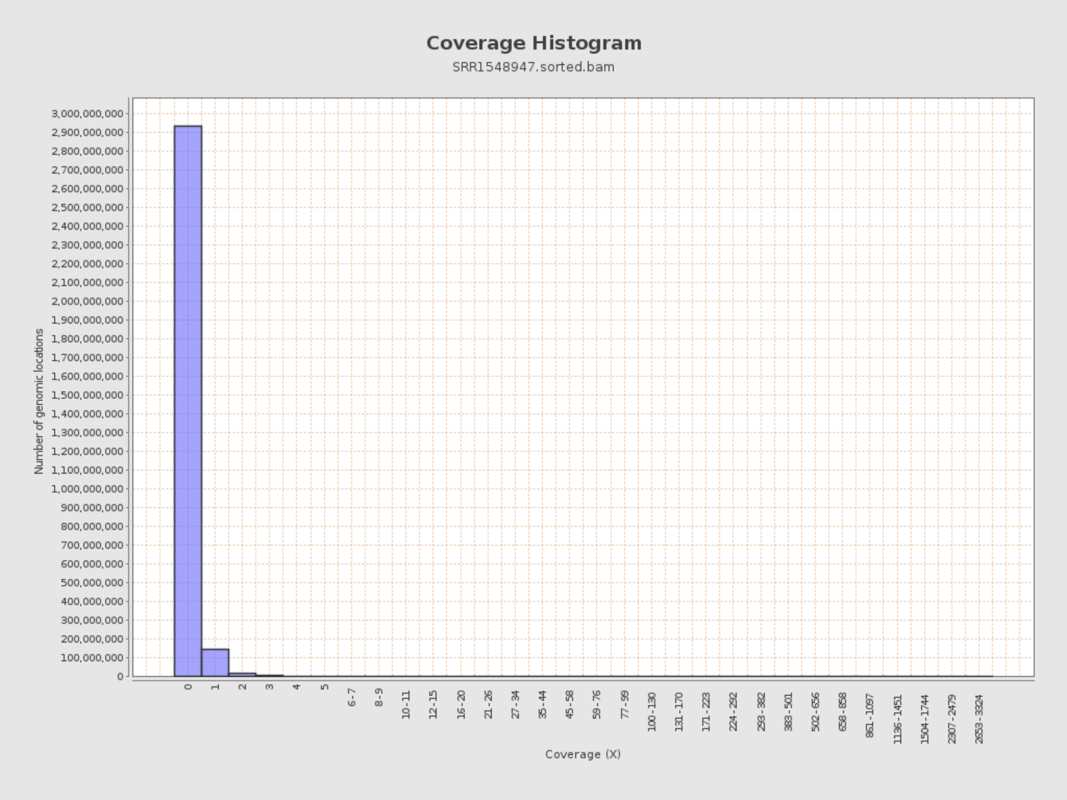
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15238151	0.0611	1.0964
chr2	243199373	16041405	0.066	0.5305
chr3	198022430	12707642	0.0642	0.2858
chr4	191154276	12464566	0.0652	0.3122
chr5	180915260	11627603	0.0643	0.2903
chr6	171115067	11067185	0.0647	0.3095
chr7	159138663	11008461	0.0692	0.9145
chr8	146364022	9852445	0.0673	1.6539

chr9	141213431	8025183	0.0568	0.5546
chr10	135534747	8965317	0.0661	0.4699
chr11	135006516	8658119	0.0641	0.4052
chr12	133851895	8688097	0.0649	0.3076
chr13	115169878	6050848	0.0525	0.251
chr14	107349540	5838517	0.0544	0.335
chr15	102531392	5332827	0.052	0.2577
chr16	90354753	5305702	0.0587	0.3264
chr17	81195210	5150279	0.0634	0.2968
chr18	78077248	5039502	0.0645	1.0154
chr19	59128983	4215850	0.0713	1.0436
chr20	63025520	3846512	0.061	0.2964
chr21	48129895	2379923	0.0494	0.3323
chr22	51304566	2183262	0.0426	0.3184
chrMT	16571	8597	0.5188	0.9916
chrX	155270560	6904817	0.0445	0.3386
chrY	59373566	1761605	0.0297	0.3025

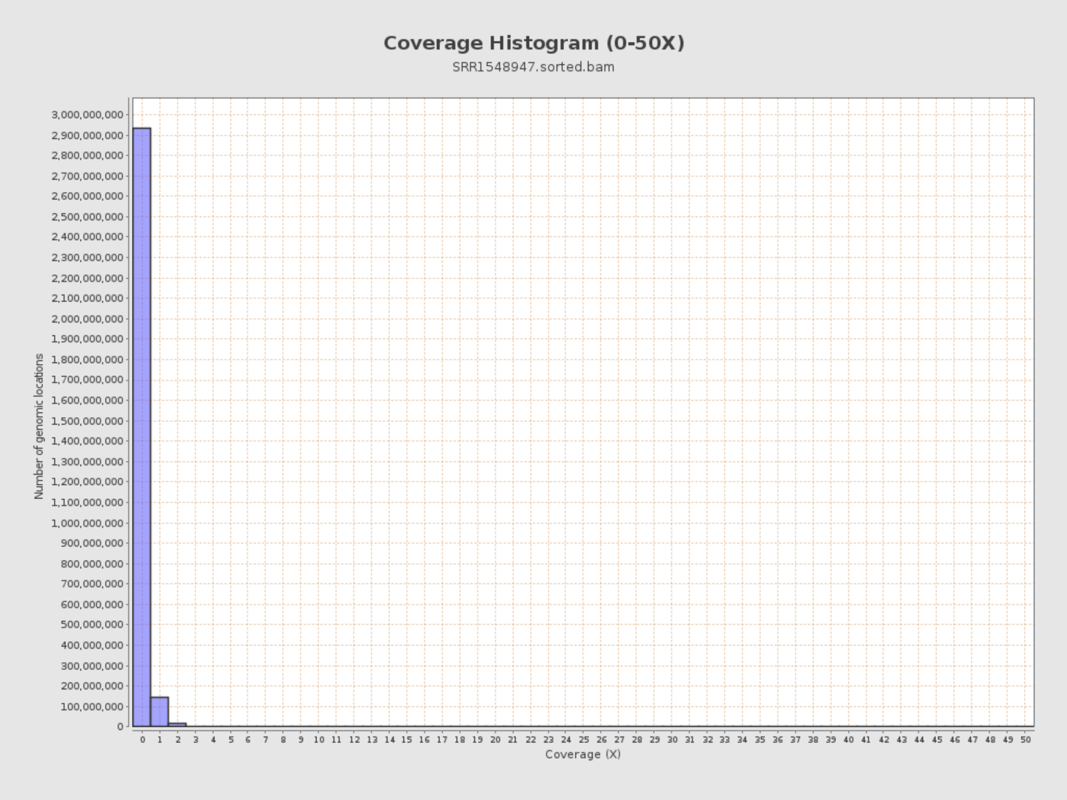
3. Results : Coverage across reference



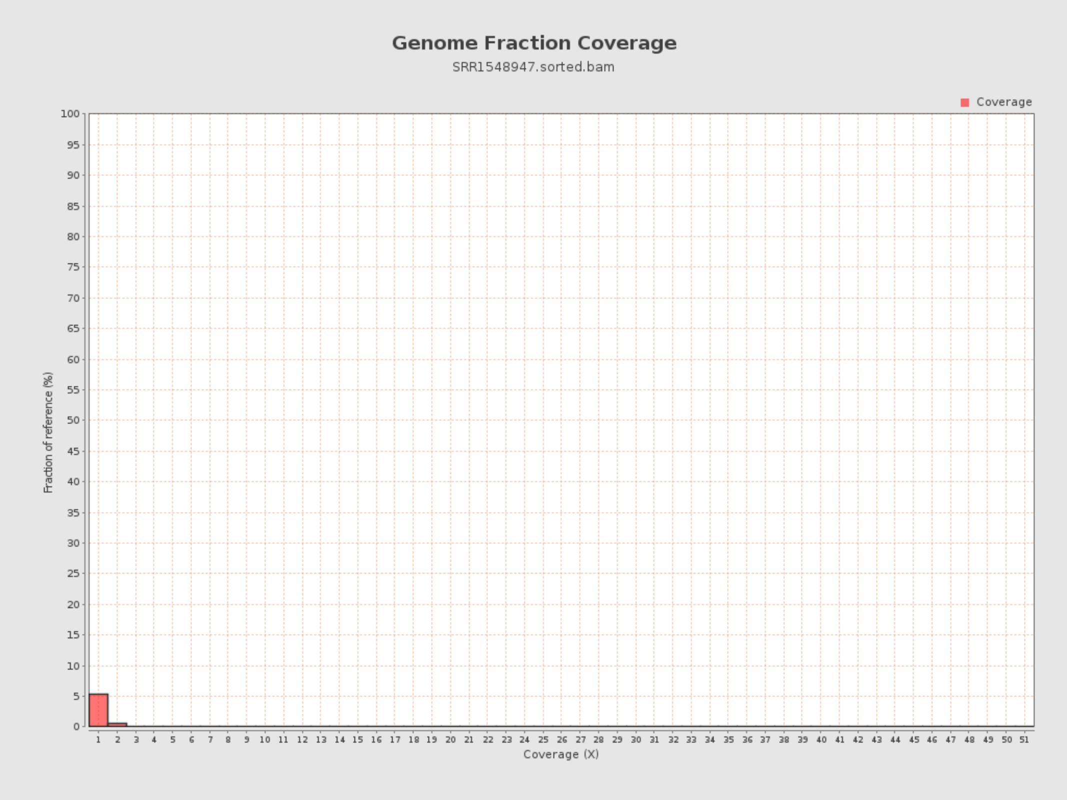
4. Results : Coverage Histogram



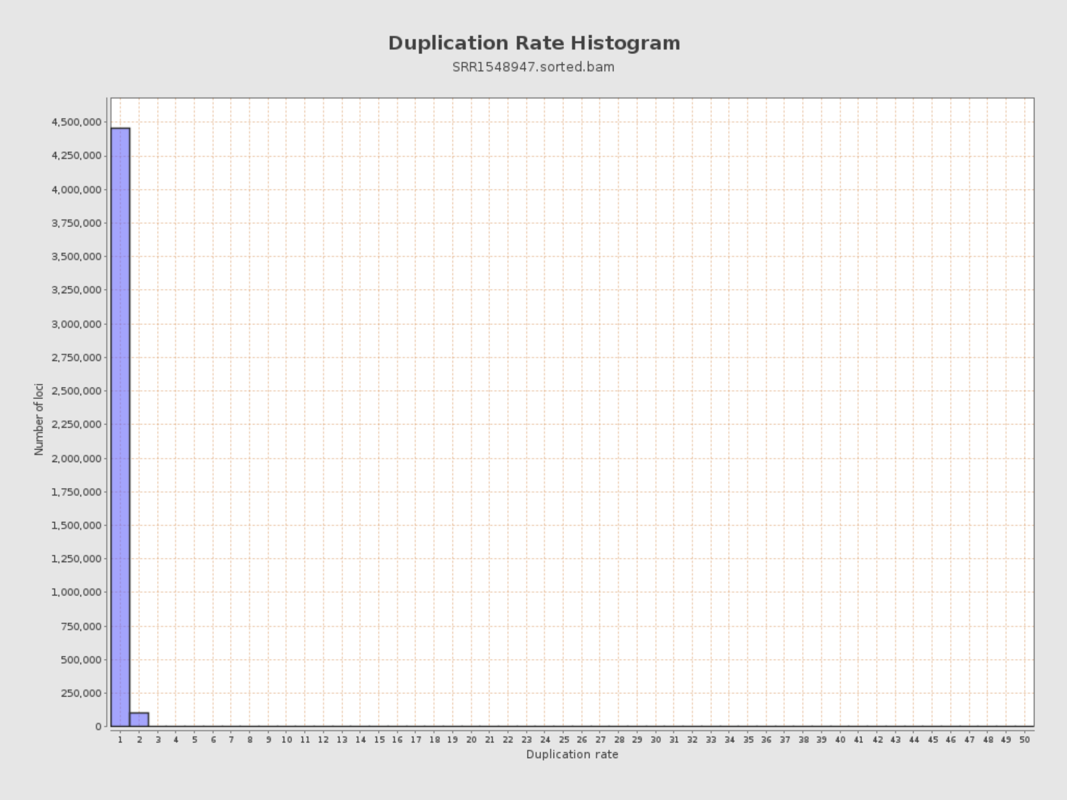
5. Results : Coverage Histogram (0-50X)



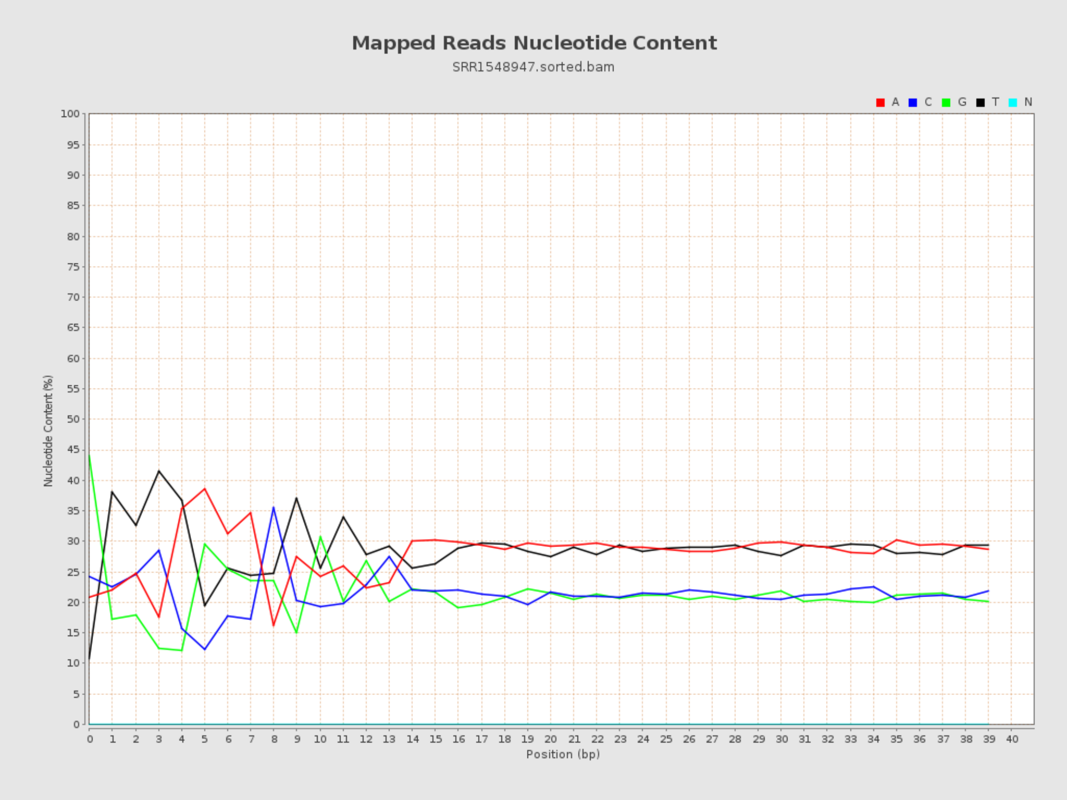
6. Results : Genome Fraction Coverage



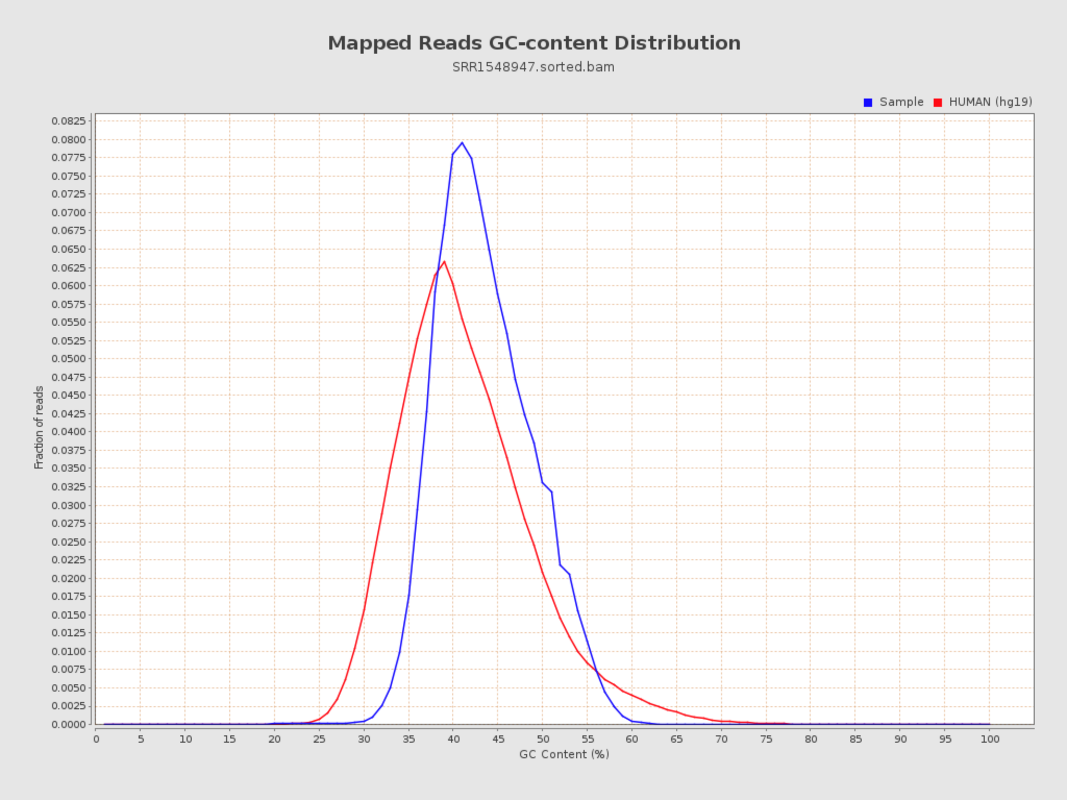
7. Results : Duplication Rate Histogram



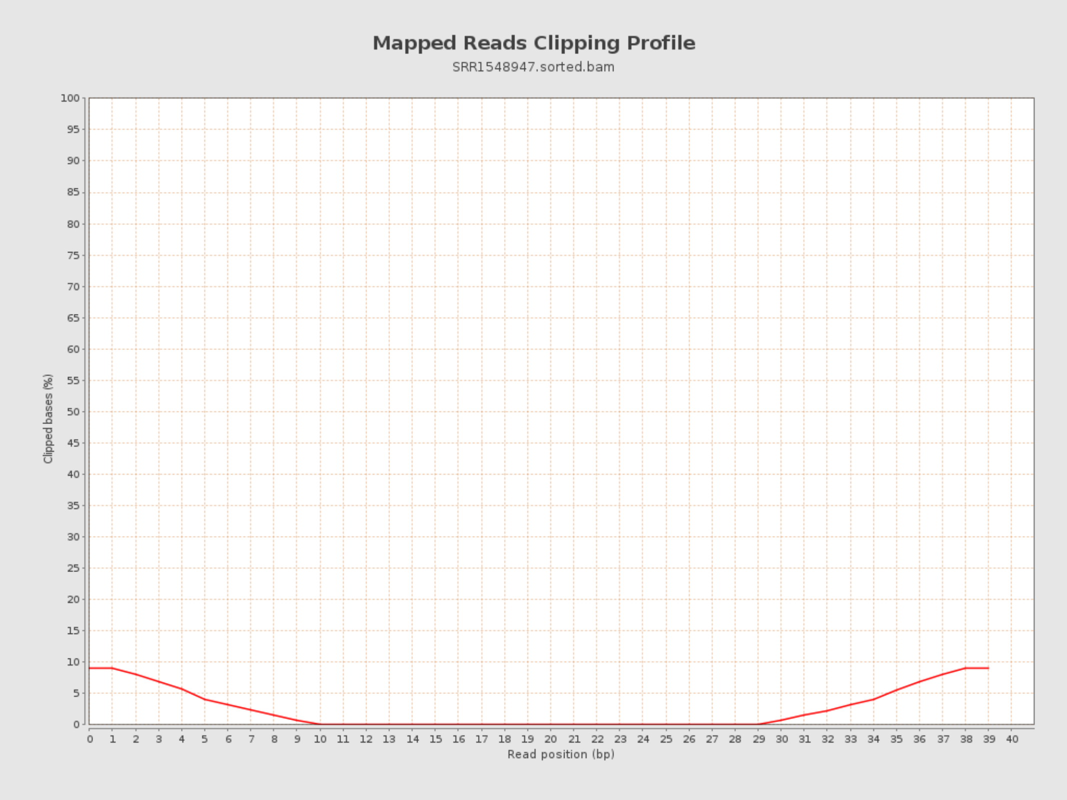
8. Results : Mapped Reads Nucleotide Content



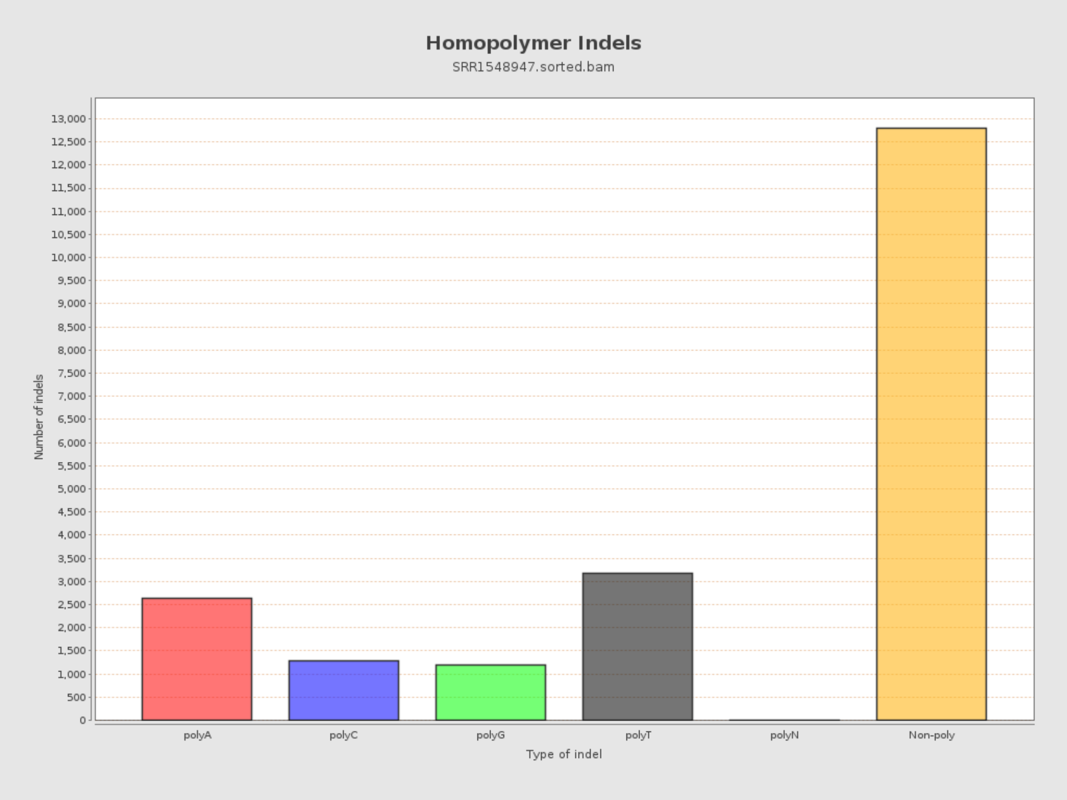
9. Results : Mapped Reads GC-content Distribution



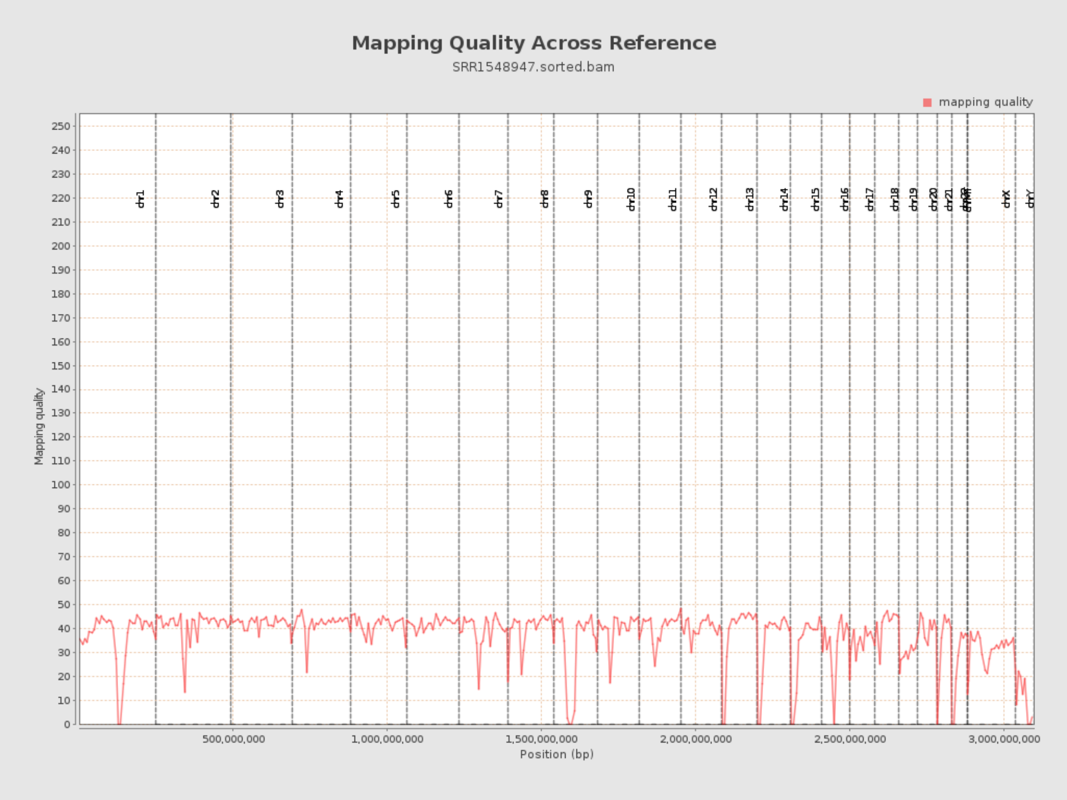
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram