Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 14:51:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548946.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_SRR1548946 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548946.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 14:51:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548946.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,449,915
Mapped reads	3,793,076 / 85.24%
Unmapped reads	656,839 / 14.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	156,211 / 3.51%
Duplication rate	3.16%
Clipped reads	241,046 / 5.42%

2.2. ACGT Content

Number/percentage of A's	42,716,731 / 28.41%
Number/percentage of C's	32,075,558 / 21.33%
Number/percentage of T's	43,412,600 / 28.87%
Number/percentage of G's	32,145,974 / 21.38%
Number/percentage of N's	1,266 / 0%
GC Percentage	42.71%

2.3. Coverage

Mean	0.0486
Standard Deviation	0.7164

2.4. Mapping Quality

Mean Mapping Quality	44.19

2.5. Mismatches and indels

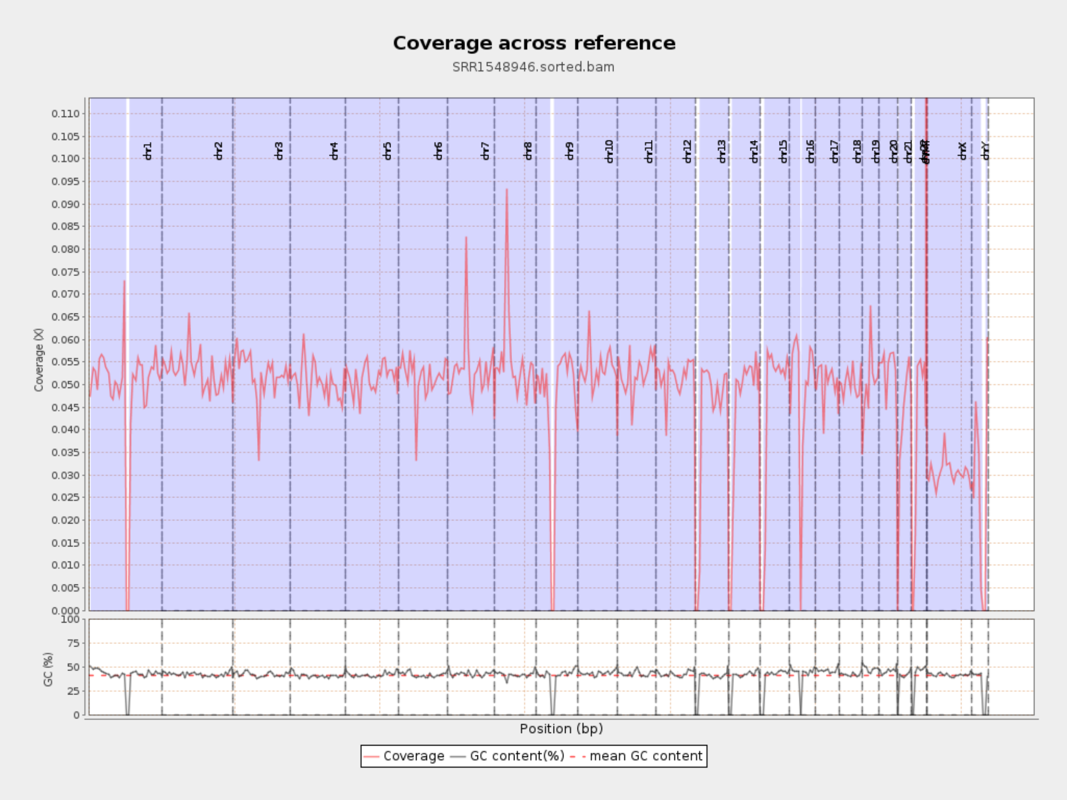
General error rate	0.23%
Mismatches	338,312
Insertions	4,127
Mapped reads with at least one insertion	0.11%
Deletions	10,709
Mapped reads with at least one deletion	0.28%
Homopolymer indels	42.59%

2.6. Chromosome stats

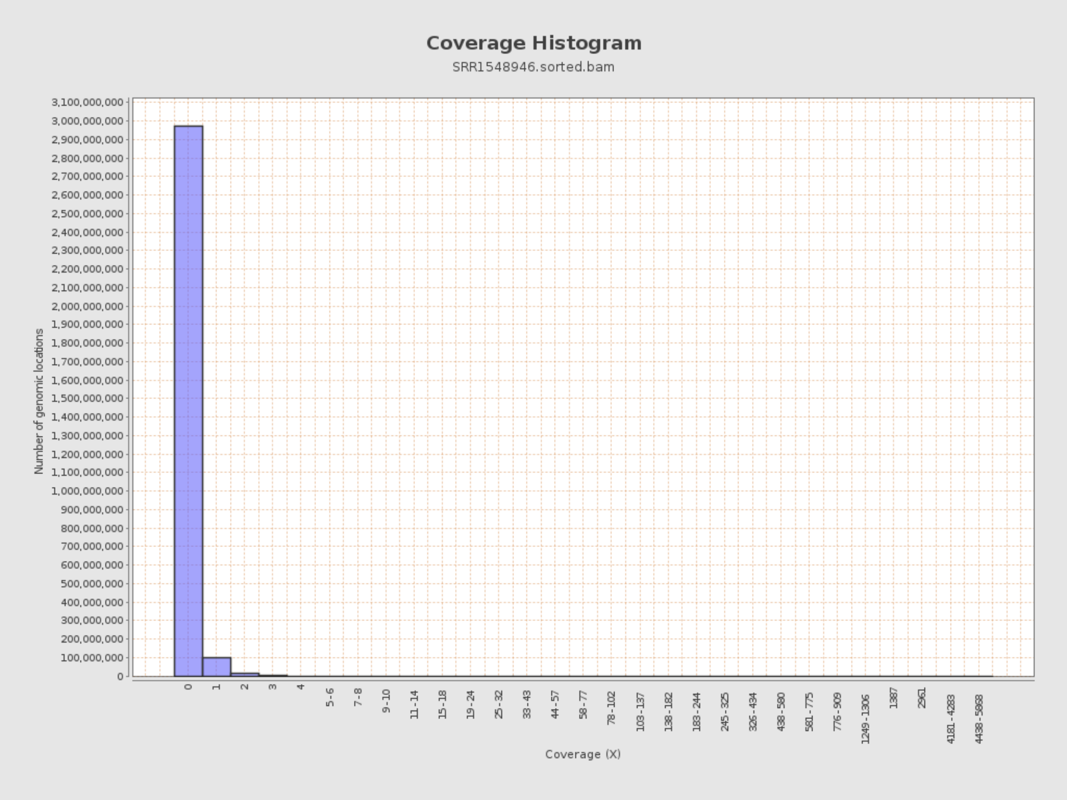
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12205142	0.049	0.7067
chr2	243199373	12942281	0.0532	0.3291
chr3	198022430	10336489	0.0522	0.2711
chr4	191154276	9625068	0.0504	0.2746
chr5	180915260	9327070	0.0516	0.2698
chr6	171115067	8838749	0.0517	0.2753
chr7	159138663	8533269	0.0536	0.5476
chr8	146364022	8060076	0.0551	2.846

chr9	141213431	6413972	0.0454	0.2979
chr10	135534747	7264157	0.0536	0.3341
chr11	135006516	7059905	0.0523	0.3361
chr12	133851895	6913332	0.0516	0.273
chr13	115169878	4784586	0.0415	0.24
chr14	107349540	4639016	0.0432	0.2603
chr15	102531392	4483065	0.0437	0.246
chr16	90354753	4408675	0.0488	0.2714
chr17	81195210	4088170	0.0503	0.2751
chr18	78077248	3924159	0.0503	0.4863
chr19	59128983	3014503	0.051	0.5486
chr20	63025520	3372631	0.0535	0.2794
chr21	48129895	1986916	0.0413	0.2683
chr22	51304566	1889782	0.0368	0.3
chrMT	16571	17714	1.069	1.548
chrX	155270560	4765282	0.0307	0.2329
chrY	59373566	1472517	0.0248	0.3182

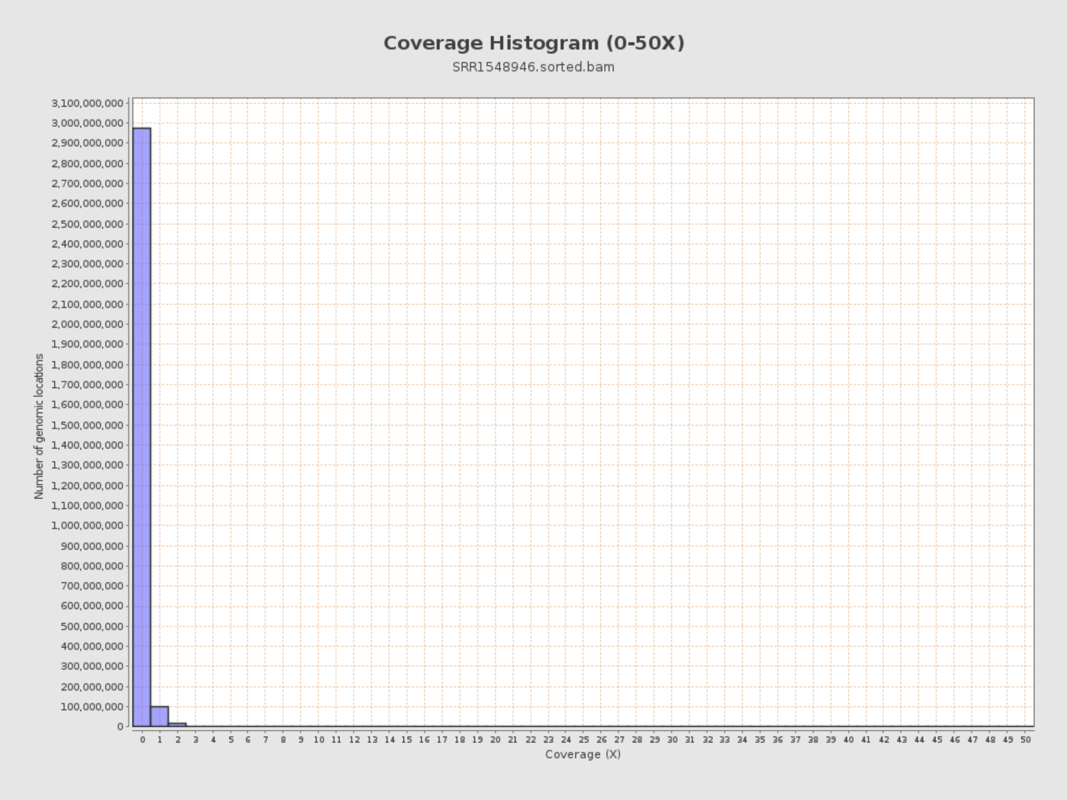
3. Results : Coverage across reference



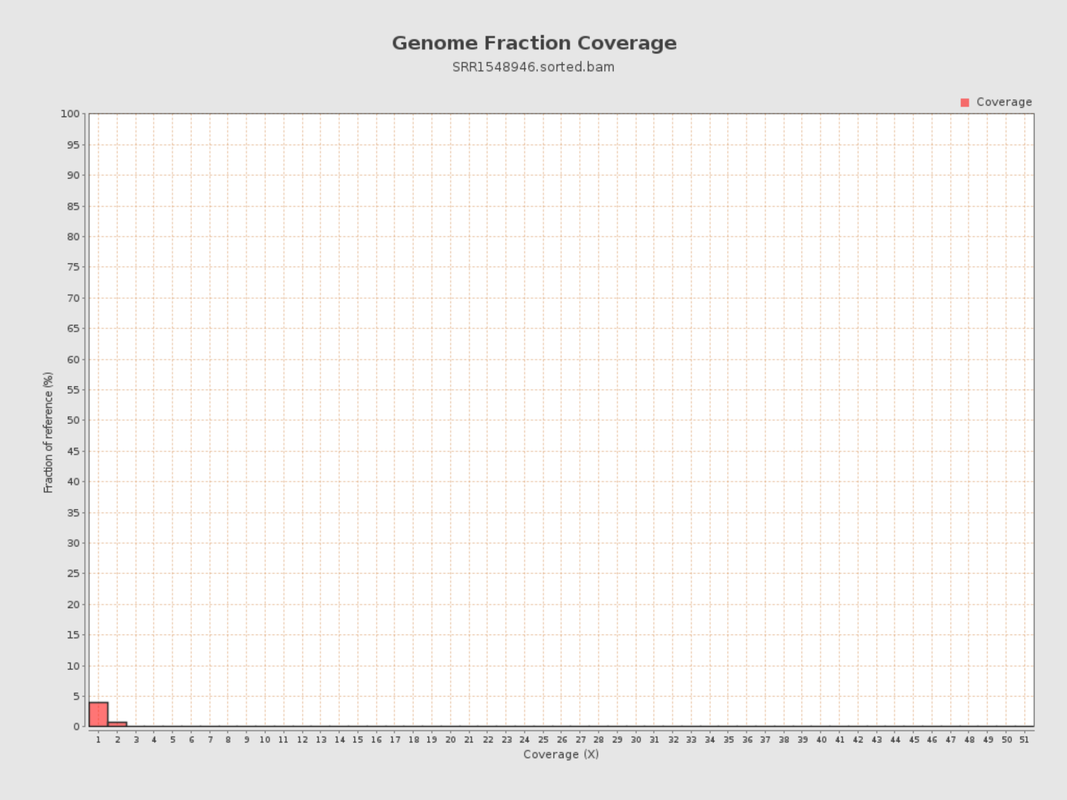
4. Results : Coverage Histogram



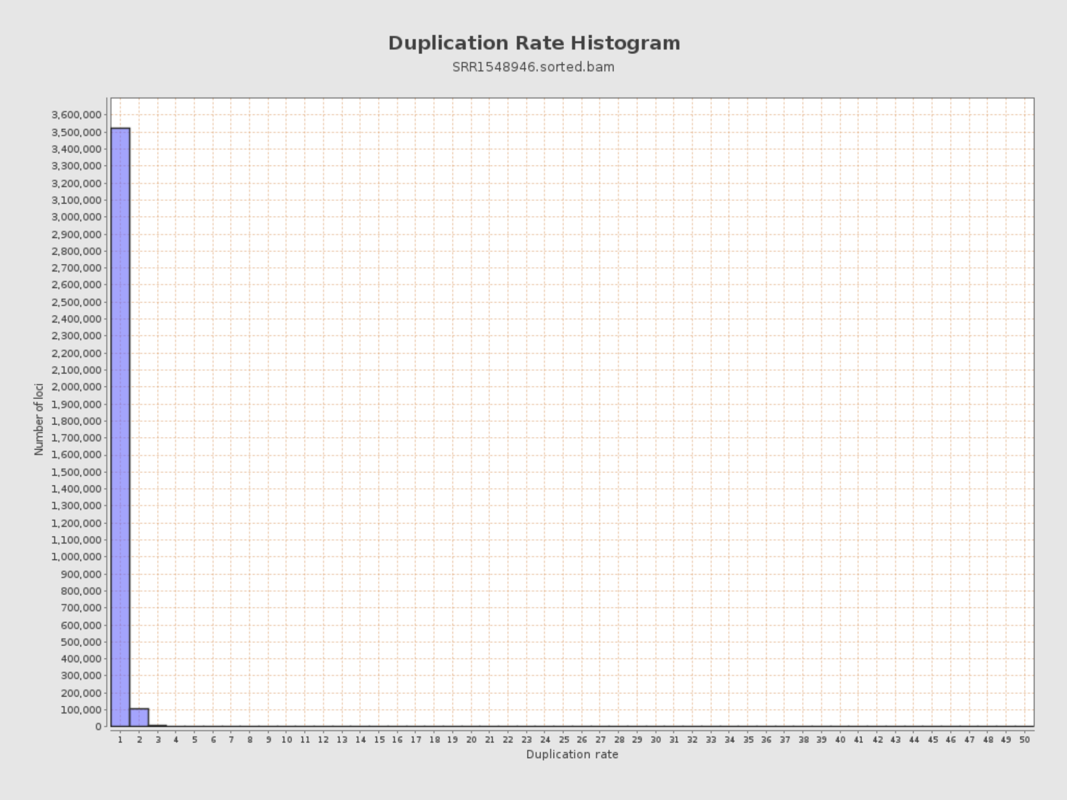
5. Results : Coverage Histogram (0-50X)



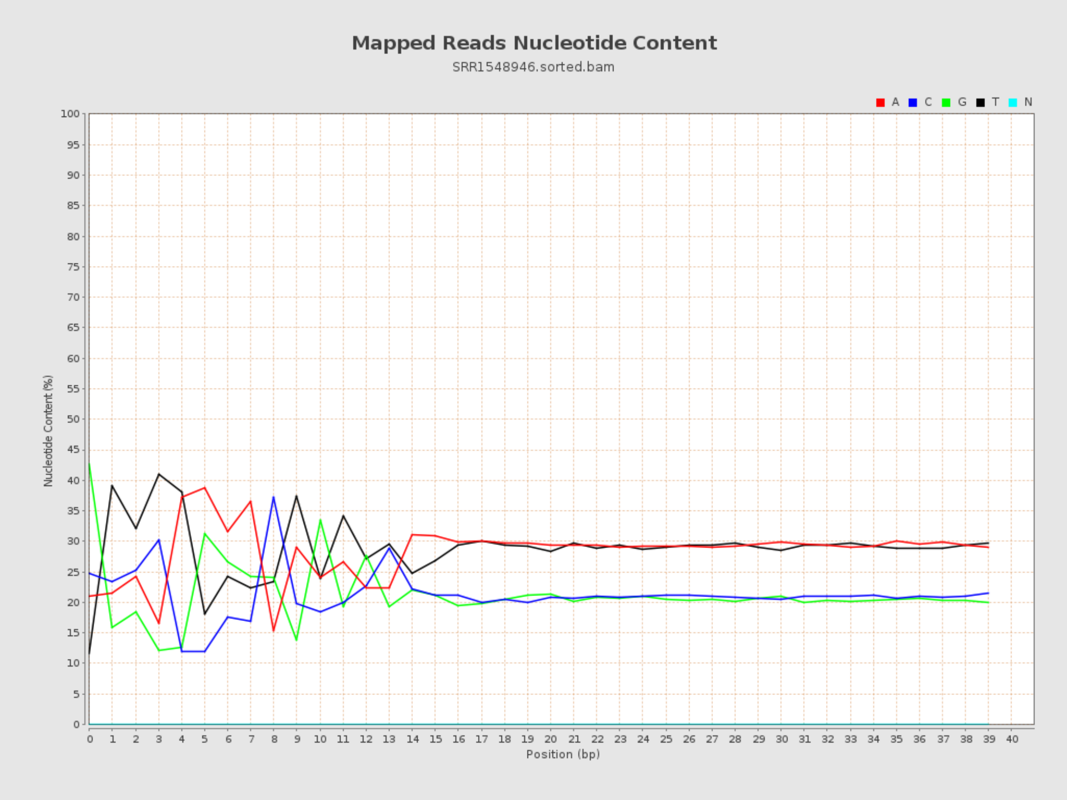
6. Results : Genome Fraction Coverage



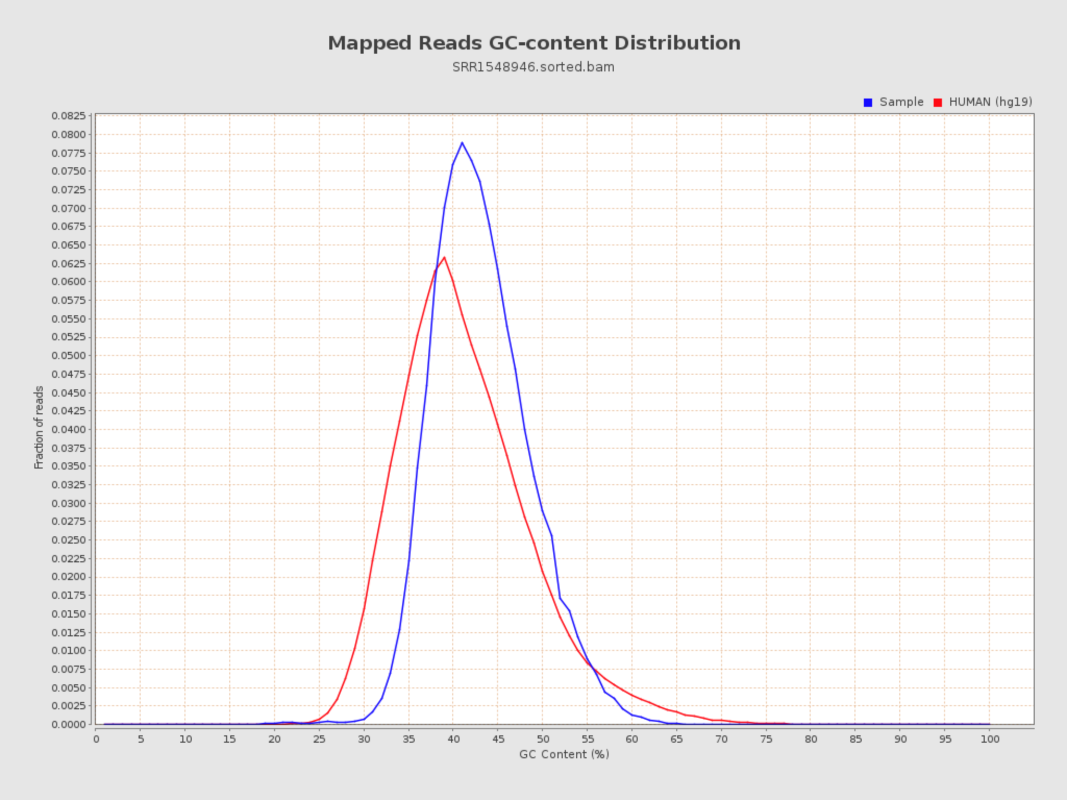
7. Results : Duplication Rate Histogram



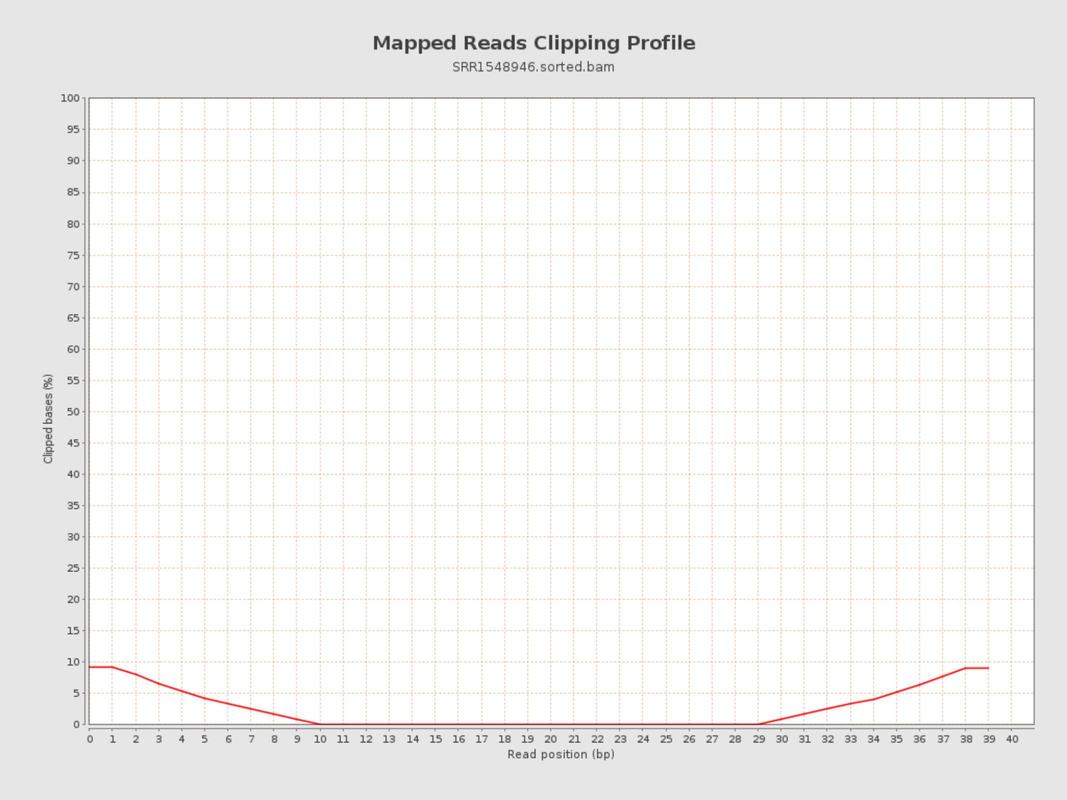
8. Results : Mapped Reads Nucleotide Content



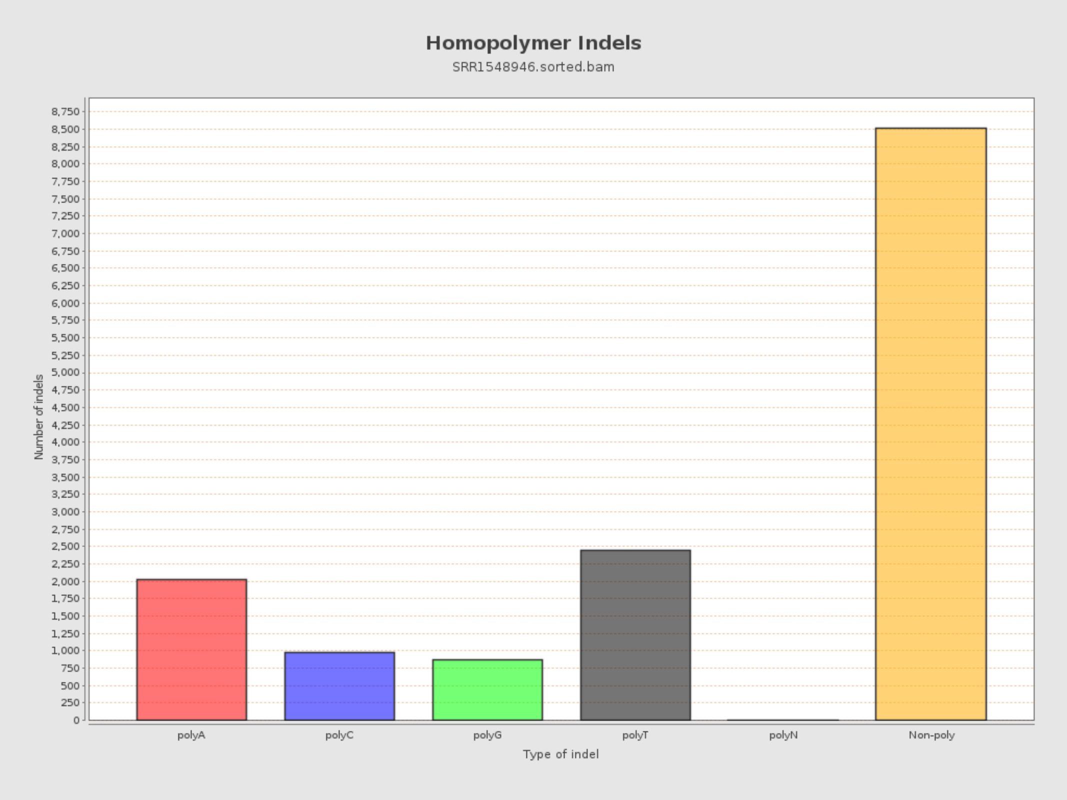
9. Results : Mapped Reads GC-content Distribution



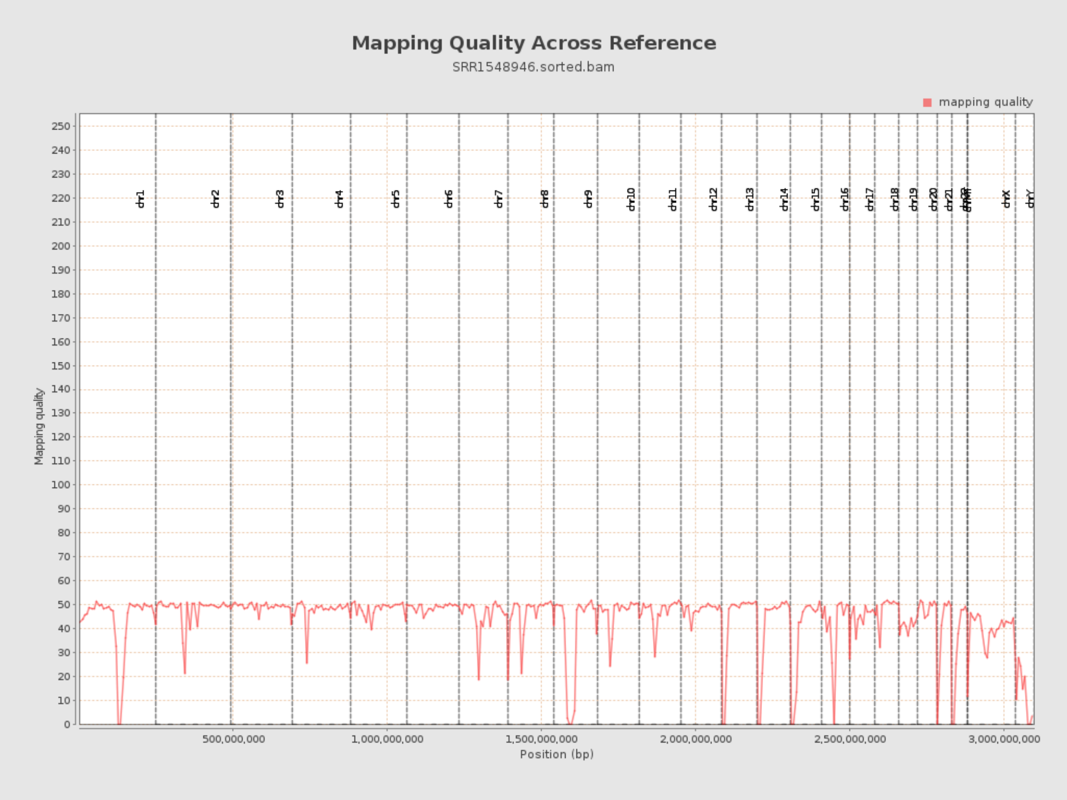
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram