

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:30:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549095.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_SRR1549095 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549095.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:30:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549095.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,689,476
Mapped reads	6,699,257 / 87.12%
Unmapped reads	990,219 / 12.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	231,717 / 3.01%
Duplication rate	2.26%
Clipped reads	317,929 / 4.13%

2.2. ACGT Content

Number/percentage of A's	79,673,997 / 29.94%
Number/percentage of C's	53,634,253 / 20.16%
Number/percentage of T's	80,611,044 / 30.3%
Number/percentage of G's	52,093,063 / 19.58%
Number/percentage of N's	63,886 / 0.02%
GC Percentage	39.74%

2.3. Coverage

Mean	0.086
Standard Deviation	0.8106

2.4. Mapping Quality

Mean Mapping Quality	43.94
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2.5. Mismatches and indels

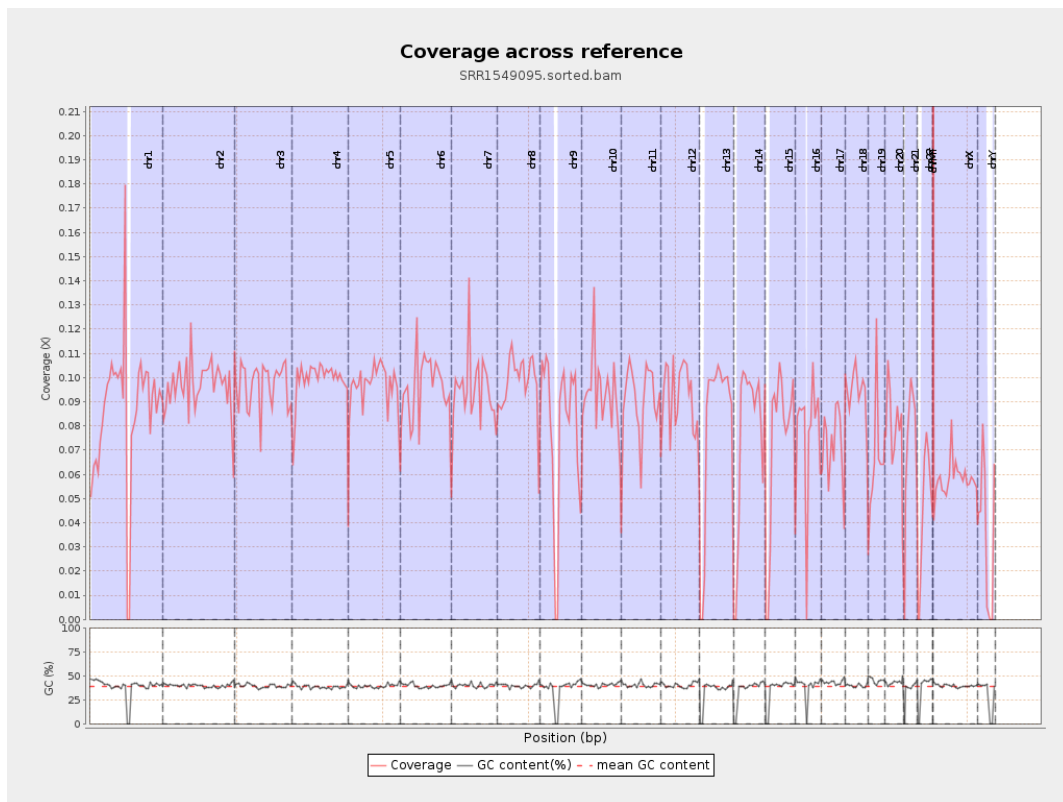
General error rate	0.4%
Mismatches	1,050,259
Insertions	6,094
Mapped reads with at least one insertion	0.09%
Deletions	19,470
Mapped reads with at least one deletion	0.29%
Homopolymer indels	45.16%

2.6. Chromosome stats

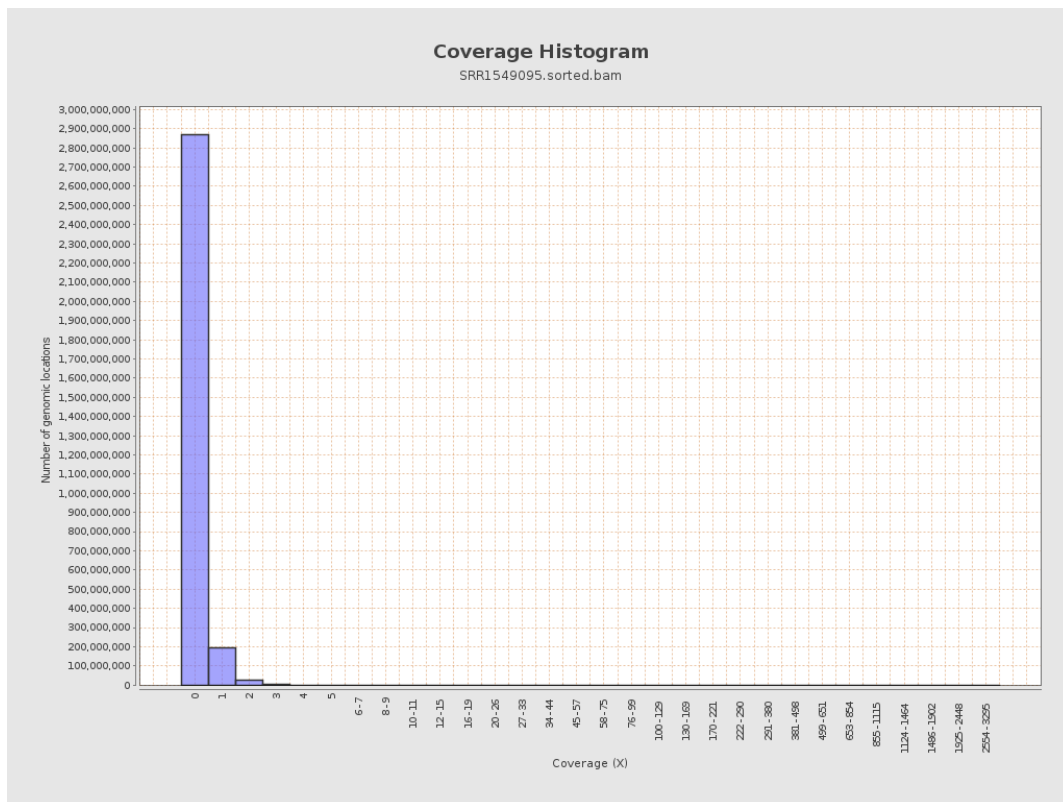
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21489884	0.0862	1.928
chr2	243199373	23549937	0.0968	0.5221
chr3	198022430	19254631	0.0972	0.3579
chr4	191154276	18964888	0.0992	0.3641
chr5	180915260	17394967	0.0961	0.361
chr6	171115067	16507694	0.0965	0.4418
chr7	159138663	15019580	0.0944	0.7866
chr8	146364022	14353348	0.0981	1.6469

chr9	141213431	11274701	0.0798	0.5055
chr10	135534747	12614071	0.0931	0.59
chr11	135006516	12309225	0.0912	0.516
chr12	133851895	12284163	0.0918	0.3638
chr13	115169878	9316587	0.0809	0.3158
chr14	107349540	8224668	0.0766	0.3684
chr15	102531392	7440257	0.0726	0.3007
chr16	90354753	6740539	0.0746	0.3796
chr17	81195210	5896678	0.0726	0.3487
chr18	78077248	7386756	0.0946	0.9957
chr19	59128983	3993770	0.0675	1.4394
chr20	63025520	5086222	0.0807	0.3324
chr21	48129895	3423804	0.0711	0.3462
chr22	51304566	2363869	0.0461	0.2761
chrMT	16571	19786	1.194	1.6733
chrX	155270560	8976166	0.0578	0.35
chrY	59373566	2214597	0.0373	0.3394

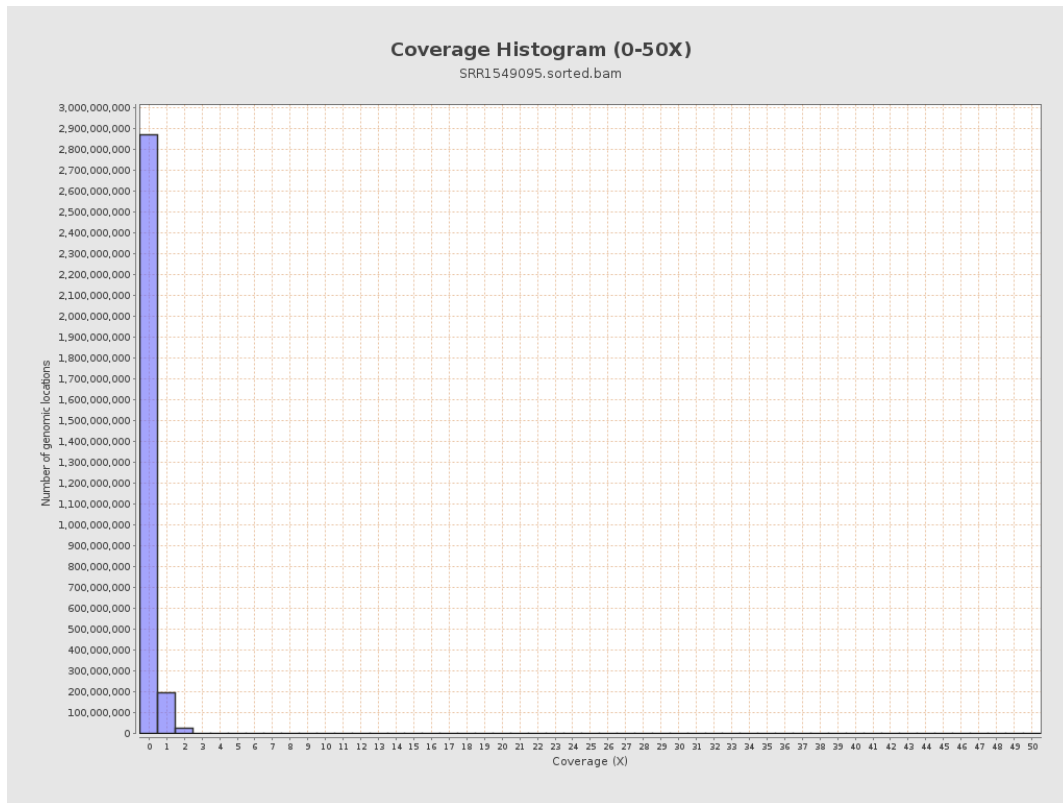
3. Results : Coverage across reference



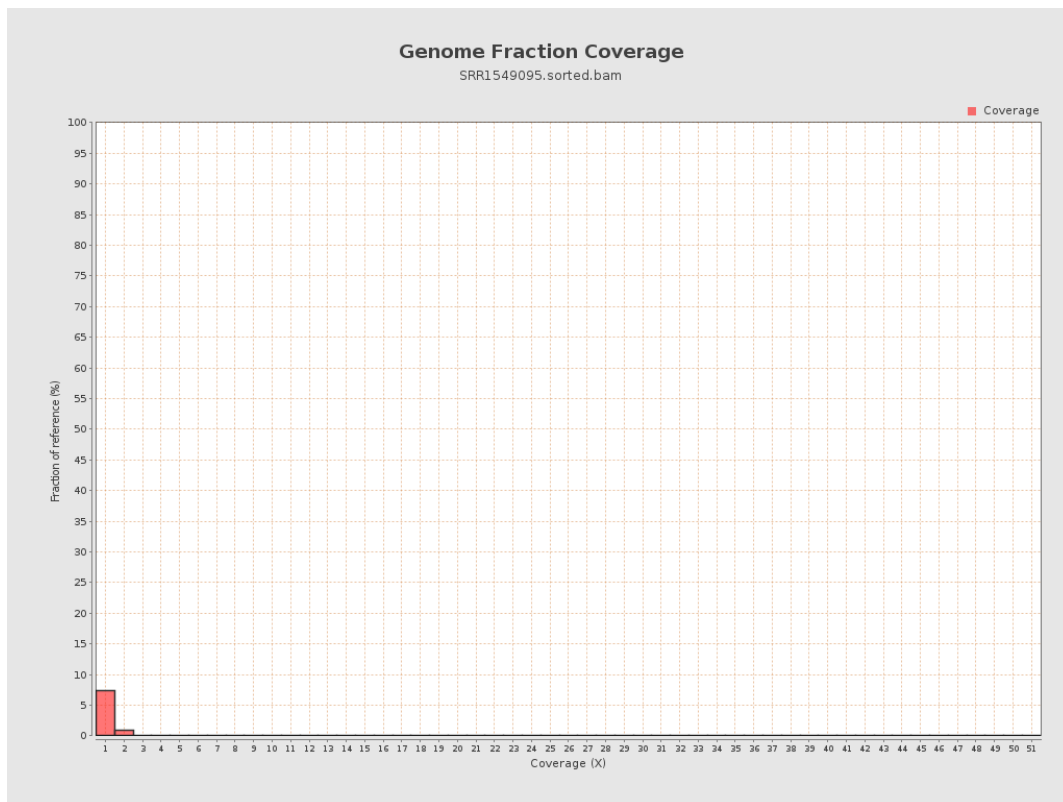
4. Results : Coverage Histogram



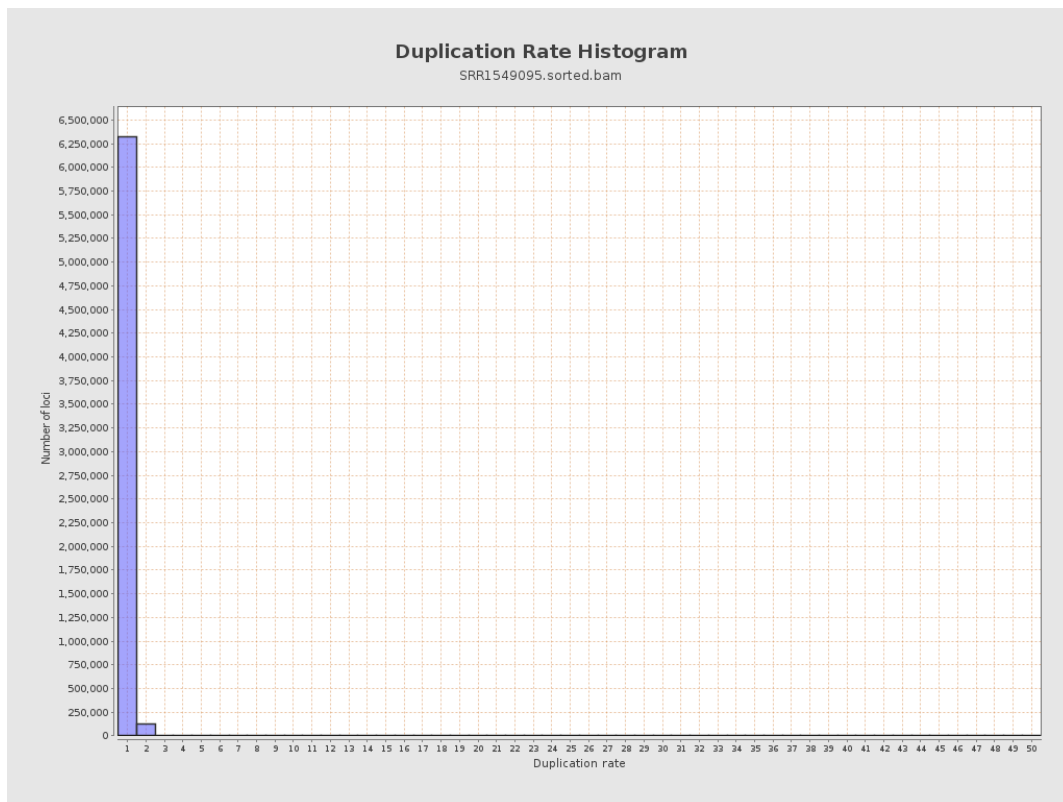
5. Results : Coverage Histogram (0-50X)



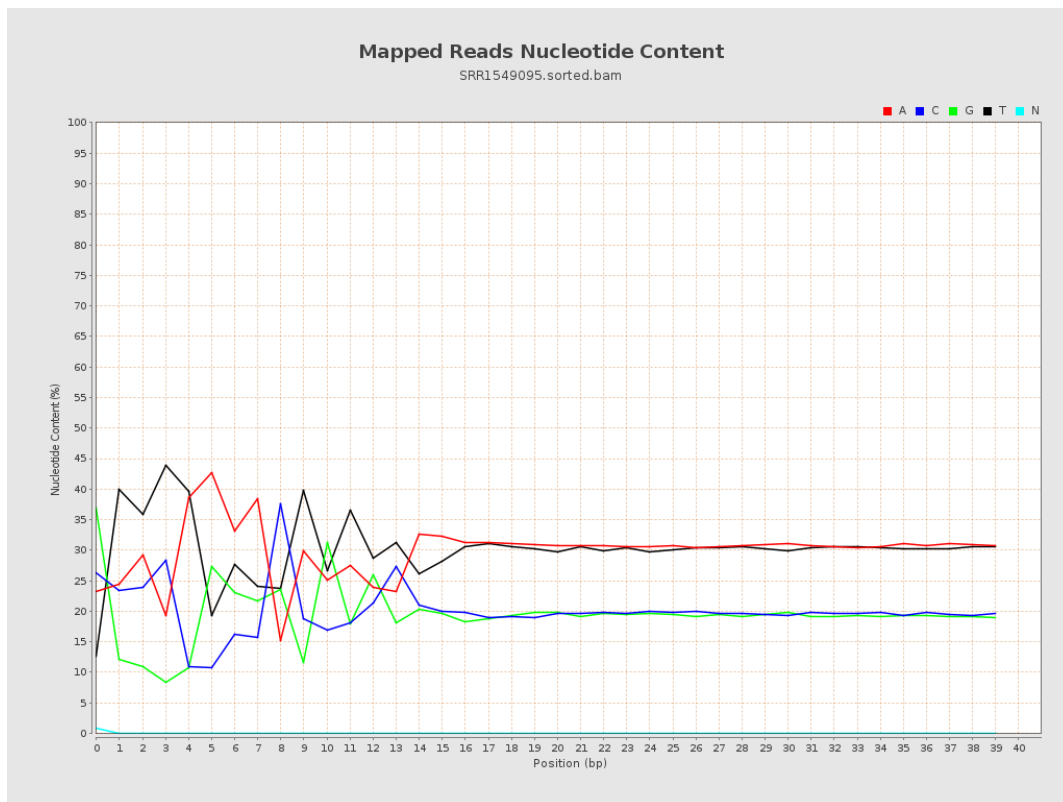
6. Results : Genome Fraction Coverage



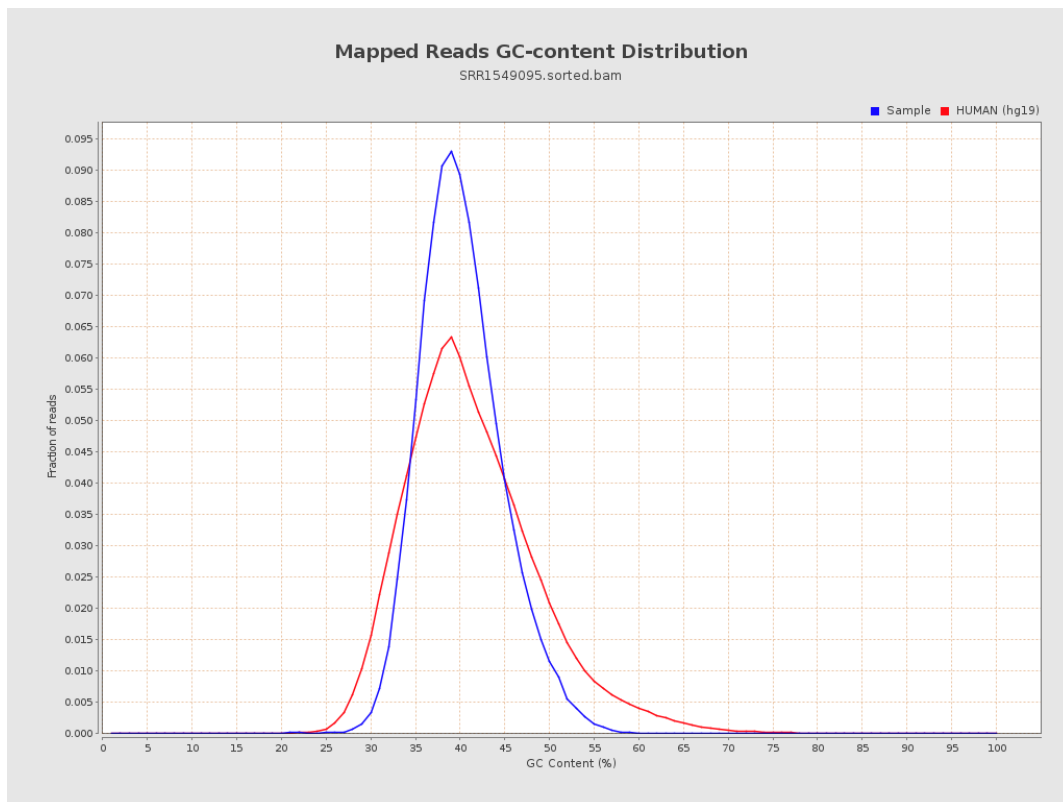
7. Results : Duplication Rate Histogram



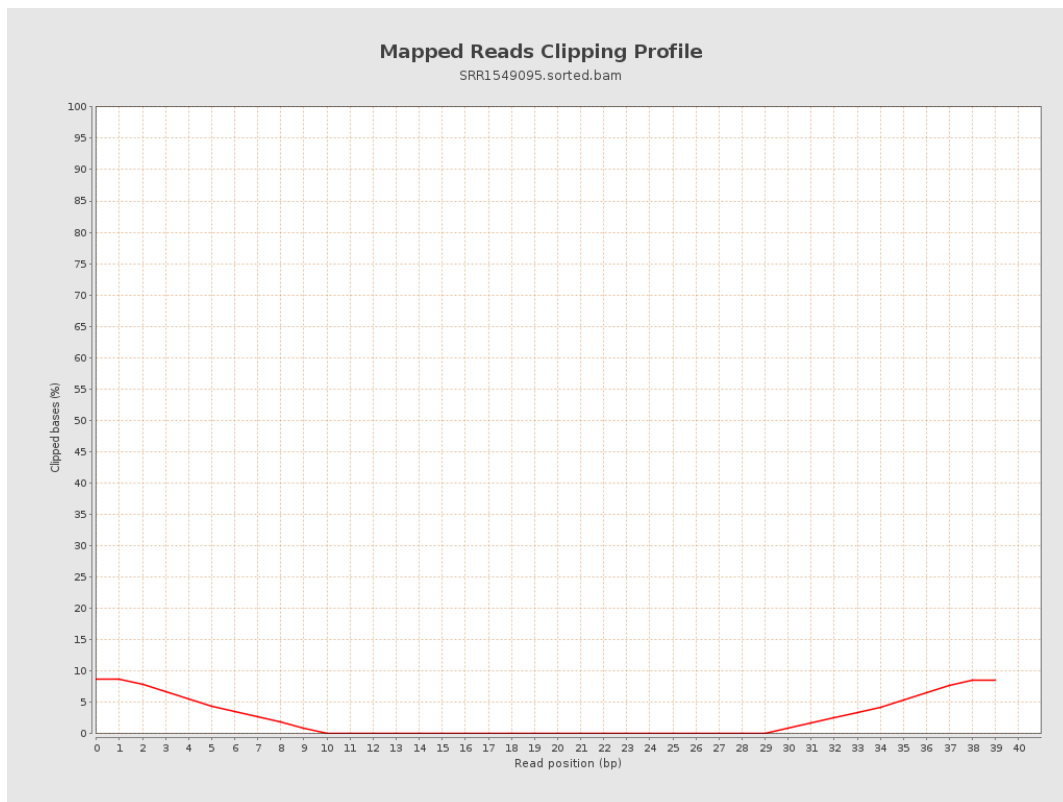
8. Results : Mapped Reads Nucleotide Content



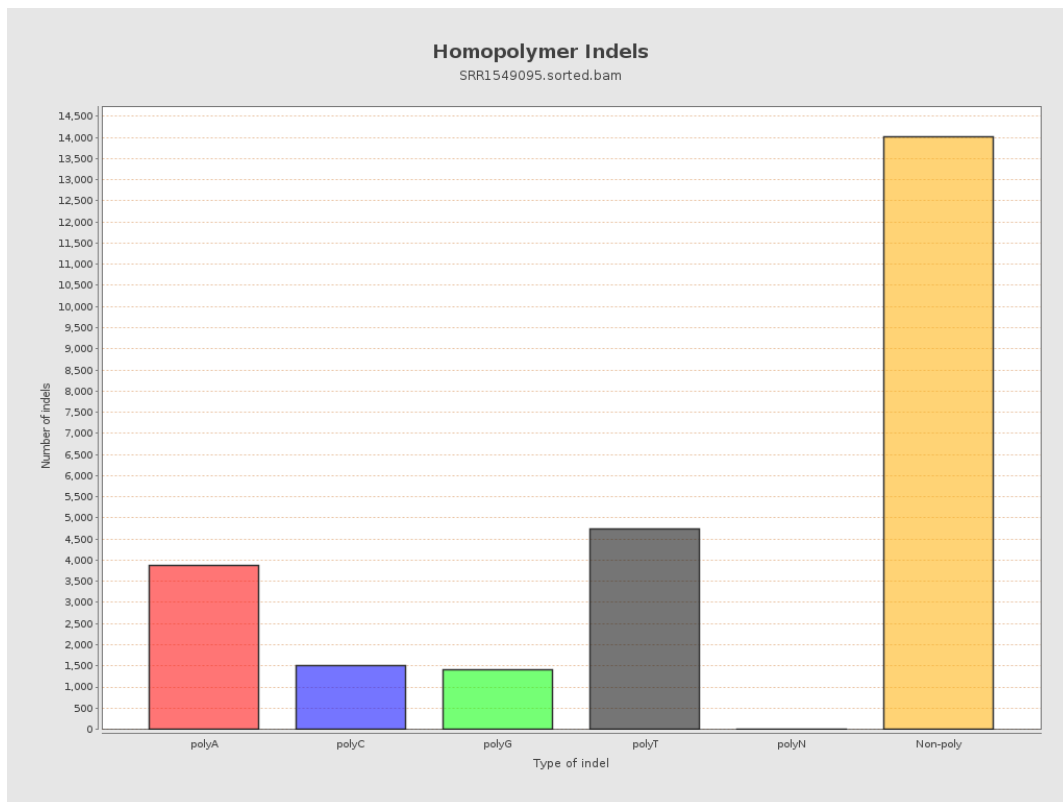
9. Results : Mapped Reads GC-content Distribution



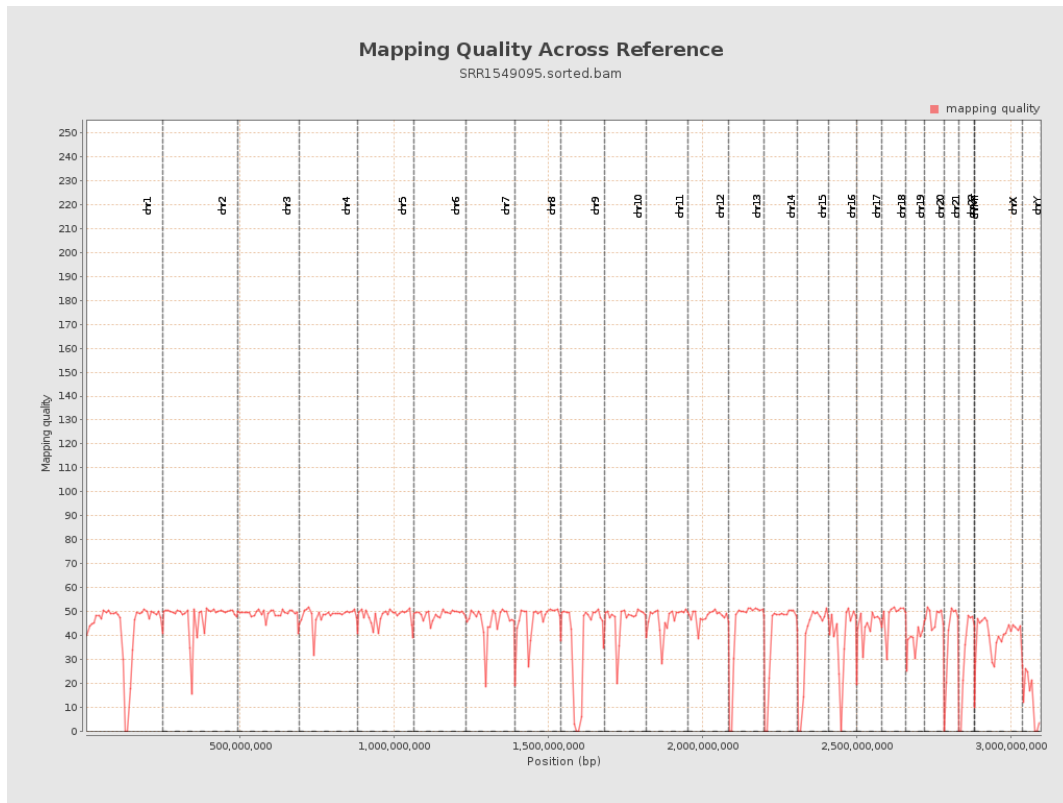
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

