Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:43:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080949.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_SRR3080949 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080949.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:43:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080949.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,561,113
Mapped reads	3,245,324 / 91.13%
Unmapped reads	315,789 / 8.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,024 / 0.98%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	130,223 / 3.66%
Duplication rate	3.05%
Clipped reads	1,099,750 / 30.88%

2.2. ACGT Content

Number/percentage of A's	65,239,427 / 29.09%
Number/percentage of C's	39,855,778 / 17.77%
Number/percentage of T's	71,665,857 / 31.95%
Number/percentage of G's	46,458,382 / 20.71%
Number/percentage of N's	1,086,430 / 0.48%
GC Percentage	38.48%

2.3. Coverage

Mean	0.0725

Standard Deviation	0.5573

2.4. Mapping Quality

Mean Mapping Quality	47.89

2.5. Mismatches and indels

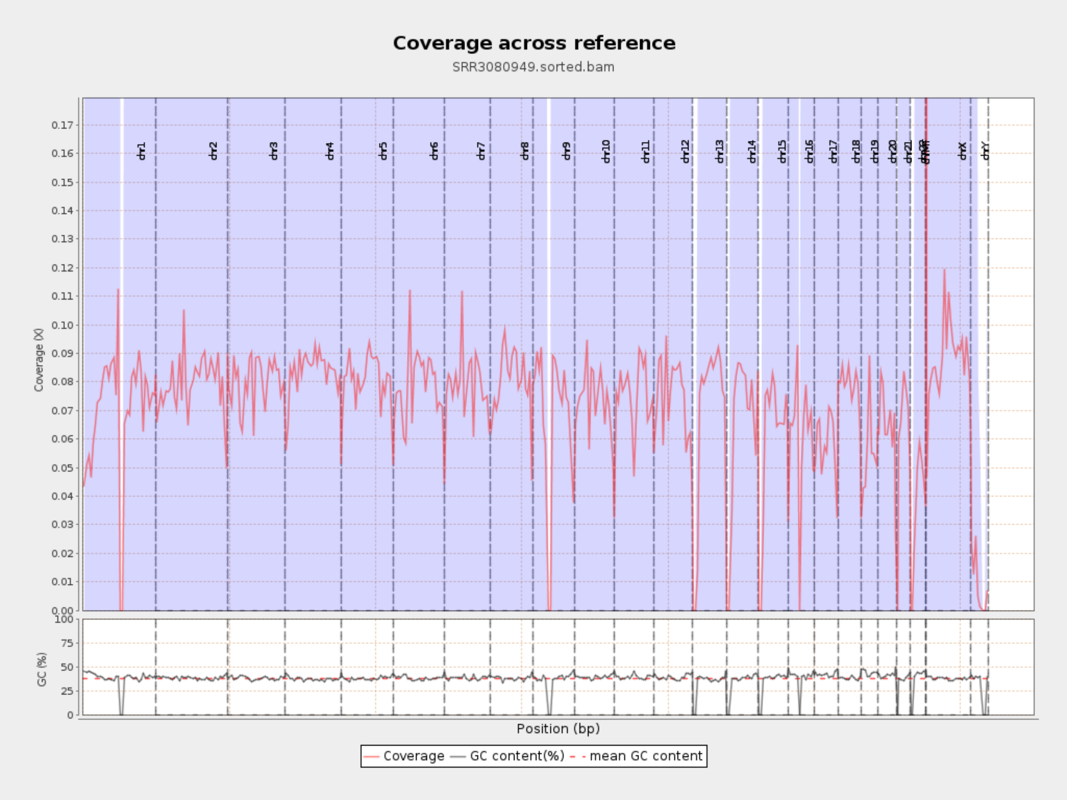
General error rate	1.14%
Mismatches	2,532,690
Insertions	17,256
Mapped reads with at least one insertion	0.53%
Deletions	50,217
Mapped reads with at least one deletion	1.53%
Homopolymer indels	50.02%

2.6. Chromosome stats

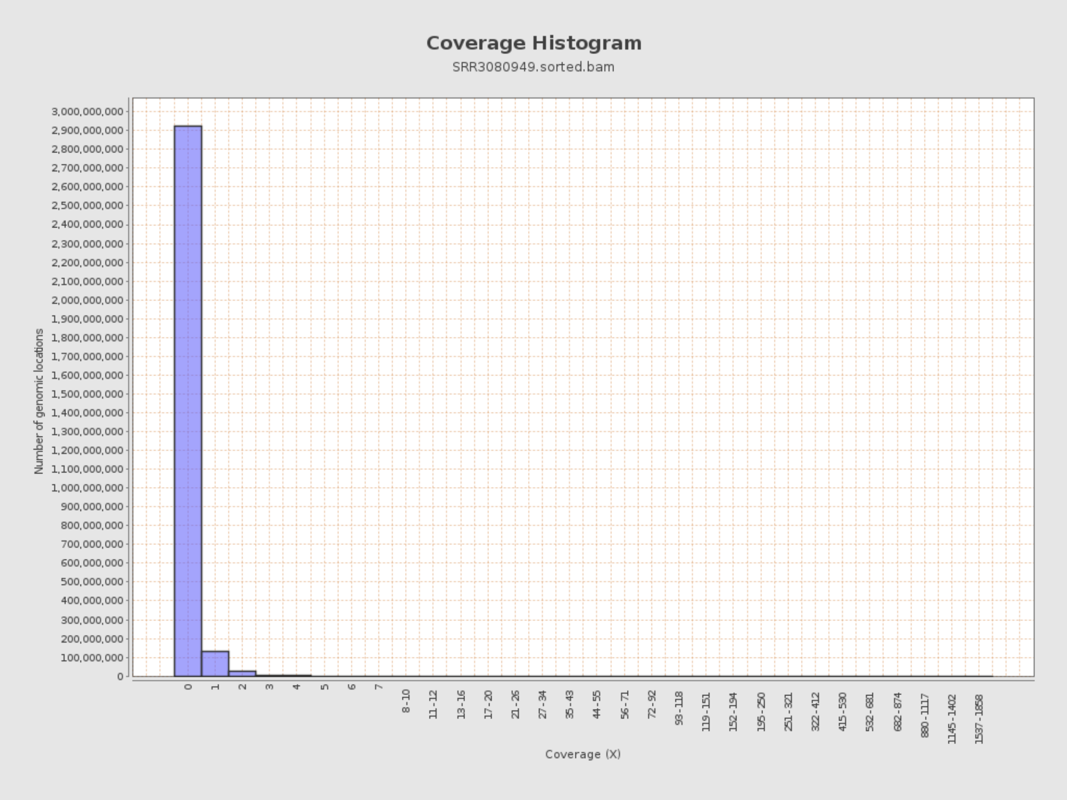
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17413966	0.0699	0.9293
chr2	243199373	19281262	0.0793	0.4936
chr3	198022430	15882716	0.0802	0.3522
chr4	191154276	16008759	0.0837	0.3742
chr5	180915260	14561771	0.0805	0.353
chr6	171115067	13578745	0.0794	0.4462
chr7	159138663	12515986	0.0786	0.7027

chr8	146364022	11761434	0.0804	1.1607
chr9	141213431	9499339	0.0673	0.502
chr10	135534747	9995682	0.0737	0.4862
chr11	135006516	10150965	0.0752	0.472
chr12	133851895	9991966	0.0746	0.3436
chr13	115169878	7919398	0.0688	0.3263
chr14	107349540	6841690	0.0637	0.3436
chr15	102531392	6027996	0.0588	0.3002
chr16	90354753	5368956	0.0594	0.3344
chr17	81195210	4780510	0.0589	0.3538
chr18	78077248	6204044	0.0795	0.9245
chr19	59128983	3288714	0.0556	0.649
chr20	63025520	4171044	0.0662	0.3376
chr21	48129895	3021694	0.0628	0.3427
chr22	51304566	1866150	0.0364	0.2337
chrMT	16571	30528	1.8423	1.7347
chrX	155270560	13706658	0.0883	0.4055
chrY	59373566	519384	0.0087	0.1776

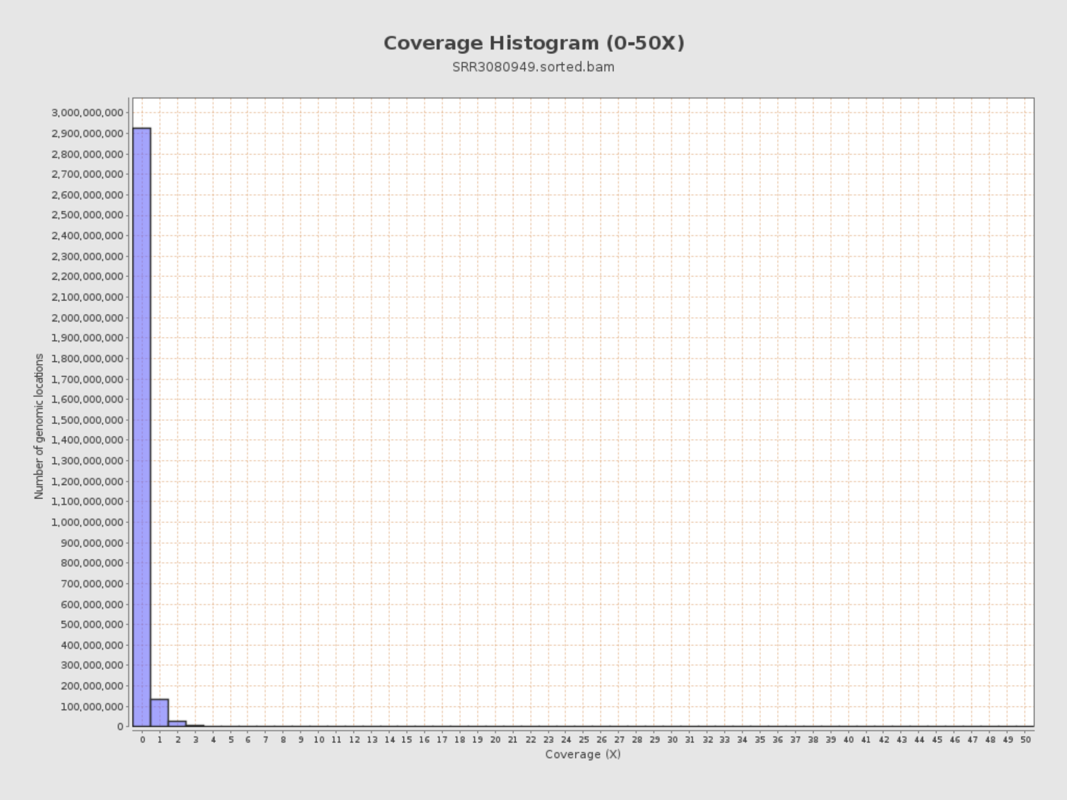
3. Results : Coverage across reference



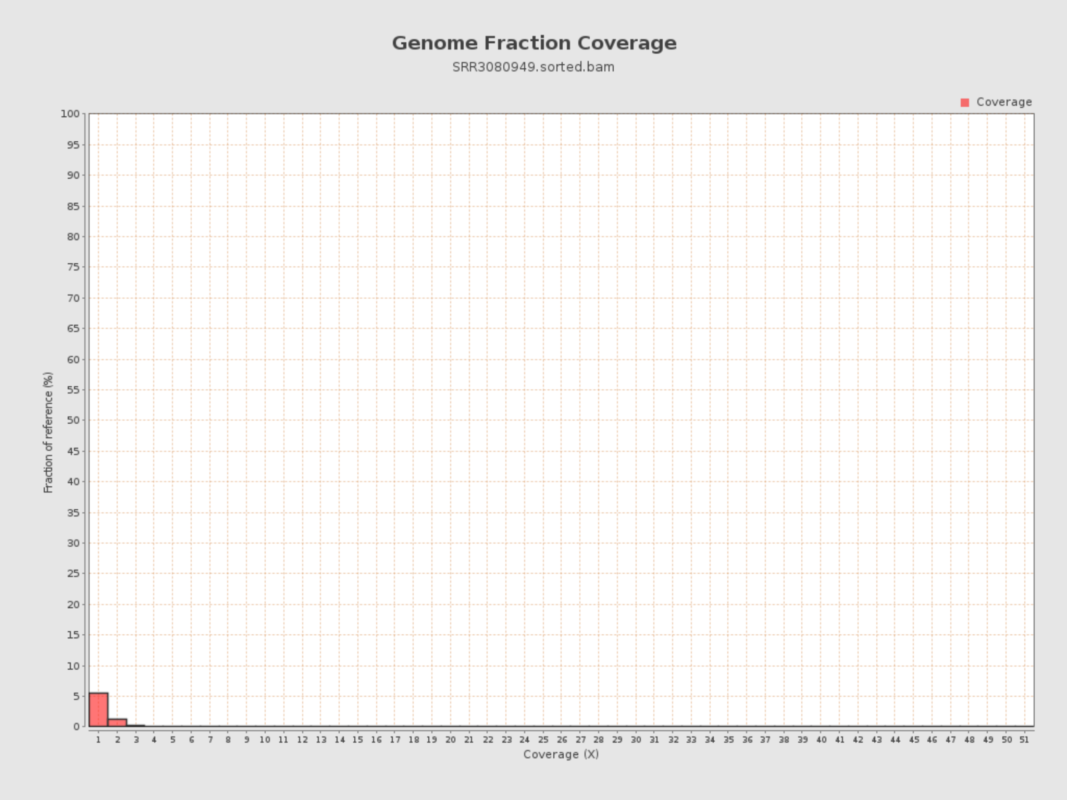
4. Results : Coverage Histogram



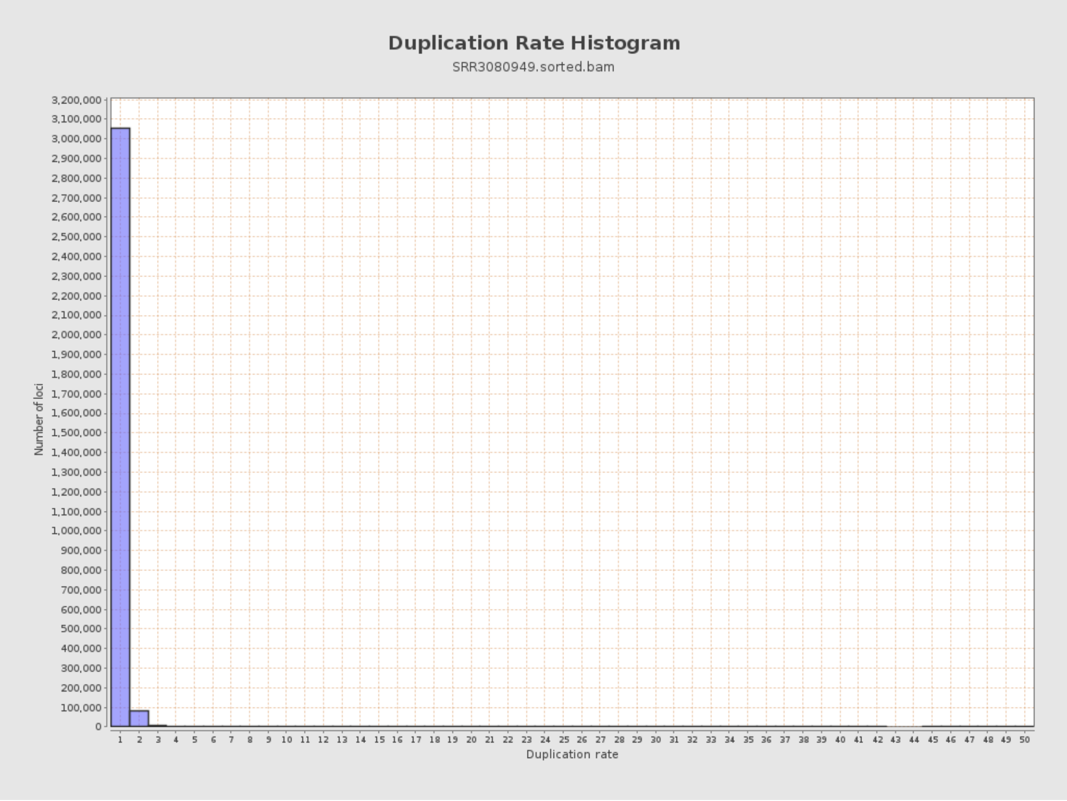
5. Results : Coverage Histogram (0-50X)



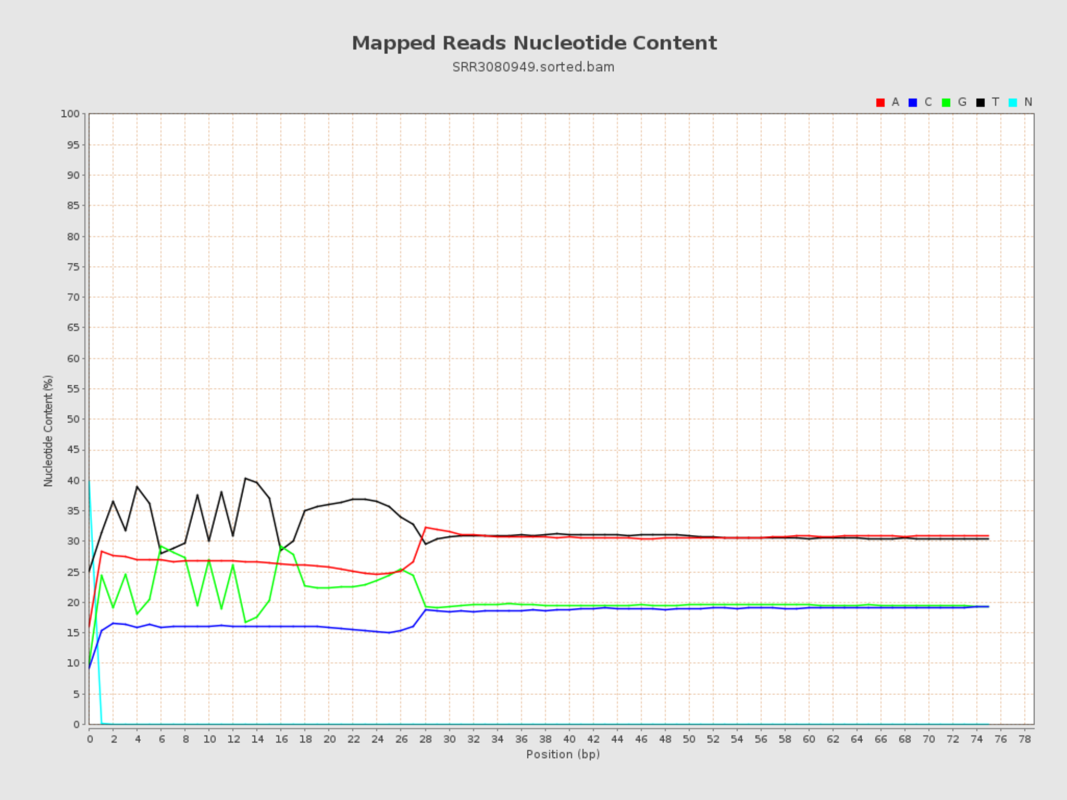
6. Results : Genome Fraction Coverage



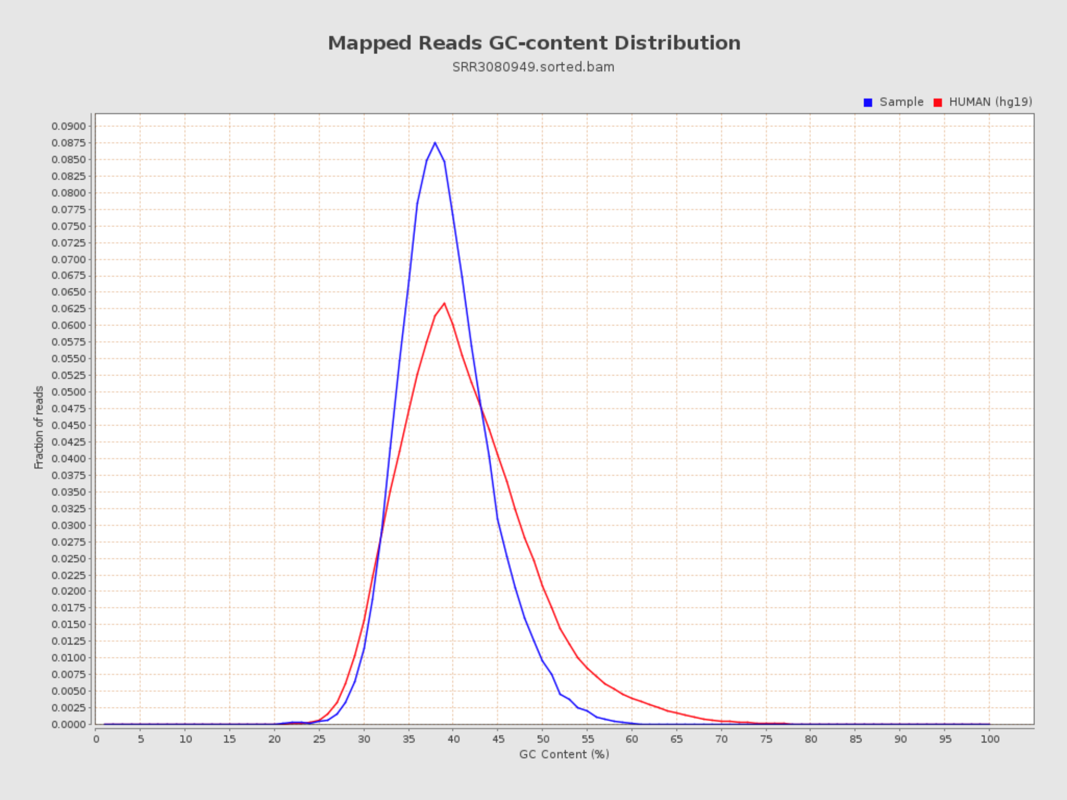
7. Results : Duplication Rate Histogram



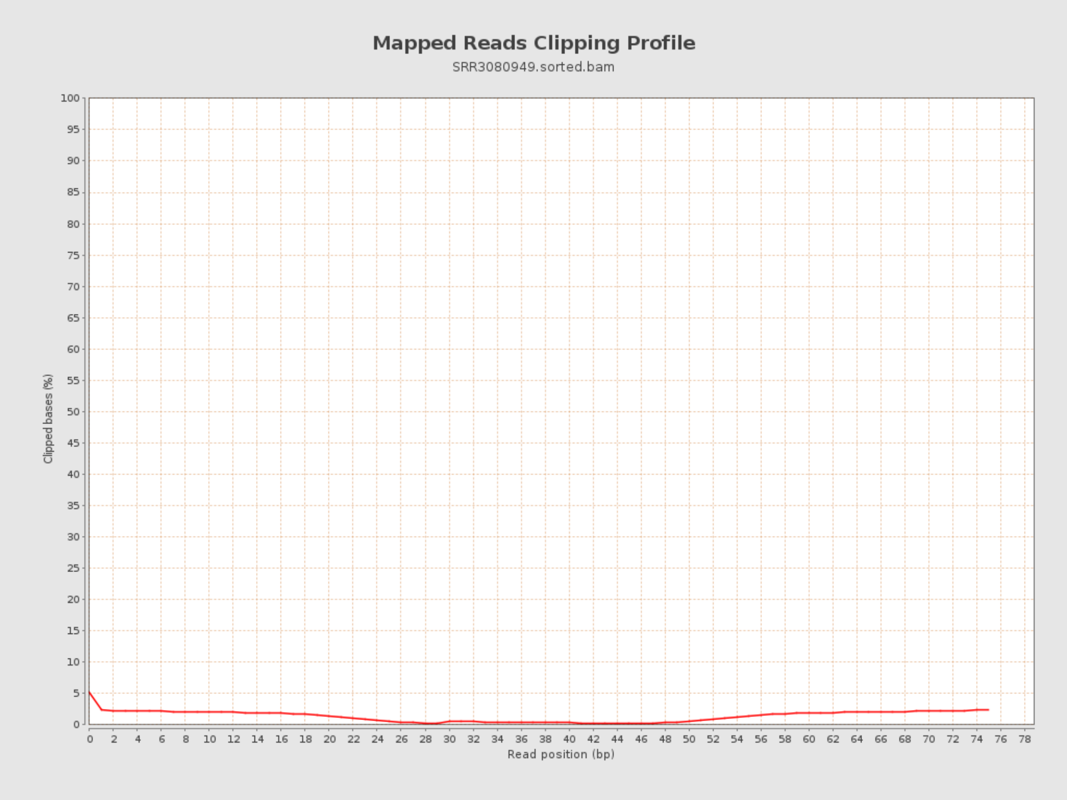
8. Results : Mapped Reads Nucleotide Content



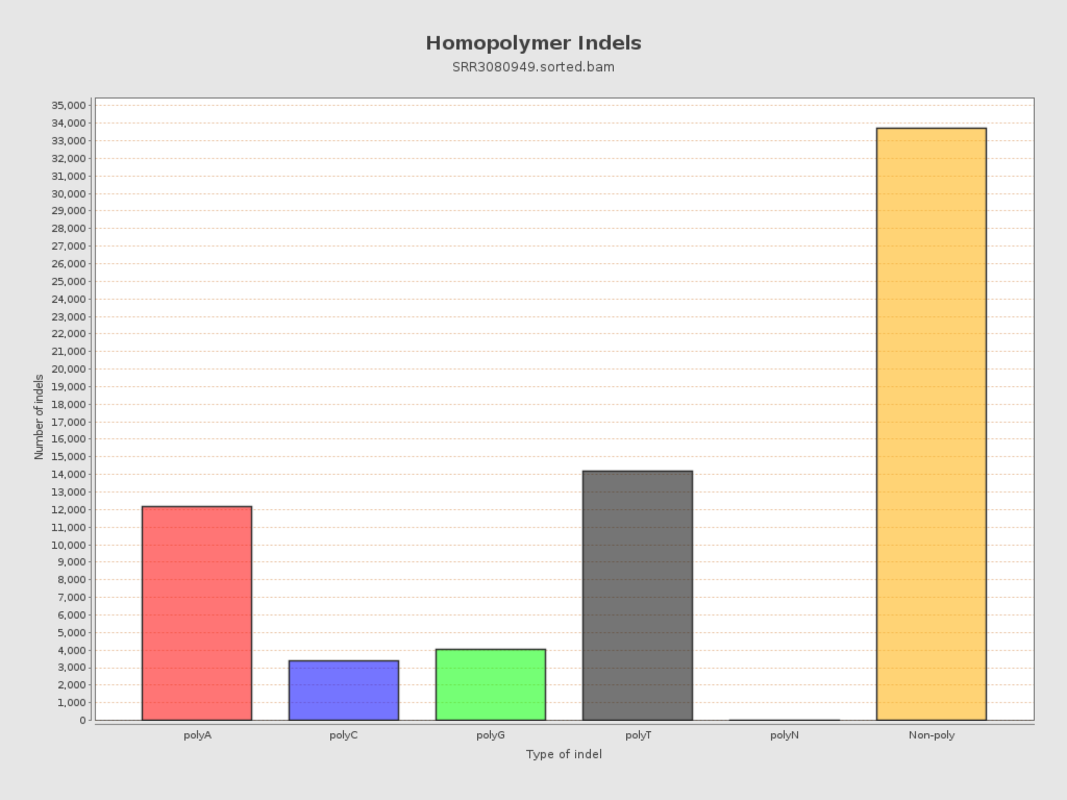
9. Results : Mapped Reads GC-content Distribution



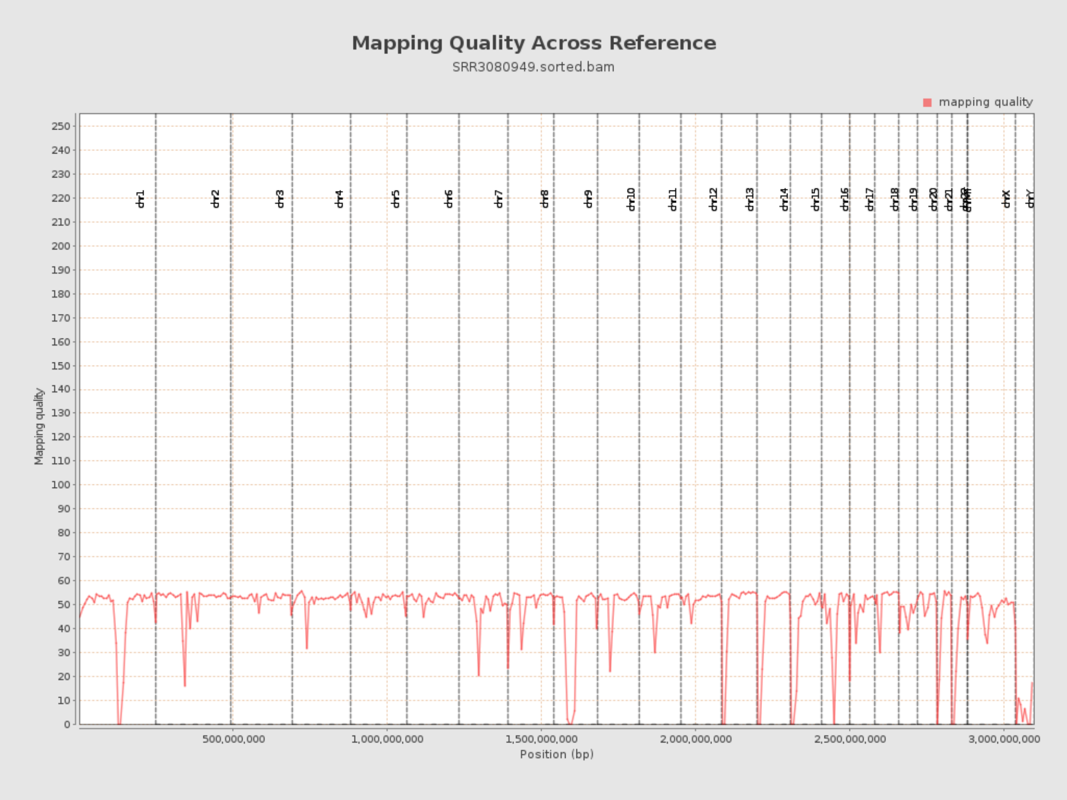
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram