Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:27:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081949.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_SRR3081949 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081949.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:27:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081949.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,157,668
Mapped reads	2,908,153 / 92.1%
Unmapped reads	249,515 / 7.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,653 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	144,037 / 4.56%
Duplication rate	3.78%
Clipped reads	1,029,891 / 32.62%

2.2. ACGT Content

Number/percentage of A's	57,191,789 / 28.65%
Number/percentage of C's	36,722,051 / 18.39%
Number/percentage of T's	63,409,229 / 31.76%
Number/percentage of G's	42,285,101 / 21.18%
Number/percentage of N's	25,690 / 0.01%
GC Percentage	39.58%

2.3. Coverage

Mean	0.0645

Standard Deviation	0.54

2.4. Mapping Quality

Mean Mapping Quality	46.6

2.5. Mismatches and indels

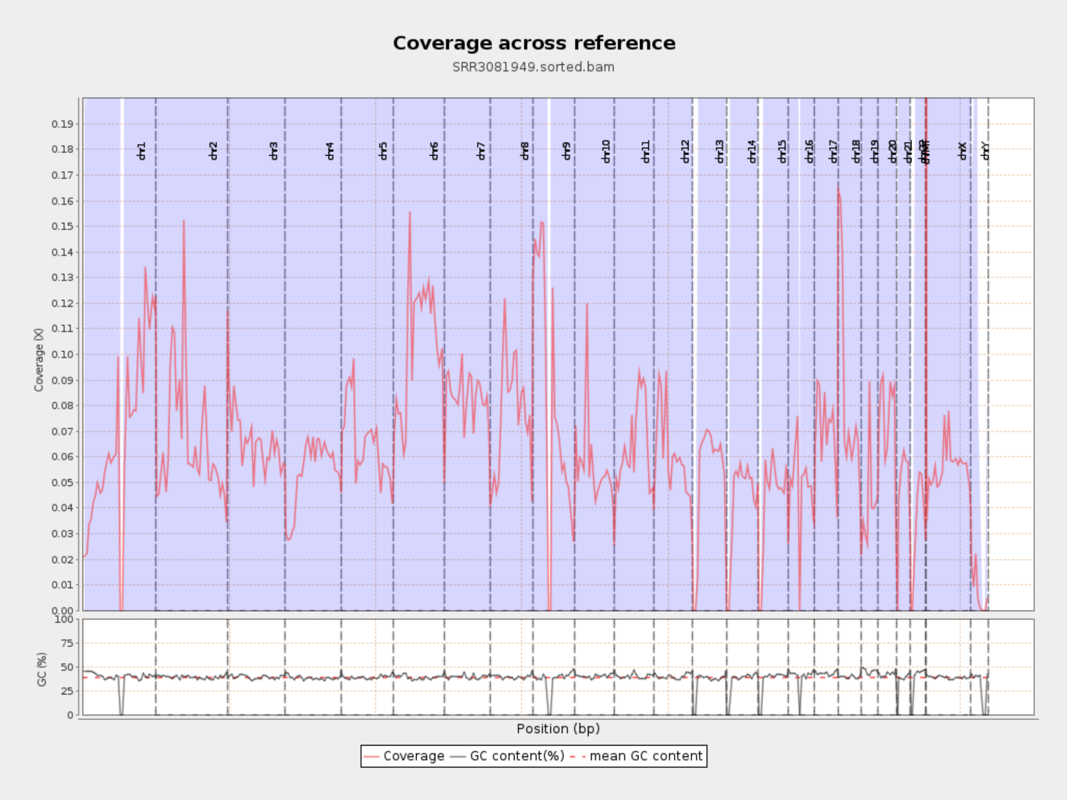
General error rate	0.78%
Mismatches	1,527,452
Insertions	14,312
Mapped reads with at least one insertion	0.49%
Deletions	42,766
Mapped reads with at least one deletion	1.46%
Homopolymer indels	48.31%

2.6. Chromosome stats

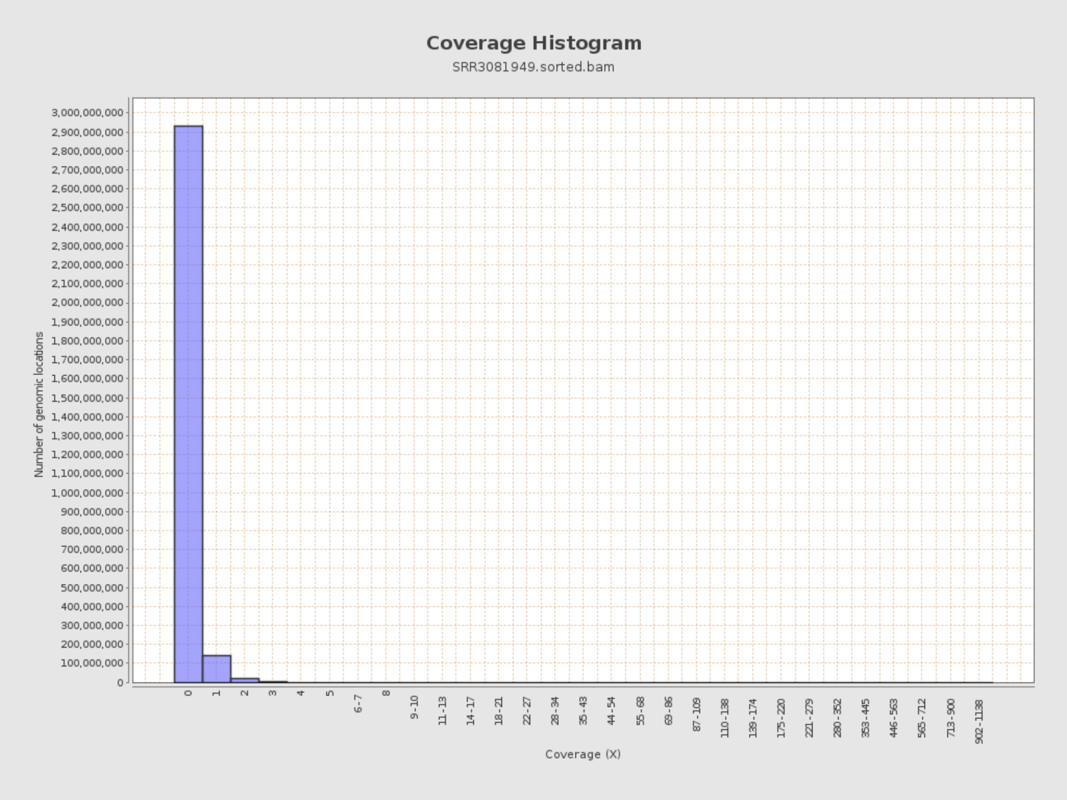
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16915109	0.0679	0.9008
chr2	243199373	16267662	0.0669	0.786
chr3	198022430	13235874	0.0668	0.3051
chr4	191154276	10358899	0.0542	0.292
chr5	180915260	11843359	0.0655	0.2982
chr6	171115067	18025926	0.1053	0.4815
chr7	159138663	13217103	0.0831	0.5674

chr8	146364022	11221475	0.0767	0.8267
chr9	141213431	11427915	0.0809	0.6166
chr10	135534747	7762669	0.0573	0.5478
chr11	135006516	8696484	0.0644	0.4061
chr12	133851895	8152650	0.0609	0.3014
chr13	115169878	6077593	0.0528	0.2625
chr14	107349540	4639727	0.0432	0.2786
chr15	102531392	4381002	0.0427	0.2374
chr16	90354753	4241406	0.0469	0.3109
chr17	81195210	5837421	0.0719	0.3418
chr18	78077248	6672994	0.0855	0.9366
chr19	59128983	2500348	0.0423	0.7538
chr20	63025520	4888603	0.0776	0.3335
chr21	48129895	2294887	0.0477	0.2811
chr22	51304566	1704226	0.0332	0.2058
chrMT	16571	230376	13.9024	7.5084
chrX	155270560	8697148	0.056	0.3374
chrY	59373566	418813	0.0071	0.165

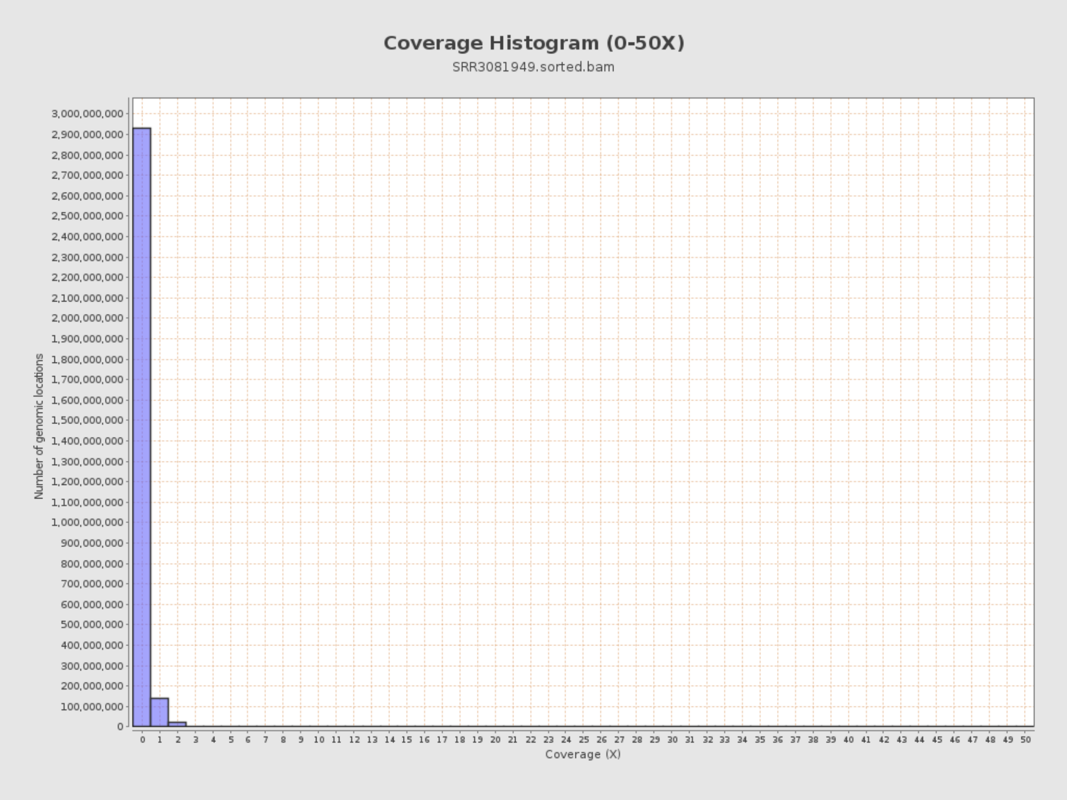
3. Results : Coverage across reference



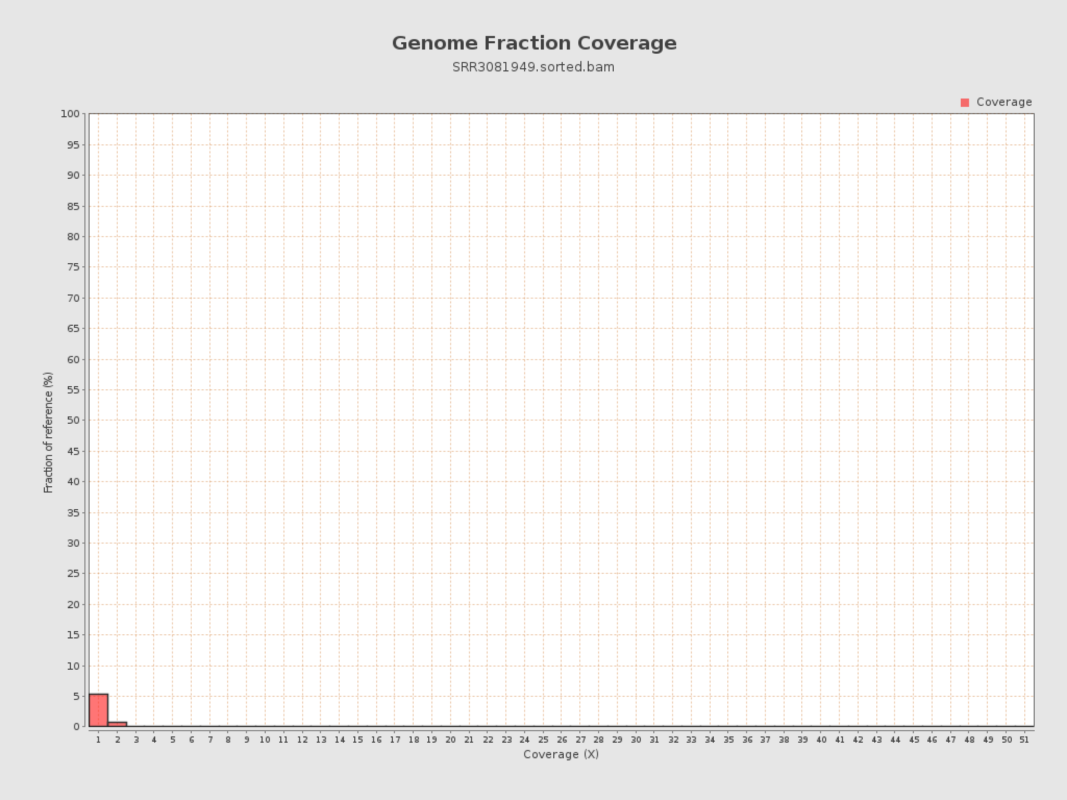
4. Results : Coverage Histogram



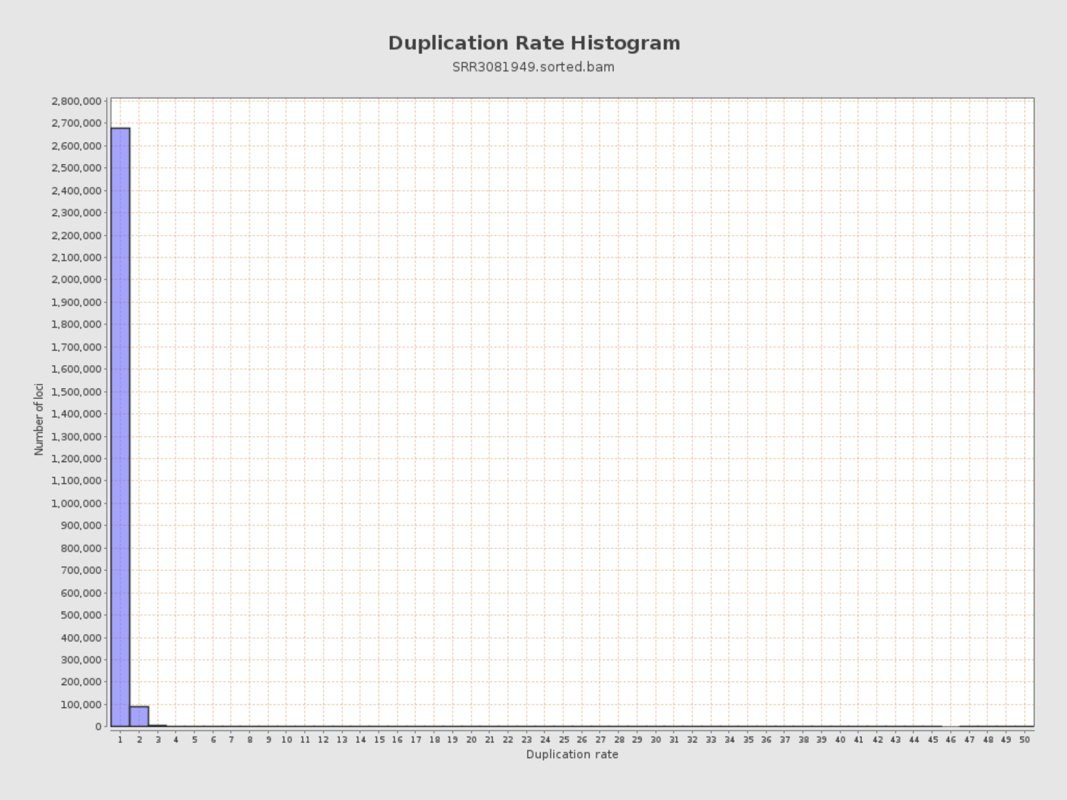
5. Results : Coverage Histogram (0-50X)



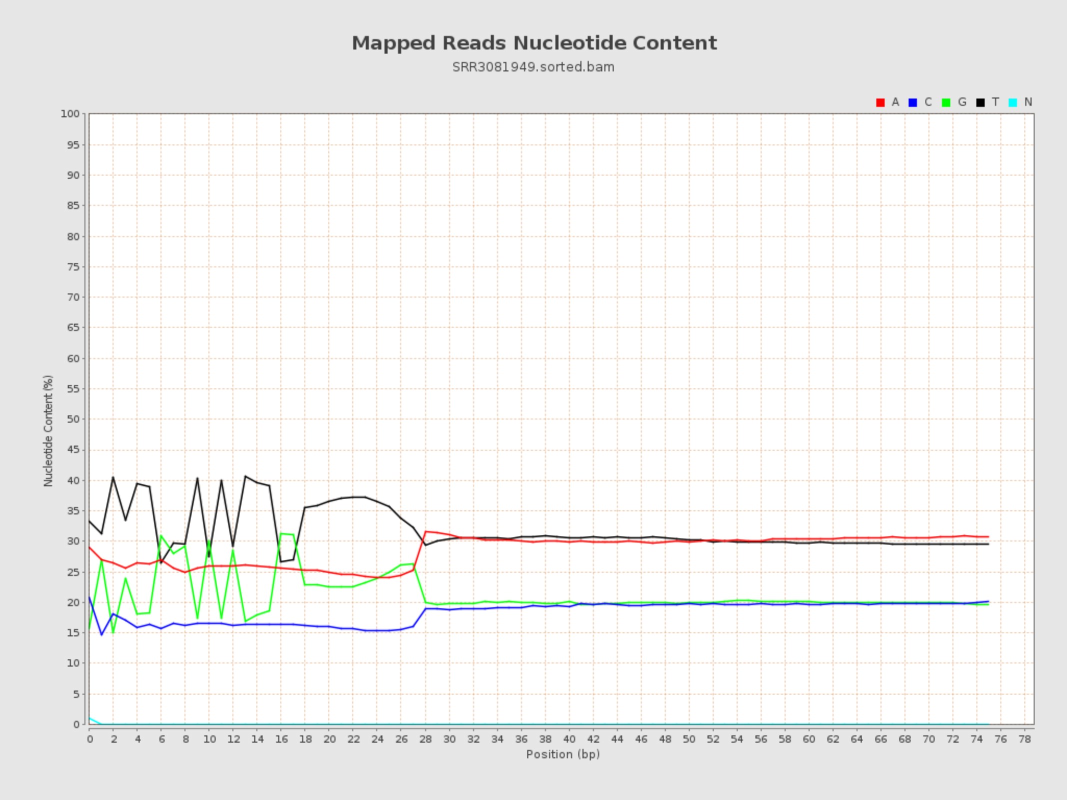
6. Results : Genome Fraction Coverage



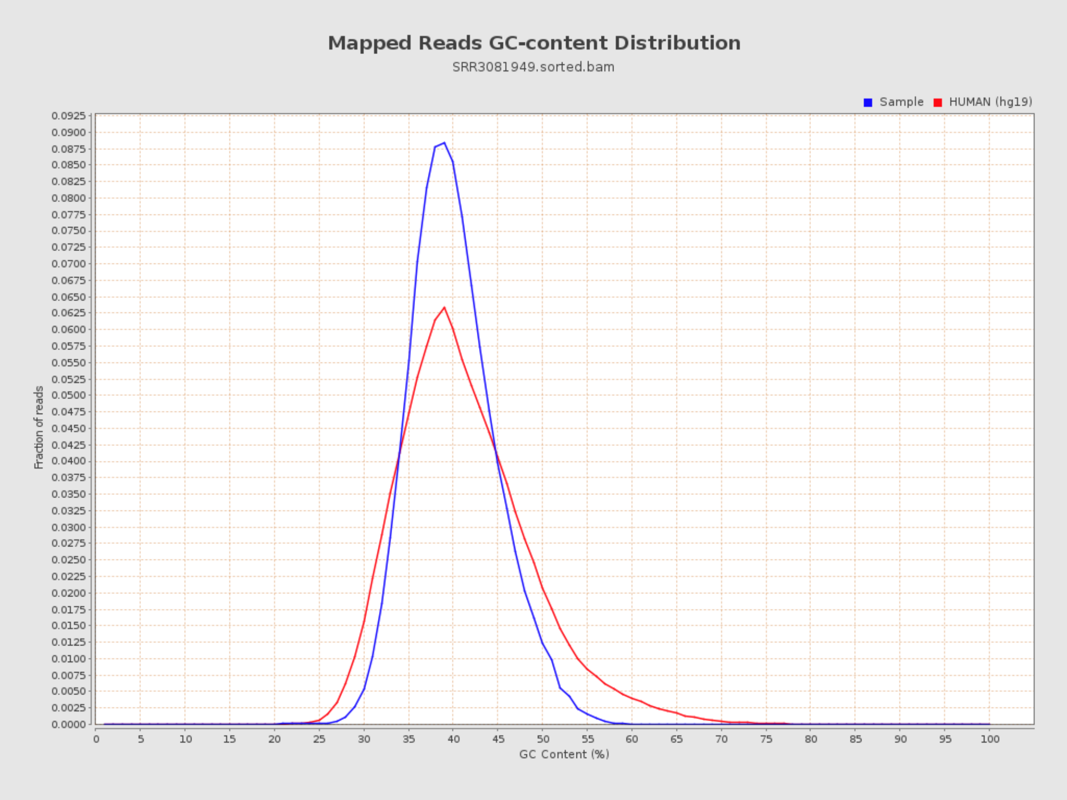
7. Results : Duplication Rate Histogram



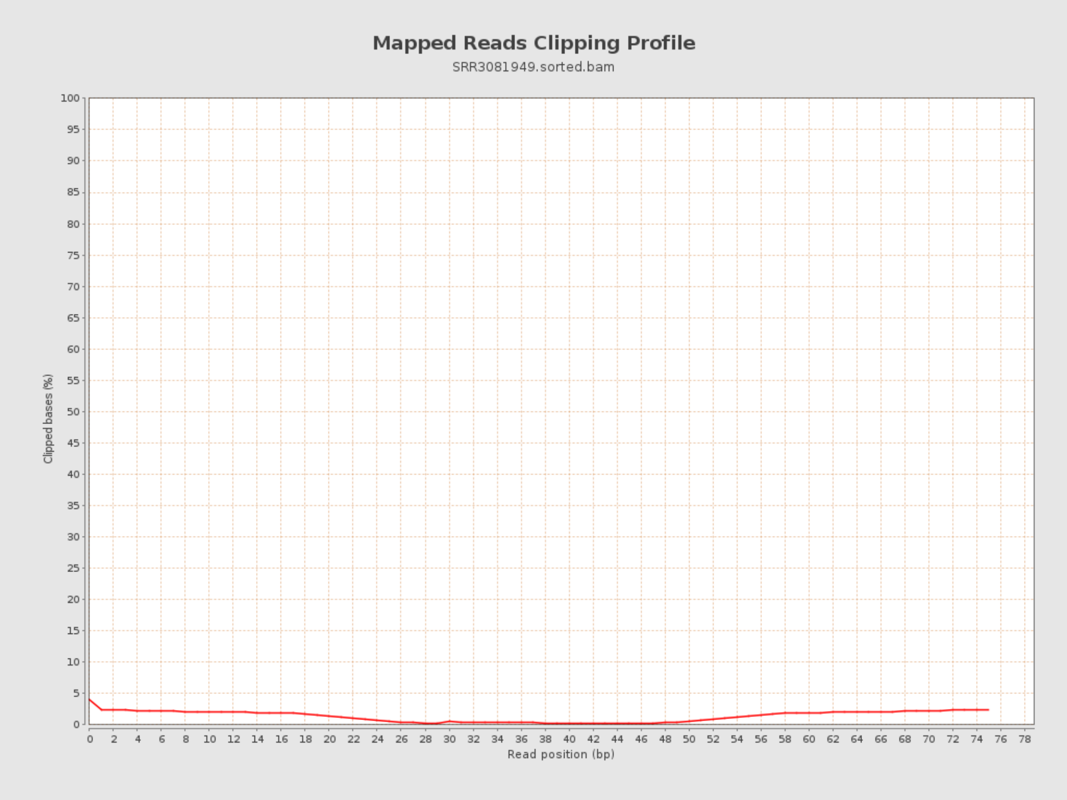
8. Results : Mapped Reads Nucleotide Content



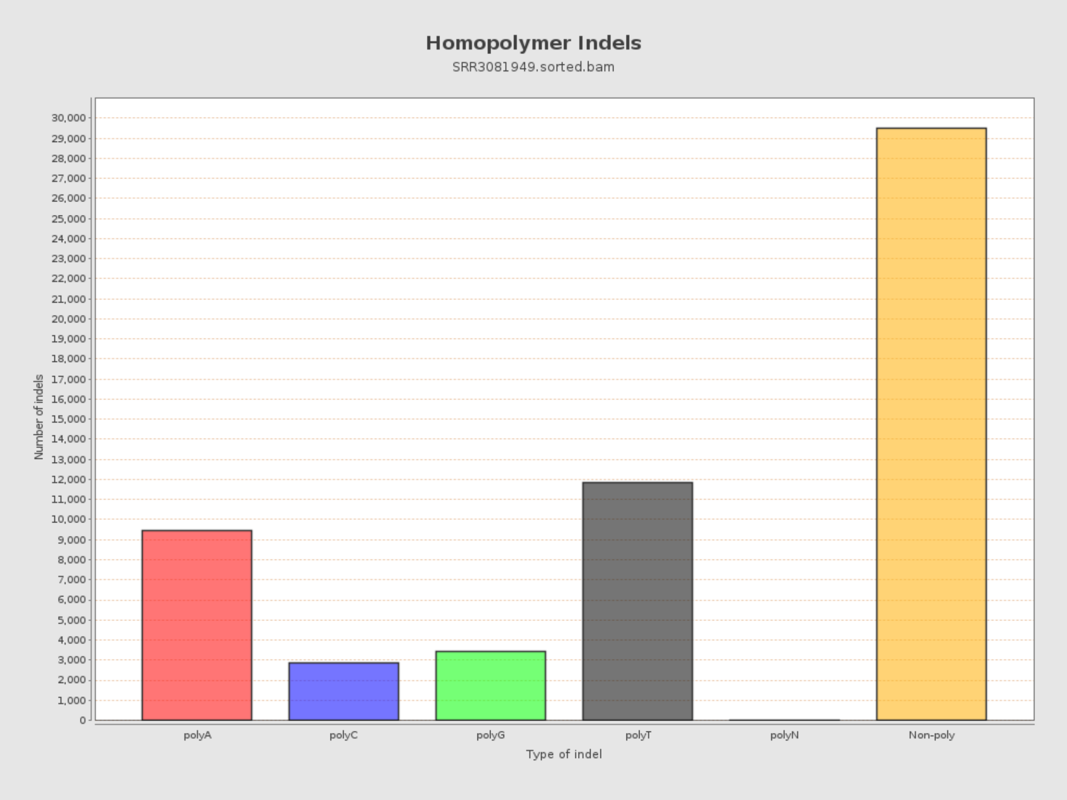
9. Results : Mapped Reads GC-content Distribution



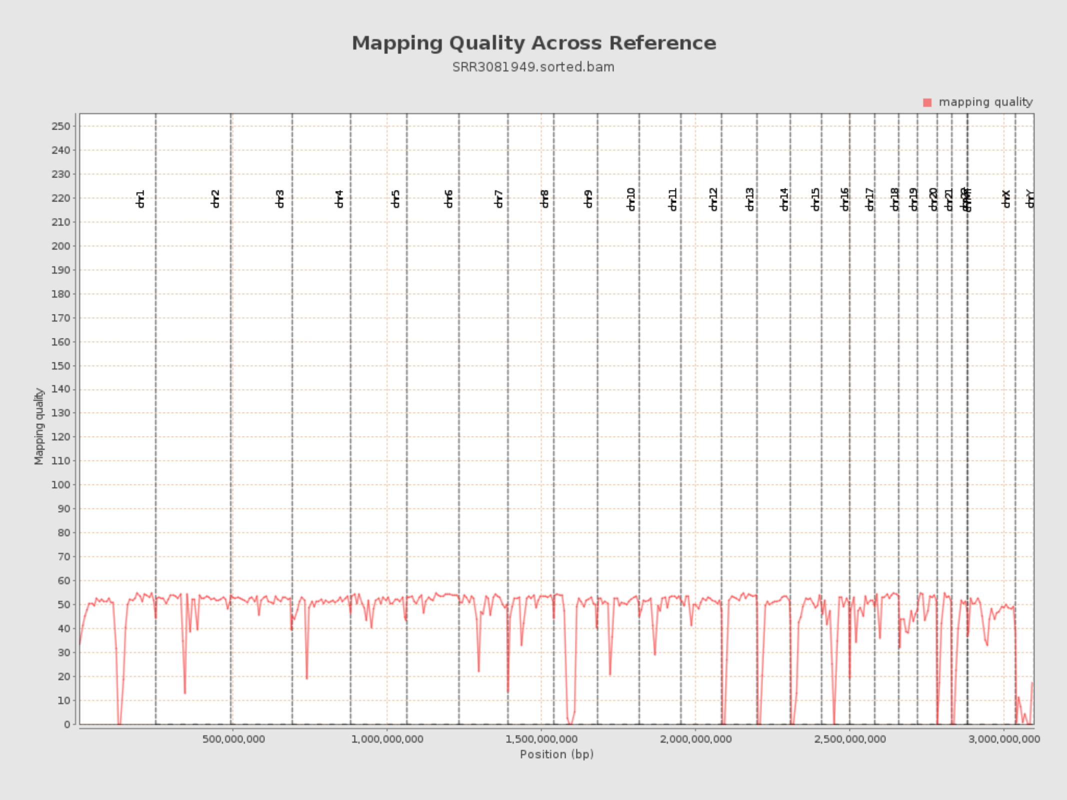
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram