Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 17:30:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084849.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_SRR3084849 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084849.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 17:30:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084849.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,774,113
Mapped reads	2,486,554 / 89.63%
Unmapped reads	287,559 / 10.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,712 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	139,863 / 5.04%
Duplication rate	4.78%
Clipped reads	826,579 / 29.8%

2.2. ACGT Content

Number/percentage of A's	50,407,304 / 29.22%
Number/percentage of C's	31,358,477 / 18.18%
Number/percentage of T's	55,762,257 / 32.33%
Number/percentage of G's	34,945,290 / 20.26%
Number/percentage of N's	27,106 / 0.02%
GC Percentage	38.44%

2.3. Coverage

Mean	0.0557

Standard Deviation	0.4539

2.4. Mapping Quality

Mean Mapping Quality	48.39

2.5. Mismatches and indels

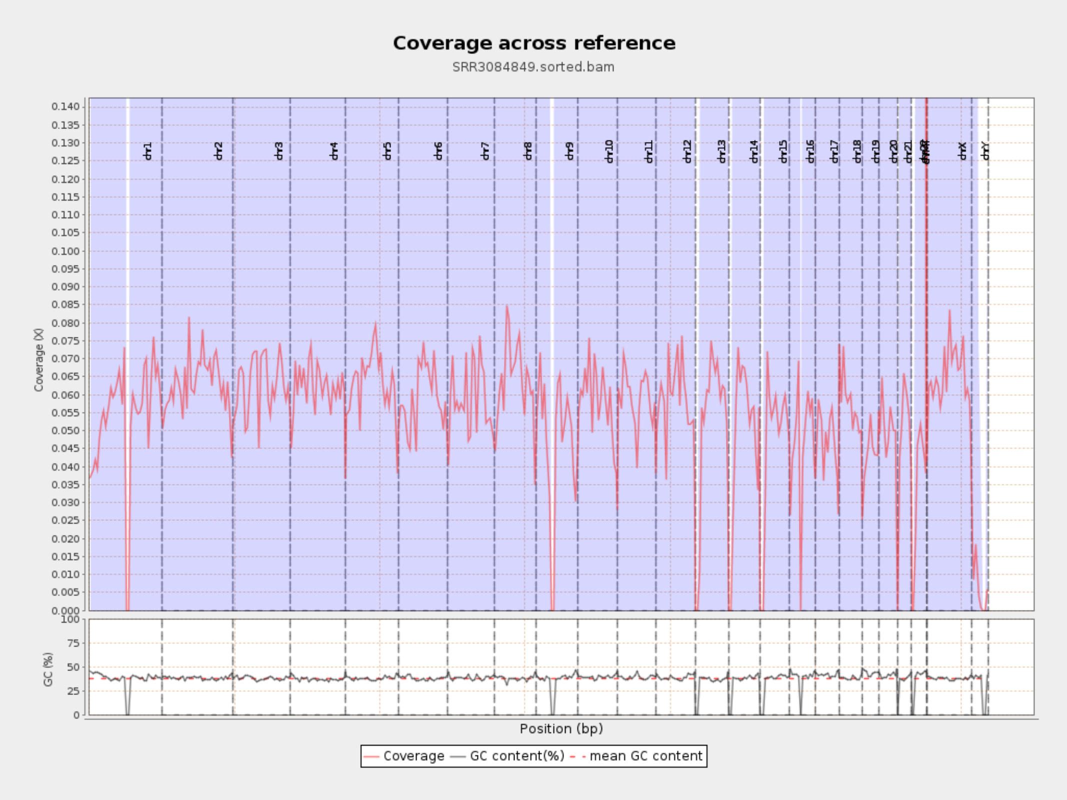
General error rate	0.83%
Mismatches	1,398,638
Insertions	13,610
Mapped reads with at least one insertion	0.54%
Deletions	37,255
Mapped reads with at least one deletion	1.48%
Homopolymer indels	48.58%

2.6. Chromosome stats

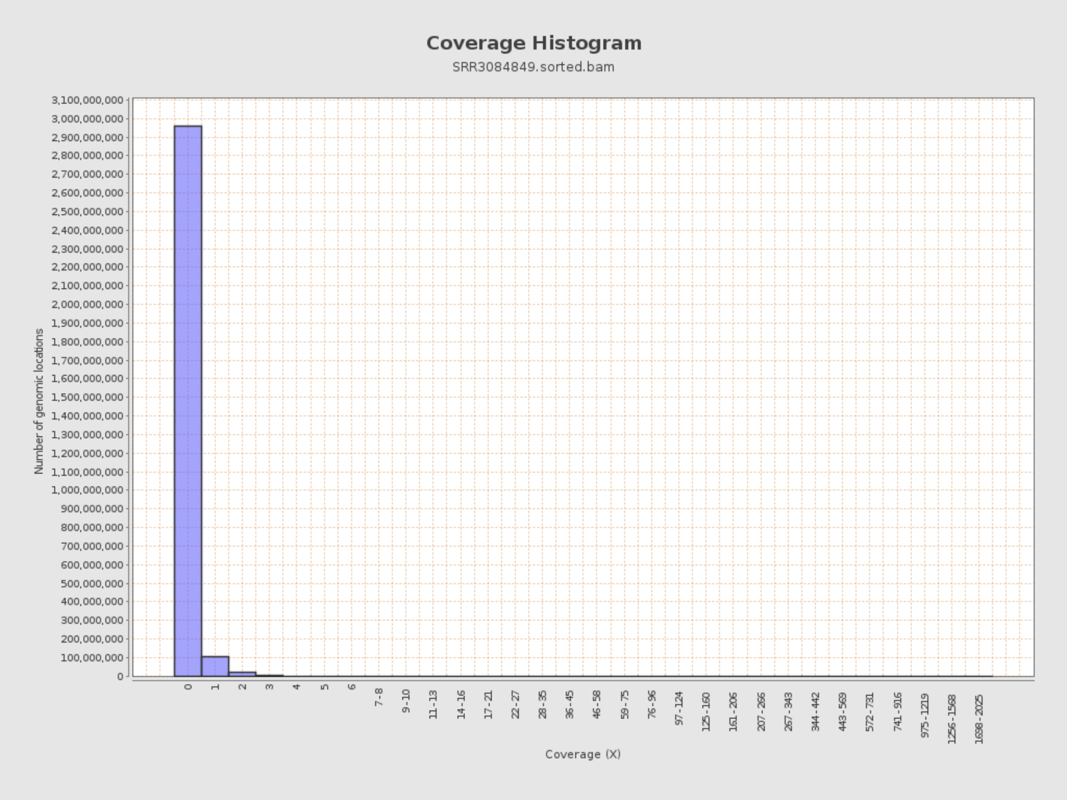
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13392618	0.0537	0.5316
chr2	243199373	15380916	0.0632	0.3935
chr3	198022430	12453551	0.0629	0.3056
chr4	191154276	11914750	0.0623	0.3089
chr5	180915260	11490240	0.0635	0.307
chr6	171115067	10085149	0.0589	0.2997
chr7	159138663	9400032	0.0591	0.4249

chr8	146364022	9301013	0.0635	1.3054
chr9	141213431	6626102	0.0469	0.3539
chr10	135534747	7961032	0.0587	0.3817
chr11	135006516	7917334	0.0586	0.3462
chr12	133851895	7919016	0.0592	0.2975
chr13	115169878	5929255	0.0515	0.277
chr14	107349540	5164389	0.0481	0.2799
chr15	102531392	4807982	0.0469	0.2622
chr16	90354753	4205512	0.0465	0.2891
chr17	81195210	3776485	0.0465	0.2734
chr18	78077248	4520731	0.0579	0.7043
chr19	59128983	2596665	0.0439	0.4044
chr20	63025520	3163460	0.0502	0.2803
chr21	48129895	2317052	0.0481	0.2762
chr22	51304566	1657052	0.0323	0.2145
chrMT	16571	155811	9.4026	5.5504
chrX	155270560	10051049	0.0647	0.3244
chrY	59373566	378994	0.0064	0.1349

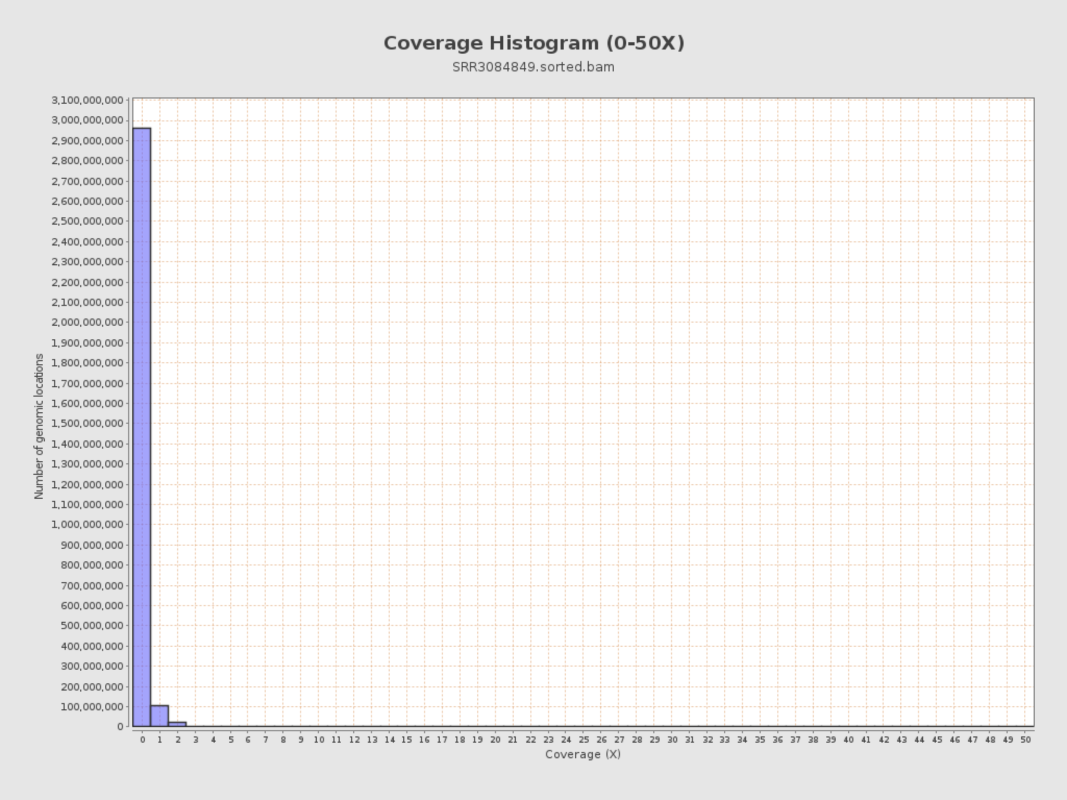
3. Results : Coverage across reference



4. Results : Coverage Histogram



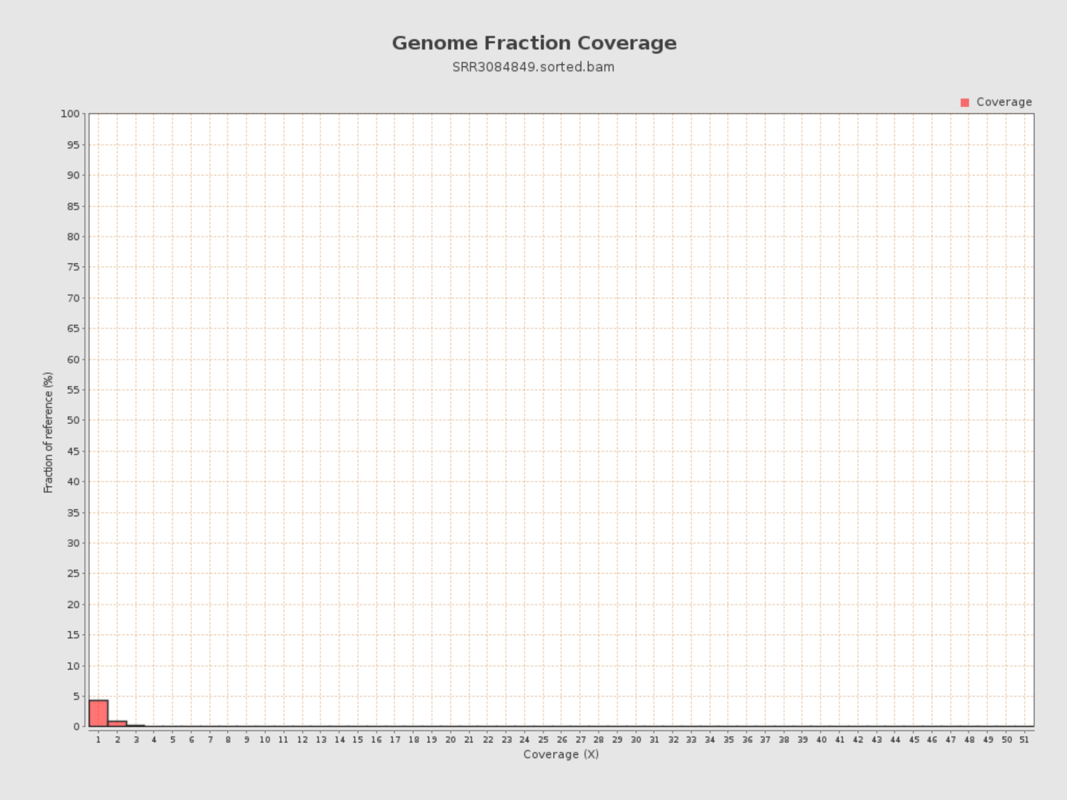
5. Results : Coverage Histogram (0-50X)



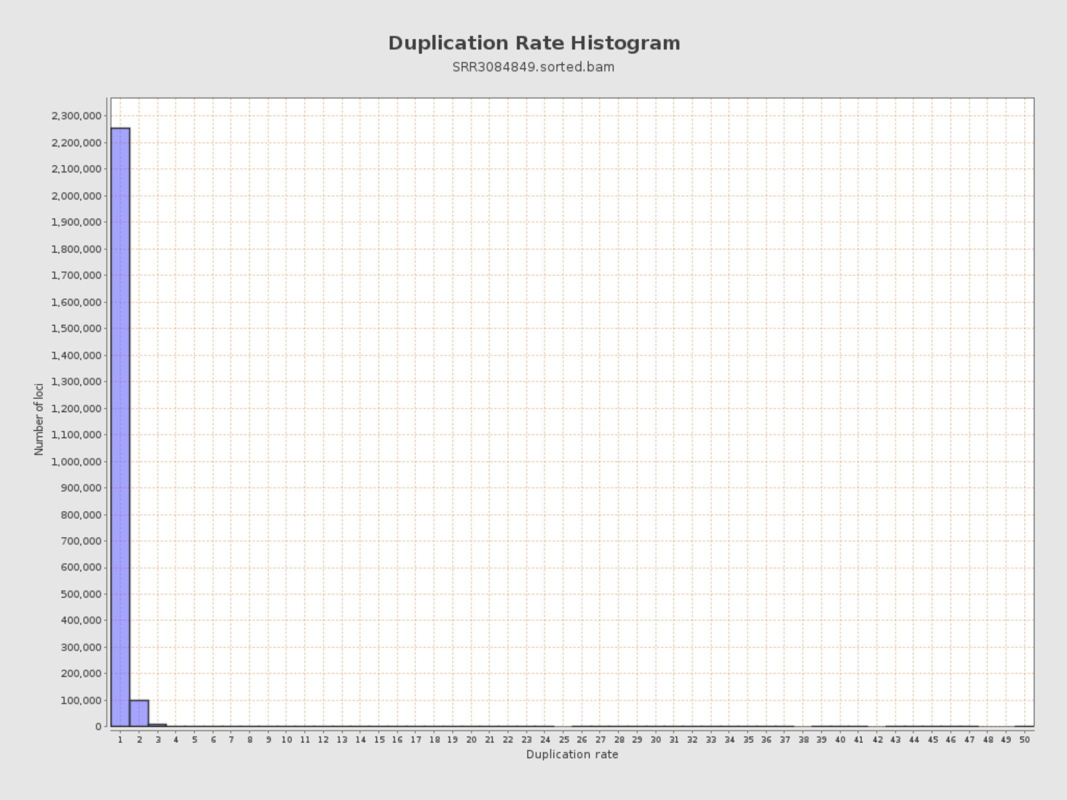
Coverage Histogram (0-50X)

SRR3084849.sorted.bam

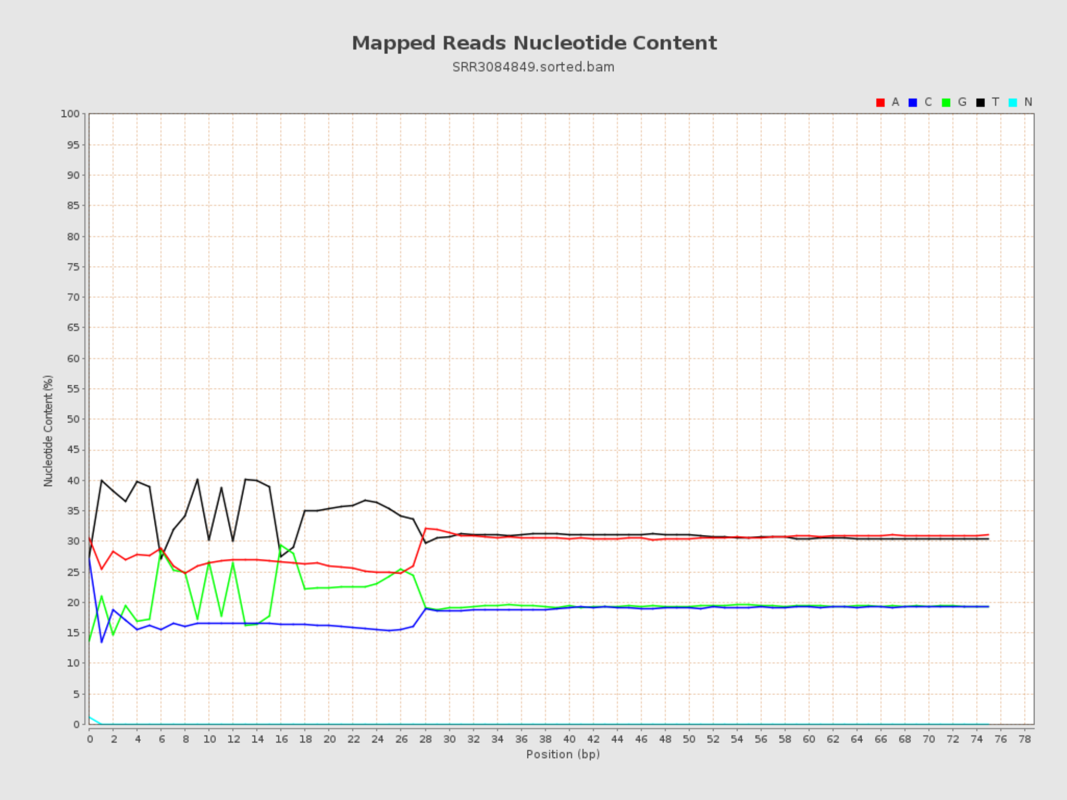
6. Results : Genome Fraction Coverage



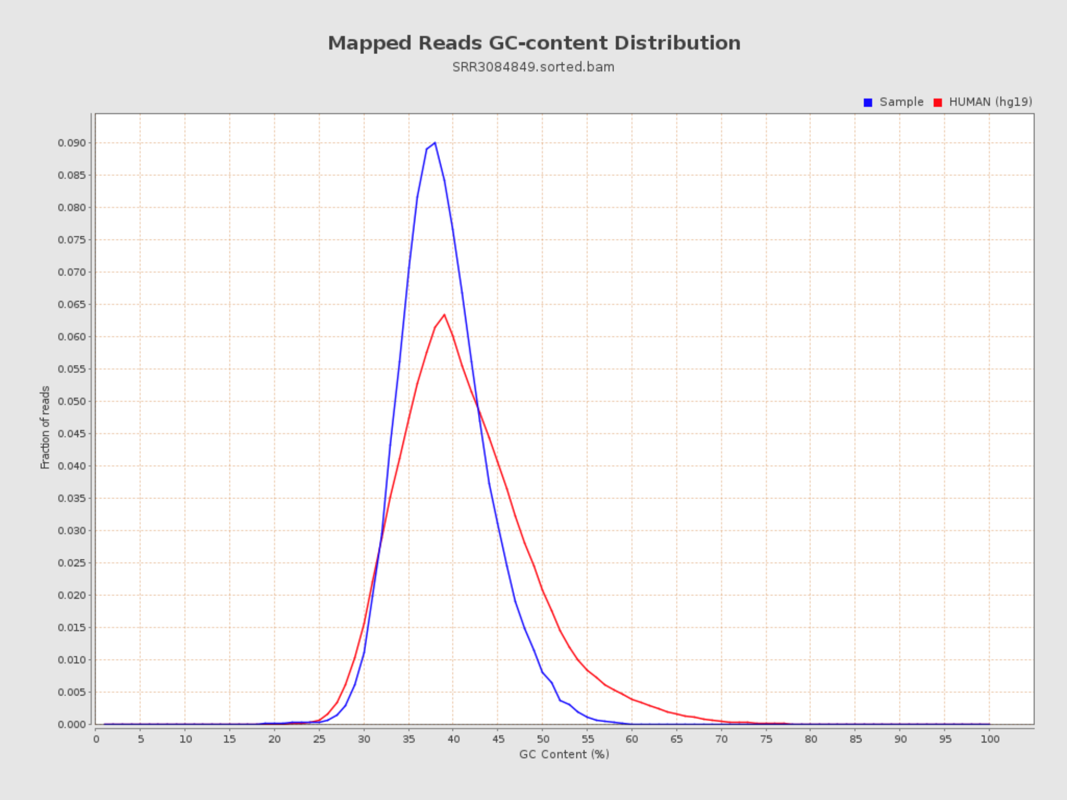
7. Results : Duplication Rate Histogram



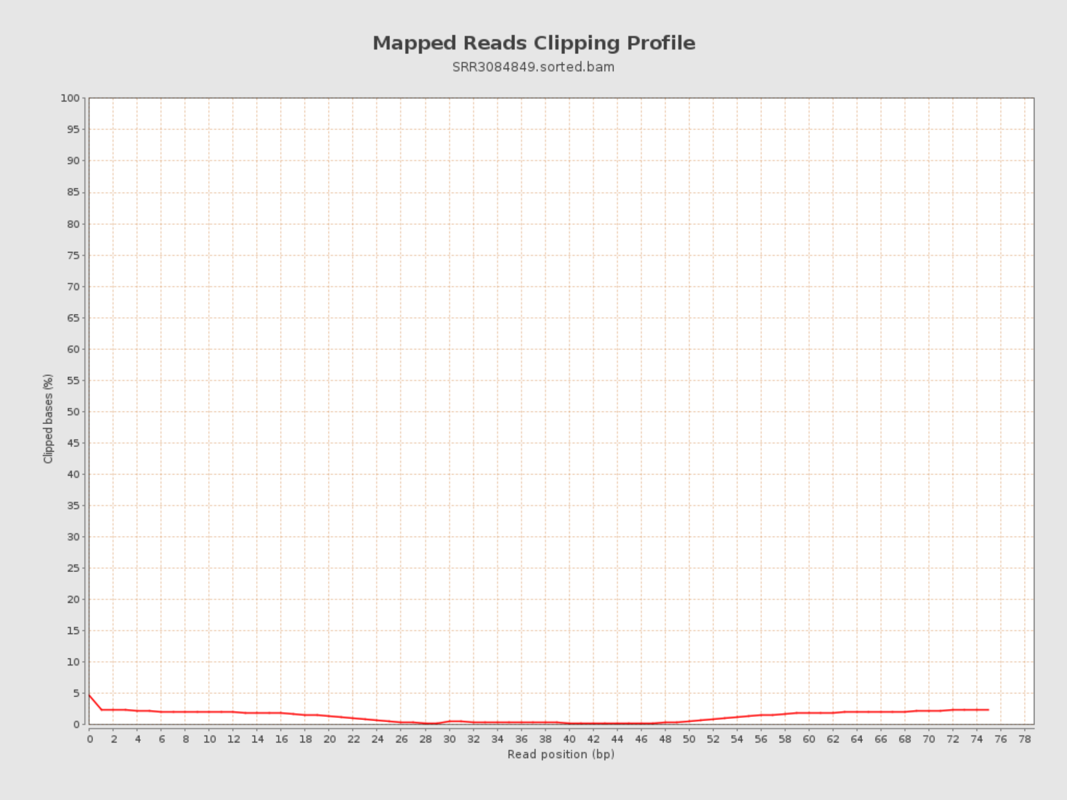
8. Results : Mapped Reads Nucleotide Content



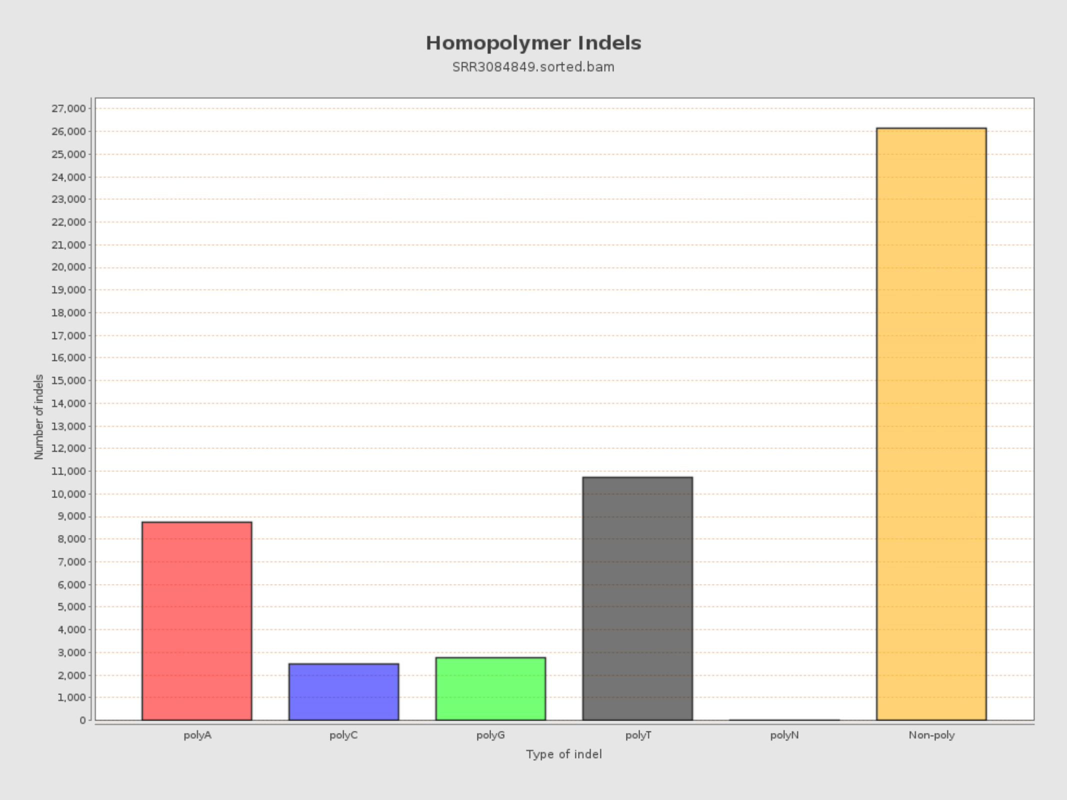
9. Results : Mapped Reads GC-content Distribution



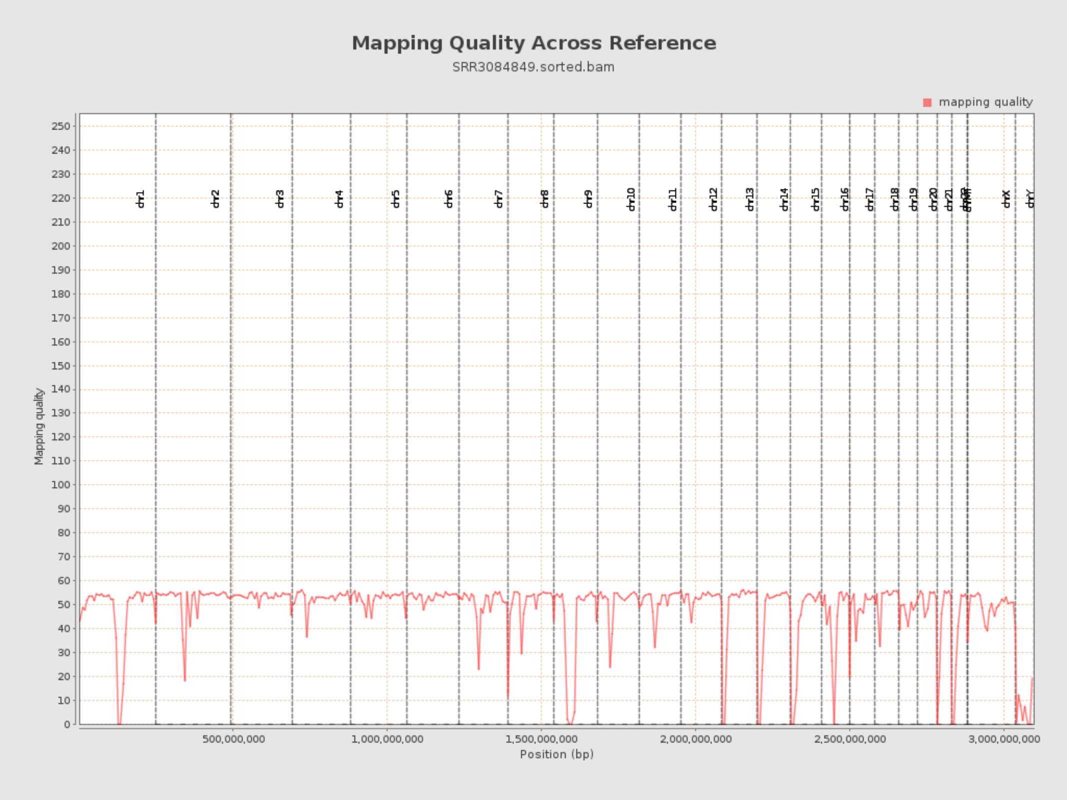
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram