Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:49:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004087.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_SRR6004087 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004087.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:49:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004087.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,905,862
Mapped reads	2,593,471 / 89.25%
Unmapped reads	312,391 / 10.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,475 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	185,826 / 6.39%
Duplication rate	5.52%
Clipped reads	1,290,062 / 44.4%

2.2. ACGT Content

Number/percentage of A's	47,433,618 / 27.93%
Number/percentage of C's	30,317,418 / 17.85%
Number/percentage of T's	54,775,884 / 32.25%
Number/percentage of G's	37,214,733 / 21.91%
Number/percentage of N's	80,160 / 0.05%
GC Percentage	39.77%

2.3. Coverage

Mean	0.0549

Standard Deviation	0.5484

2.4. Mapping Quality

Mean Mapping Quality	46.06

2.5. Mismatches and indels

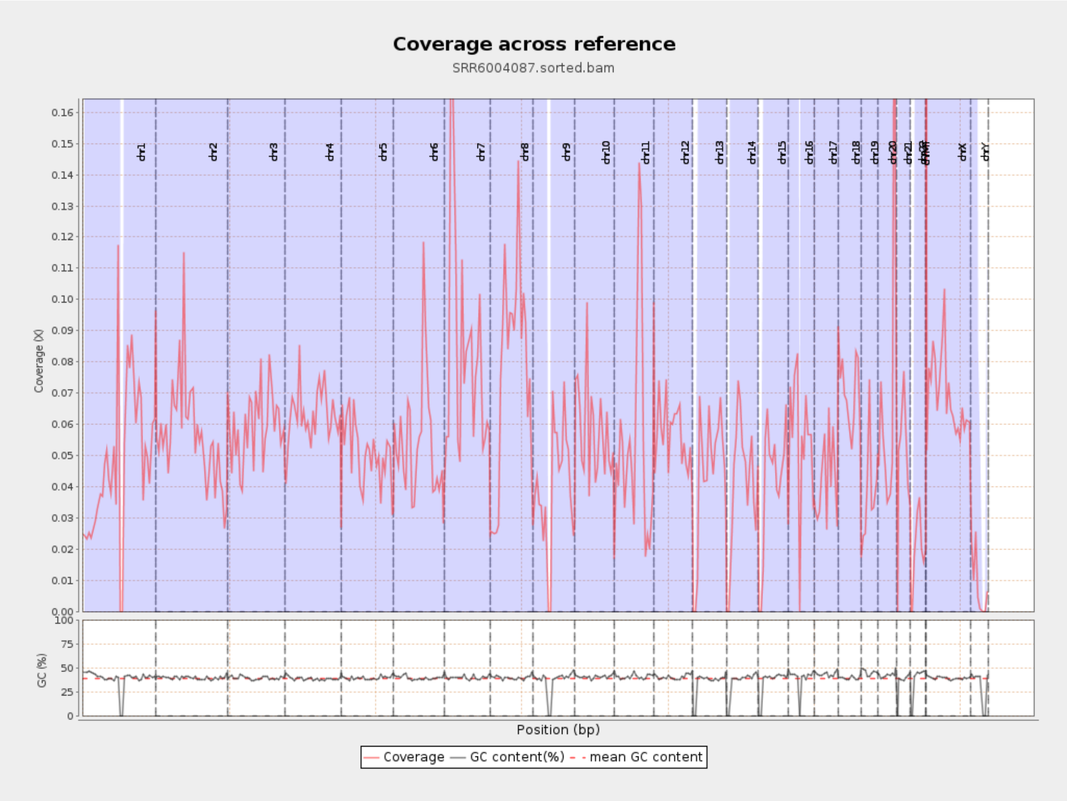
General error rate	0.86%
Mismatches	1,444,228
Insertions	13,076
Mapped reads with at least one insertion	0.5%
Deletions	53,005
Mapped reads with at least one deletion	2.02%
Homopolymer indels	45.03%

2.6. Chromosome stats

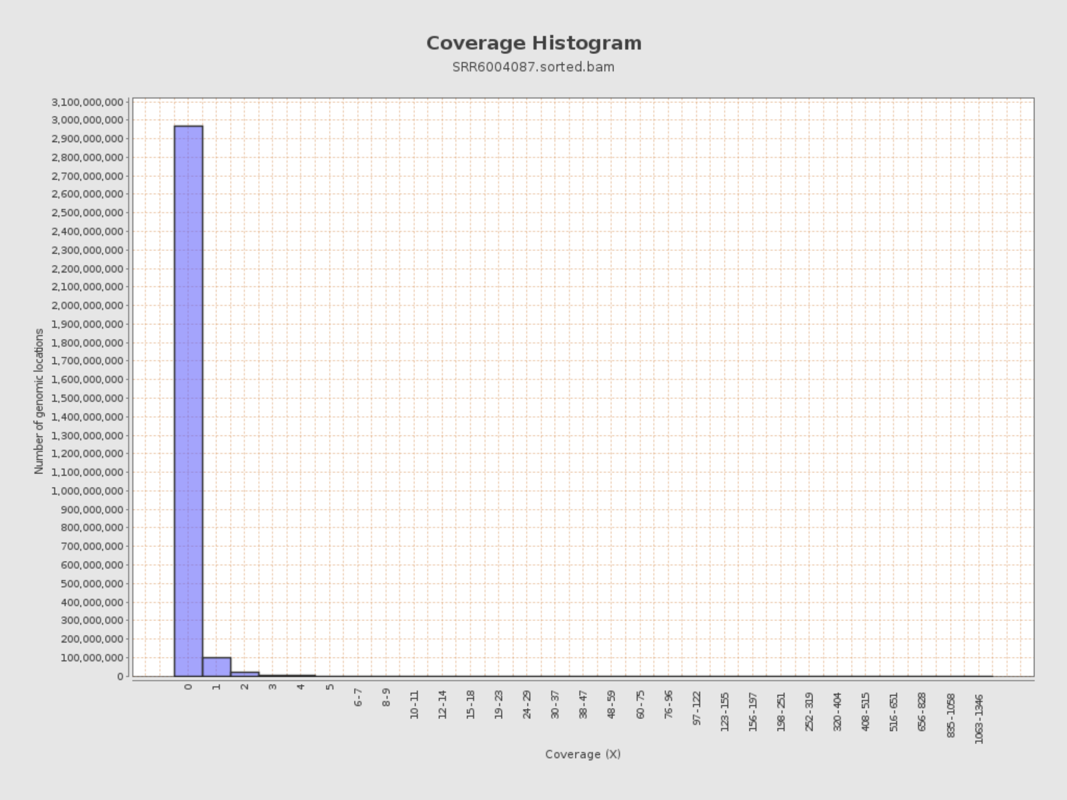
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11995969	0.0481	1.0216
chr2	243199373	13722480	0.0564	0.6127
chr3	198022430	11753185	0.0594	0.309
chr4	191154276	12099958	0.0633	0.3454
chr5	180915260	9176687	0.0507	0.2917
chr6	171115067	9316614	0.0544	0.3401
chr7	159138663	12988723	0.0816	0.7402

chr8	146364022	11279588	0.0771	0.8853
chr9	141213431	5672040	0.0402	0.4867
chr10	135534747	7849706	0.0579	0.4936
chr11	135006516	7191725	0.0533	0.4439
chr12	133851895	7537990	0.0563	0.3141
chr13	115169878	5200830	0.0452	0.2672
chr14	107349540	4448158	0.0414	0.301
chr15	102531392	4184739	0.0408	0.2575
chr16	90354753	4854261	0.0537	0.3513
chr17	81195210	3432001	0.0423	0.2964
chr18	78077248	5511596	0.0706	0.9973
chr19	59128983	2282142	0.0386	0.7328
chr20	63025520	4884849	0.0775	0.386
chr21	48129895	2351855	0.0489	0.31
chr22	51304566	988863	0.0193	0.1675
chrMT	16571	22505	1.3581	1.6708
chrX	155270560	10681092	0.0688	0.394
chrY	59373566	482117	0.0081	0.1783

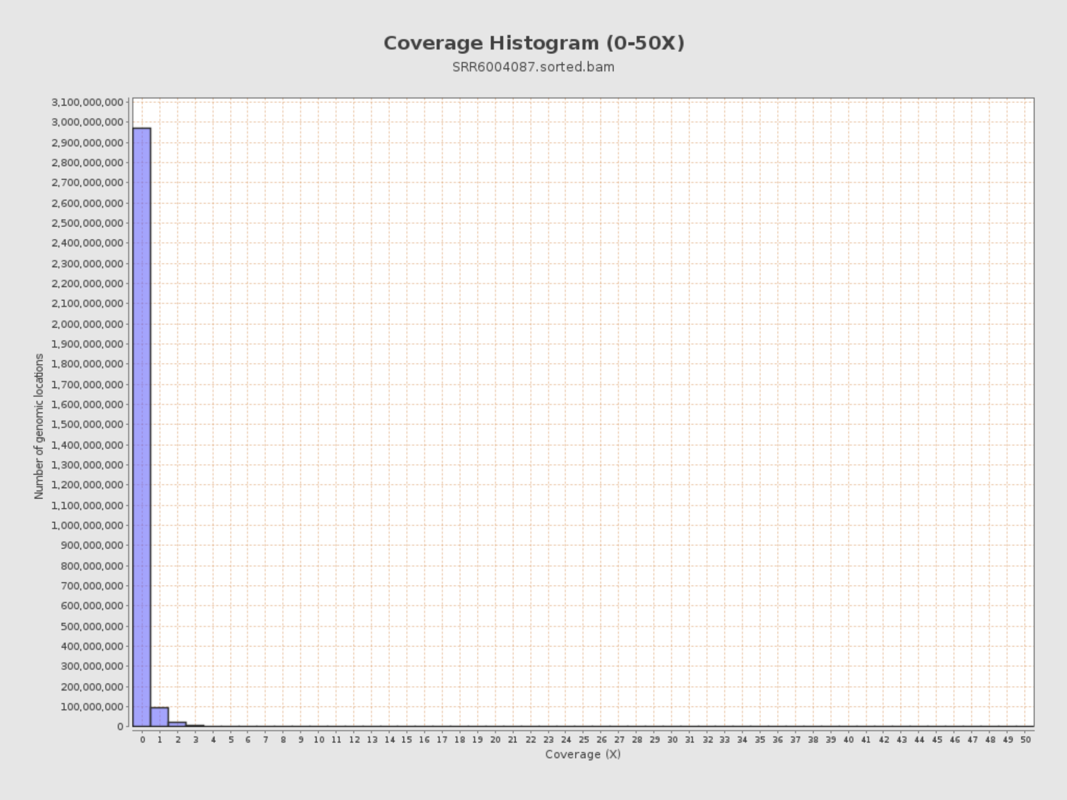
3. Results : Coverage across reference



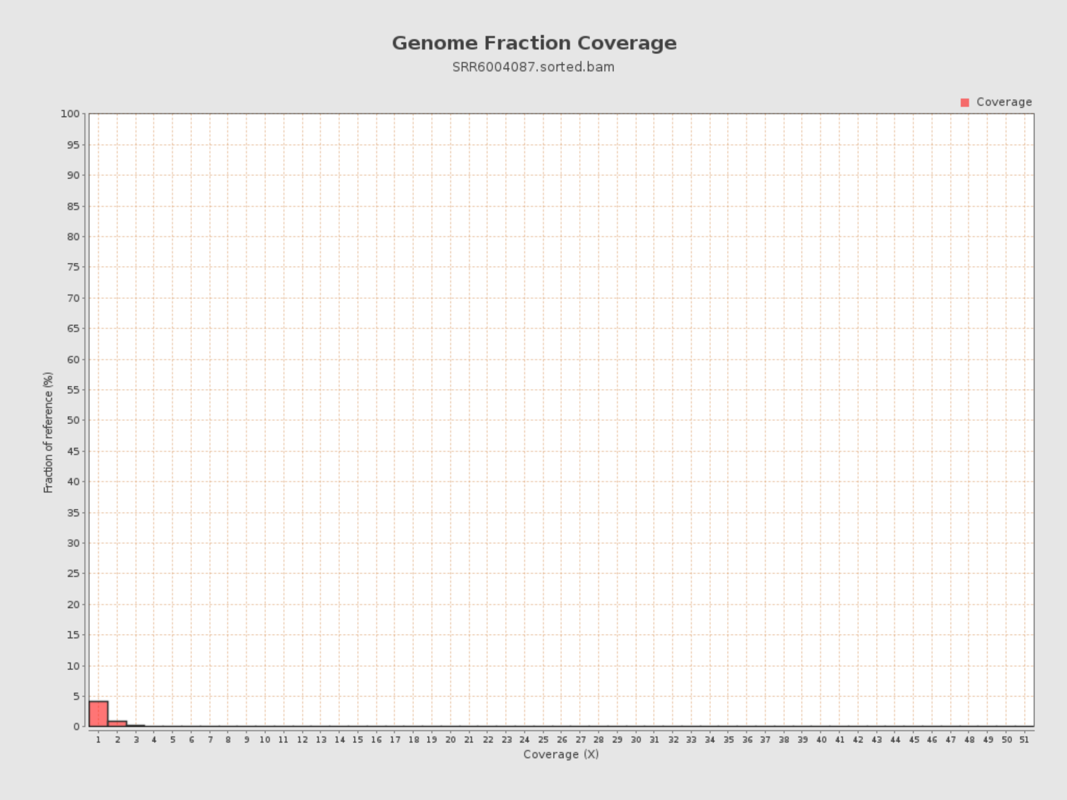
4. Results : Coverage Histogram



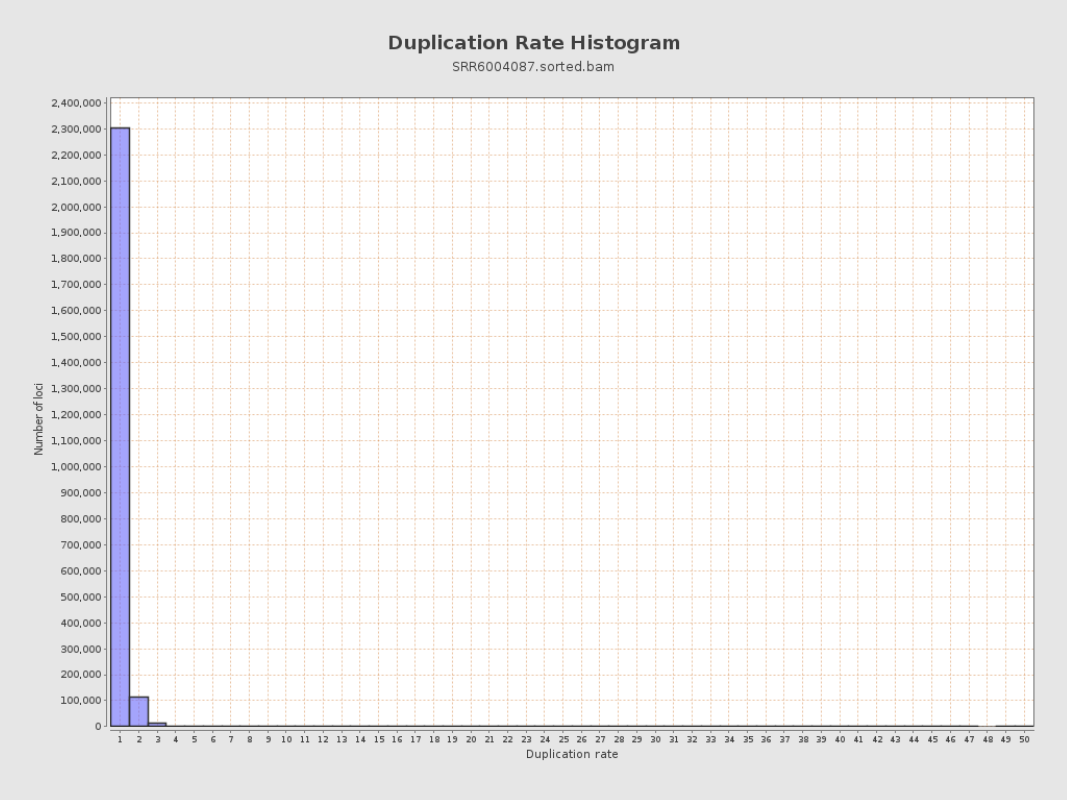
5. Results : Coverage Histogram (0-50X)



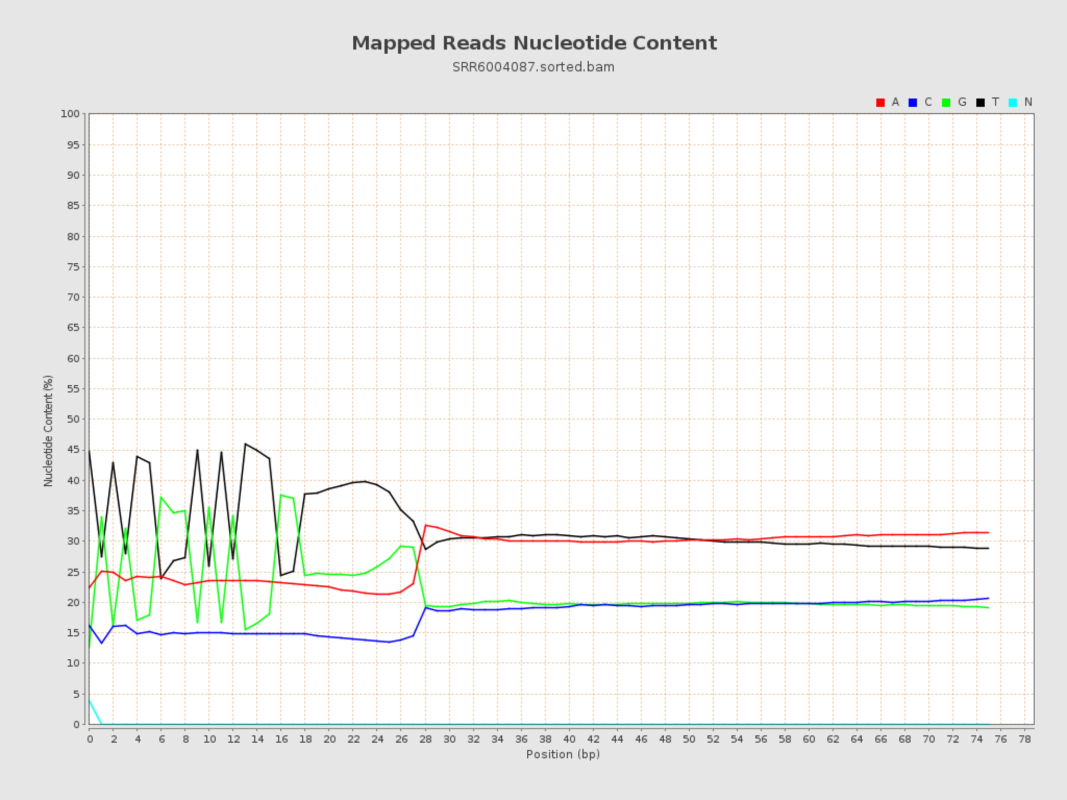
6. Results : Genome Fraction Coverage



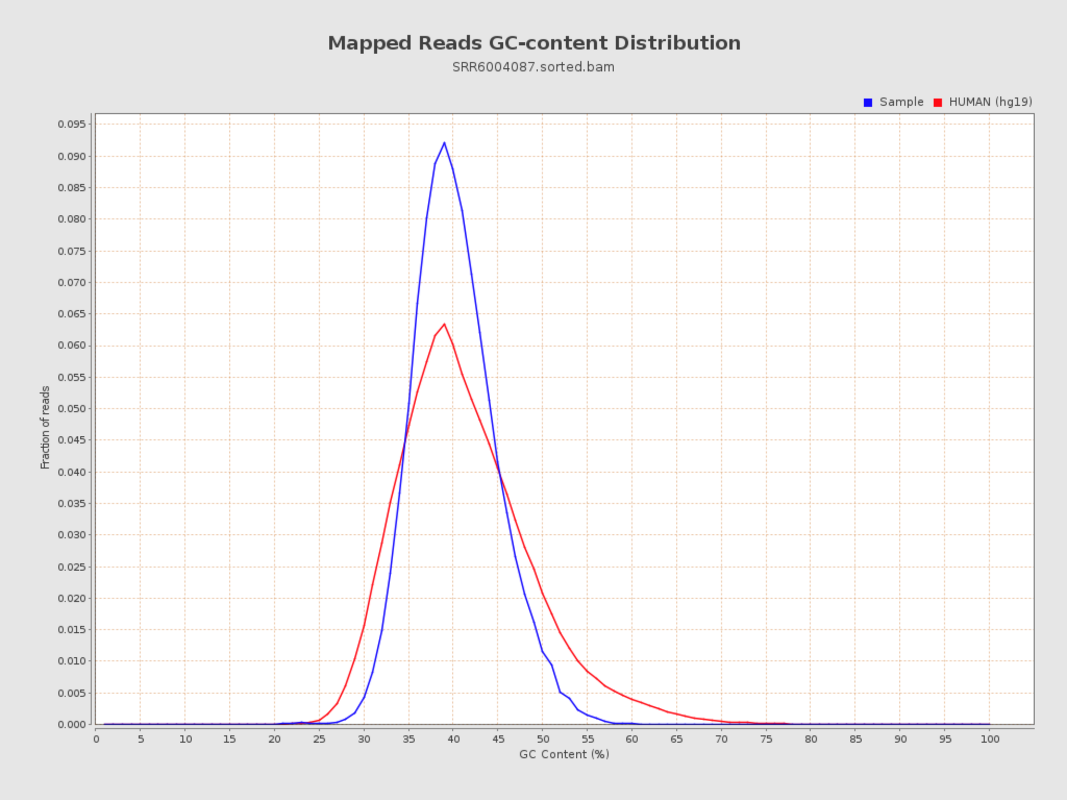
7. Results : Duplication Rate Histogram



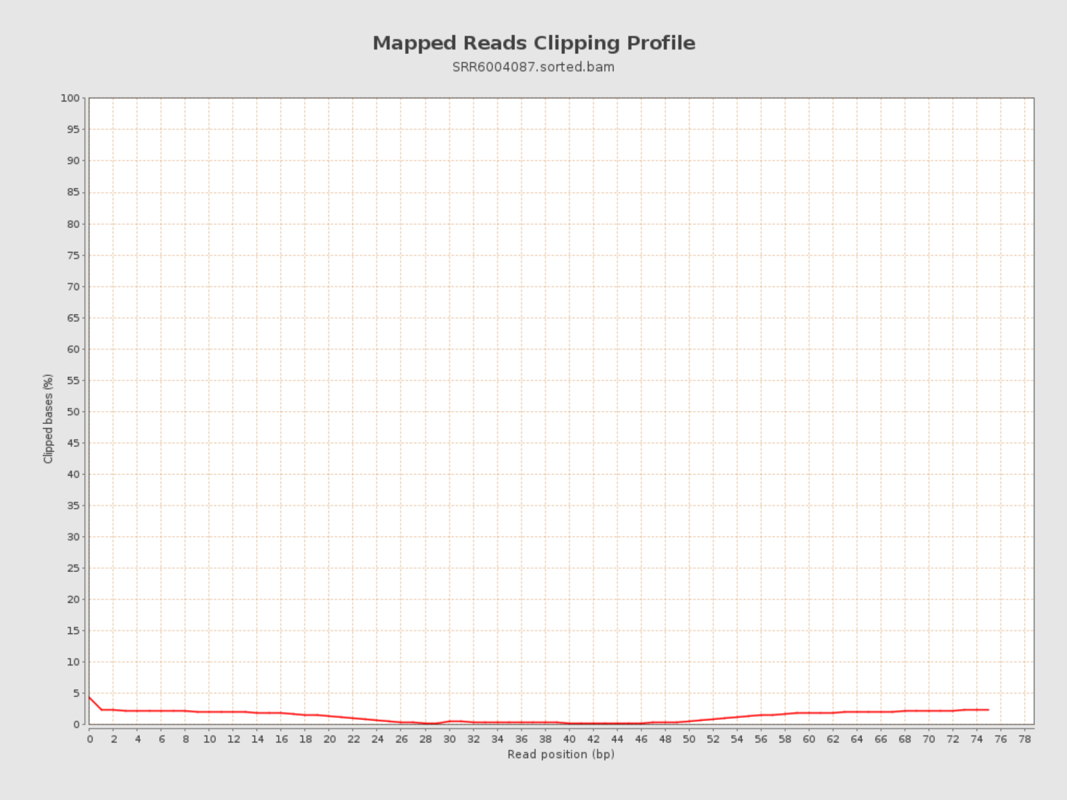
8. Results : Mapped Reads Nucleotide Content



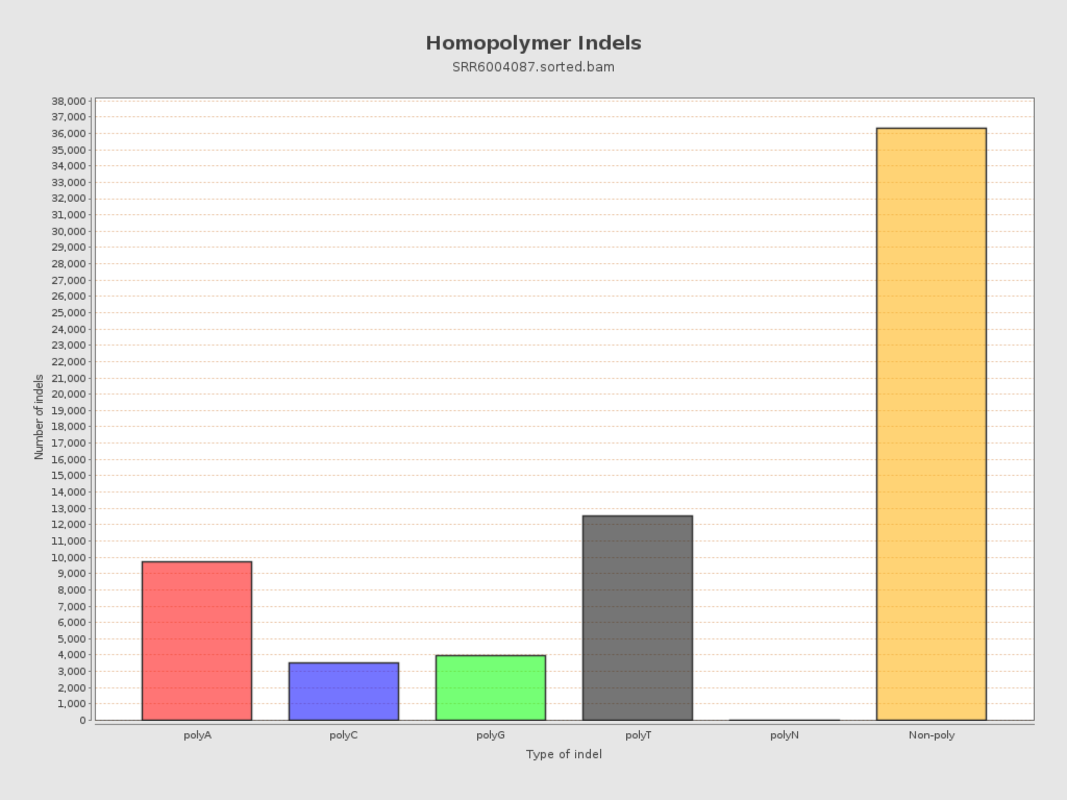
9. Results : Mapped Reads GC-content Distribution



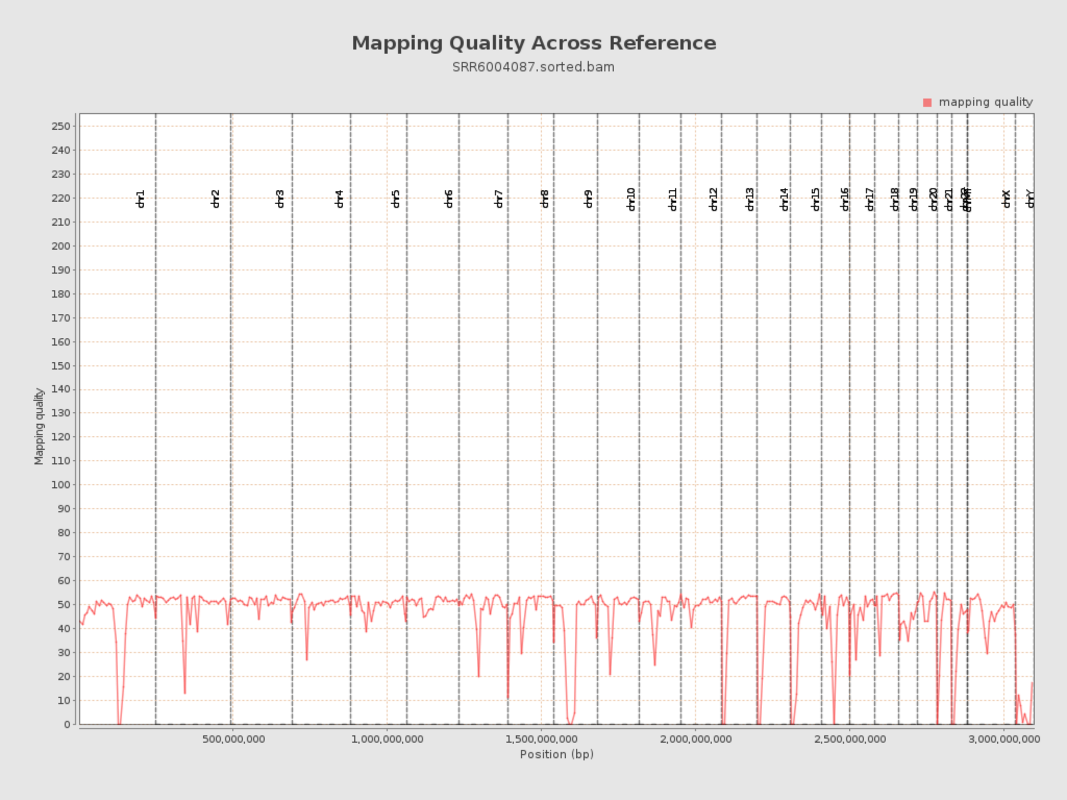
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram