Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:30:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084890.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_SRR3084890 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084890.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:30:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084890.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,885,239
Mapped reads	2,598,114 / 90.05%
Unmapped reads	287,125 / 9.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,887 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	122,231 / 4.24%
Duplication rate	3.77%
Clipped reads	869,424 / 30.13%

2.2. ACGT Content

Number/percentage of A's	52,583,046 / 29.19%
Number/percentage of C's	32,869,907 / 18.25%
Number/percentage of T's	57,702,260 / 32.03%
Number/percentage of G's	36,975,327 / 20.52%
Number/percentage of N's	27,850 / 0.02%
GC Percentage	38.77%

2.3. Coverage

Mean	0.0582

Standard Deviation	0.4919

2.4. Mapping Quality

Mean Mapping Quality	47.54

2.5. Mismatches and indels

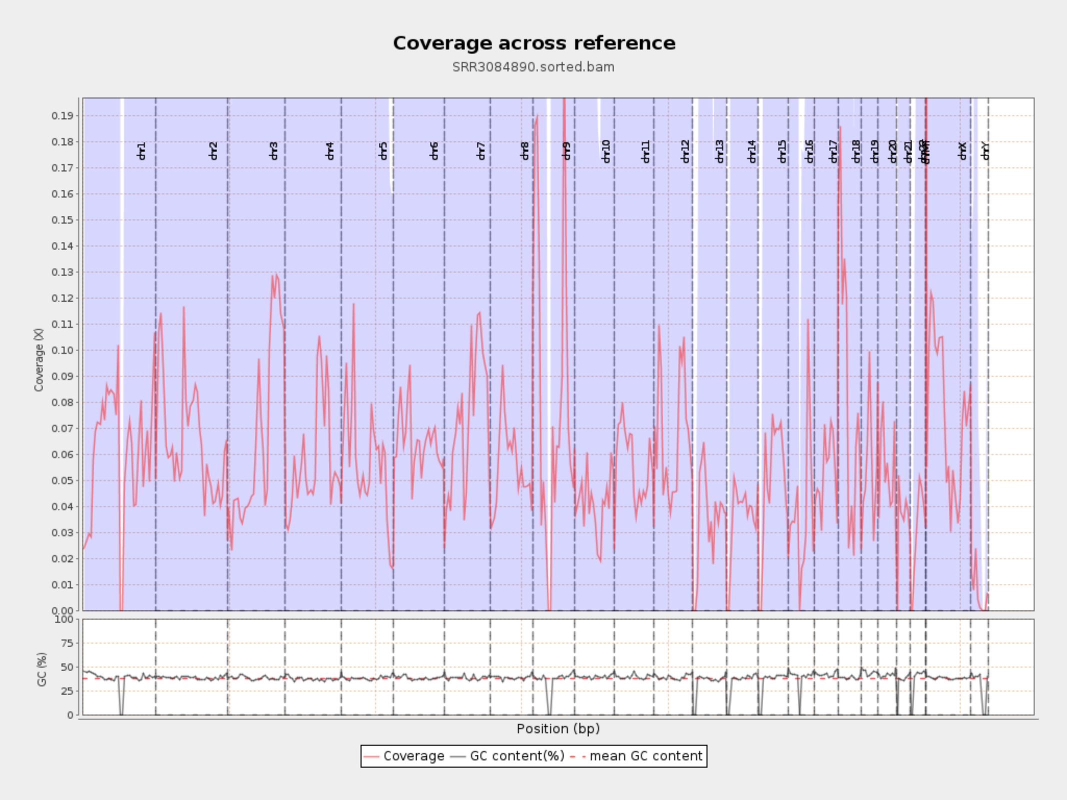
General error rate	0.86%
Mismatches	1,514,147
Insertions	14,728
Mapped reads with at least one insertion	0.56%
Deletions	38,922
Mapped reads with at least one deletion	1.48%
Homopolymer indels	48.49%

2.6. Chromosome stats

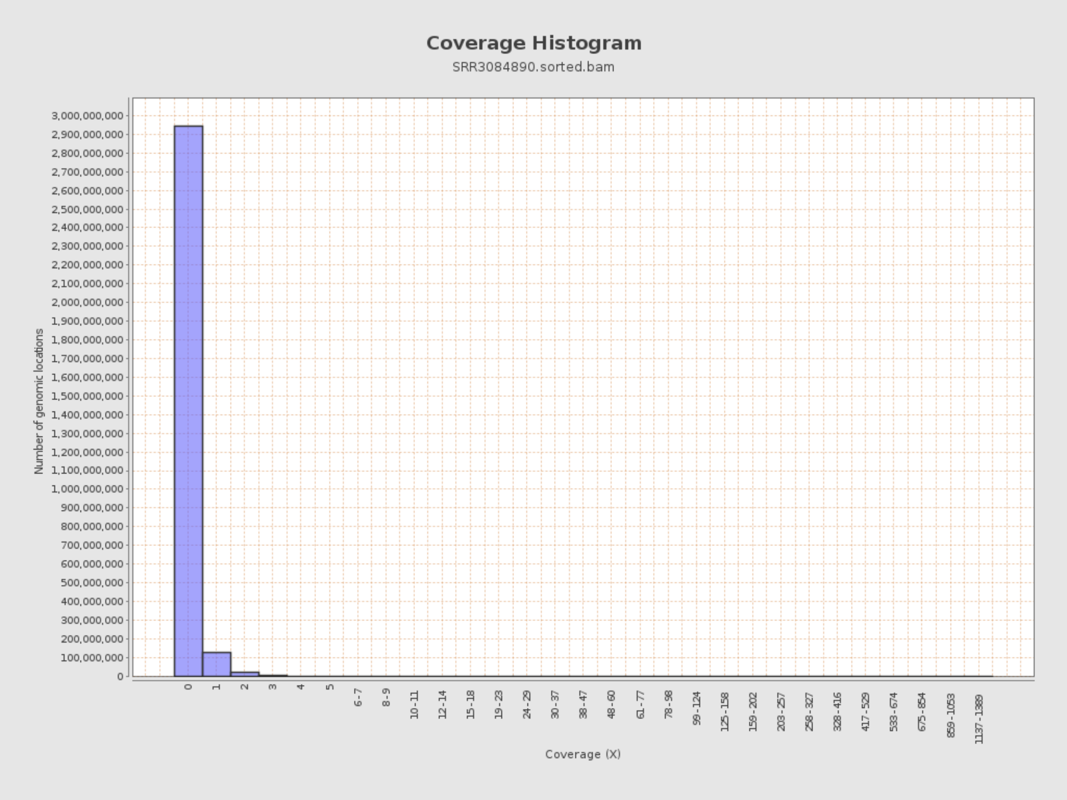
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15132468	0.0607	0.9276
chr2	243199373	16048681	0.066	0.5292
chr3	198022430	13179735	0.0666	0.2957
chr4	191154276	11139909	0.0583	0.2814
chr5	180915260	10407136	0.0575	0.2894
chr6	171115067	11185944	0.0654	0.3029
chr7	159138663	11623456	0.073	0.4533

chr8	146364022	8215559	0.0561	0.9427
chr9	141213431	11606833	0.0822	0.5282
chr10	135534747	5594424	0.0413	0.3449
chr11	135006516	7625030	0.0565	0.3672
chr12	133851895	9013822	0.0673	0.3056
chr13	115169878	3947867	0.0343	0.2083
chr14	107349540	3760548	0.035	0.2384
chr15	102531392	5021531	0.049	0.2521
chr16	90354753	3246096	0.0359	0.2659
chr17	81195210	4364851	0.0538	0.29
chr18	78077248	6894644	0.0883	0.9518
chr19	59128983	3313902	0.056	0.5677
chr20	63025520	3483250	0.0553	0.2864
chr21	48129895	1723670	0.0358	0.2443
chr22	51304566	1557466	0.0304	0.1949
chrMT	16571	27887	1.6829	1.6299
chrX	155270560	11697362	0.0753	0.3511
chrY	59373566	414704	0.007	0.2458

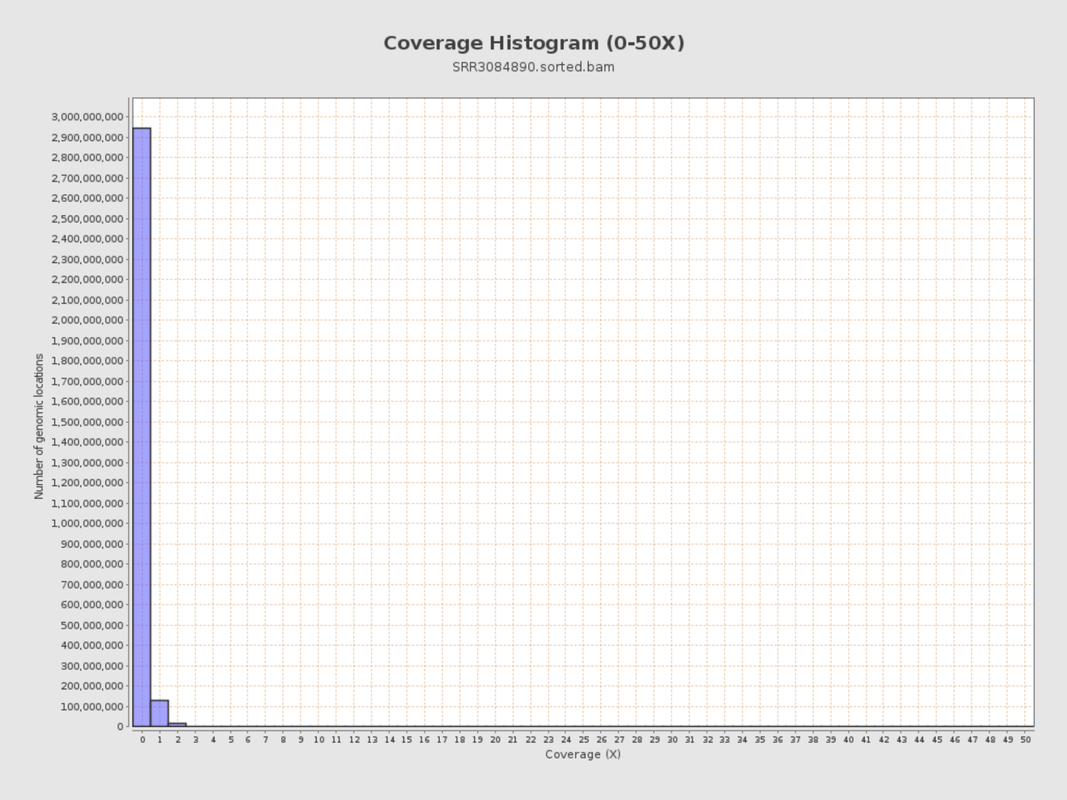
3. Results : Coverage across reference



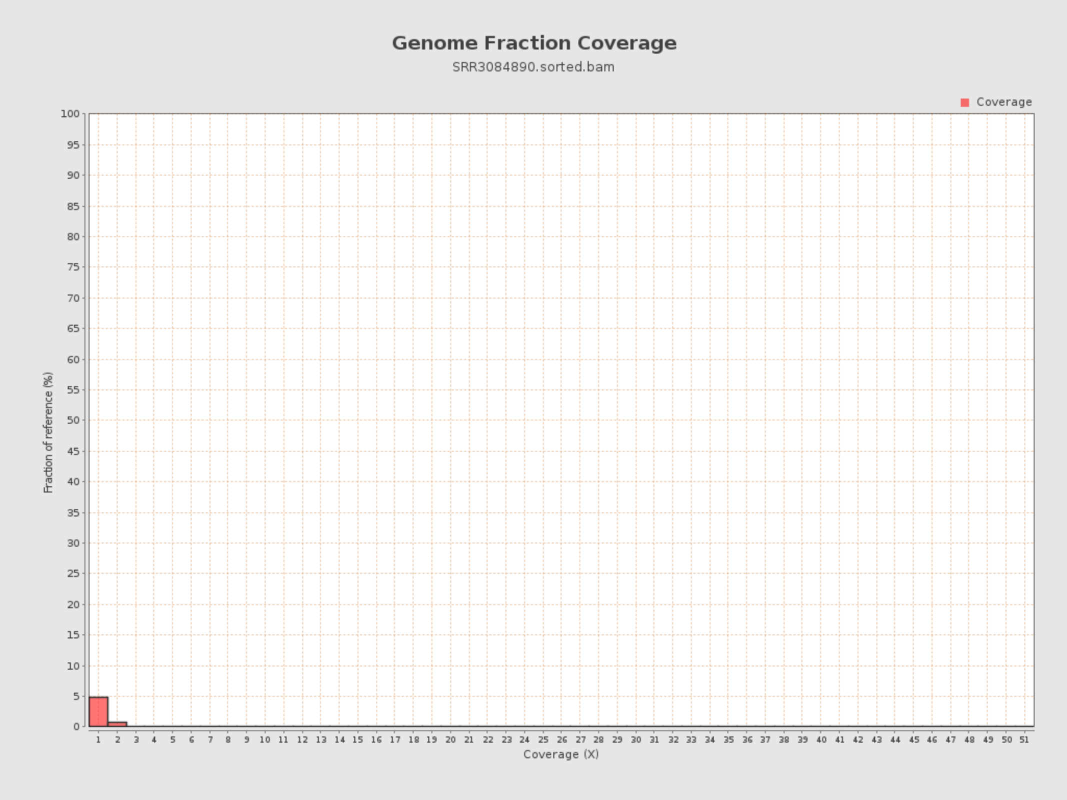
4. Results : Coverage Histogram



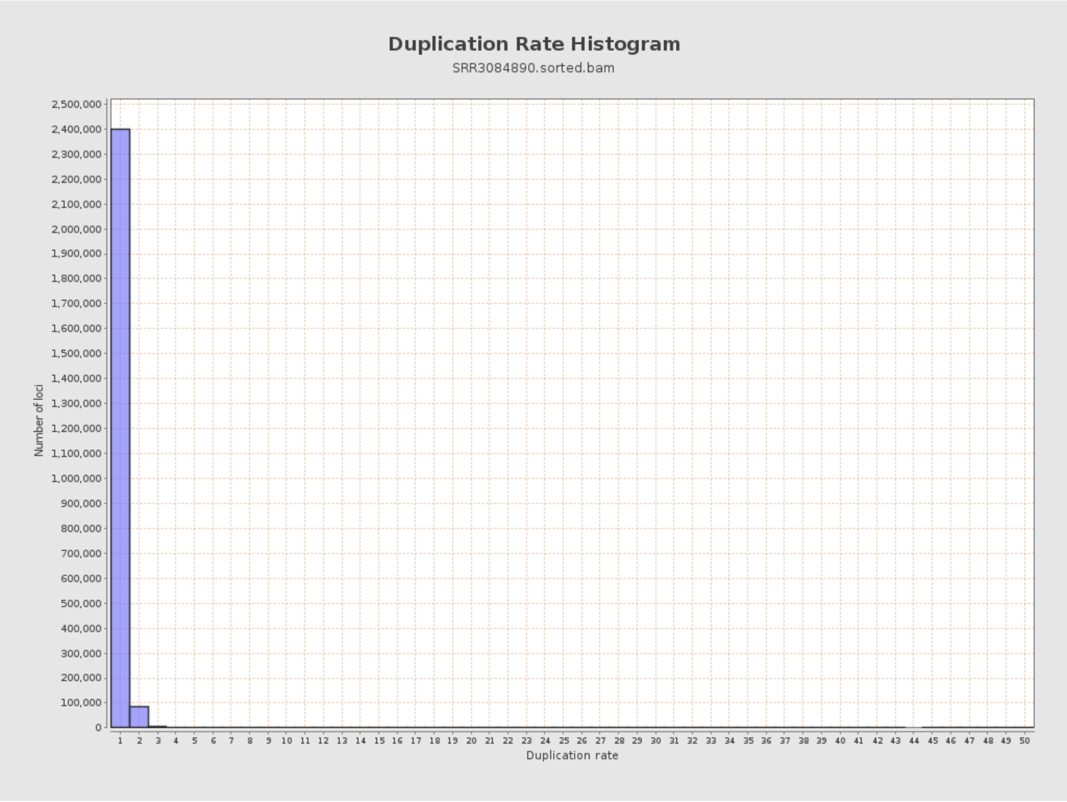
5. Results : Coverage Histogram (0-50X)



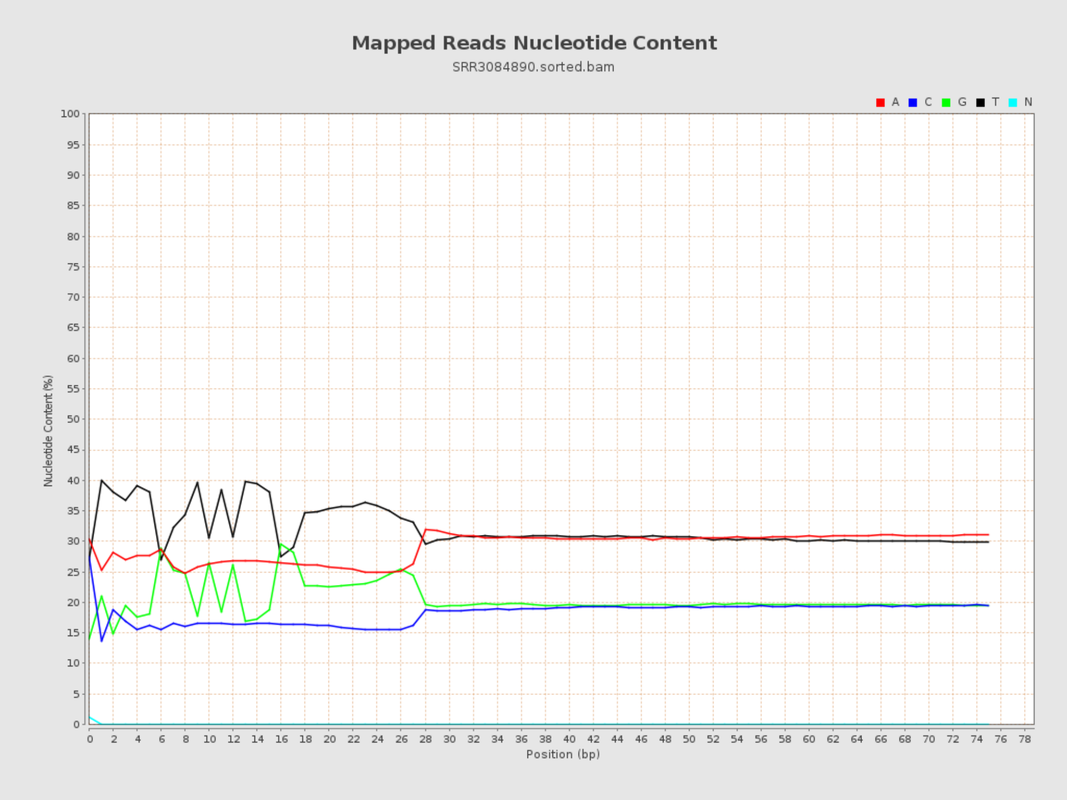
6. Results : Genome Fraction Coverage



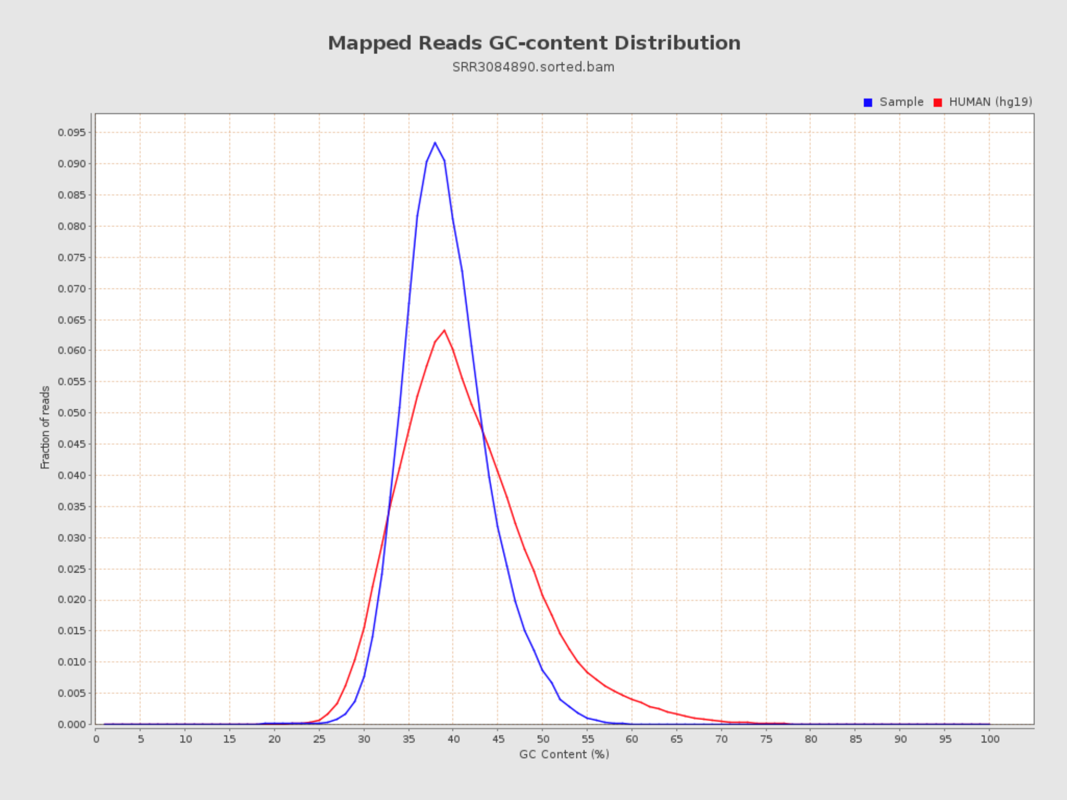
7. Results : Duplication Rate Histogram



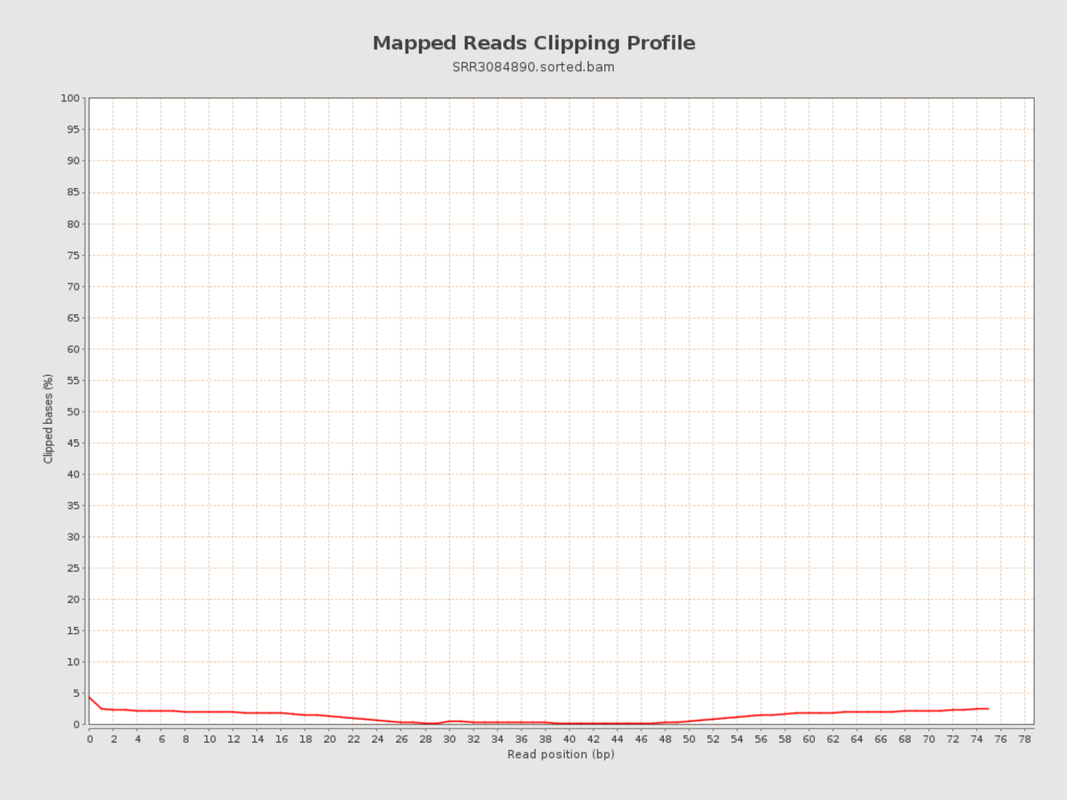
8. Results : Mapped Reads Nucleotide Content



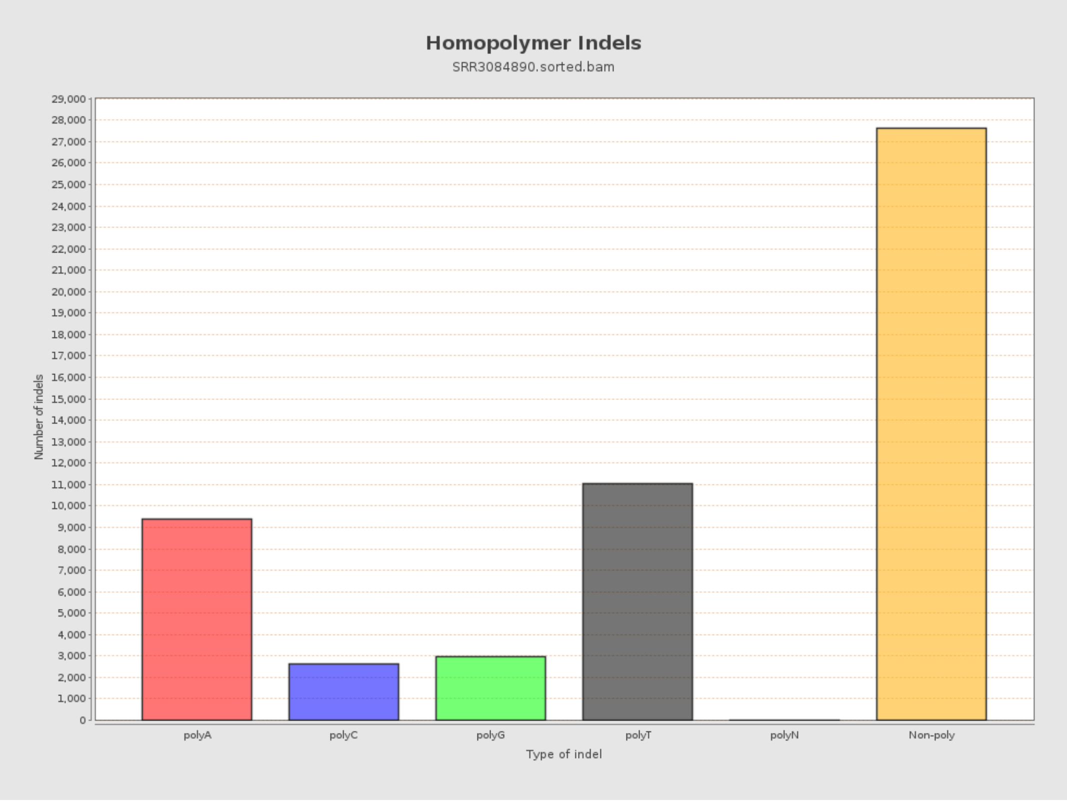
9. Results : Mapped Reads GC-content Distribution



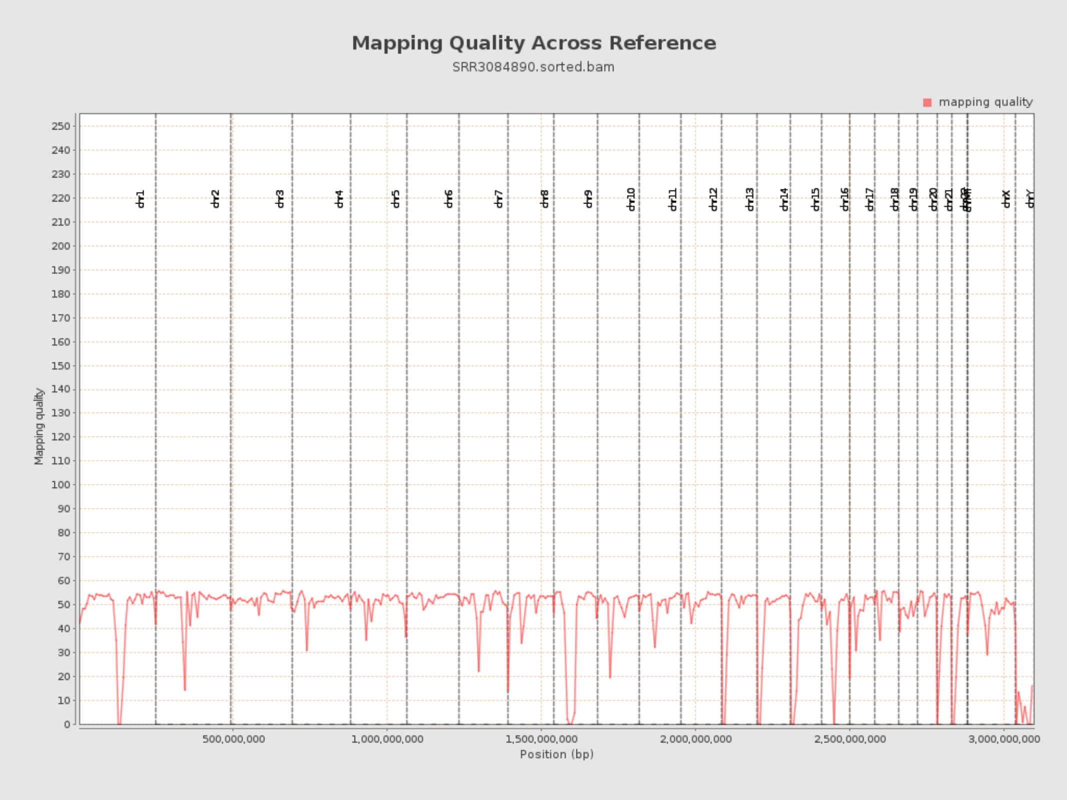
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram