Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:24:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084799.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_SRR3084799 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084799.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:24:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084799.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,350,420
Mapped reads	2,138,234 / 90.97%
Unmapped reads	212,186 / 9.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,156 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	96,763 / 4.12%
Duplication rate	3.84%
Clipped reads	960,028 / 40.84%

2.2. ACGT Content

Number/percentage of A's	38,474,605 / 26.98%
Number/percentage of C's	26,841,458 / 18.83%
Number/percentage of T's	44,609,856 / 31.29%
Number/percentage of G's	32,638,053 / 22.89%
Number/percentage of N's	20,106 / 0.01%
GC Percentage	41.72%

2.3. Coverage

Mean	0.0461

Standard Deviation	0.3265

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Mismatches and indels

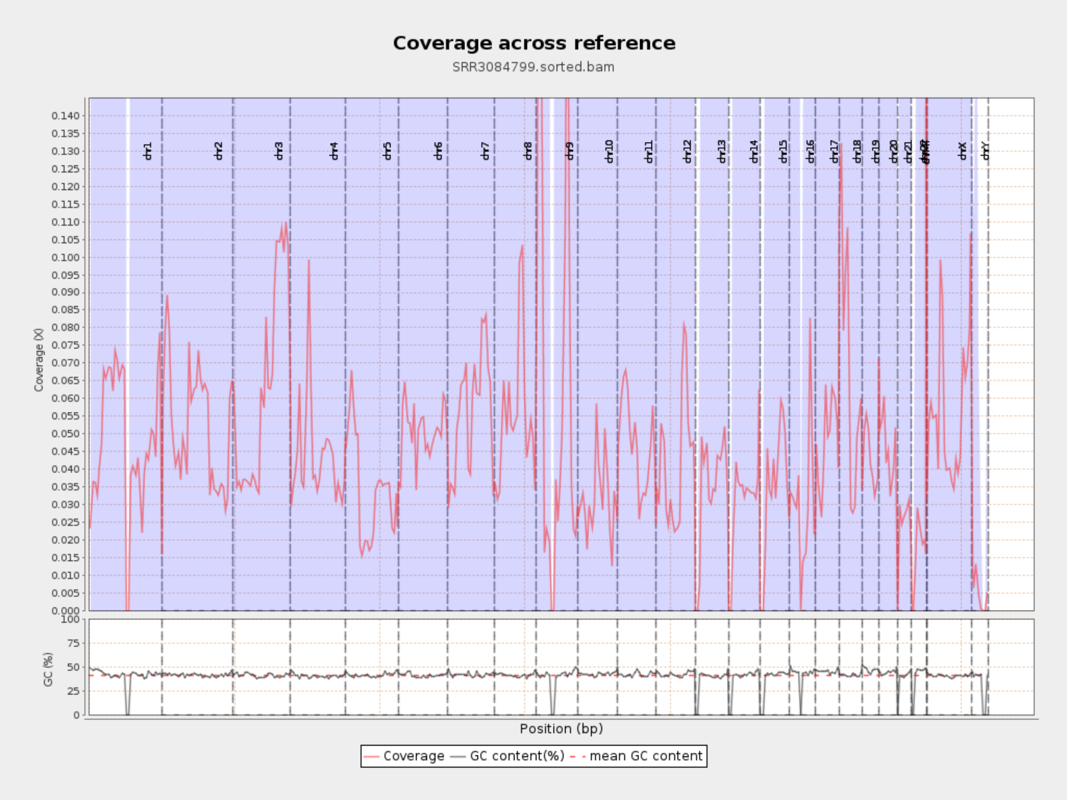
General error rate	0.78%
Mismatches	1,089,461
Insertions	11,408
Mapped reads with at least one insertion	0.53%
Deletions	32,872
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.42%

2.6. Chromosome stats

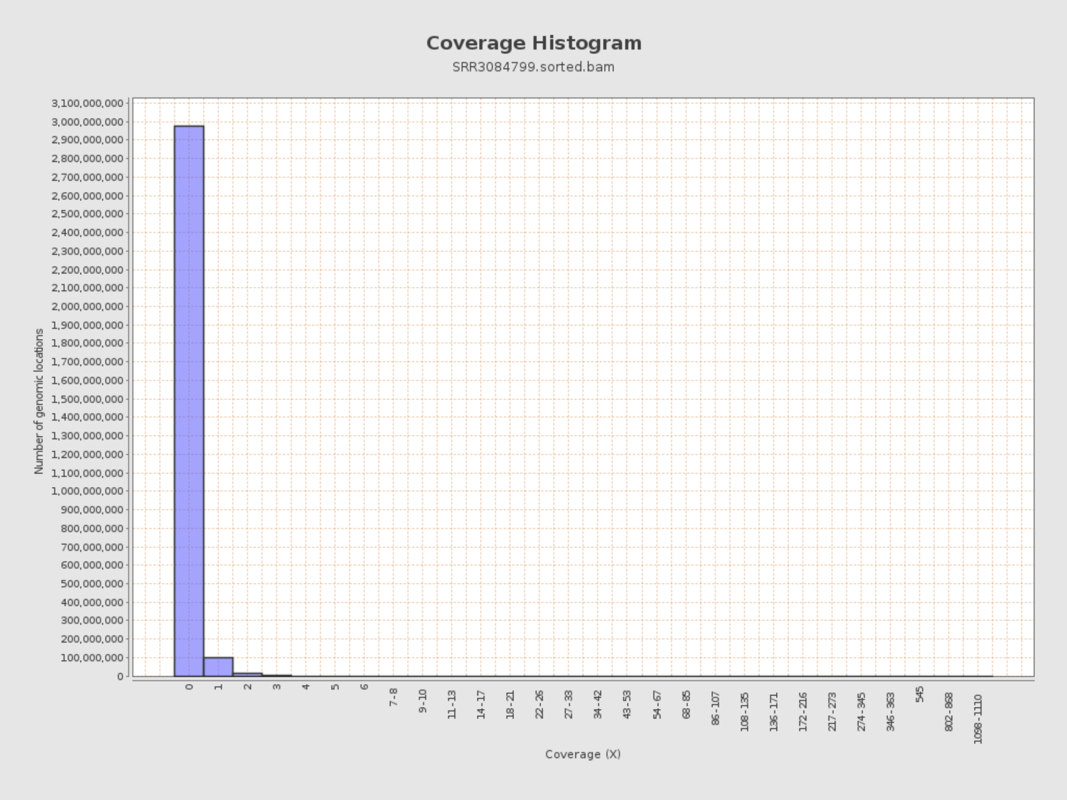
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11884643	0.0477	0.3972
chr2	243199373	12743603	0.0524	0.5705
chr3	198022430	12505365	0.0632	0.2932
chr4	191154276	8463886	0.0443	0.2489
chr5	180915260	6192611	0.0342	0.2144
chr6	171115067	8622737	0.0504	0.2854
chr7	159138663	9071437	0.057	0.4302

chr8	146364022	7976275	0.0545	0.32
chr9	141213431	9565676	0.0677	0.3728
chr10	135534747	4290199	0.0317	0.2228
chr11	135006516	6321460	0.0468	0.3033
chr12	133851895	5652653	0.0422	0.2404
chr13	115169878	3929757	0.0341	0.2167
chr14	107349540	3203400	0.0298	0.2076
chr15	102531392	3584426	0.035	0.2328
chr16	90354753	2806037	0.0311	0.2136
chr17	81195210	3950618	0.0487	0.2611
chr18	78077248	5377834	0.0689	0.4701
chr19	59128983	2624768	0.0444	0.3273
chr20	63025520	2892234	0.0459	0.2516
chr21	48129895	1179934	0.0245	0.1866
chr22	51304566	828882	0.0162	0.1447
chrMT	16571	16836	1.016	1.214
chrX	155270560	8661515	0.0558	0.2869
chrY	59373566	291388	0.0049	0.0998

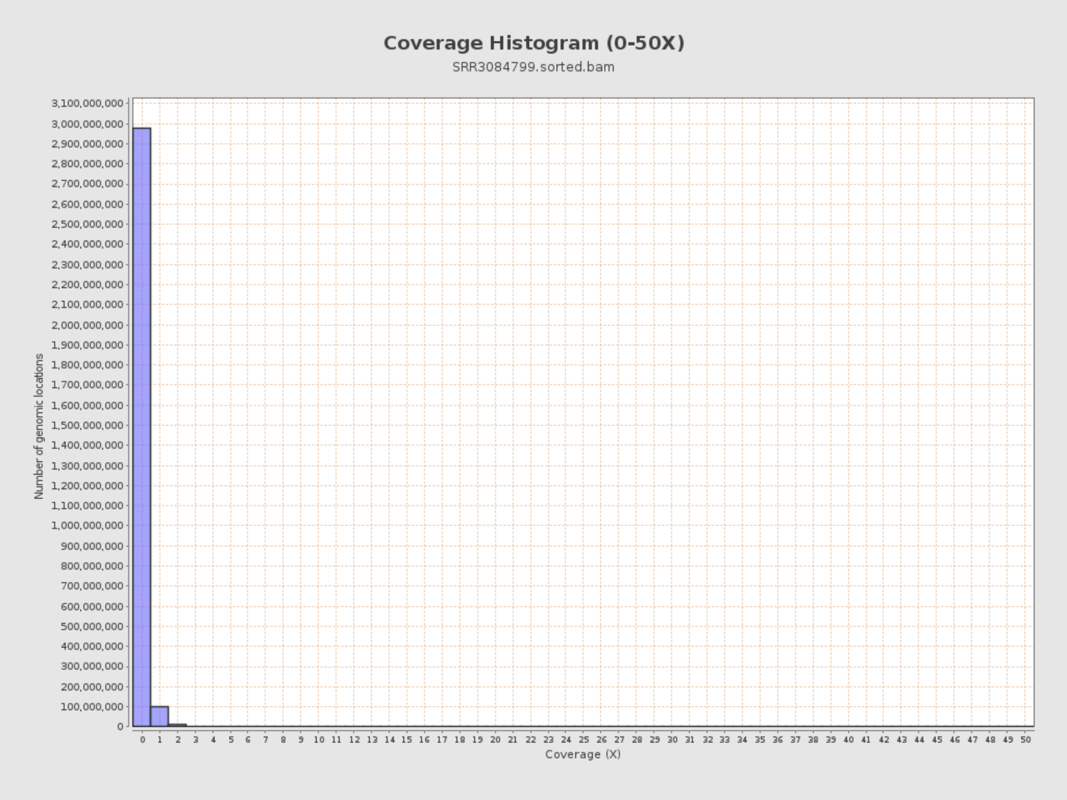
3. Results : Coverage across reference



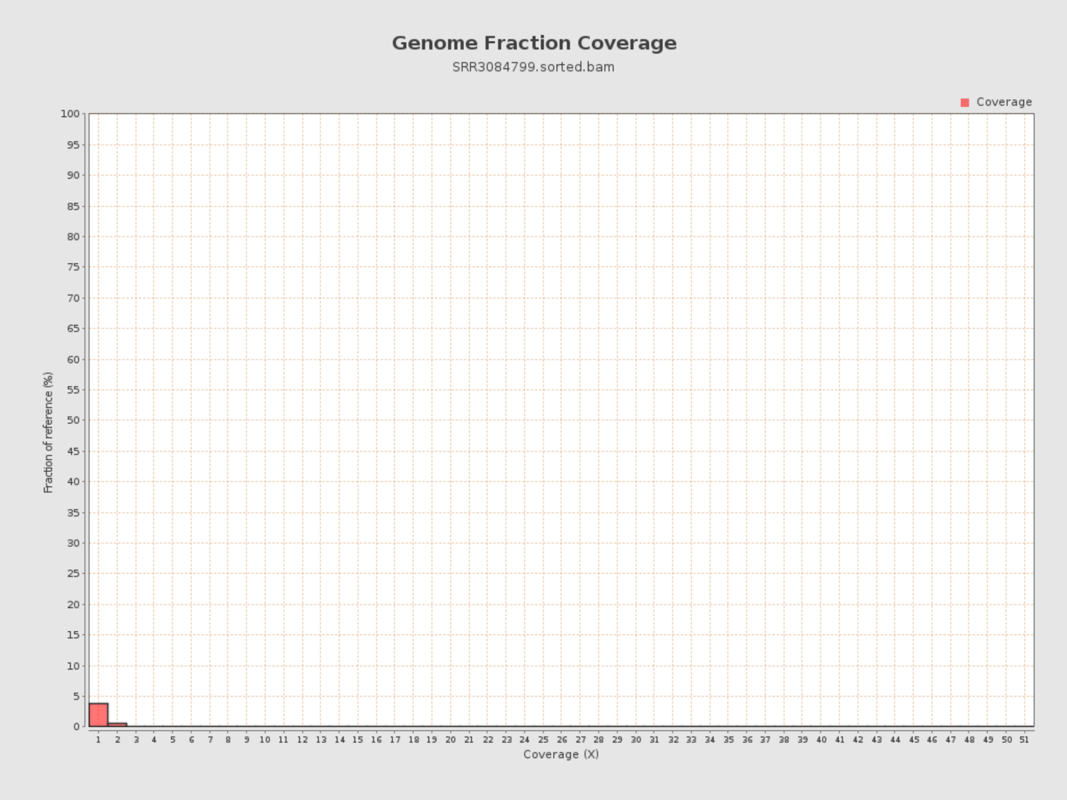
4. Results : Coverage Histogram



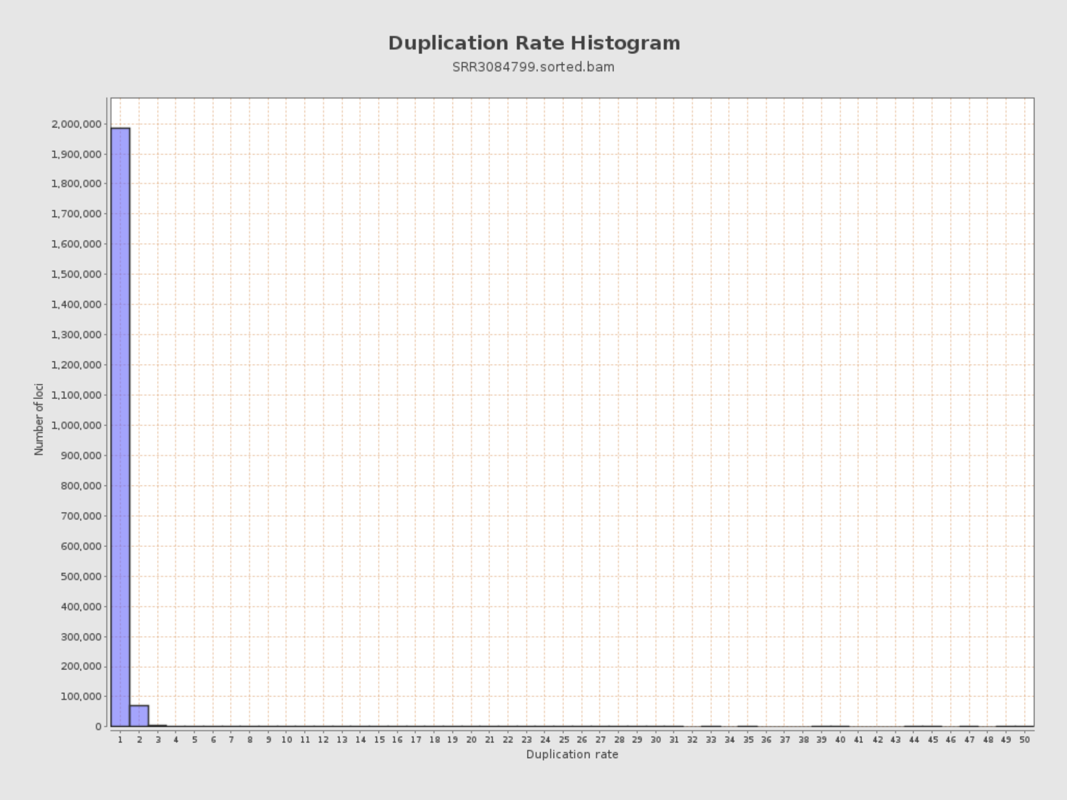
5. Results : Coverage Histogram (0-50X)



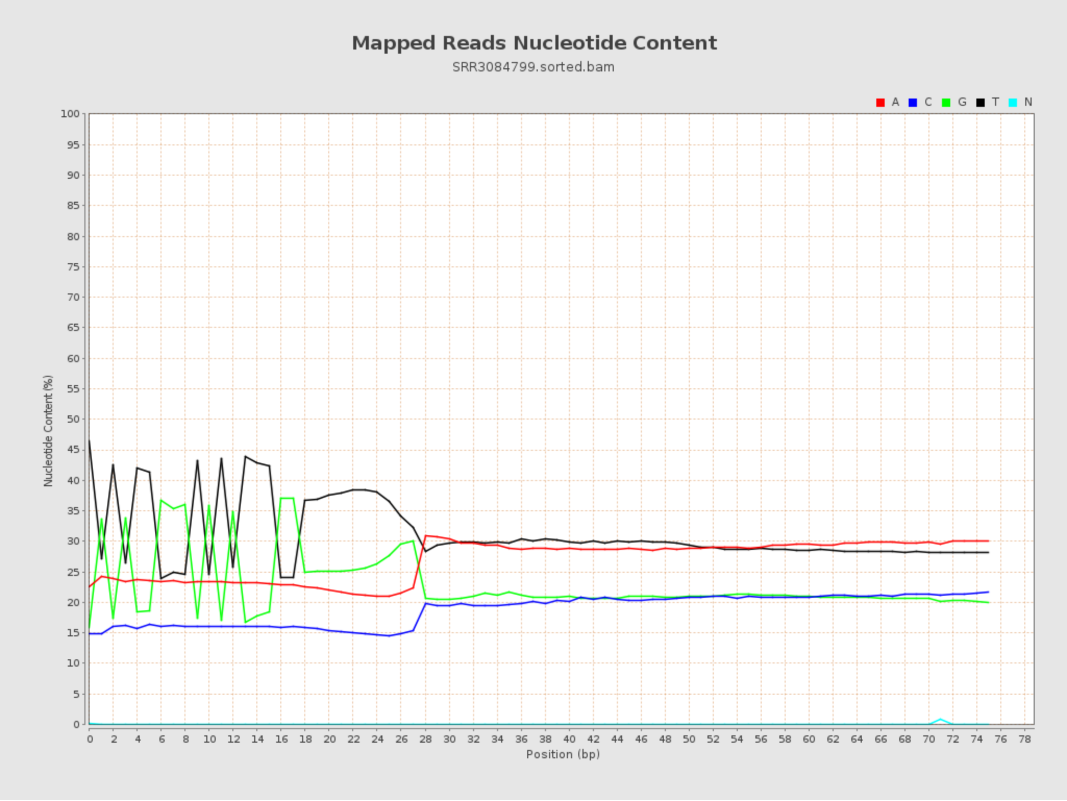
6. Results : Genome Fraction Coverage



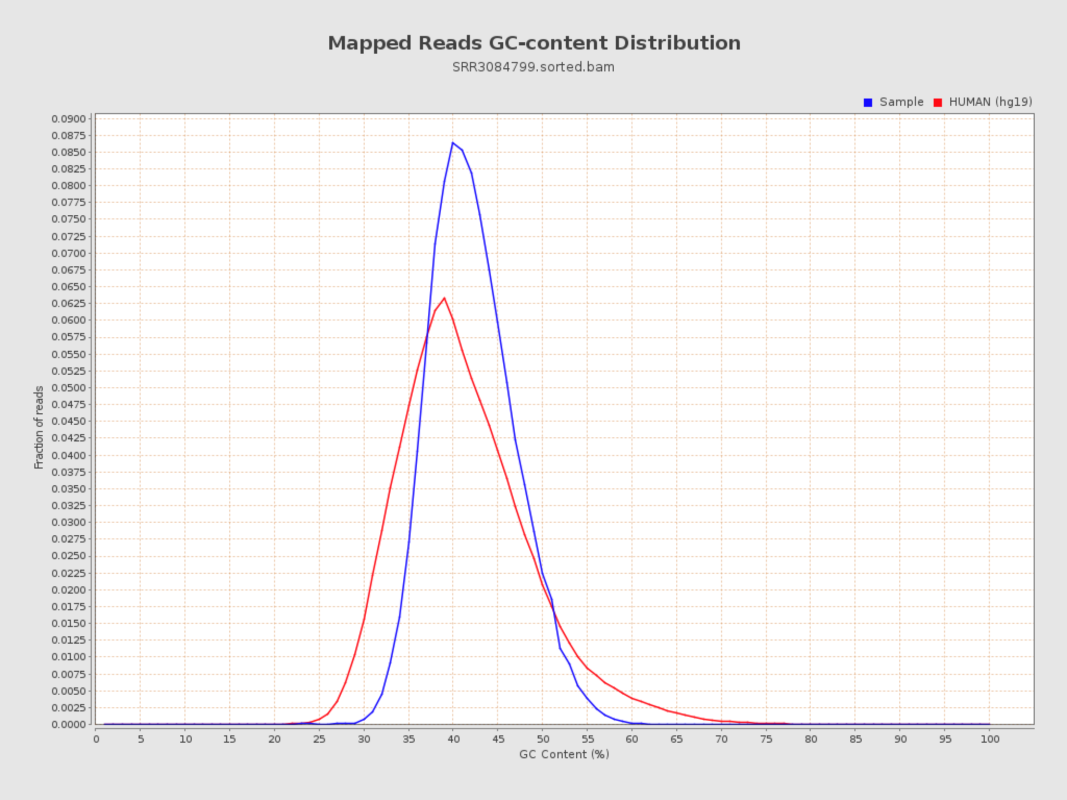
7. Results : Duplication Rate Histogram



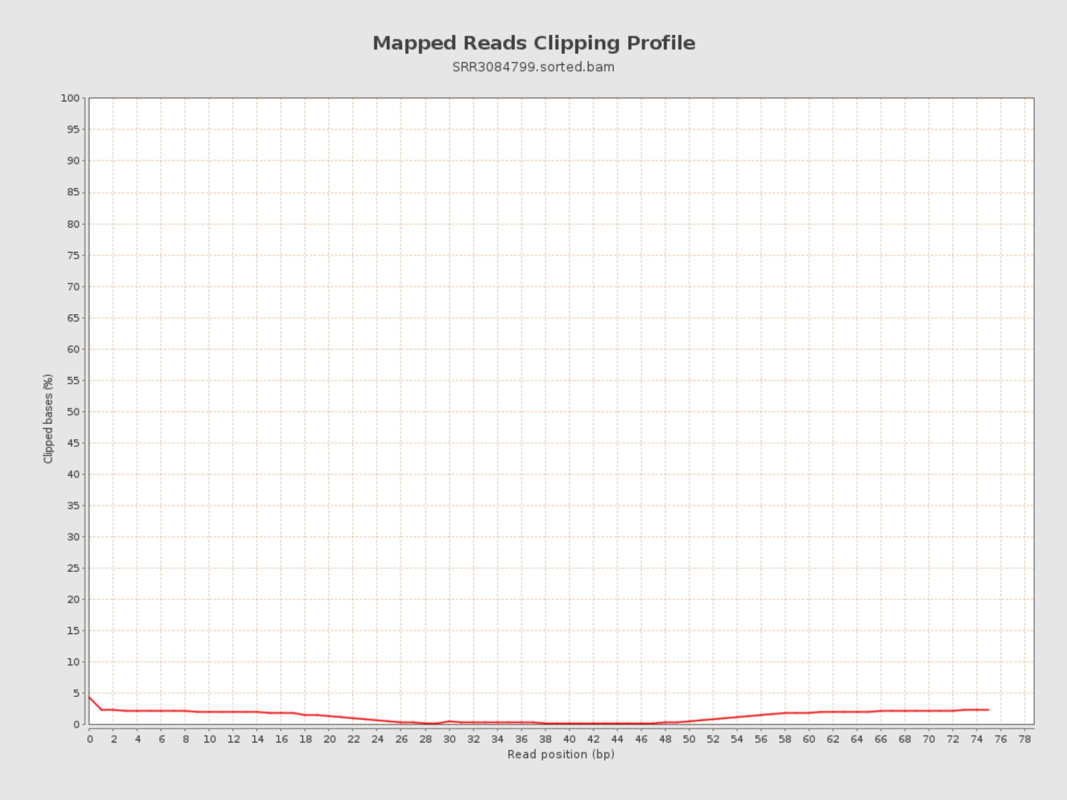
8. Results : Mapped Reads Nucleotide Content



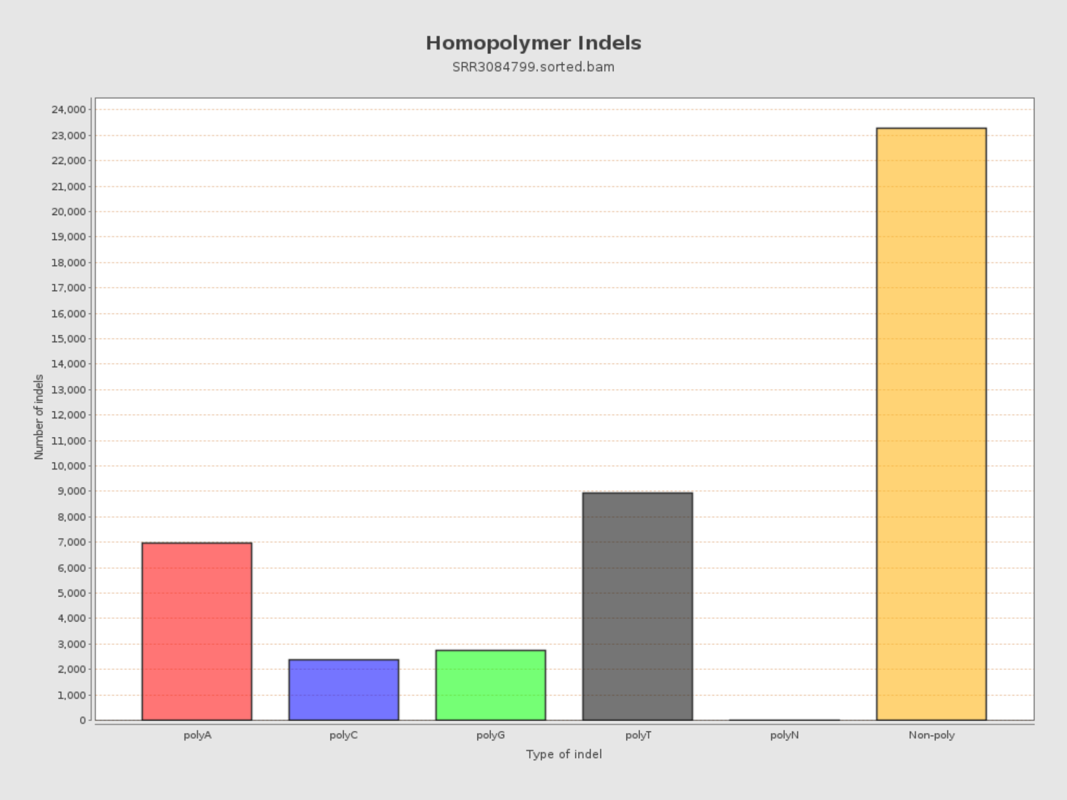
9. Results : Mapped Reads GC-content Distribution



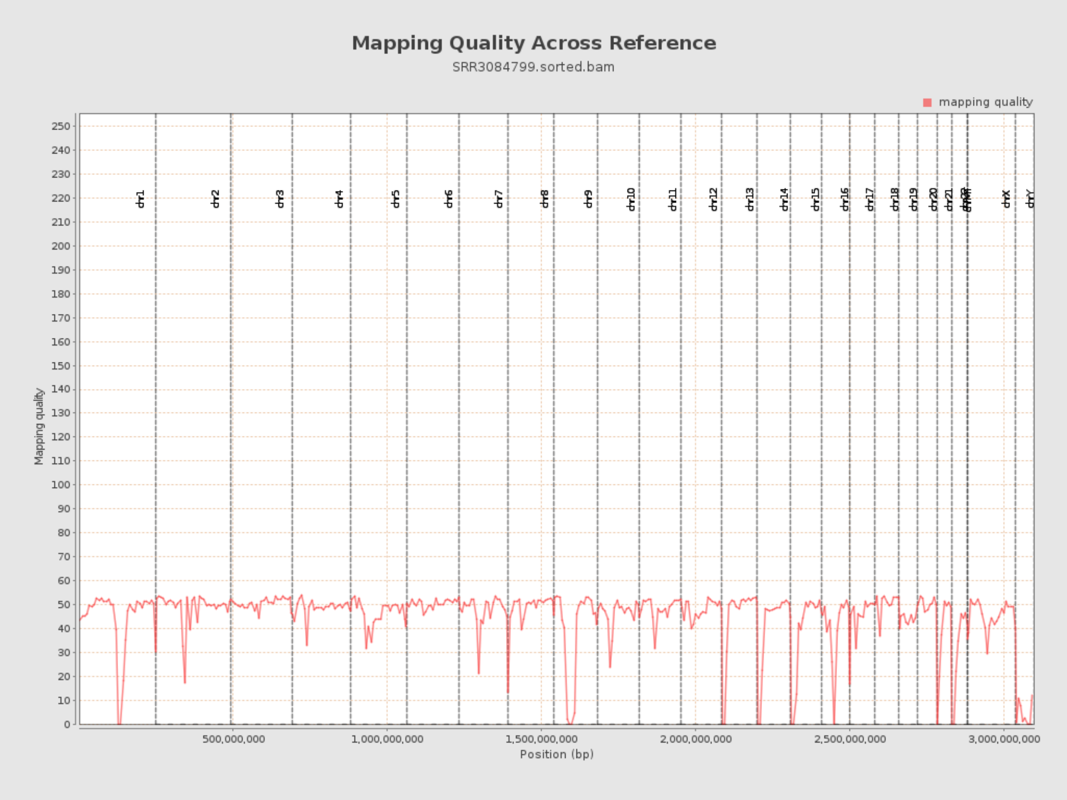
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram