Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 17:53:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084855.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_SRR3084855 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084855.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 17:53:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084855.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,494,702
Mapped reads	2,252,855 / 90.31%
Unmapped reads	241,847 / 9.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,772 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	120,892 / 4.85%
Duplication rate	4.62%
Clipped reads	733,893 / 29.42%

2.2. ACGT Content

Number/percentage of A's	45,769,118 / 29.15%
Number/percentage of C's	28,873,392 / 18.39%
Number/percentage of T's	50,529,960 / 32.18%
Number/percentage of G's	31,805,470 / 20.26%
Number/percentage of N's	25,518 / 0.02%
GC Percentage	38.65%

2.3. Coverage

Mean	0.0507

Standard Deviation	0.4087

2.4. Mapping Quality

Mean Mapping Quality	48.4

2.5. Mismatches and indels

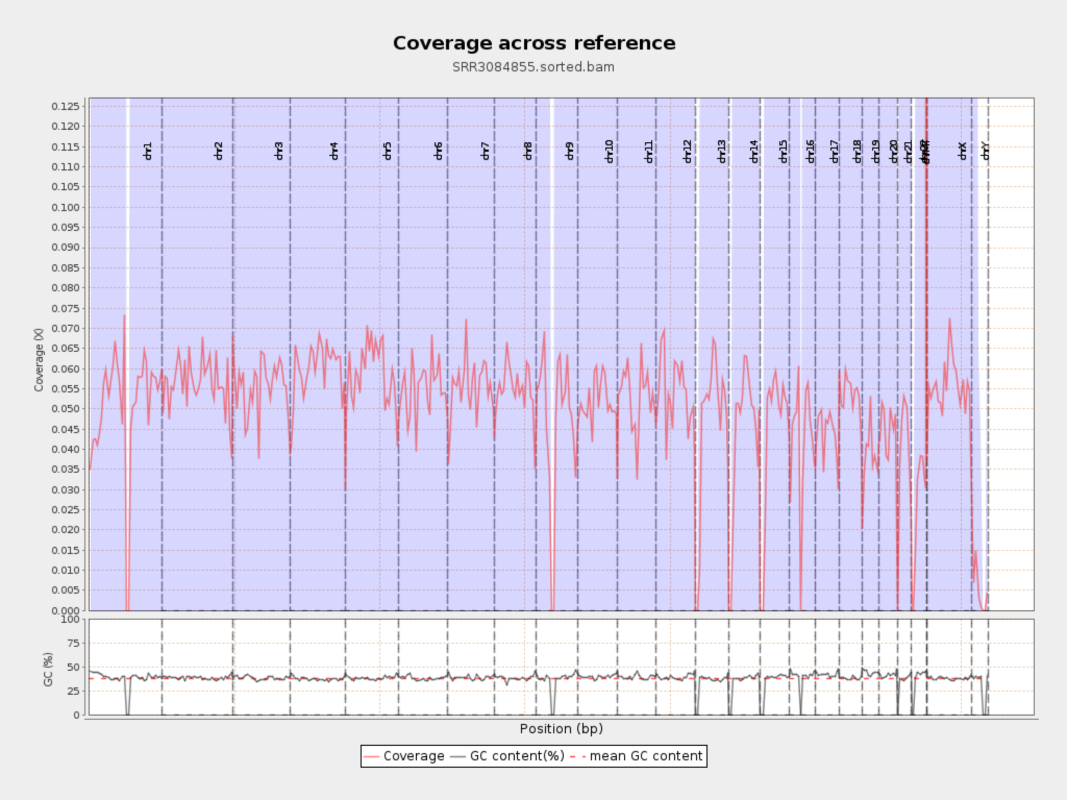
General error rate	0.82%
Mismatches	1,265,987
Insertions	12,445
Mapped reads with at least one insertion	0.55%
Deletions	34,025
Mapped reads with at least one deletion	1.49%
Homopolymer indels	48.6%

2.6. Chromosome stats

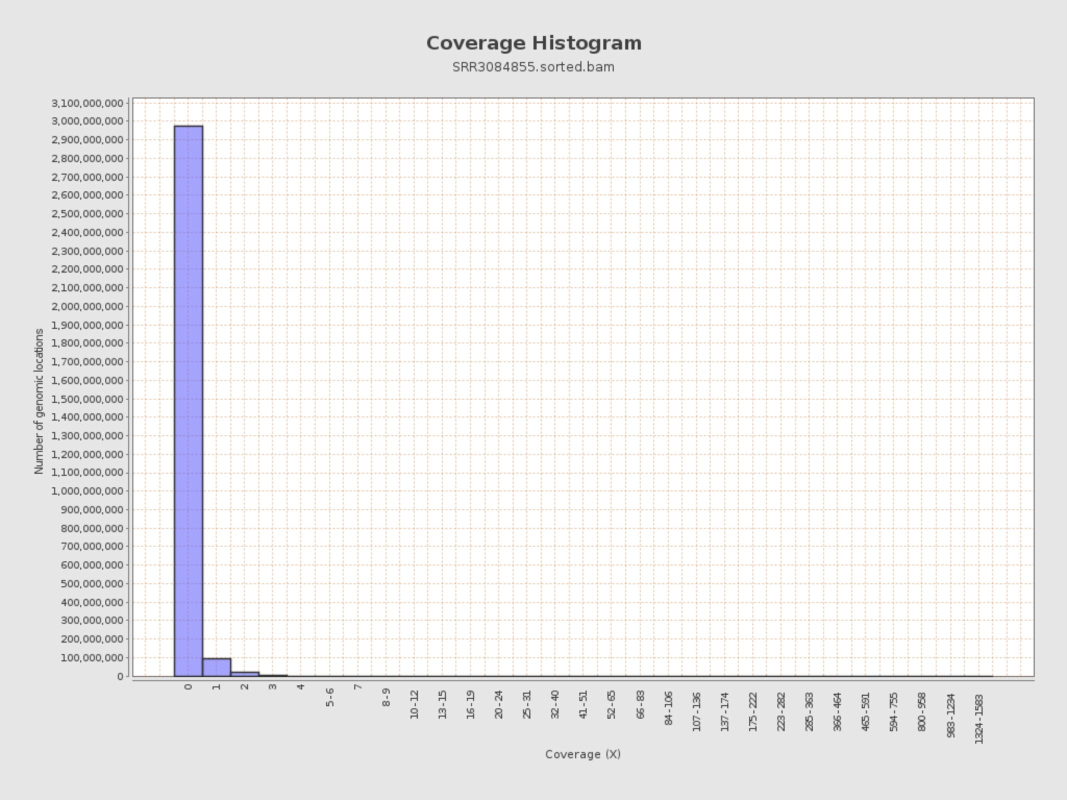
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12677246	0.0509	0.5992
chr2	243199373	13725179	0.0564	0.3449
chr3	198022430	11023319	0.0557	0.2929
chr4	191154276	11505568	0.0602	0.3109
chr5	180915260	10652897	0.0589	0.3031
chr6	171115067	9430612	0.0551	0.2955
chr7	159138663	8877398	0.0558	0.3842

chr8	146364022	8038945	0.0549	1.0545
chr9	141213431	6606971	0.0468	0.3174
chr10	135534747	7070326	0.0522	0.3268
chr11	135006516	7125953	0.0528	0.3103
chr12	133851895	7215381	0.0539	0.2889
chr13	115169878	5265748	0.0457	0.2659
chr14	107349540	4602428	0.0429	0.2666
chr15	102531392	4448876	0.0434	0.2569
chr16	90354753	3823197	0.0423	0.2678
chr17	81195210	3535096	0.0435	0.2686
chr18	78077248	4197747	0.0538	0.5377
chr19	59128983	2299244	0.0389	0.4096
chr20	63025520	2798753	0.0444	0.2656
chr21	48129895	1855533	0.0386	0.2516
chr22	51304566	1264410	0.0246	0.1899
chrMT	16571	103651	6.255	3.856
chrX	155270560	8595976	0.0554	0.2996
chrY	59373566	322817	0.0054	0.1087

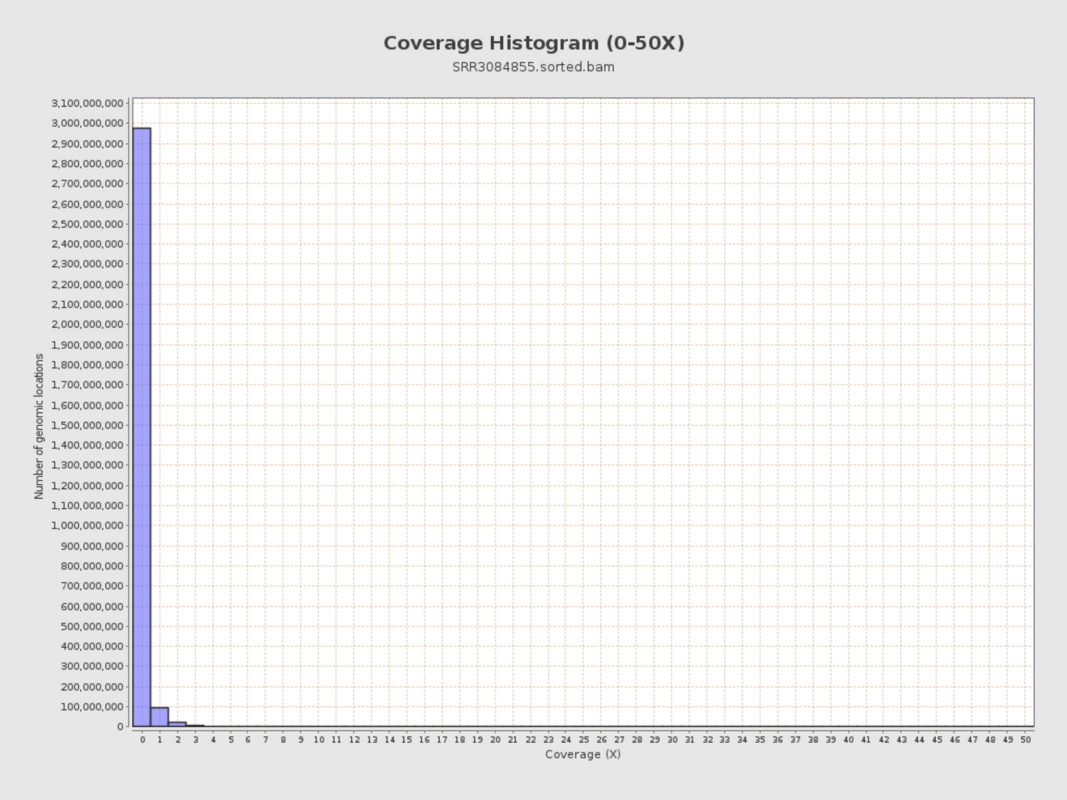
3. Results : Coverage across reference



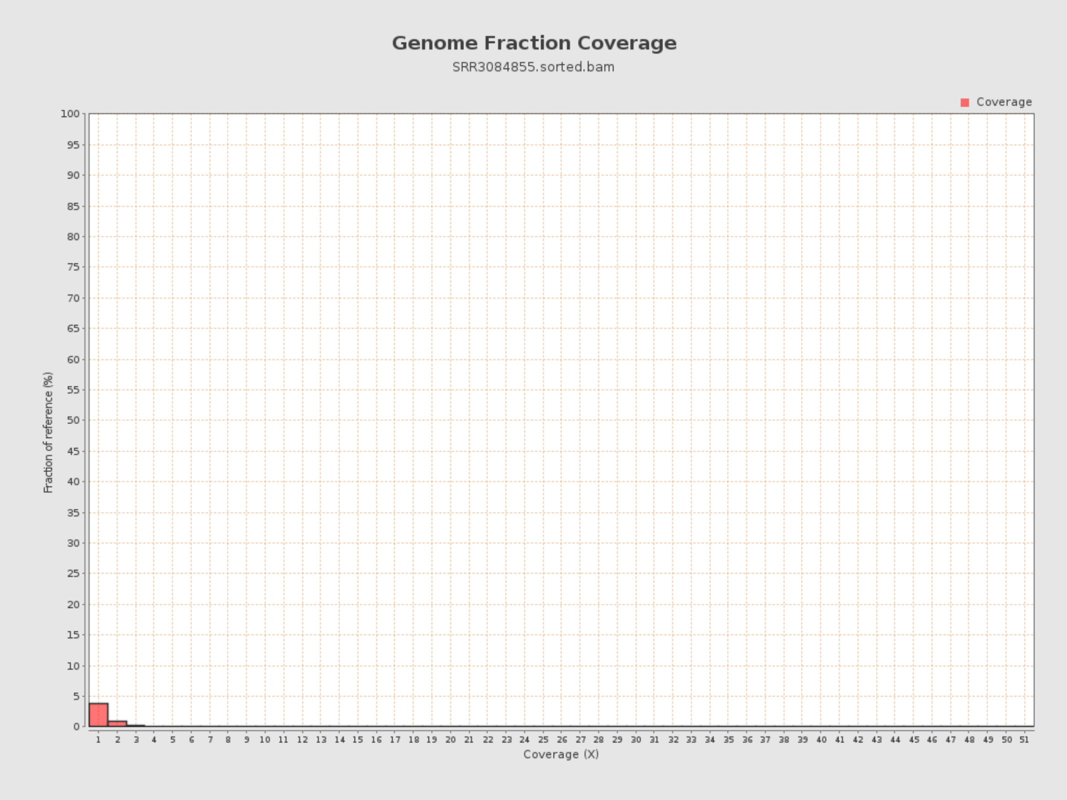
4. Results : Coverage Histogram



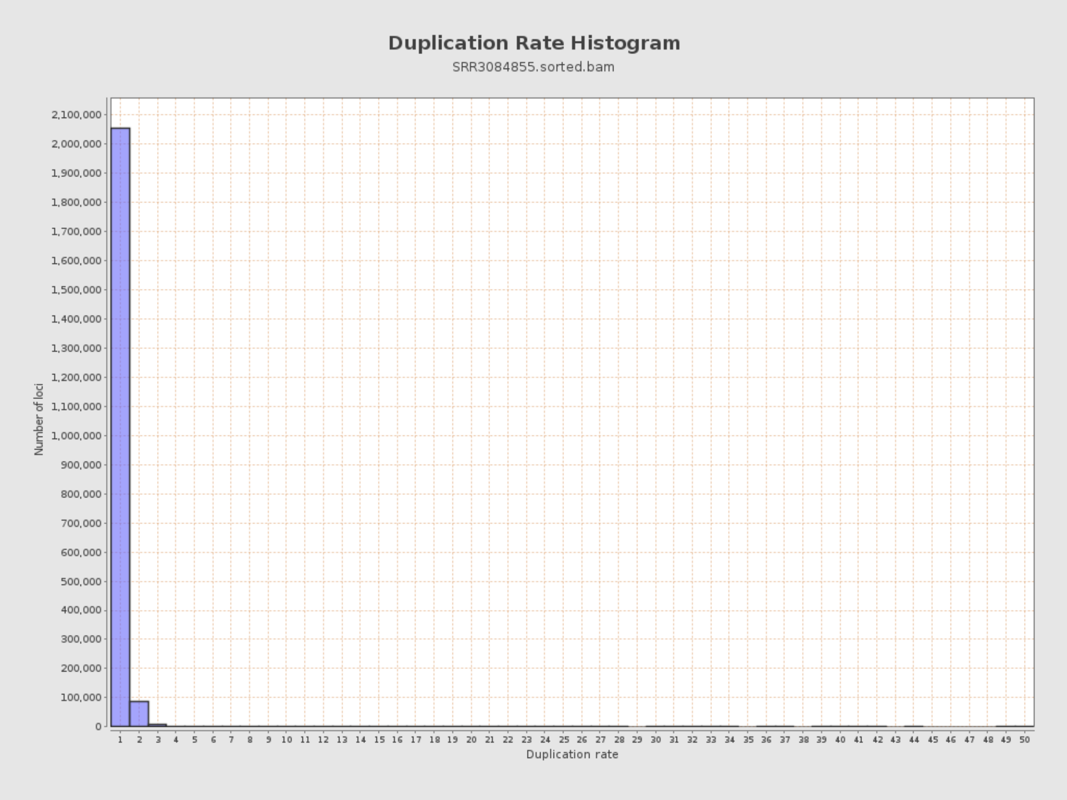
5. Results : Coverage Histogram (0-50X)



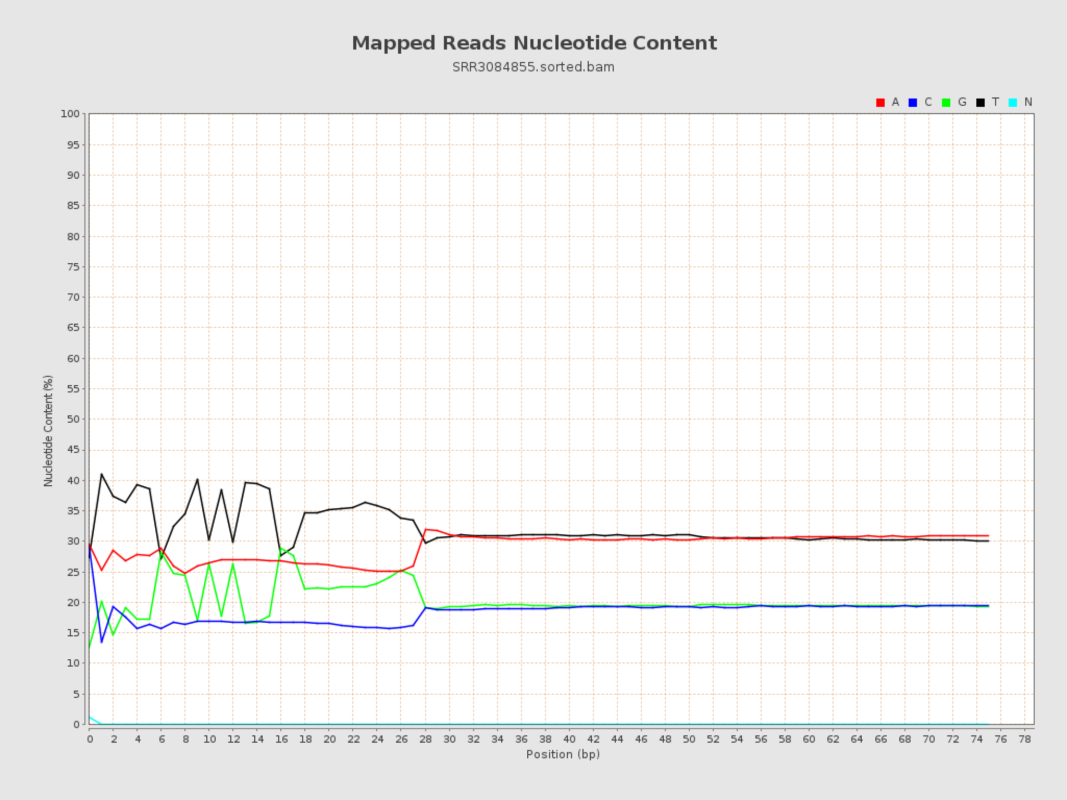
6. Results : Genome Fraction Coverage



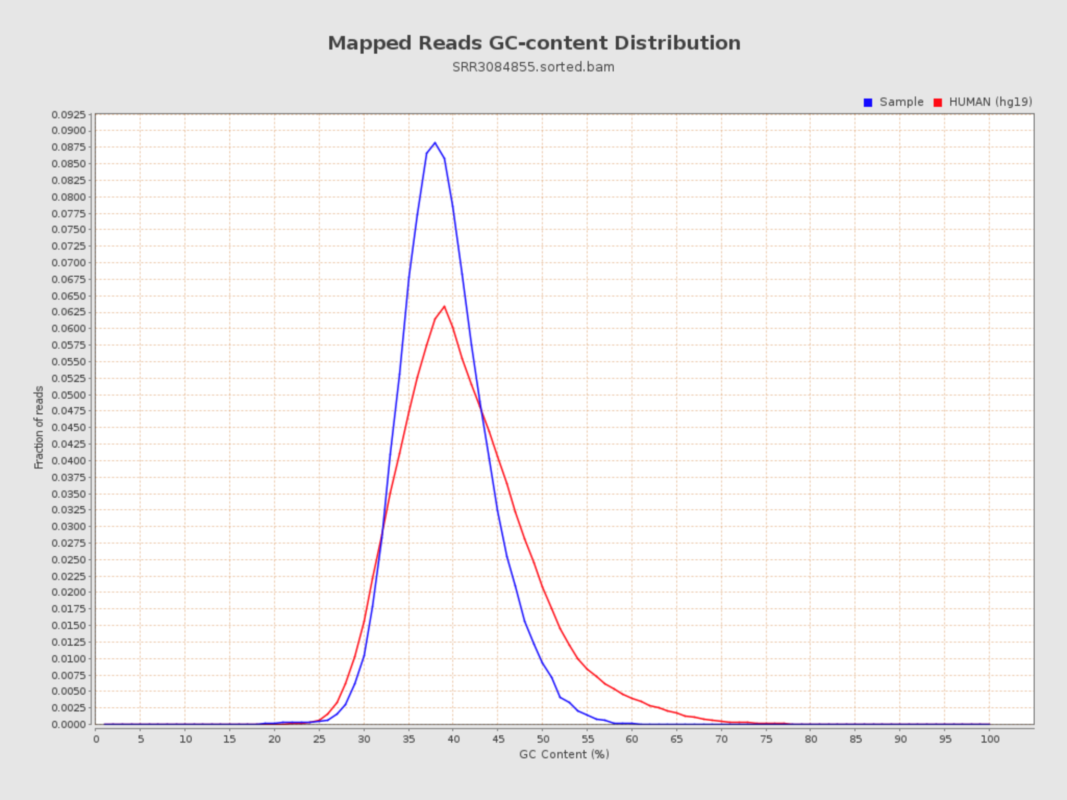
7. Results : Duplication Rate Histogram



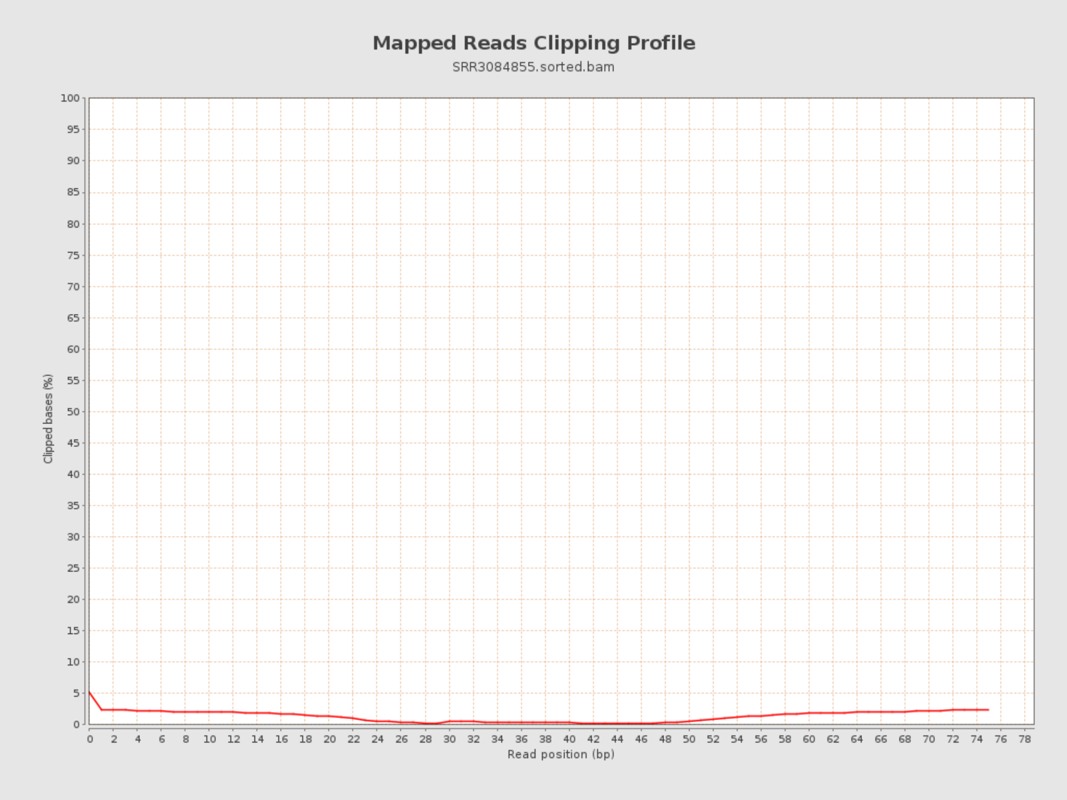
8. Results : Mapped Reads Nucleotide Content



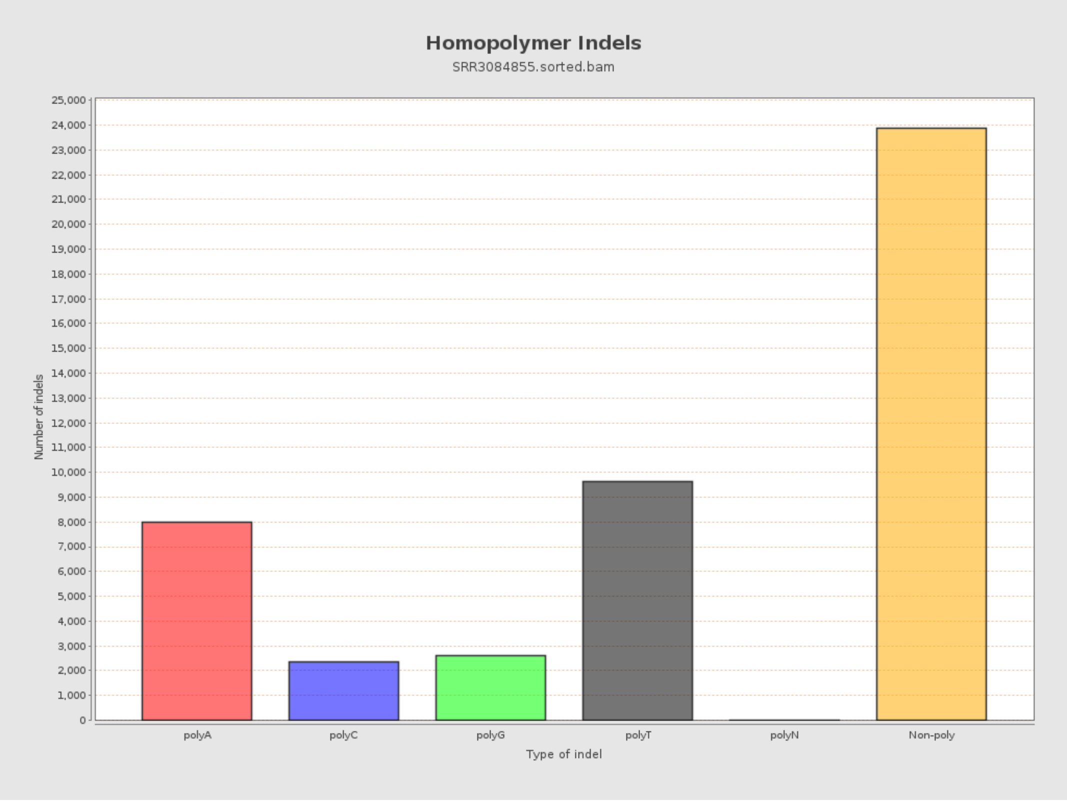
9. Results : Mapped Reads GC-content Distribution



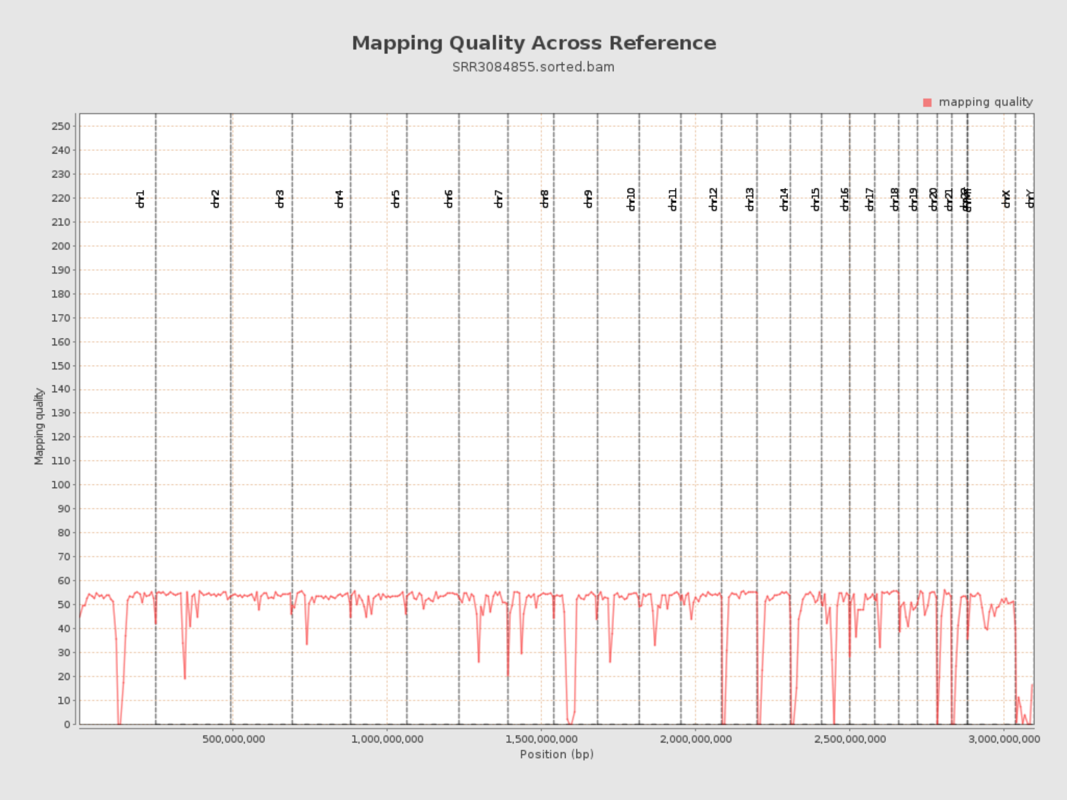
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram