Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:09:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084344.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_SRR3084344 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084344.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:09:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084344.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,910,641
Mapped reads	2,631,222 / 90.4%
Unmapped reads	279,419 / 9.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,210 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	99,390 / 3.41%
Duplication rate	3.23%
Clipped reads	1,203,005 / 41.33%

2.2. ACGT Content

Number/percentage of A's	49,373,374 / 28.11%
Number/percentage of C's	33,919,648 / 19.31%
Number/percentage of T's	53,862,170 / 30.66%
Number/percentage of G's	38,287,575 / 21.79%
Number/percentage of N's	229,216 / 0.13%
GC Percentage	41.1%

2.3. Coverage

Mean	0.0568

Standard Deviation	0.3503

2.4. Mapping Quality

Mean Mapping Quality	46.14

2.5. Mismatches and indels

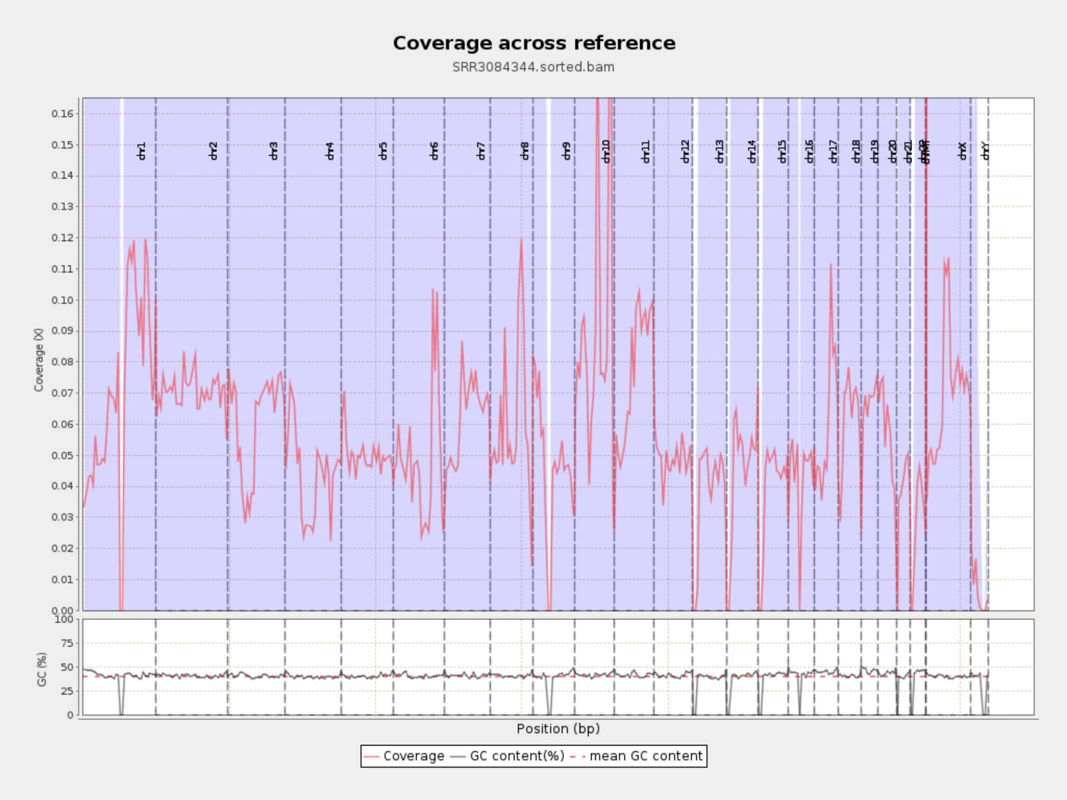
General error rate	1.02%
Mismatches	1,774,797
Insertions	11,911
Mapped reads with at least one insertion	0.45%
Deletions	36,176
Mapped reads with at least one deletion	1.36%
Homopolymer indels	47.35%

2.6. Chromosome stats

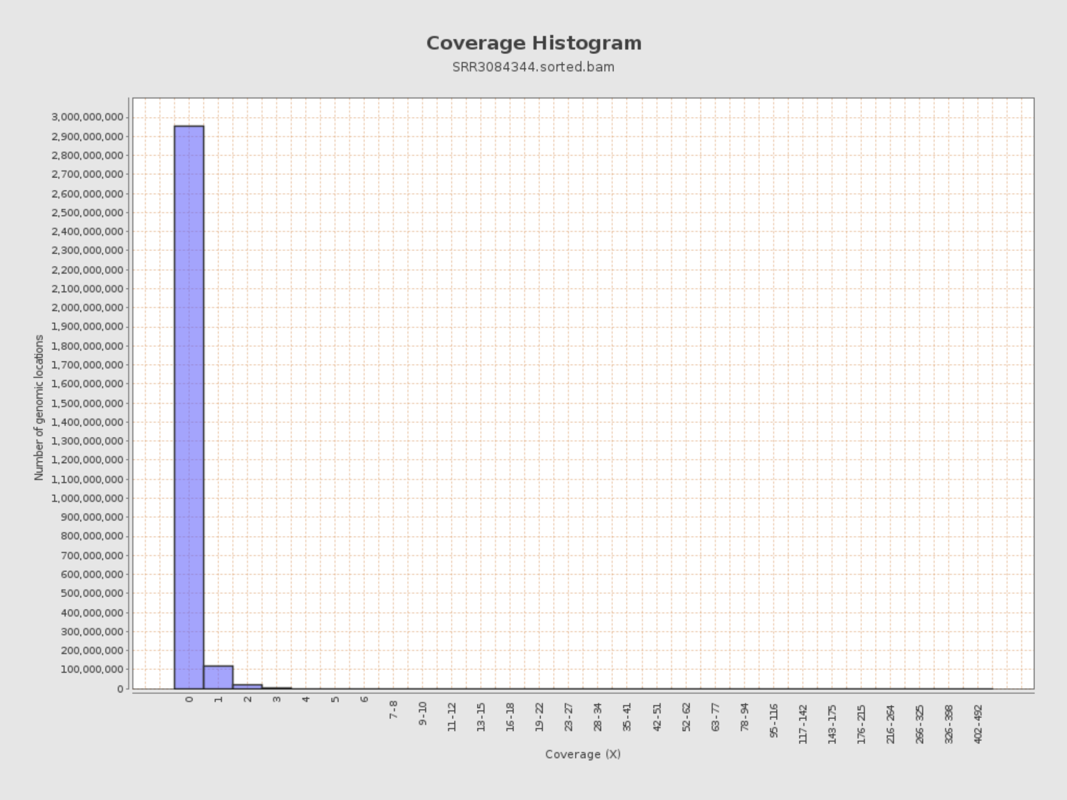
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17426337	0.0699	0.5259
chr2	243199373	17234005	0.0709	0.4026
chr3	198022430	12007545	0.0606	0.2911
chr4	191154276	8371407	0.0438	0.2532
chr5	180915260	9071014	0.0501	0.2613
chr6	171115067	8443005	0.0493	0.2886
chr7	159138663	9935182	0.0624	0.4887

chr8	146364022	8729937	0.0596	0.3621
chr9	141213431	6485135	0.0459	0.3036
chr10	135534747	12555427	0.0926	0.4491
chr11	135006516	10271537	0.0761	0.3812
chr12	133851895	6526723	0.0488	0.2589
chr13	115169878	4352239	0.0378	0.2264
chr14	107349540	4768691	0.0444	0.2559
chr15	102531392	3886489	0.0379	0.233
chr16	90354753	3802879	0.0421	0.2591
chr17	81195210	4974888	0.0613	0.3136
chr18	78077248	4790948	0.0614	0.4851
chr19	59128983	3913264	0.0662	0.4041
chr20	63025520	3605370	0.0572	0.2835
chr21	48129895	1846653	0.0384	0.2402
chr22	51304566	1423567	0.0277	0.1939
chrMT	16571	33061	1.9951	1.8758
chrX	155270560	10918457	0.0703	0.3381
chrY	59373566	361454	0.0061	0.1191

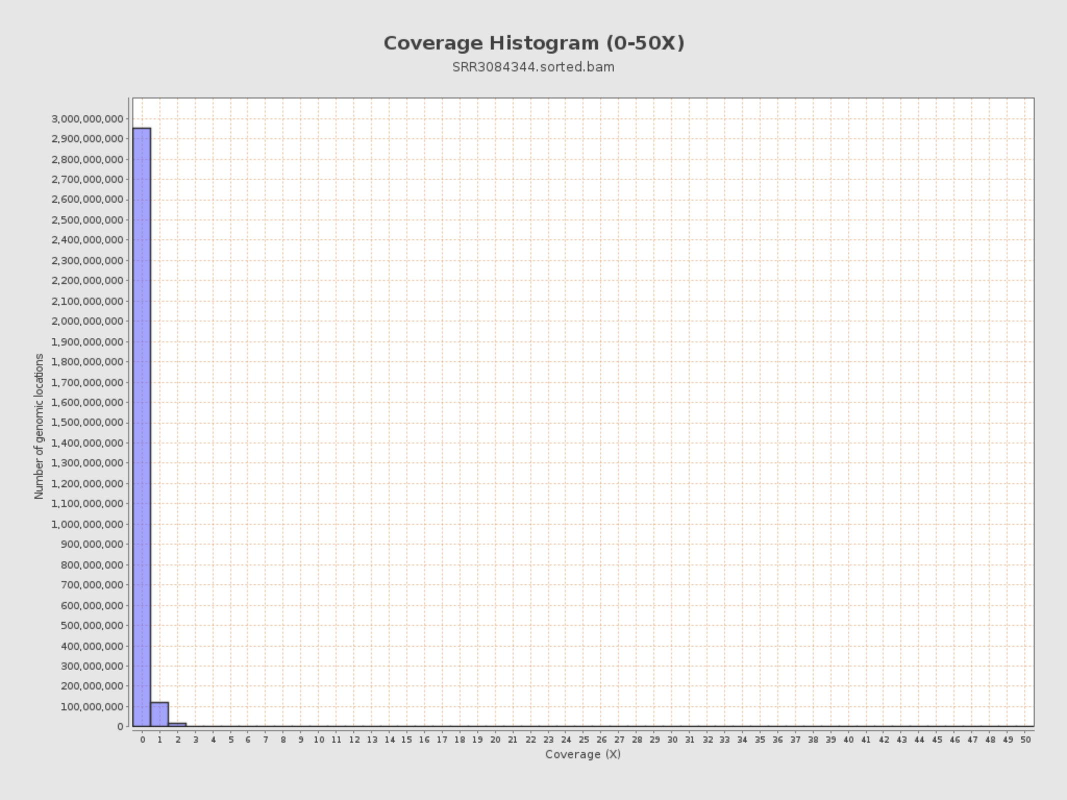
3. Results : Coverage across reference



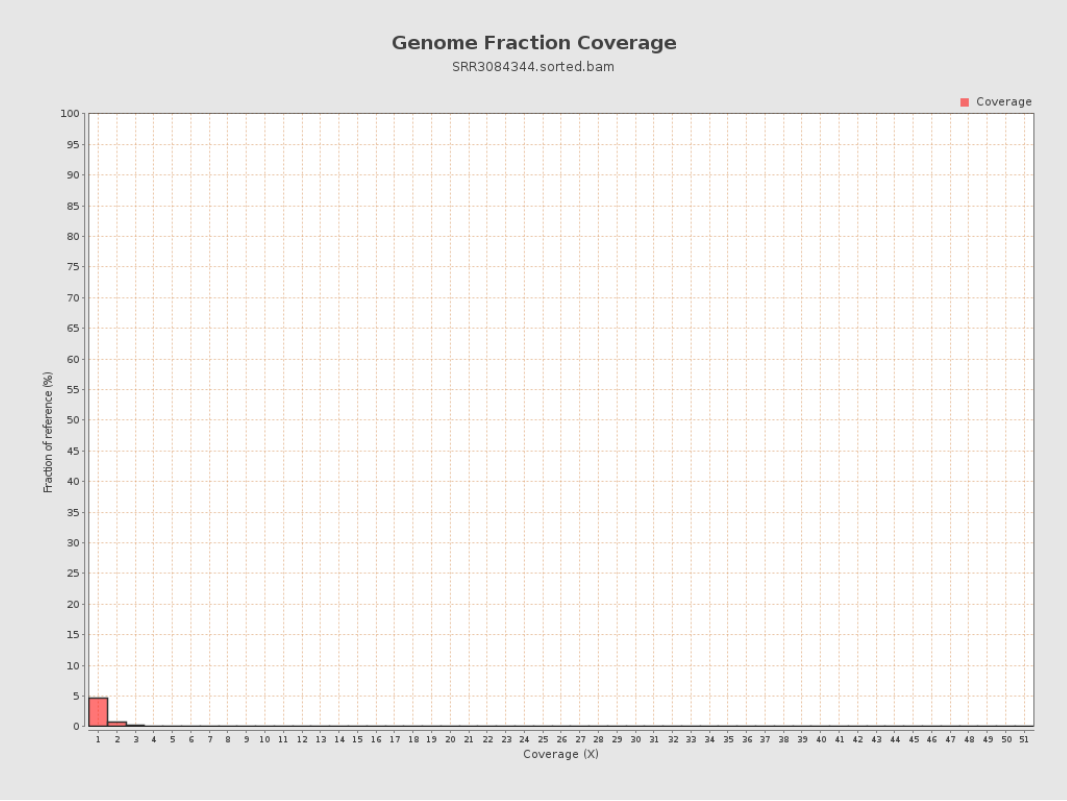
4. Results : Coverage Histogram



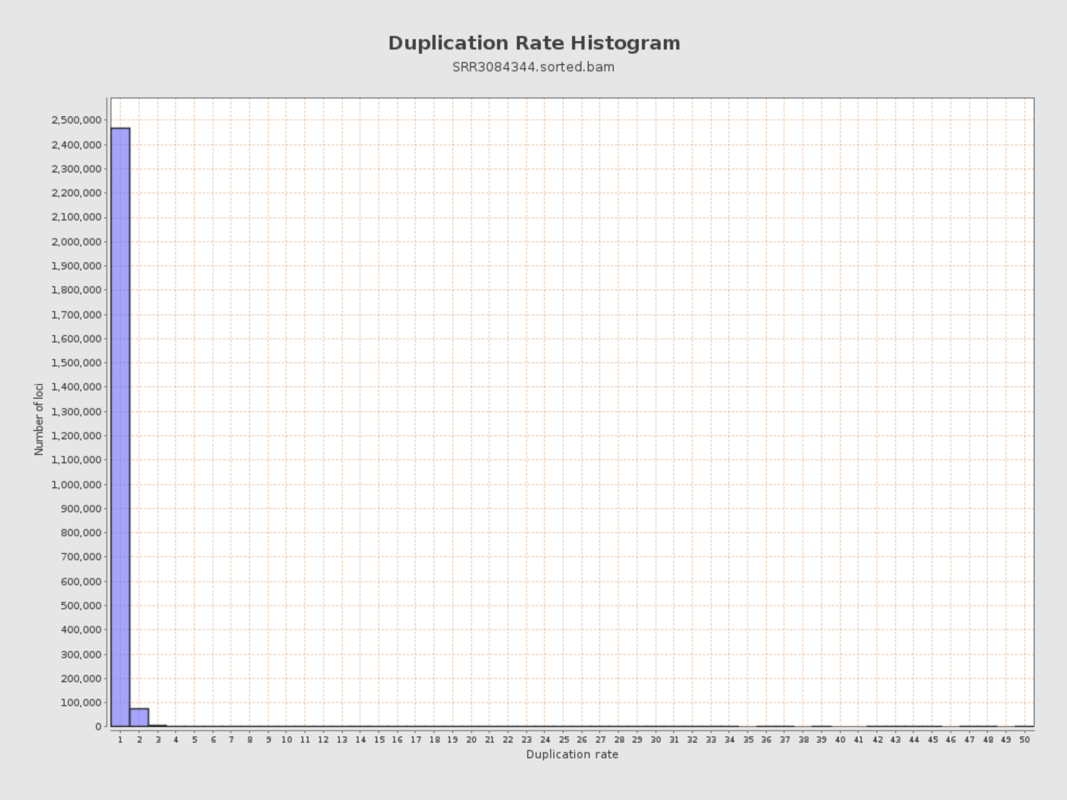
5. Results : Coverage Histogram (0-50X)



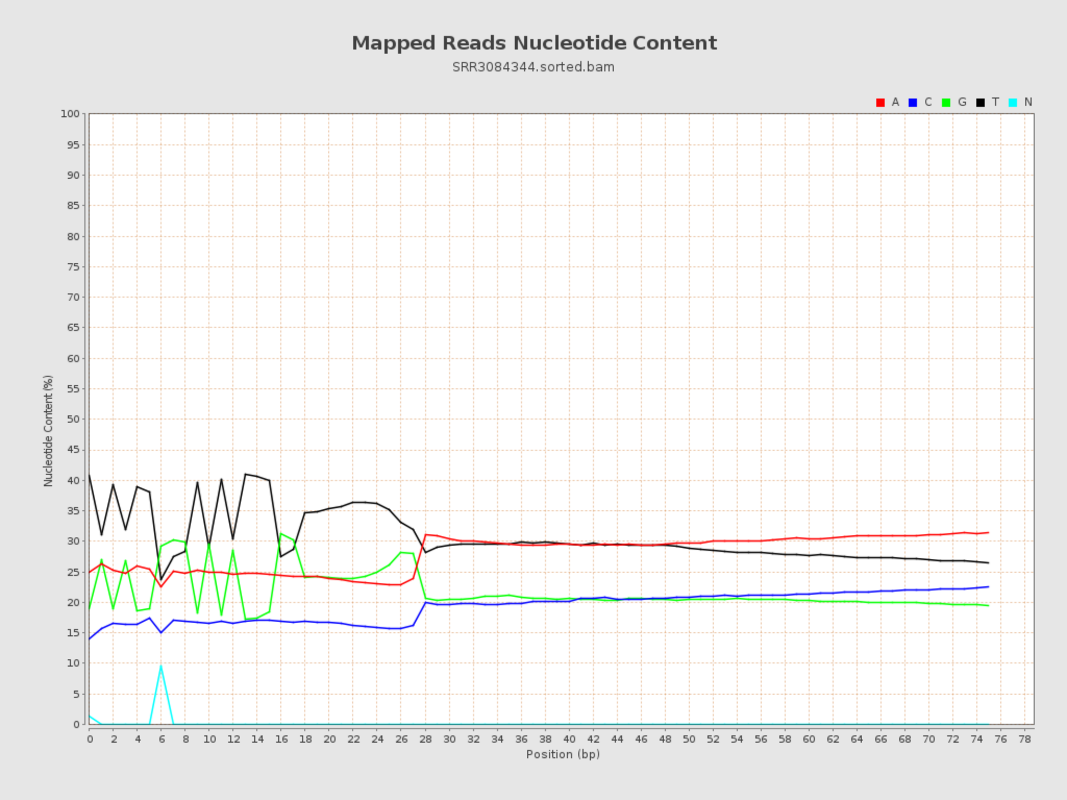
6. Results : Genome Fraction Coverage



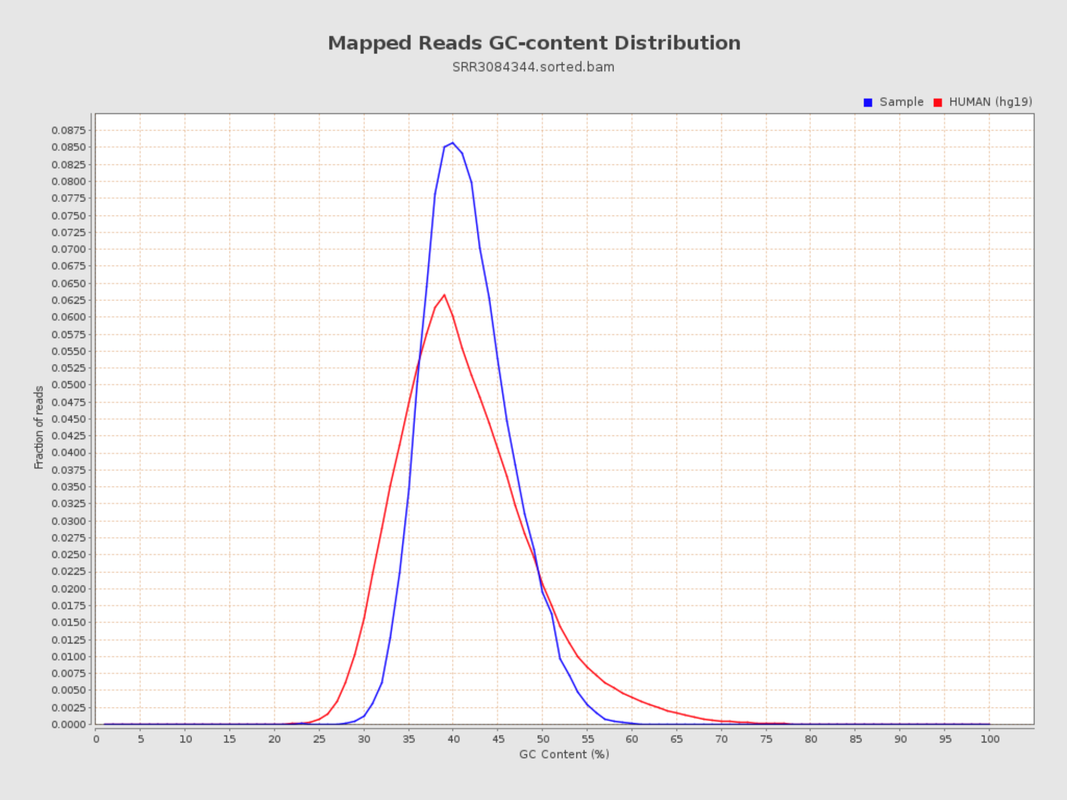
7. Results : Duplication Rate Histogram



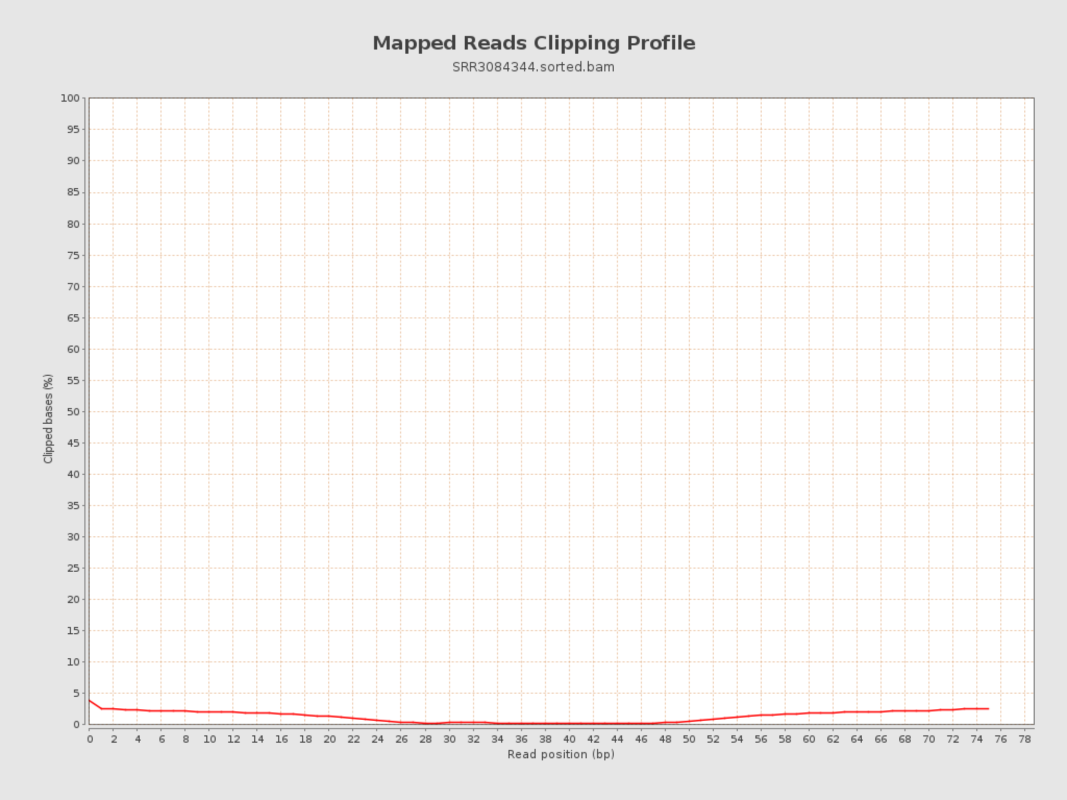
8. Results : Mapped Reads Nucleotide Content



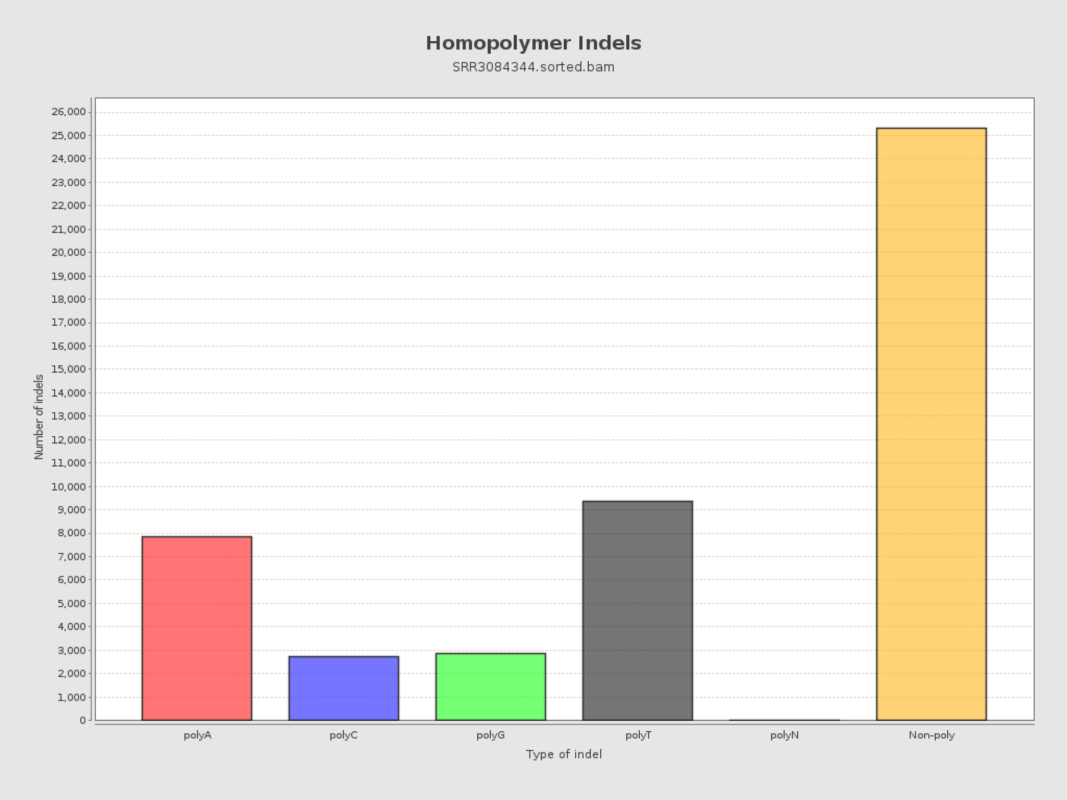
9. Results : Mapped Reads GC-content Distribution



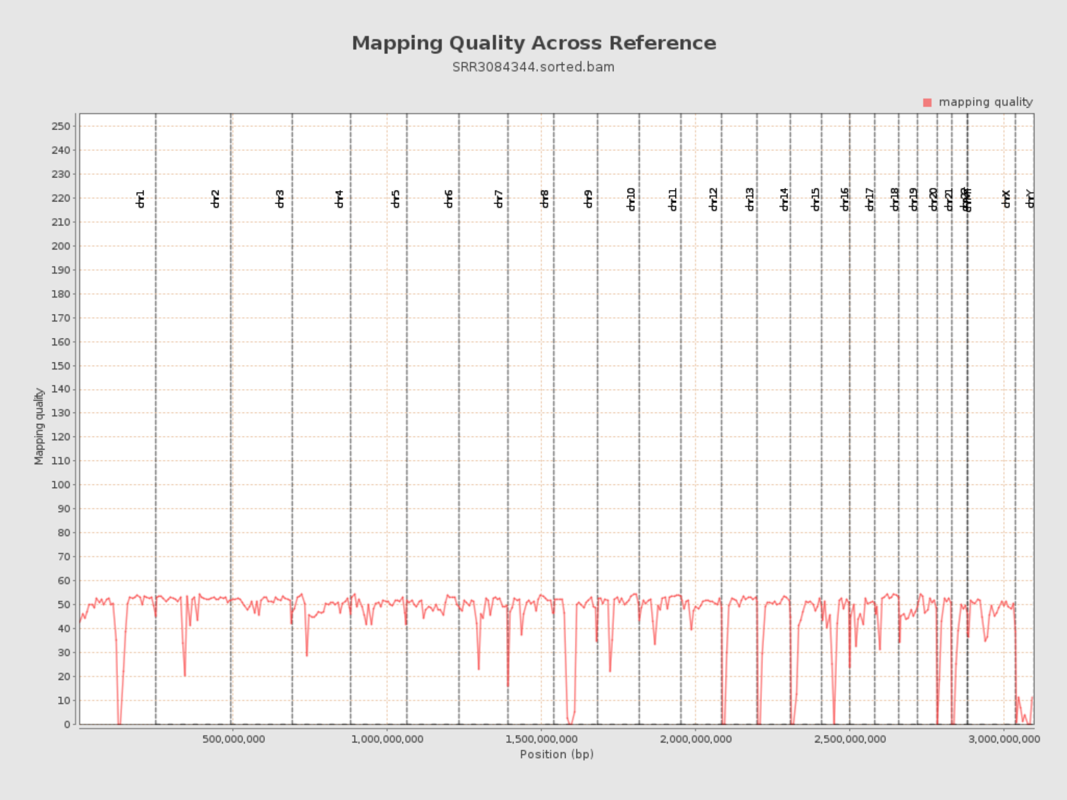
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram