Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:13:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084885.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_SRR3084885 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084885.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:13:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084885.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,591,654
Mapped reads	1,433,018 / 90.03%
Unmapped reads	158,636 / 9.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,497 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	58,502 / 3.68%
Duplication rate	3.32%
Clipped reads	651,098 / 40.91%

2.2. ACGT Content

Number/percentage of A's	25,712,770 / 26.98%
Number/percentage of C's	17,823,091 / 18.7%
Number/percentage of T's	30,022,842 / 31.51%
Number/percentage of G's	21,719,239 / 22.79%
Number/percentage of N's	13,469 / 0.01%
GC Percentage	41.5%

2.3. Coverage

Mean	0.0308

Standard Deviation	0.2691

2.4. Mapping Quality

Mean Mapping Quality	45.23

2.5. Mismatches and indels

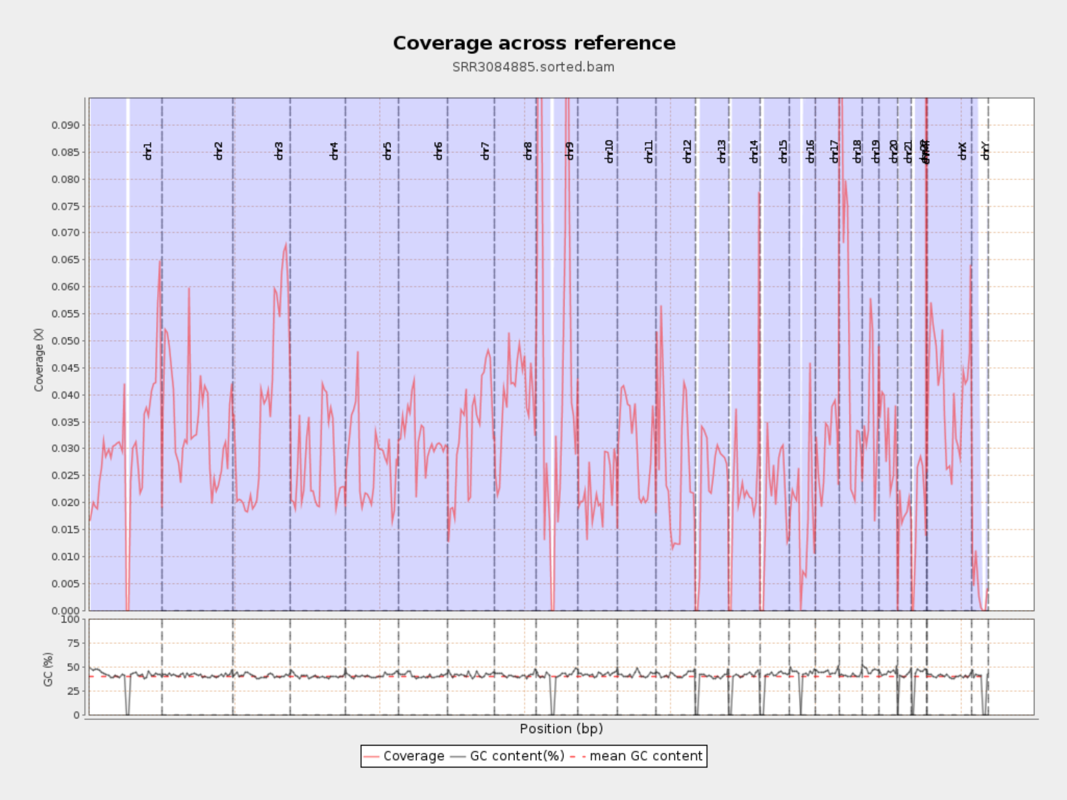
General error rate	0.8%
Mismatches	746,734
Insertions	7,825
Mapped reads with at least one insertion	0.54%
Deletions	22,798
Mapped reads with at least one deletion	1.57%
Homopolymer indels	47.95%

2.6. Chromosome stats

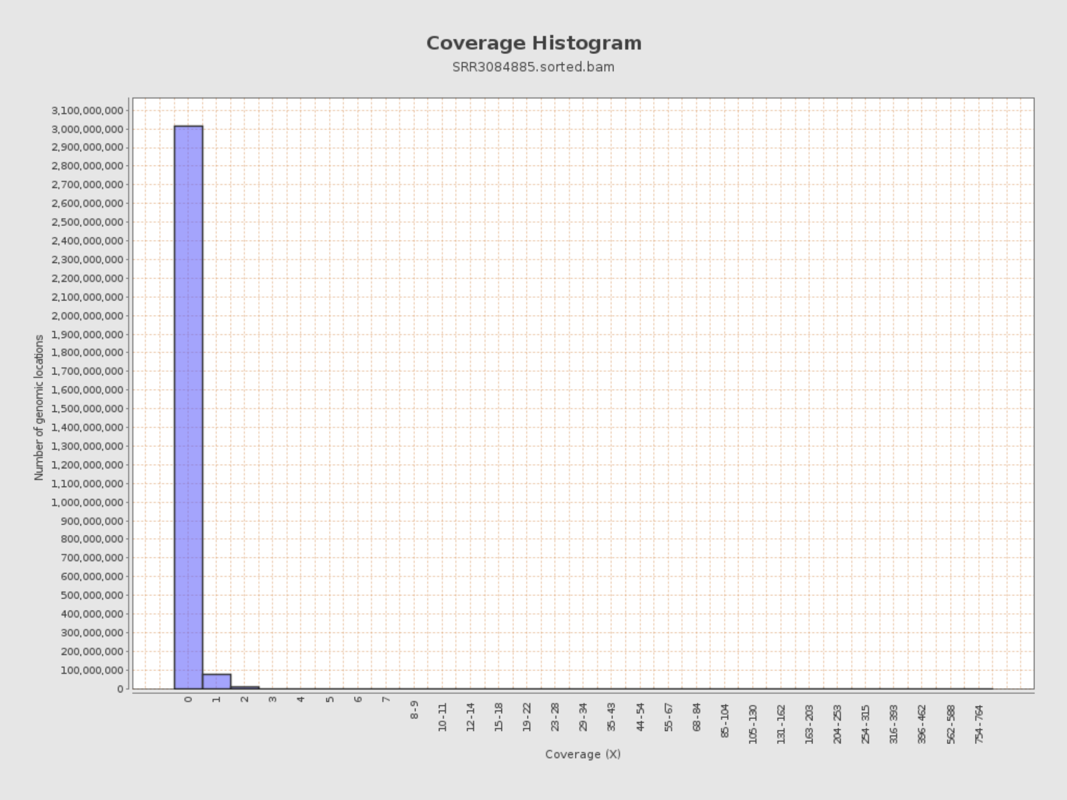
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7404781	0.0297	0.3618
chr2	243199373	8454255	0.0348	0.4584
chr3	198022430	7351125	0.0371	0.216
chr4	191154276	5177882	0.0271	0.1885
chr5	180915260	5033161	0.0278	0.1884
chr6	171115067	5495127	0.0321	0.2181
chr7	159138663	5323197	0.0335	0.2627

chr8	146364022	5699002	0.0389	0.314
chr9	141213431	6867490	0.0486	0.3245
chr10	135534747	2976848	0.022	0.19
chr11	135006516	4162587	0.0308	0.2591
chr12	133851895	3679403	0.0275	0.1888
chr13	115169878	2733651	0.0237	0.171
chr14	107349540	2209763	0.0206	0.1737
chr15	102531392	2099591	0.0205	0.1649
chr16	90354753	1634539	0.0181	0.1603
chr17	81195210	2479287	0.0305	0.2092
chr18	78077248	4109938	0.0526	0.4458
chr19	59128983	2181198	0.0369	0.3008
chr20	63025520	2069464	0.0328	0.2049
chr21	48129895	817541	0.017	0.1518
chr22	51304566	897012	0.0175	0.1452
chrMT	16571	22905	1.3822	1.4784
chrX	155270560	6222399	0.0401	0.2423
chrY	59373566	226564	0.0038	0.0908

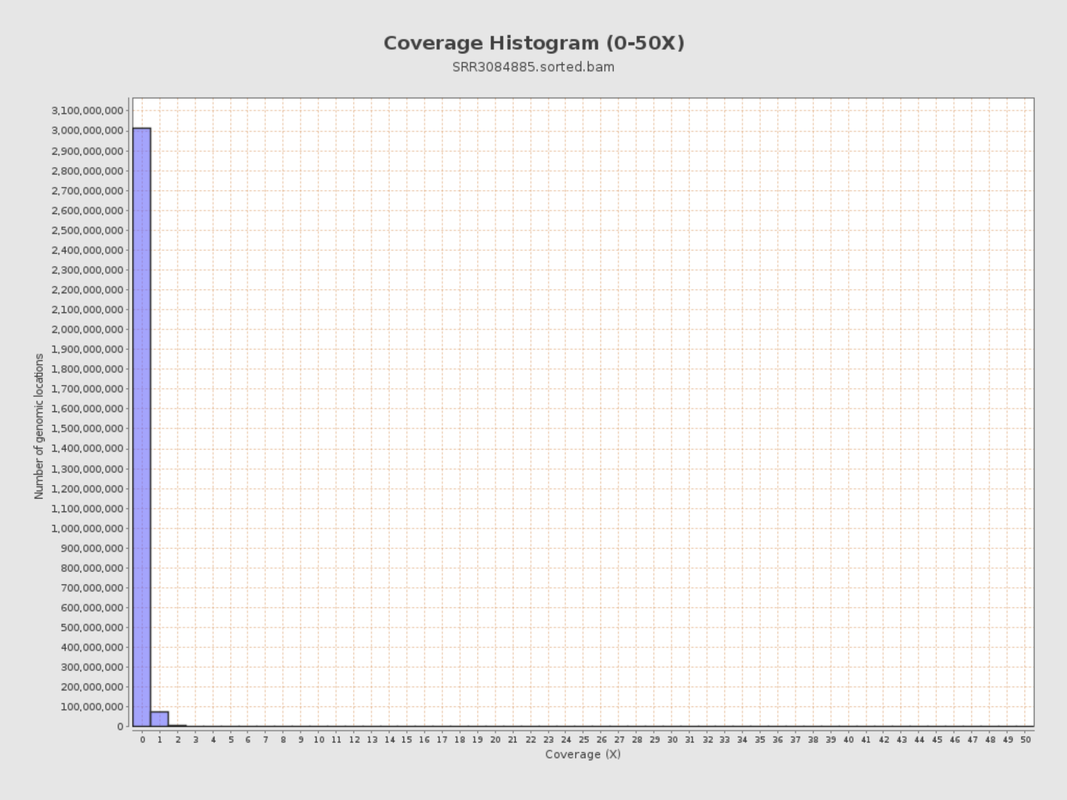
3. Results : Coverage across reference



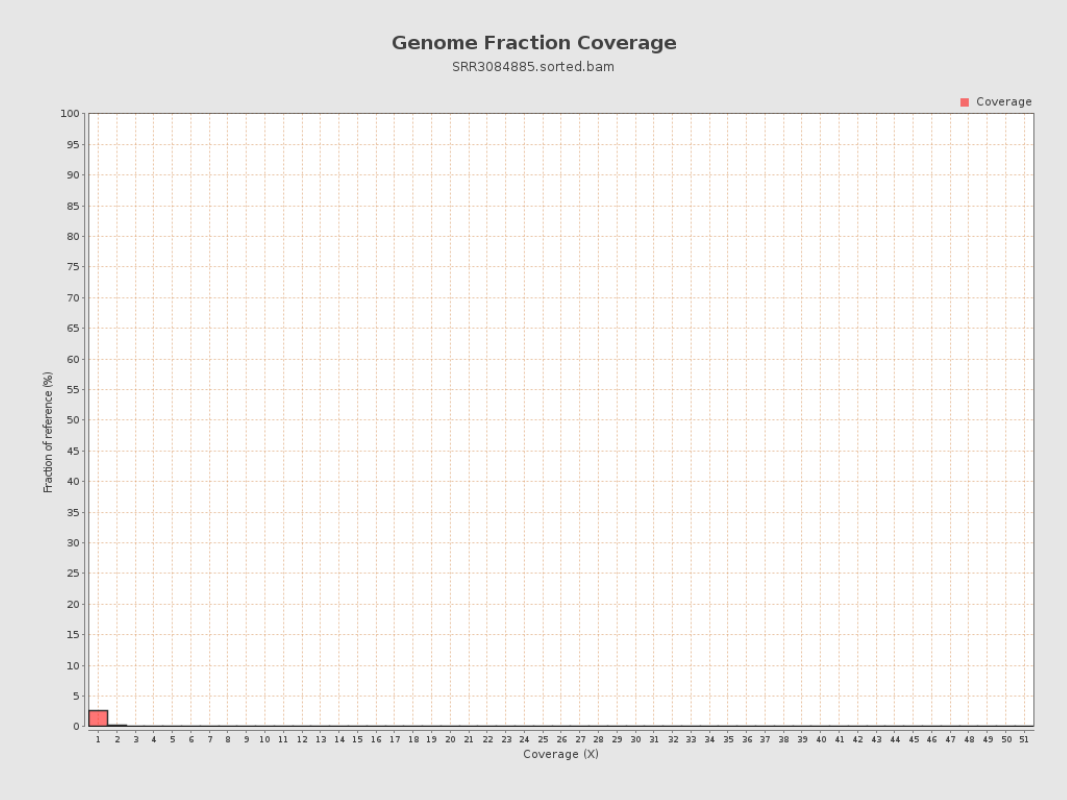
4. Results : Coverage Histogram



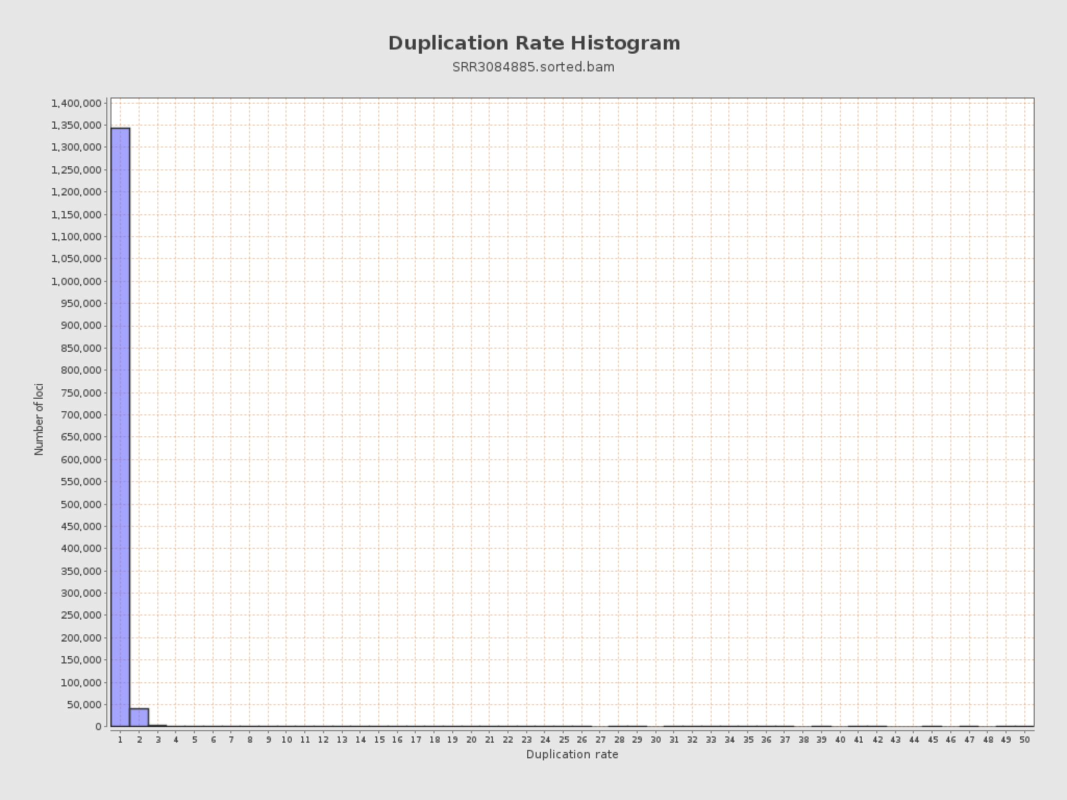
5. Results : Coverage Histogram (0-50X)



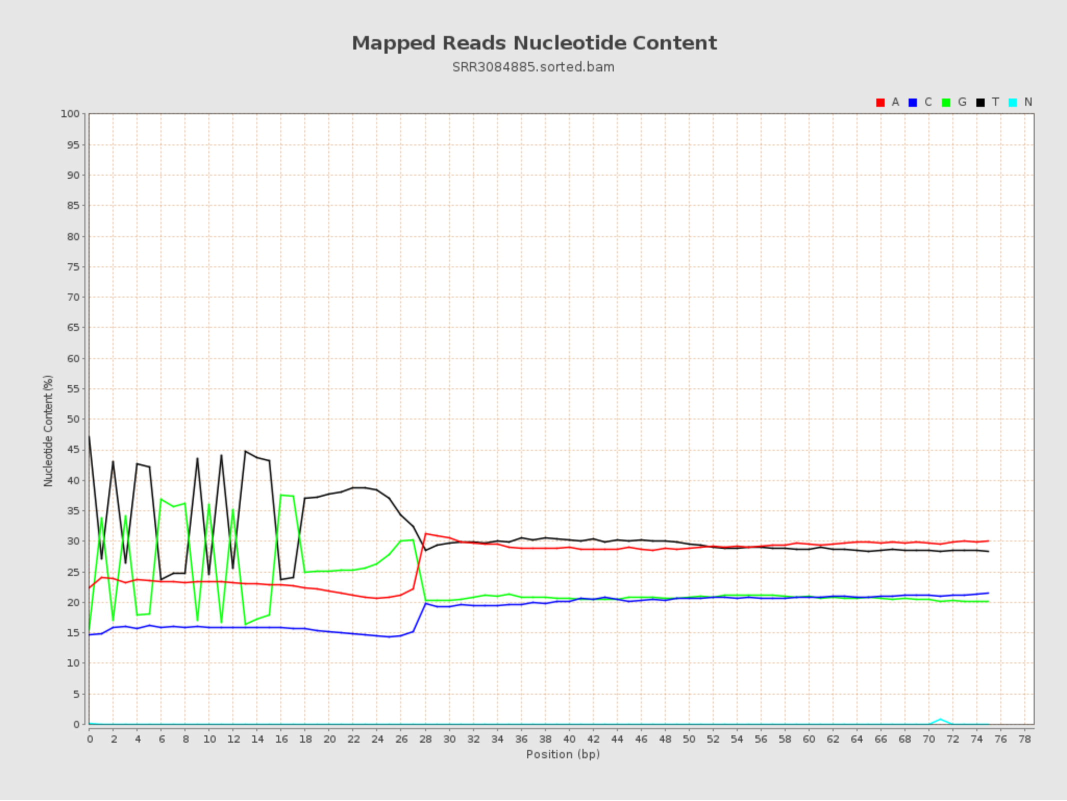
6. Results : Genome Fraction Coverage



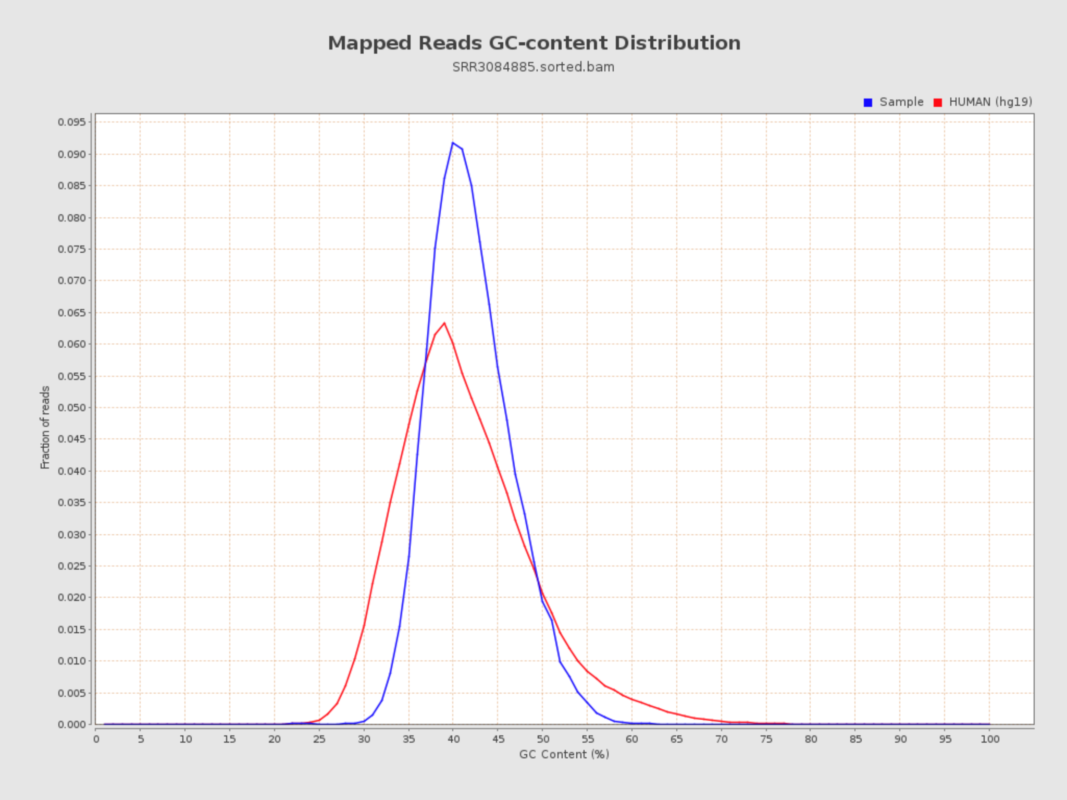
7. Results : Duplication Rate Histogram



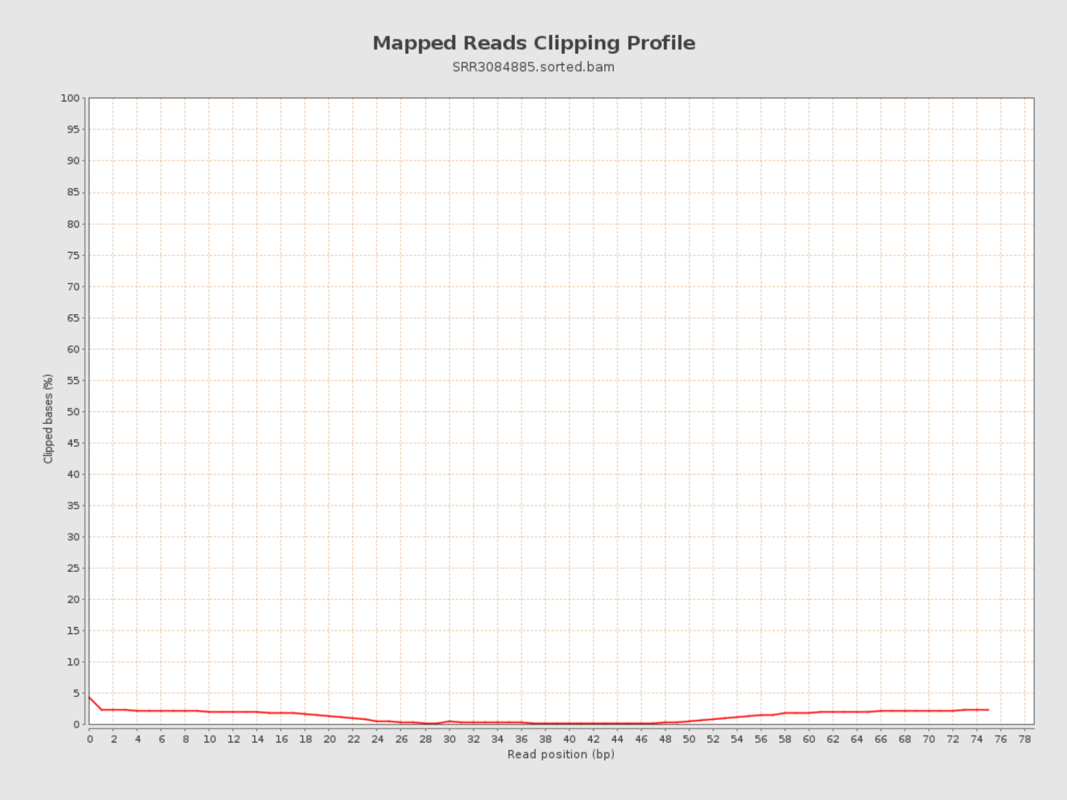
8. Results : Mapped Reads Nucleotide Content



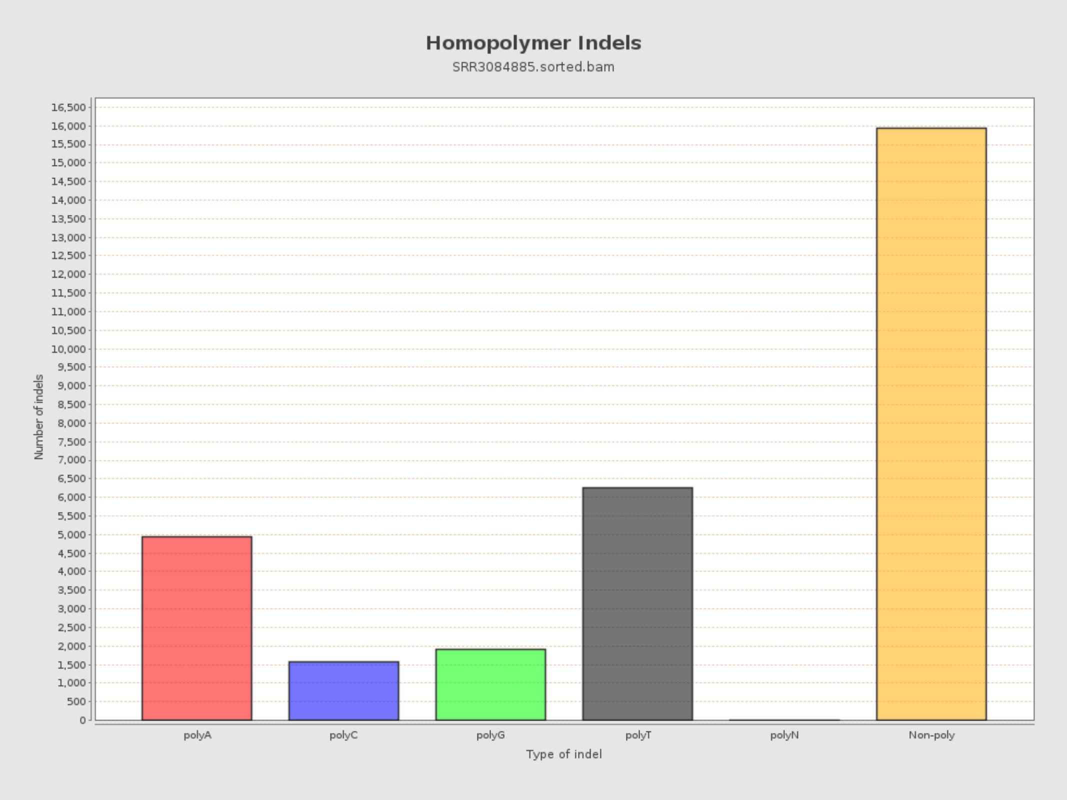
9. Results : Mapped Reads GC-content Distribution



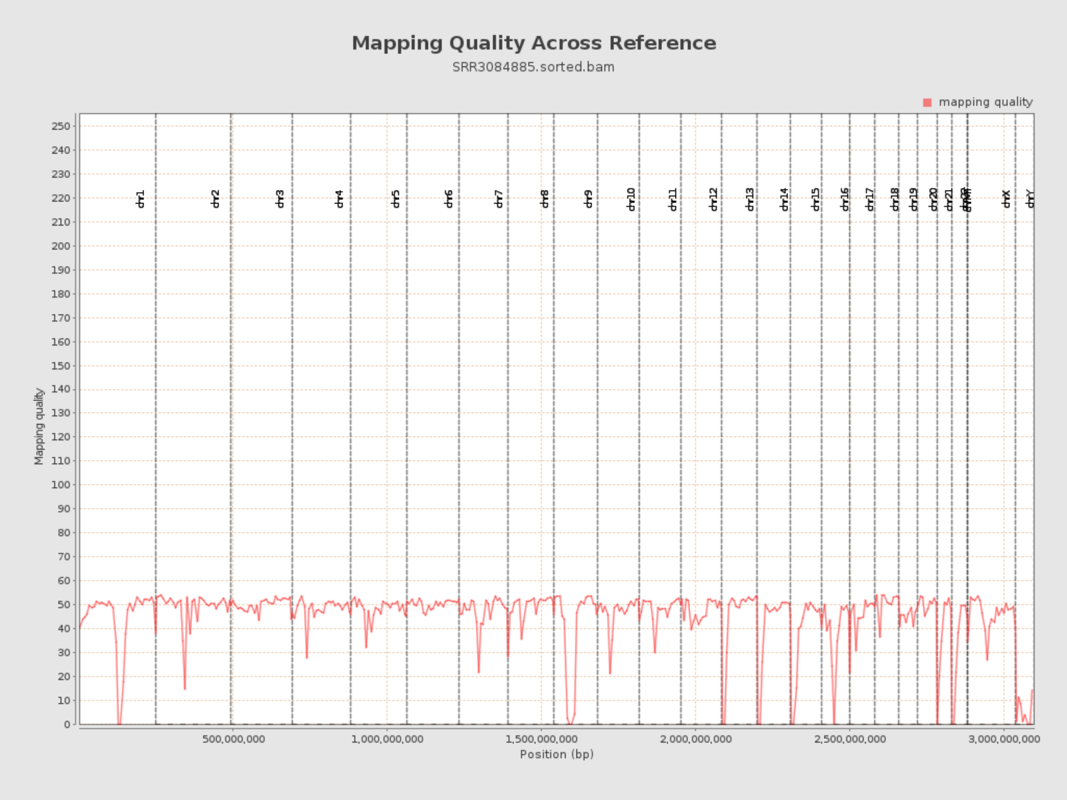
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram