Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:57:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084791.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_SRR3084791 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084791.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:57:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084791.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,685,368
Mapped reads	1,459,752 / 86.61%
Unmapped reads	225,616 / 13.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,491 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	49,684 / 2.95%
Duplication rate	2.67%
Clipped reads	722,337 / 42.86%

2.2. ACGT Content

Number/percentage of A's	26,237,317 / 27.36%
Number/percentage of C's	18,093,512 / 18.87%
Number/percentage of T's	29,802,659 / 31.08%
Number/percentage of G's	21,715,883 / 22.65%
Number/percentage of N's	36,184 / 0.04%
GC Percentage	41.52%

2.3. Coverage

Mean	0.031

Standard Deviation	0.2661

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

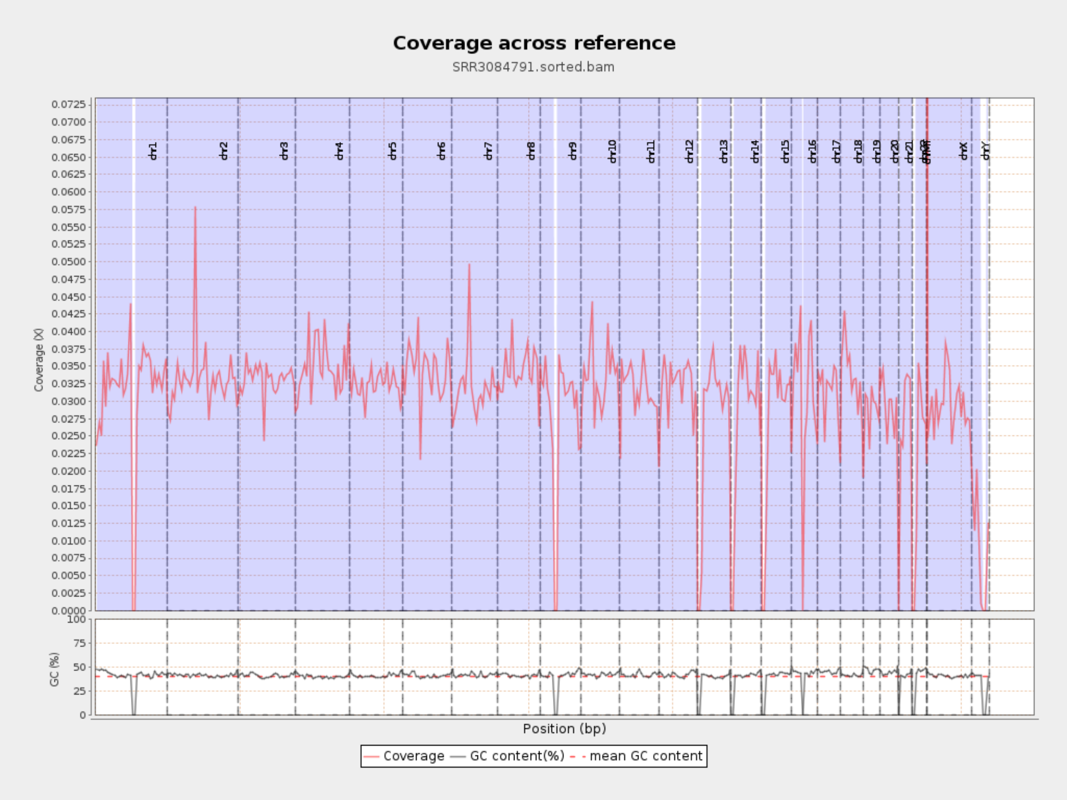
General error rate	0.89%
Mismatches	838,226
Insertions	7,793
Mapped reads with at least one insertion	0.53%
Deletions	23,148
Mapped reads with at least one deletion	1.57%
Homopolymer indels	46.97%

2.6. Chromosome stats

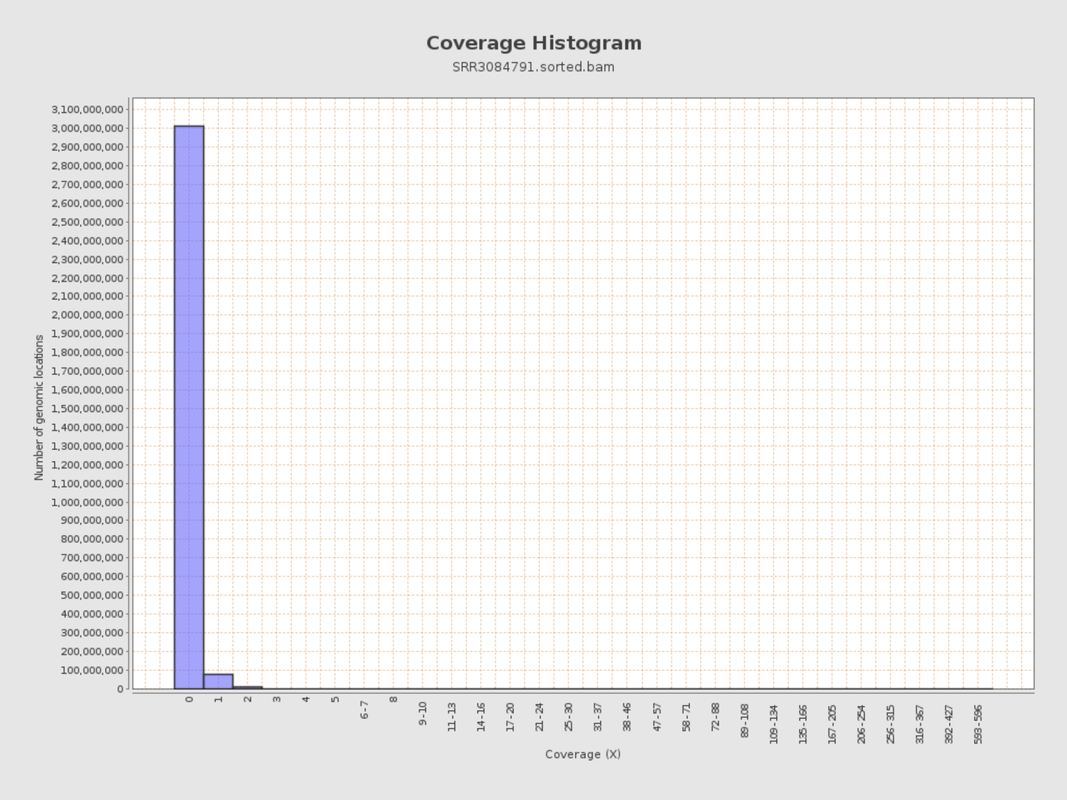
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7755168	0.0311	0.3662
chr2	243199373	8127992	0.0334	0.3829
chr3	198022430	6571477	0.0332	0.199
chr4	191154276	6664398	0.0349	0.2151
chr5	180915260	5858106	0.0324	0.1971
chr6	171115067	5871607	0.0343	0.2358
chr7	159138663	5102427	0.0321	0.3379

chr8	146364022	5020795	0.0343	0.3091
chr9	141213431	3952013	0.028	0.2537
chr10	135534747	4550508	0.0336	0.2463
chr11	135006516	4304753	0.0319	0.2513
chr12	133851895	4338096	0.0324	0.1996
chr13	115169878	3105250	0.027	0.1823
chr14	107349540	2946369	0.0274	0.1907
chr15	102531392	2761244	0.0269	0.1929
chr16	90354753	2738426	0.0303	0.2016
chr17	81195210	2547814	0.0314	0.2135
chr18	78077248	2664248	0.0341	0.448
chr19	59128983	1707177	0.0289	0.2976
chr20	63025520	1821435	0.0289	0.1956
chr21	48129895	1256068	0.0261	0.1878
chr22	51304566	1069389	0.0208	0.1592
chrMT	16571	96898	5.8474	3.7474
chrX	155270560	4572464	0.0294	0.2056
chrY	59373566	518495	0.0087	0.1238

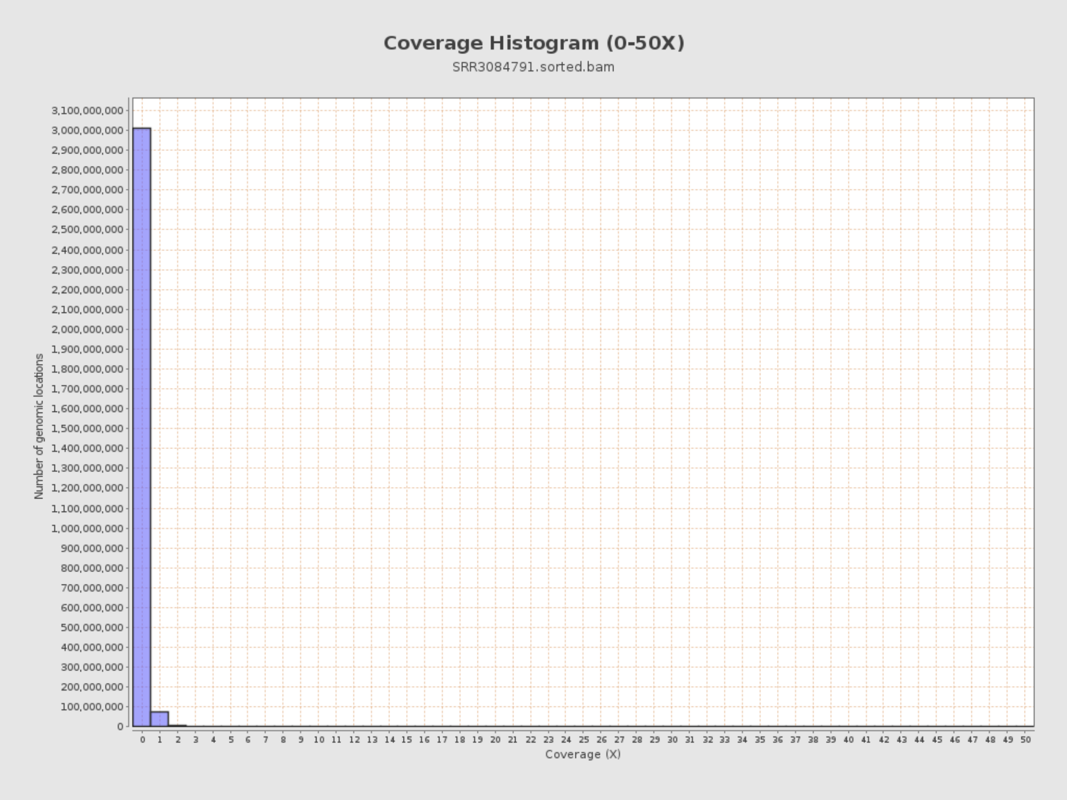
3. Results : Coverage across reference



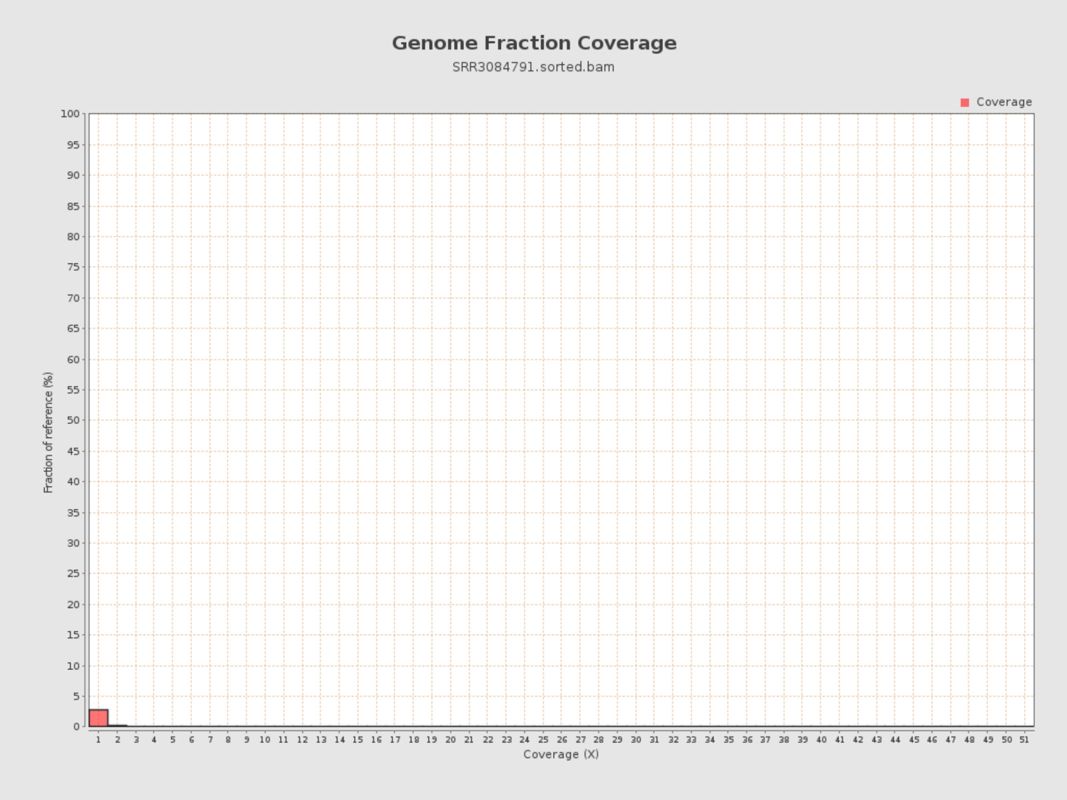
4. Results : Coverage Histogram



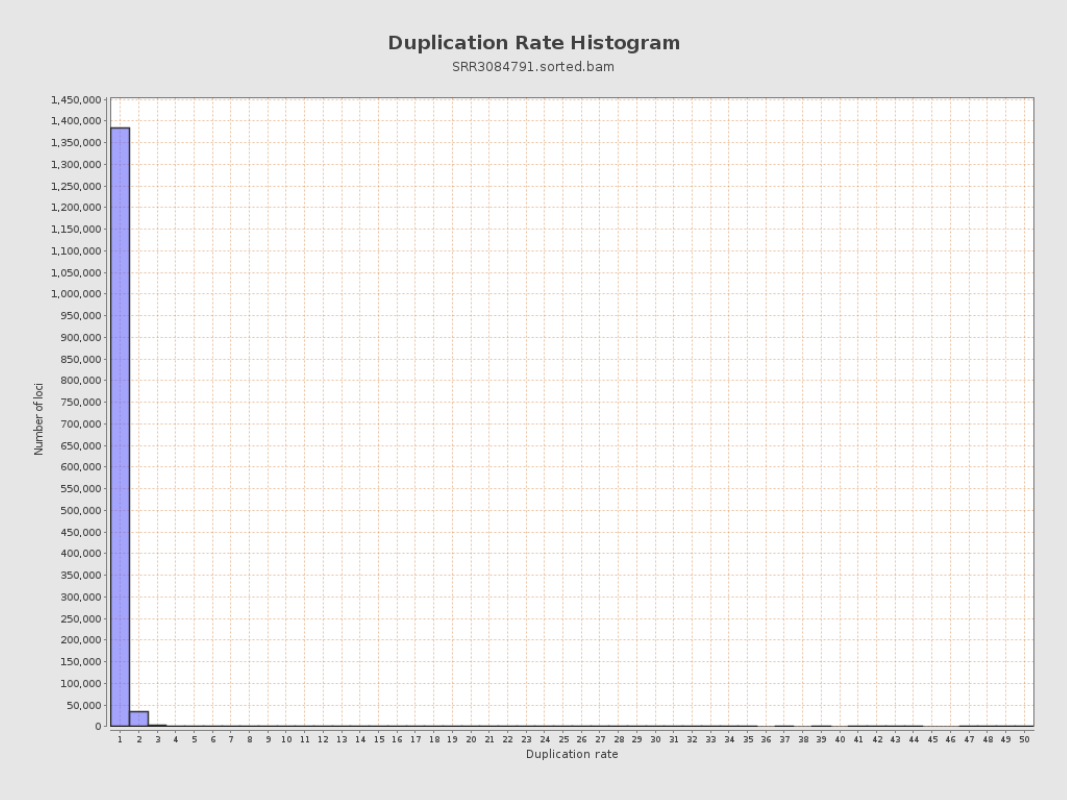
5. Results : Coverage Histogram (0-50X)



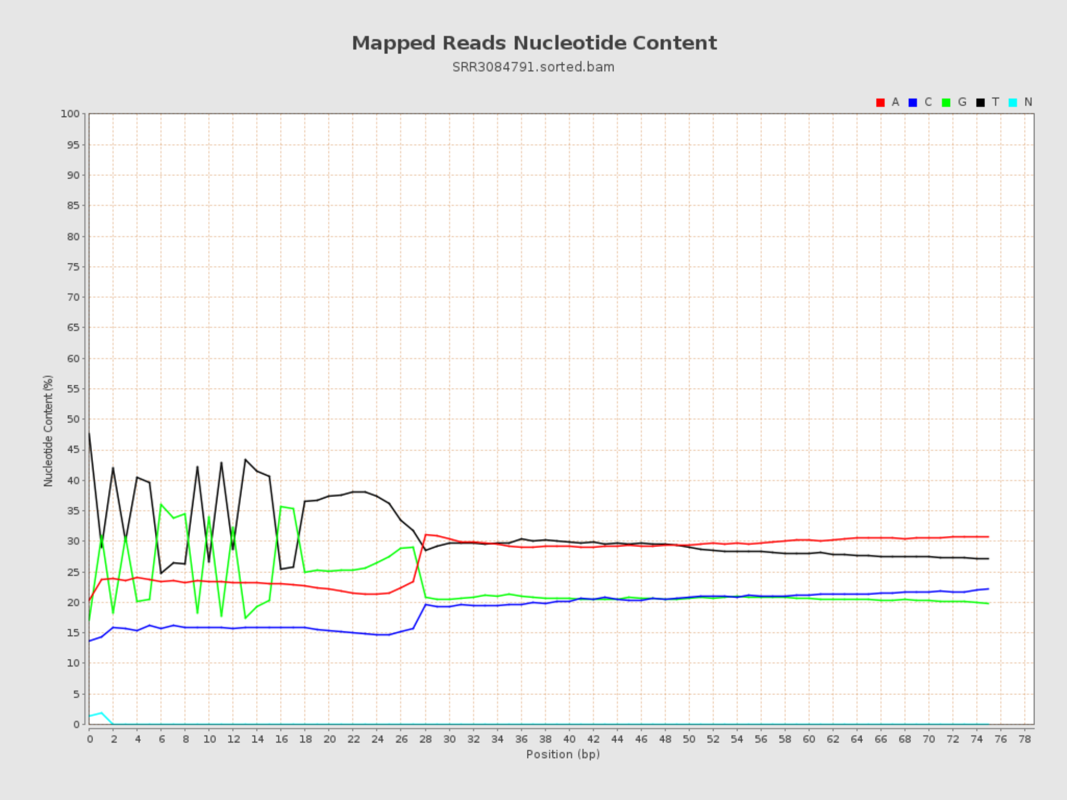
6. Results : Genome Fraction Coverage



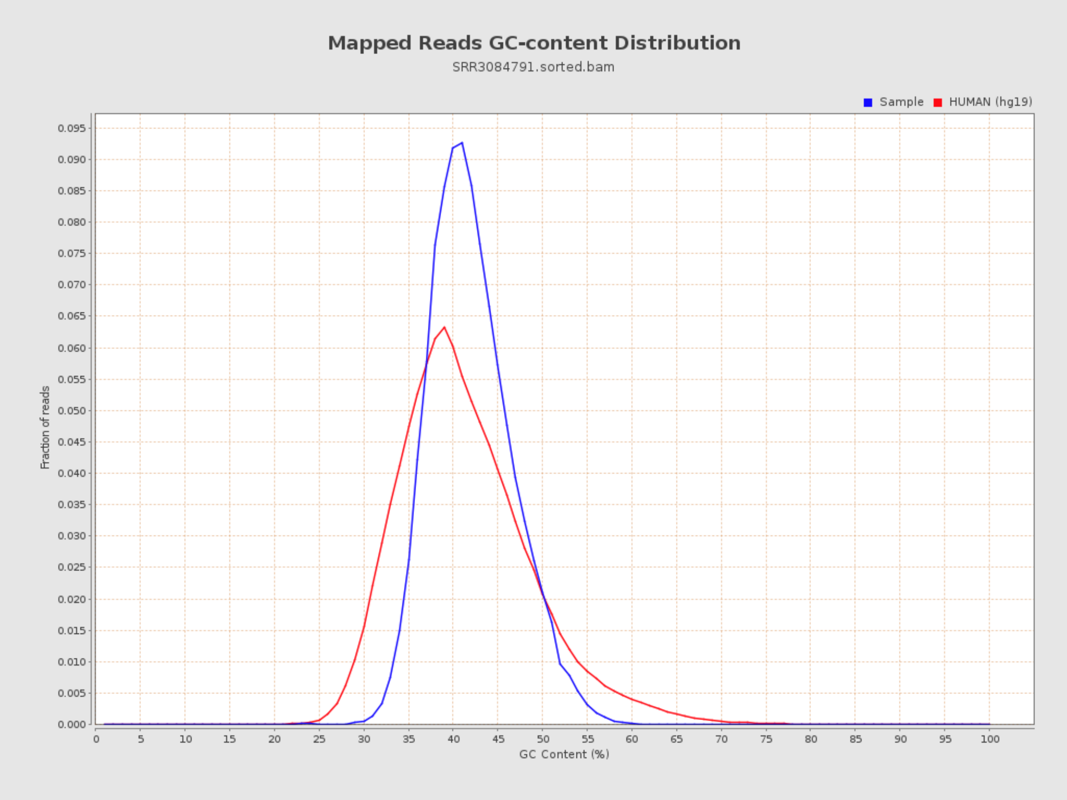
7. Results : Duplication Rate Histogram



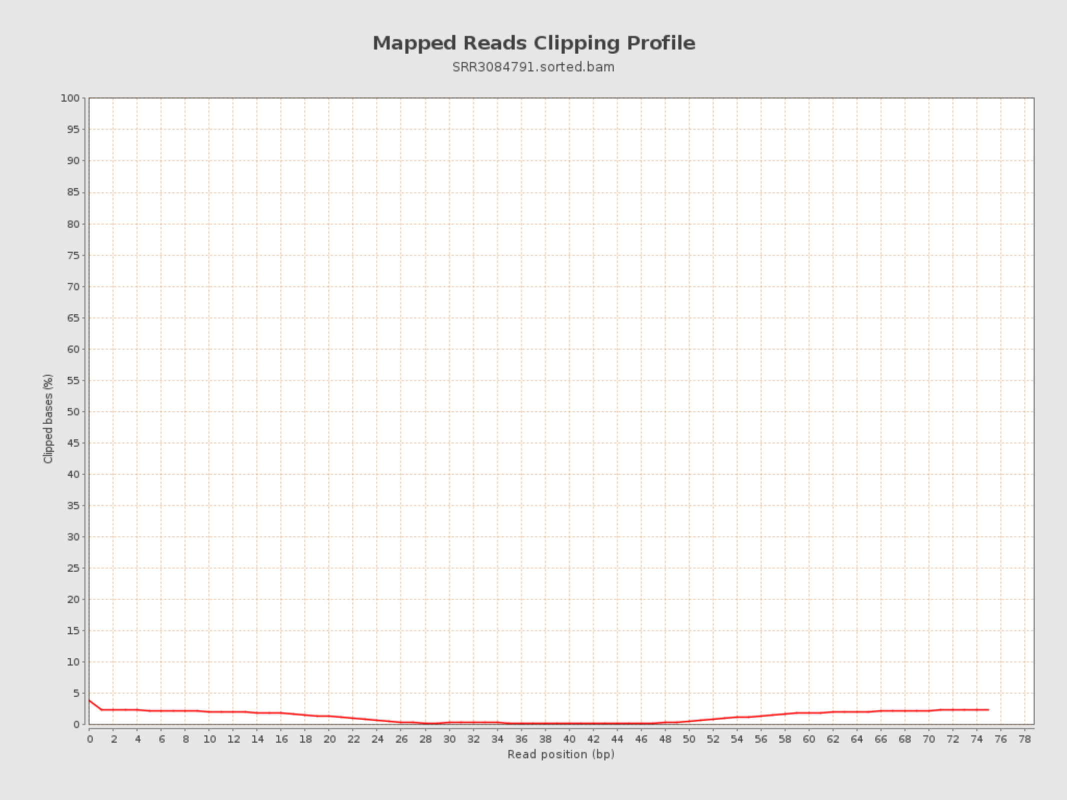
8. Results : Mapped Reads Nucleotide Content



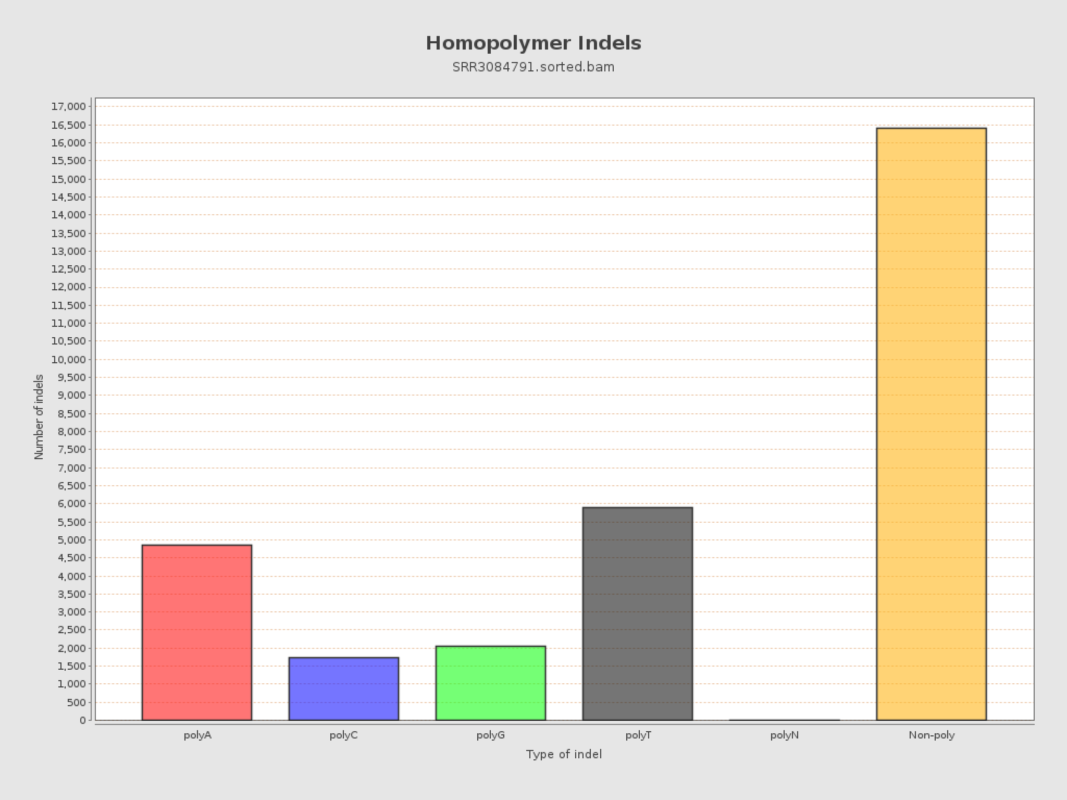
9. Results : Mapped Reads GC-content Distribution



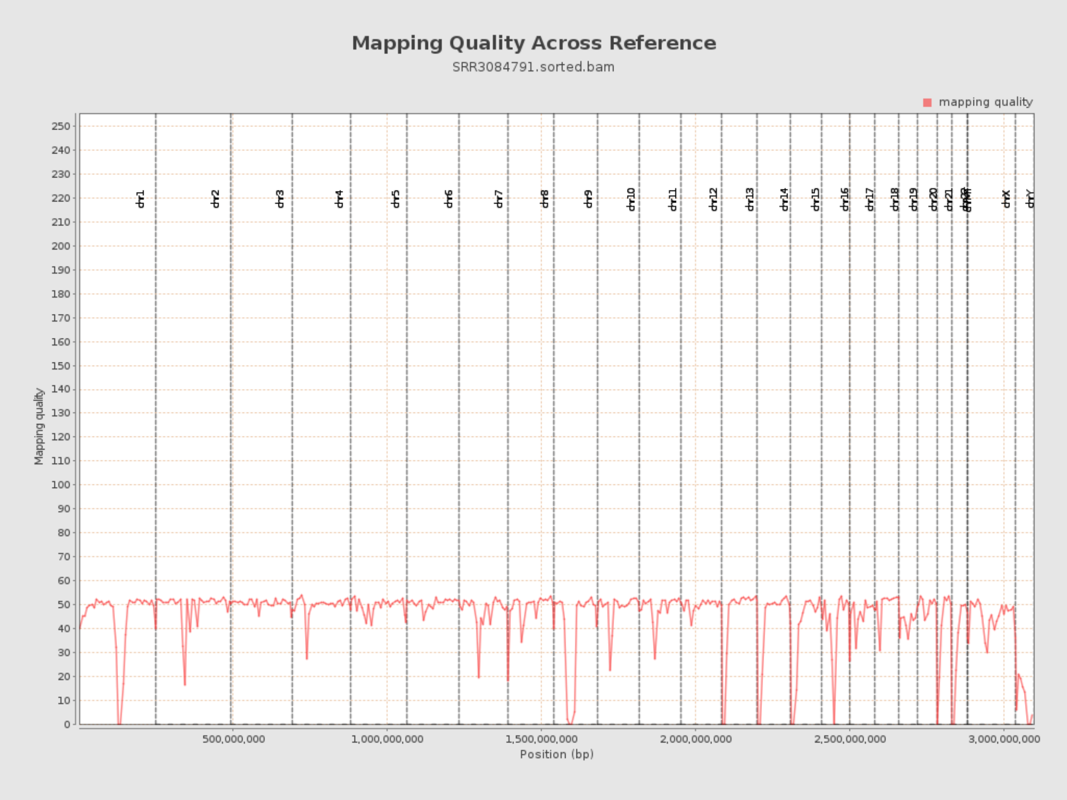
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram