Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:48:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084901.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_SRR3084901 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084901.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:48:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084901.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,405,015
Mapped reads	2,199,194 / 91.44%
Unmapped reads	205,821 / 8.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,178 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	101,749 / 4.23%
Duplication rate	3.98%
Clipped reads	813,593 / 33.83%

2.2. ACGT Content

Number/percentage of A's	42,971,863 / 28.54%
Number/percentage of C's	27,605,771 / 18.34%
Number/percentage of T's	48,070,699 / 31.93%
Number/percentage of G's	31,875,226 / 21.17%
Number/percentage of N's	23,867 / 0.02%
GC Percentage	39.51%

2.3. Coverage

Mean	0.0486

Standard Deviation	0.3535

2.4. Mapping Quality

Mean Mapping Quality	47.14

2.5. Mismatches and indels

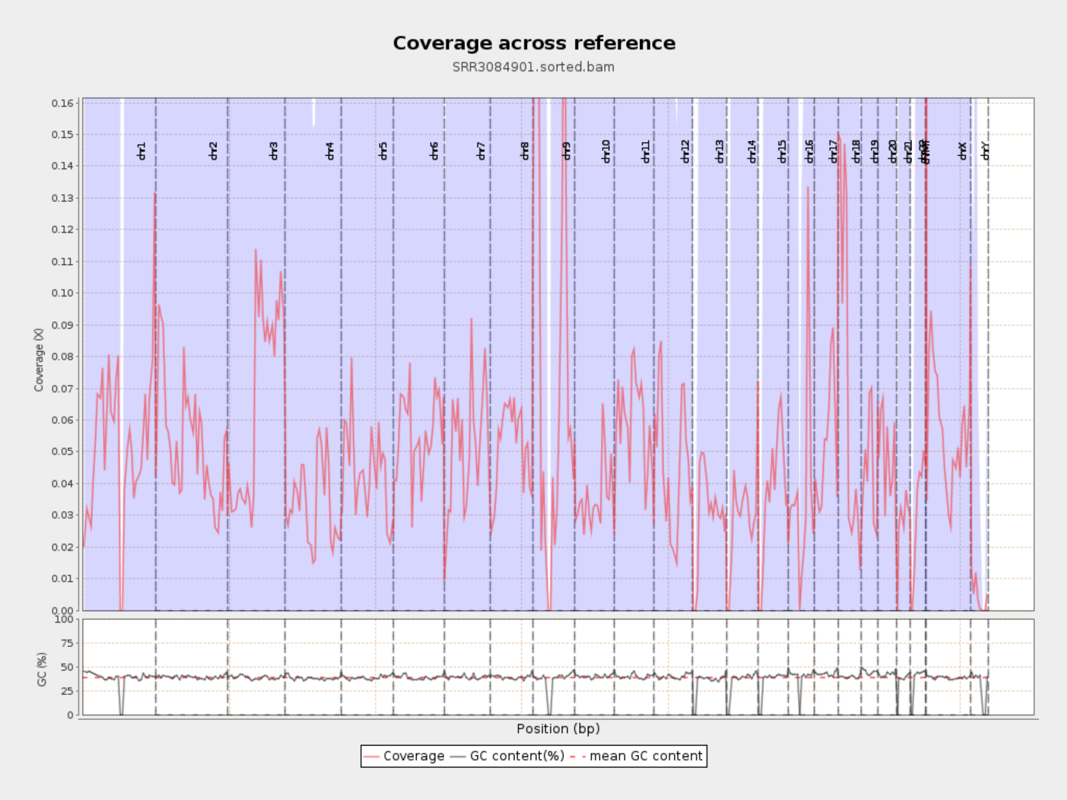
General error rate	0.82%
Mismatches	1,217,223
Insertions	11,368
Mapped reads with at least one insertion	0.51%
Deletions	33,279
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48.51%

2.6. Chromosome stats

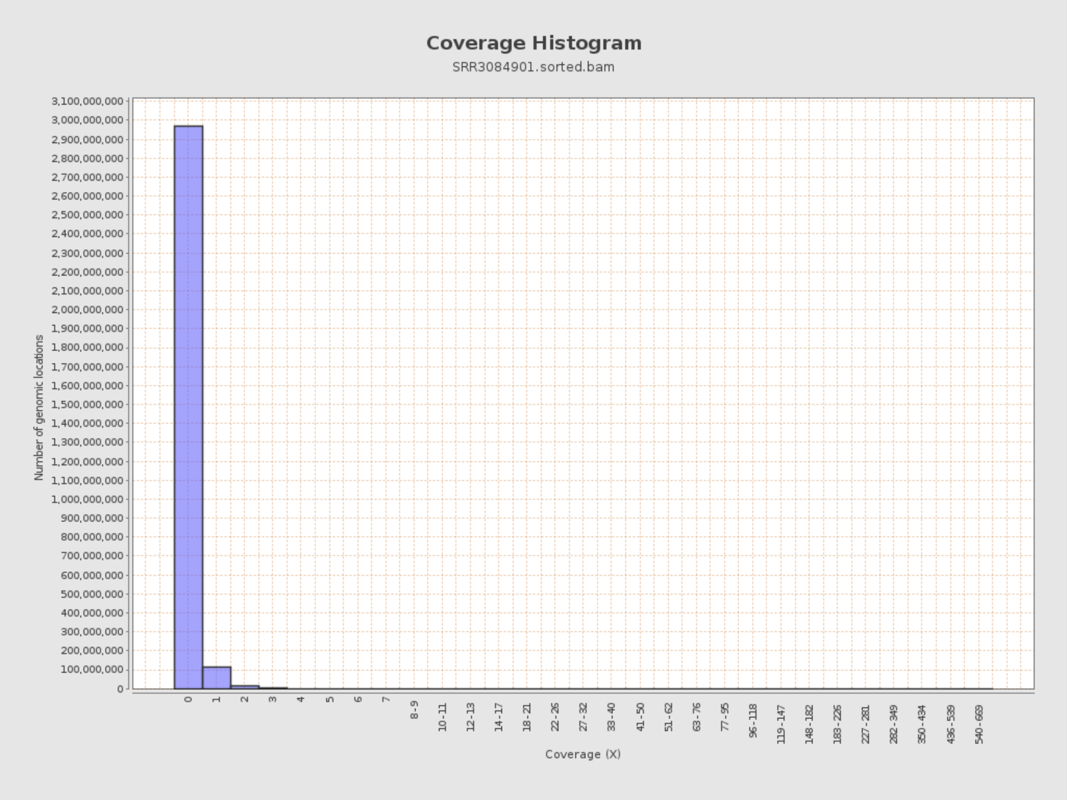
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13112955	0.0526	0.6292
chr2	243199373	12871461	0.0529	0.4254
chr3	198022430	12967463	0.0655	0.2895
chr4	191154276	6479145	0.0339	0.2098
chr5	180915260	7887502	0.0436	0.2391
chr6	171115067	9496782	0.0555	0.2729
chr7	159138663	8123454	0.051	0.3846

chr8	146364022	7559183	0.0516	0.4557
chr9	141213431	11581105	0.082	0.4355
chr10	135534747	4883573	0.036	0.2868
chr11	135006516	8019187	0.0594	0.3309
chr12	133851895	6215295	0.0464	0.2502
chr13	115169878	3457550	0.03	0.1935
chr14	107349540	2982329	0.0278	0.1957
chr15	102531392	3778352	0.0369	0.2152
chr16	90354753	3141493	0.0348	0.2305
chr17	81195210	4398152	0.0542	0.2716
chr18	78077248	5812232	0.0744	0.562
chr19	59128983	2681297	0.0453	0.4109
chr20	63025520	3115257	0.0494	0.2514
chr21	48129895	1347632	0.028	0.1989
chr22	51304566	1537099	0.03	0.1929
chrMT	16571	24820	1.4978	1.4813
chrX	155270560	8861108	0.0571	0.2897
chrY	59373566	270612	0.0046	0.1132

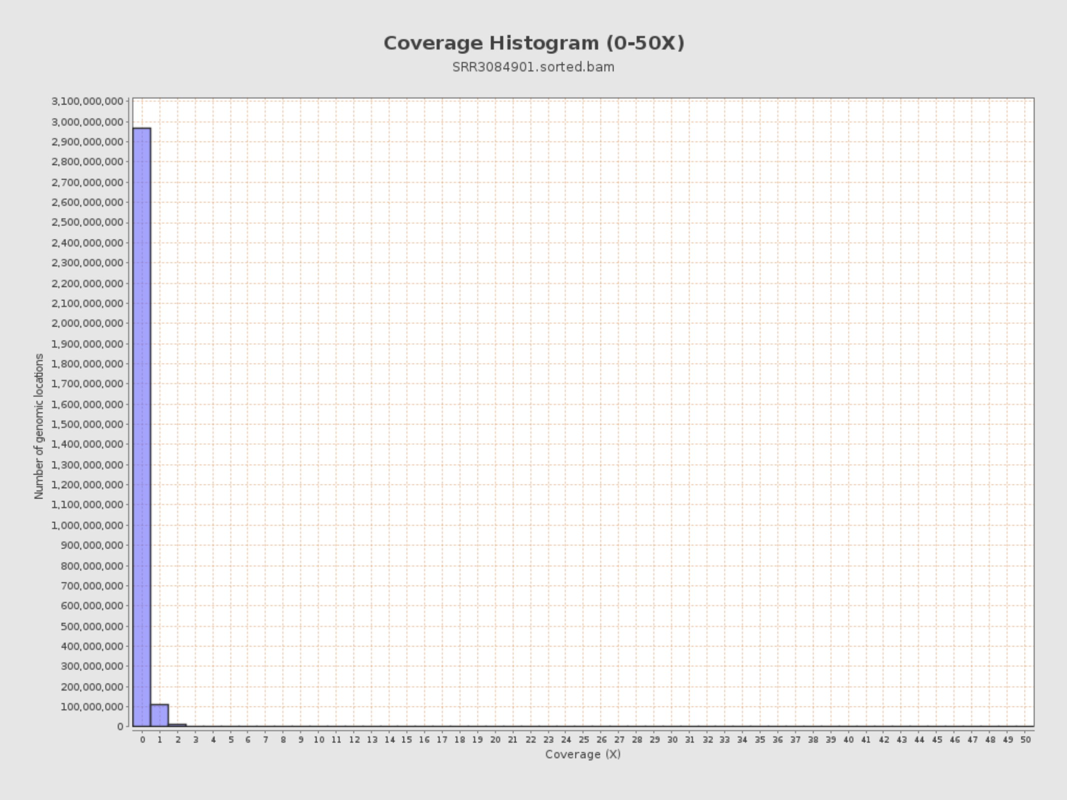
3. Results : Coverage across reference



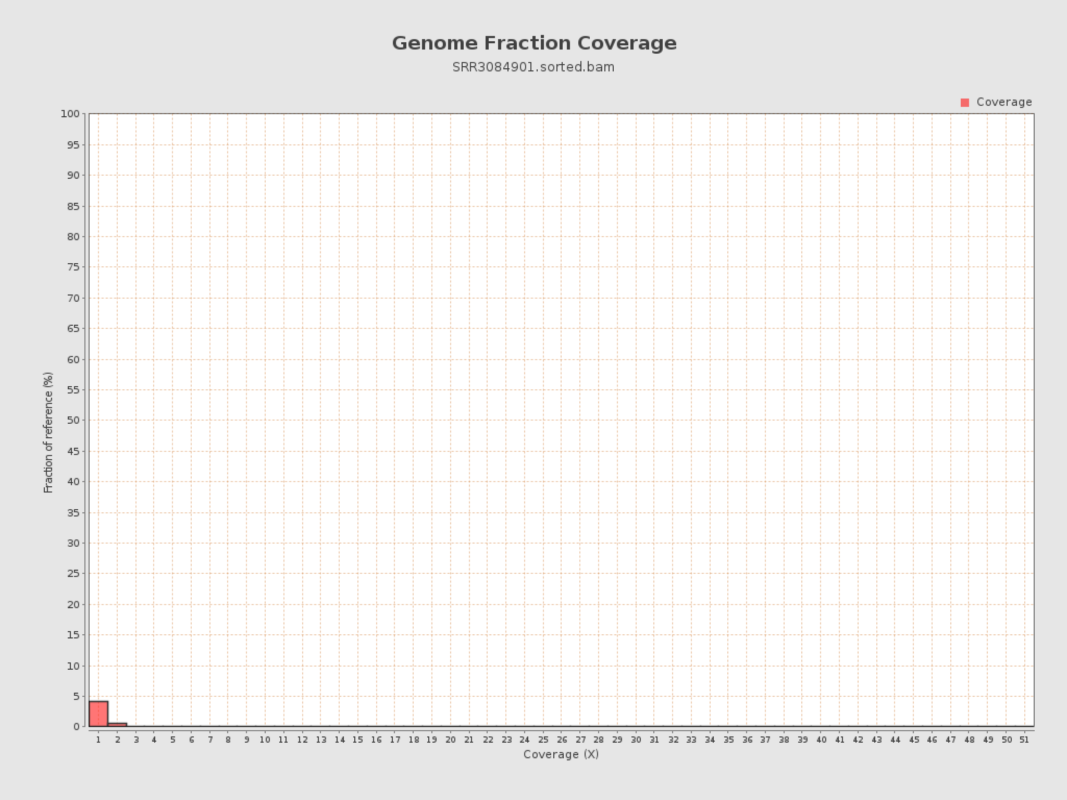
4. Results : Coverage Histogram



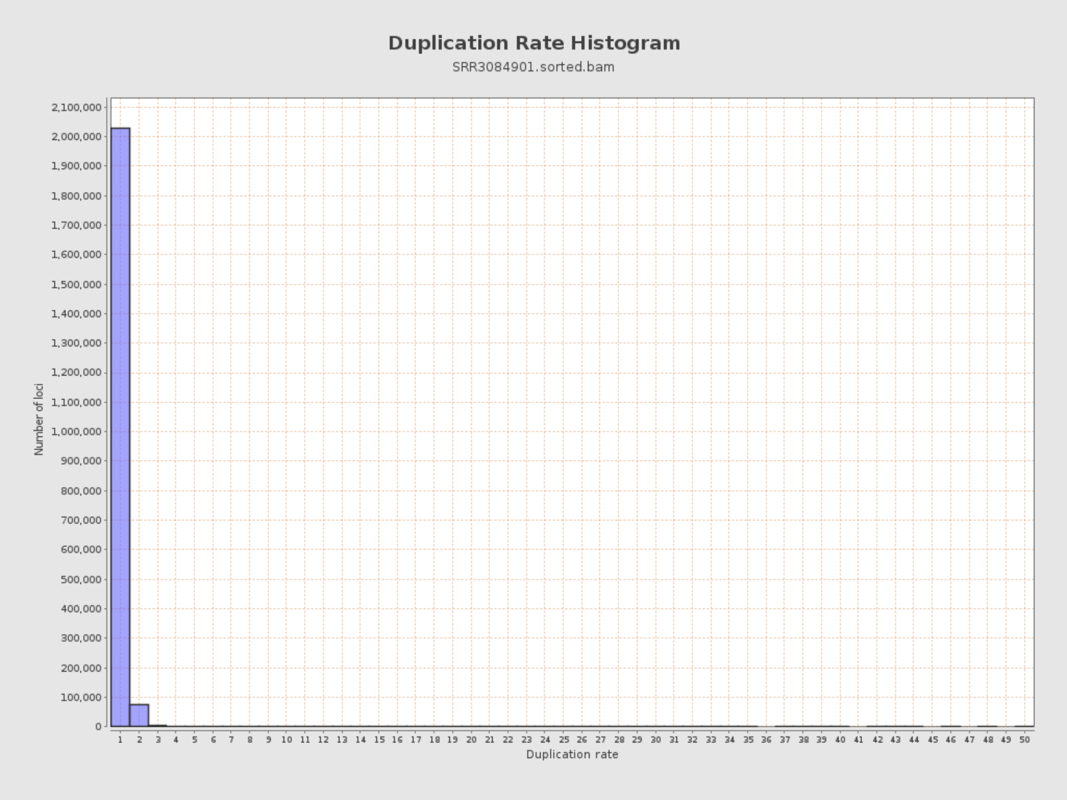
5. Results : Coverage Histogram (0-50X)



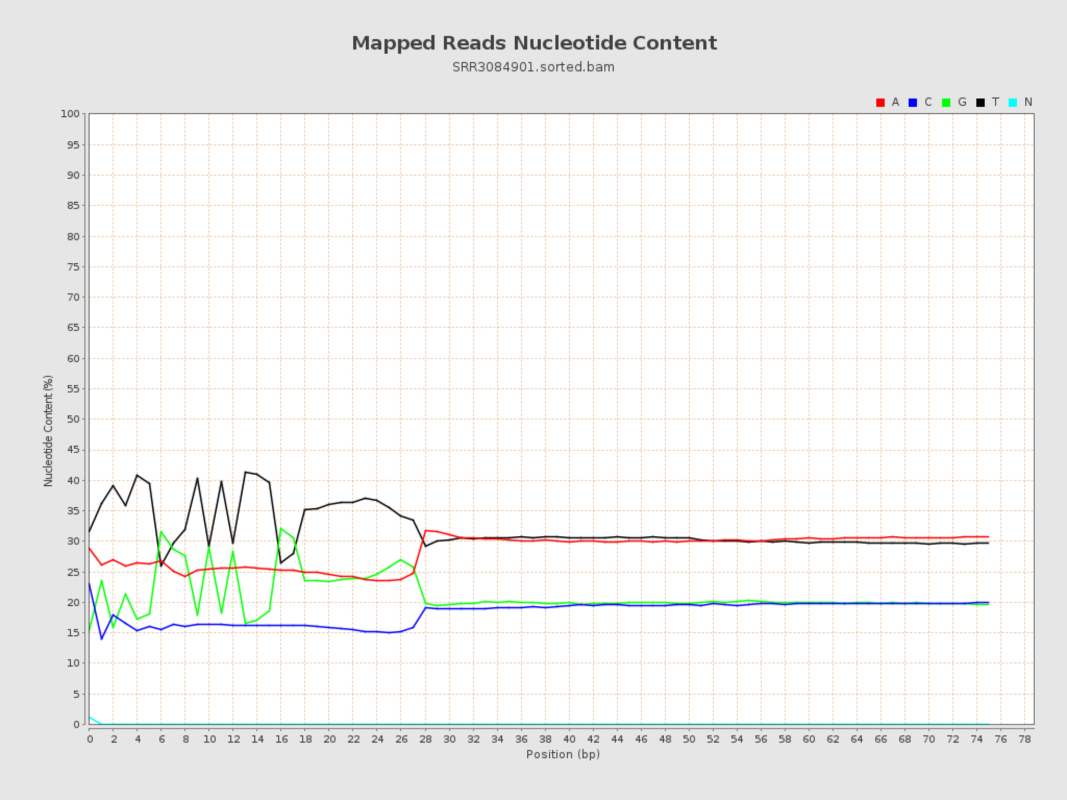
6. Results : Genome Fraction Coverage



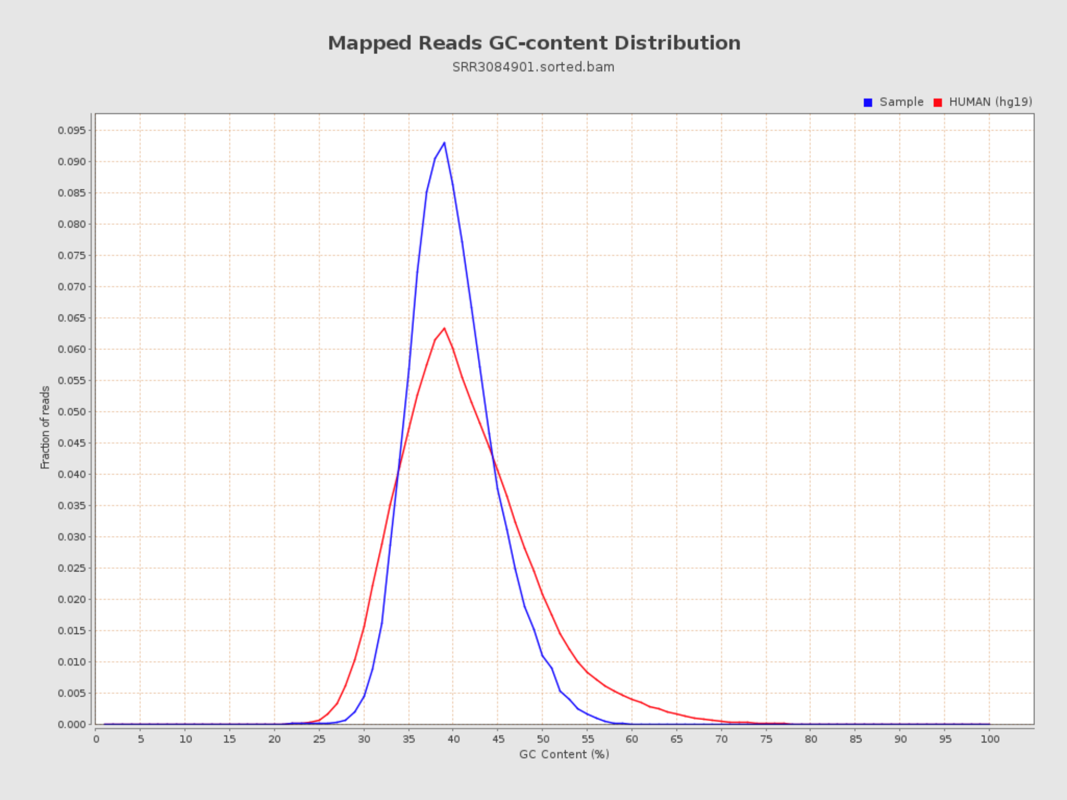
7. Results : Duplication Rate Histogram



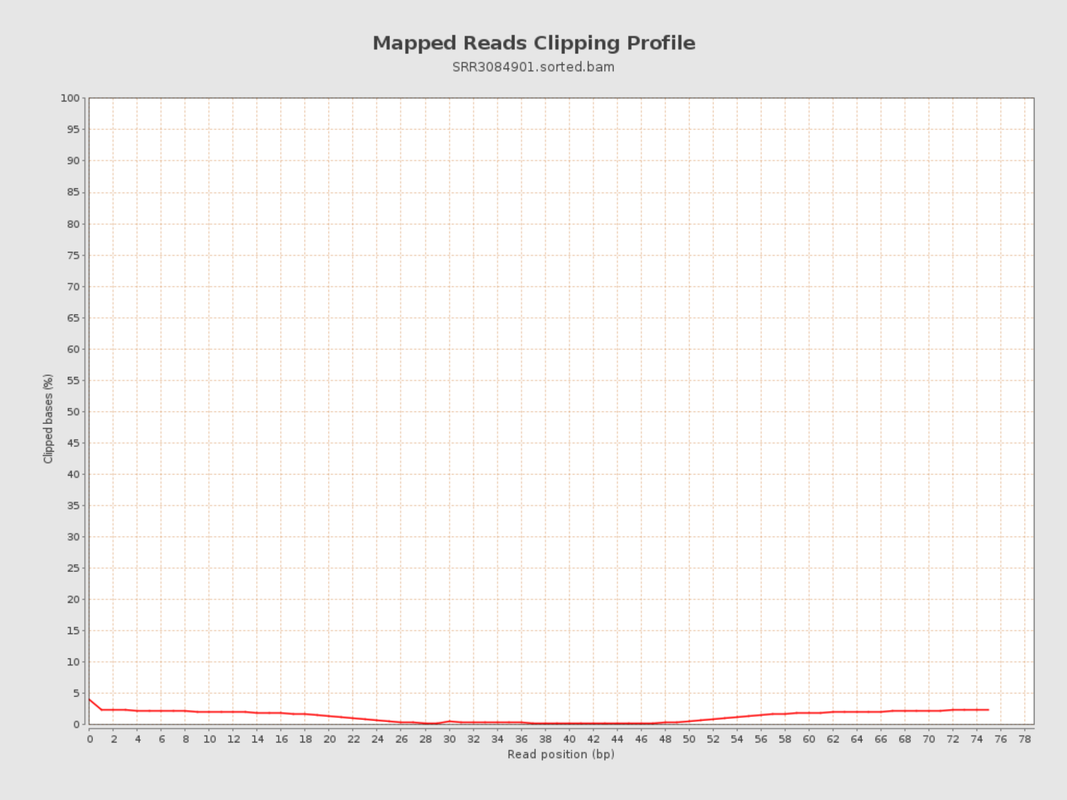
8. Results : Mapped Reads Nucleotide Content



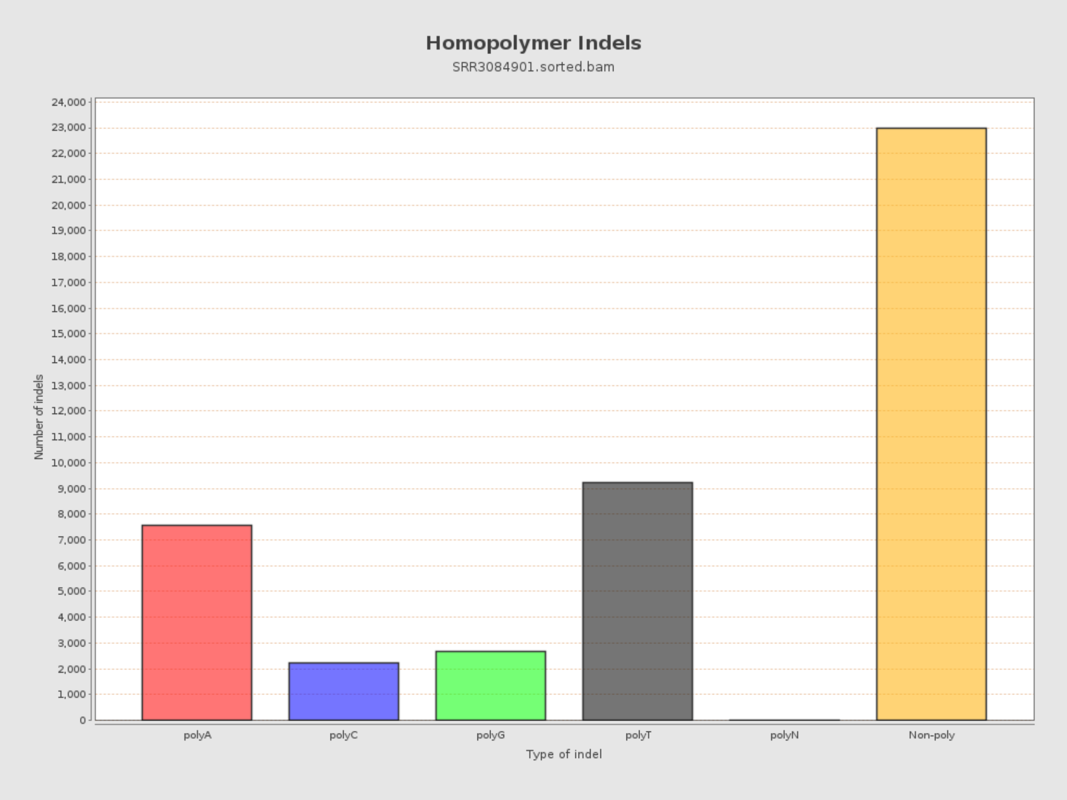
9. Results : Mapped Reads GC-content Distribution



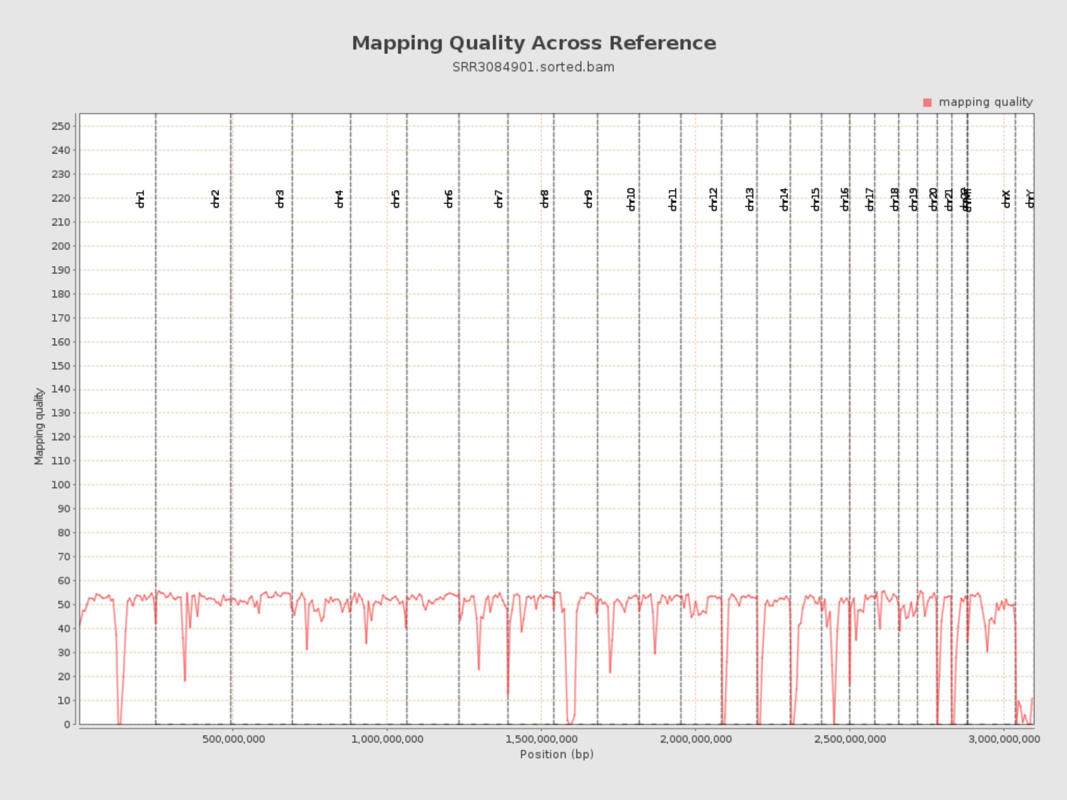
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram