Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:59:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084904.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_SRR3084904 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084904.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:59:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084904.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,896,618
Mapped reads	1,700,352 / 89.65%
Unmapped reads	196,266 / 10.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,888 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	82,322 / 4.34%
Duplication rate	4.24%
Clipped reads	675,496 / 35.62%

2.2. ACGT Content

Number/percentage of A's	32,850,762 / 28.49%
Number/percentage of C's	20,916,548 / 18.14%
Number/percentage of T's	37,086,487 / 32.16%
Number/percentage of G's	24,436,757 / 21.19%
Number/percentage of N's	17,209 / 0.01%
GC Percentage	39.33%

2.3. Coverage

Mean	0.0373

Standard Deviation	0.2854

2.4. Mapping Quality

Mean Mapping Quality	47.19

2.5. Mismatches and indels

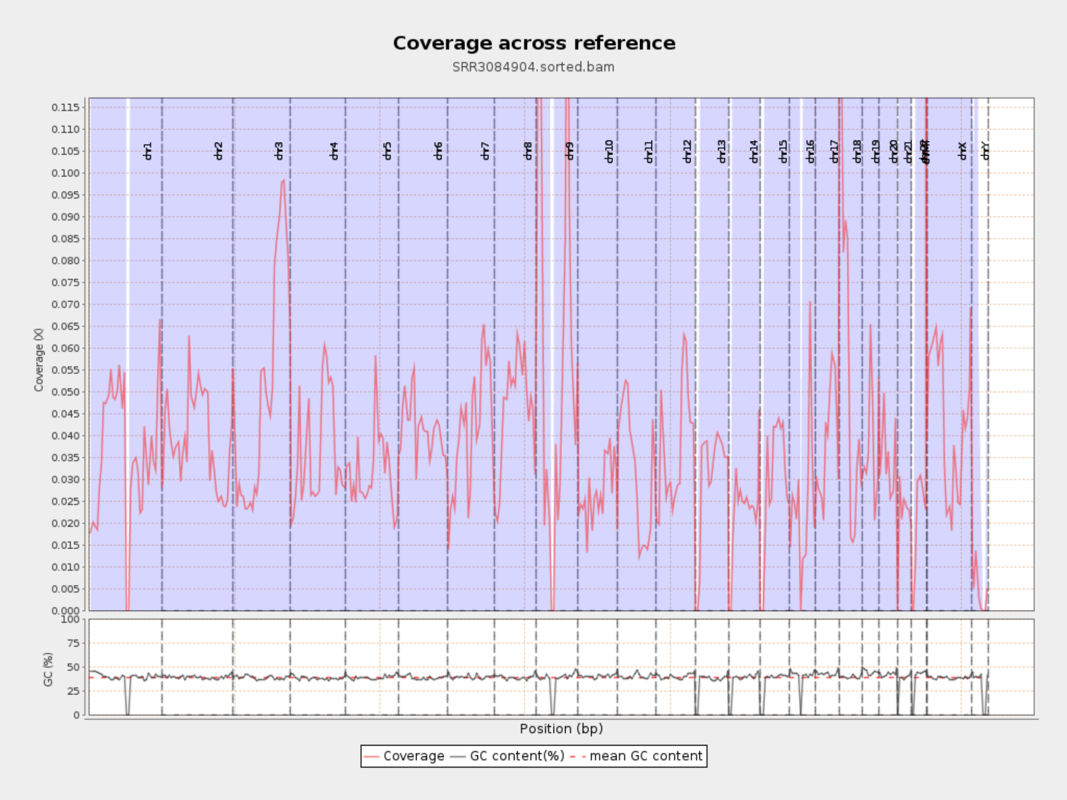
General error rate	0.83%
Mismatches	943,839
Insertions	8,648
Mapped reads with at least one insertion	0.51%
Deletions	24,828
Mapped reads with at least one deletion	1.45%
Homopolymer indels	48.87%

2.6. Chromosome stats

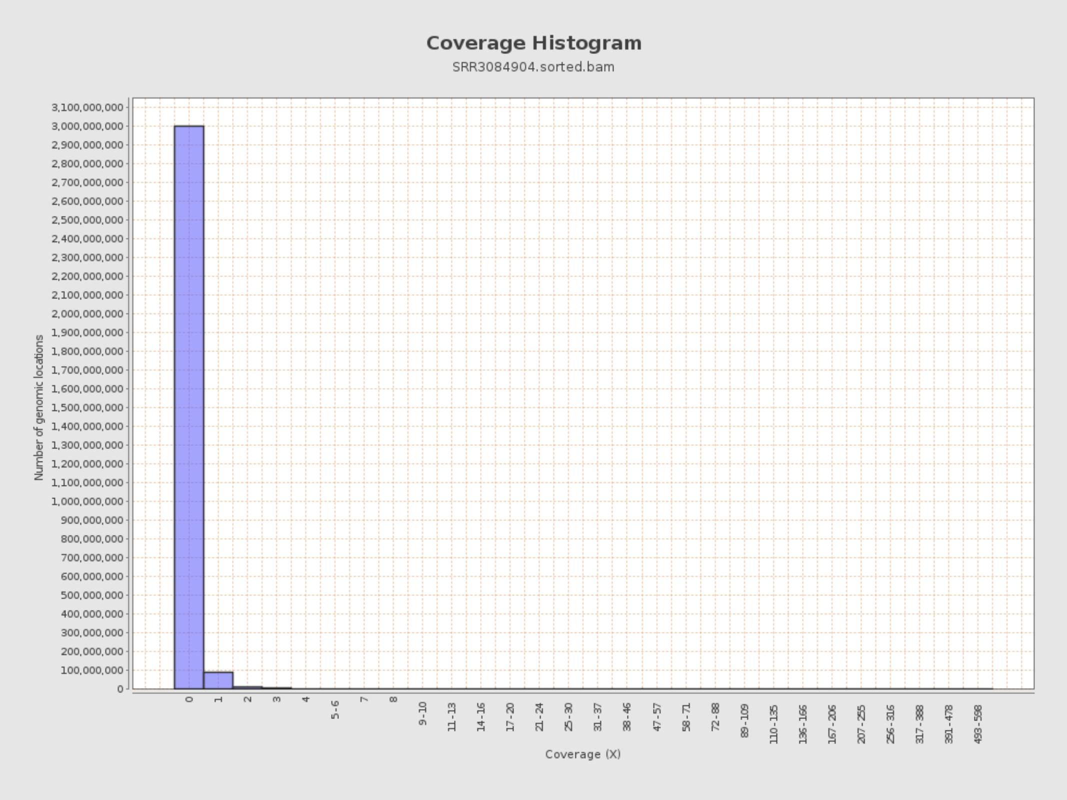
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8917913	0.0358	0.4335
chr2	243199373	9509177	0.0391	0.3235
chr3	198022430	9987503	0.0504	0.2543
chr4	191154276	6962045	0.0364	0.2171
chr5	180915260	5696440	0.0315	0.2024
chr6	171115067	7085529	0.0414	0.2394
chr7	159138663	6627950	0.0416	0.2811

chr8	146364022	6734170	0.046	0.4642
chr9	141213431	8562737	0.0606	0.3417
chr10	135534747	3678777	0.0271	0.2157
chr11	135006516	4304064	0.0319	0.2333
chr12	133851895	4952179	0.037	0.2194
chr13	115169878	3466101	0.0301	0.1949
chr14	107349540	2321538	0.0216	0.1731
chr15	102531392	2996258	0.0292	0.1921
chr16	90354753	2249395	0.0249	0.186
chr17	81195210	3174416	0.0391	0.225
chr18	78077248	4545390	0.0582	0.4959
chr19	59128983	2245702	0.038	0.3105
chr20	63025520	2202770	0.035	0.2142
chr21	48129895	1053980	0.0219	0.174
chr22	51304566	1001532	0.0195	0.1555
chrMT	16571	49912	3.012	2.2021
chrX	155270560	6762944	0.0436	0.2477
chrY	59373566	262595	0.0044	0.1204

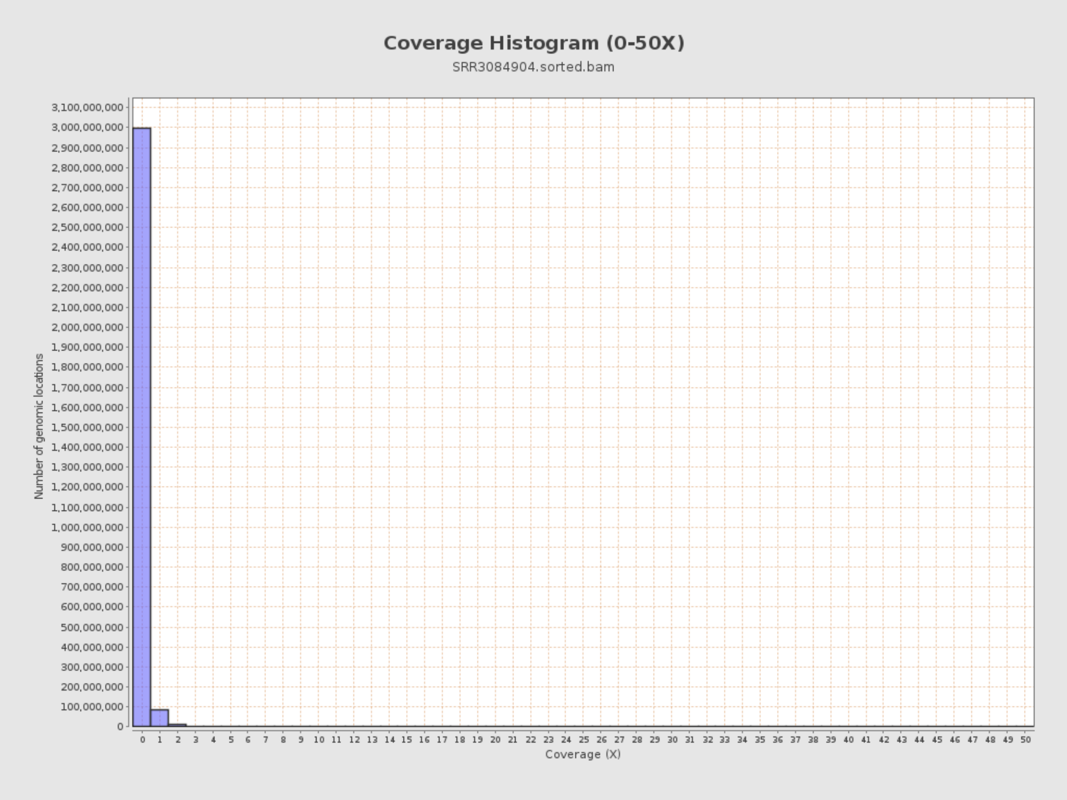
3. Results : Coverage across reference



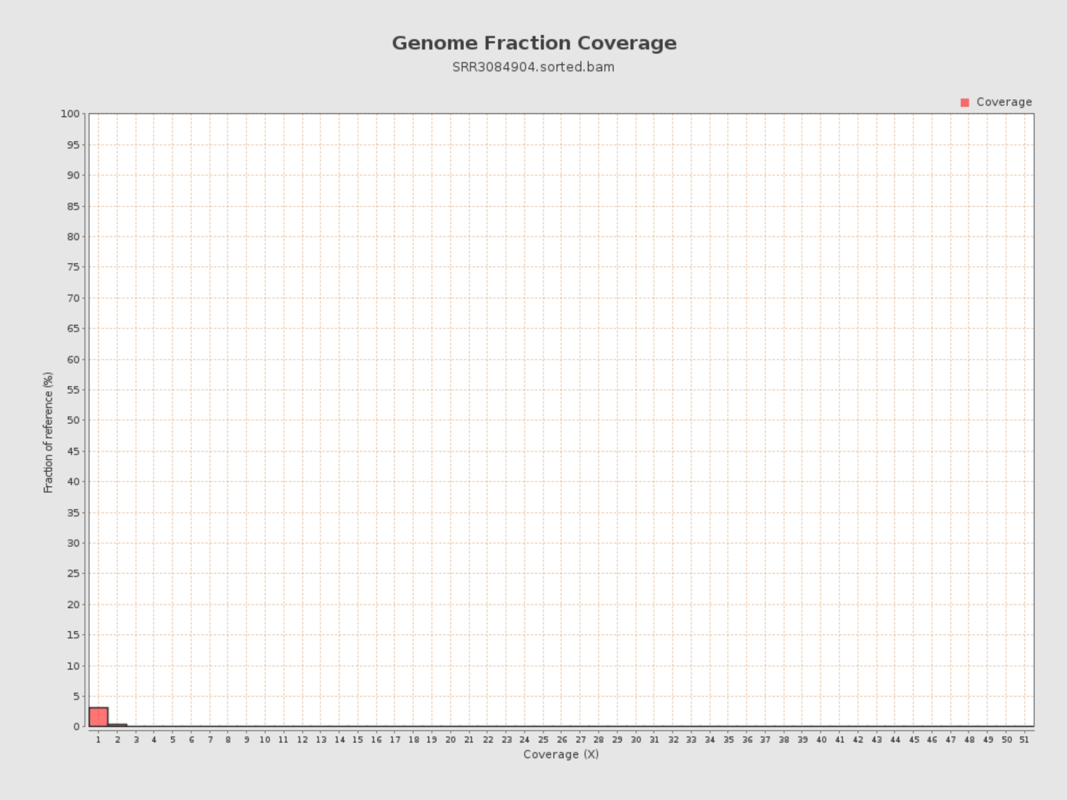
4. Results : Coverage Histogram



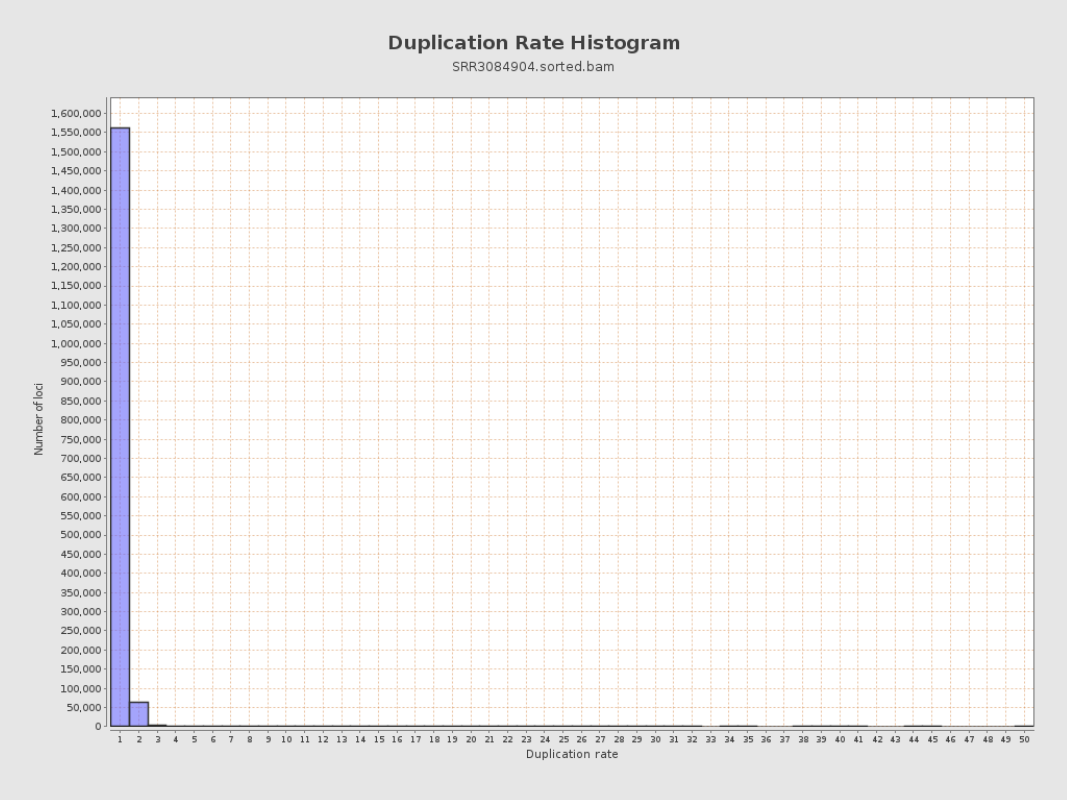
5. Results : Coverage Histogram (0-50X)



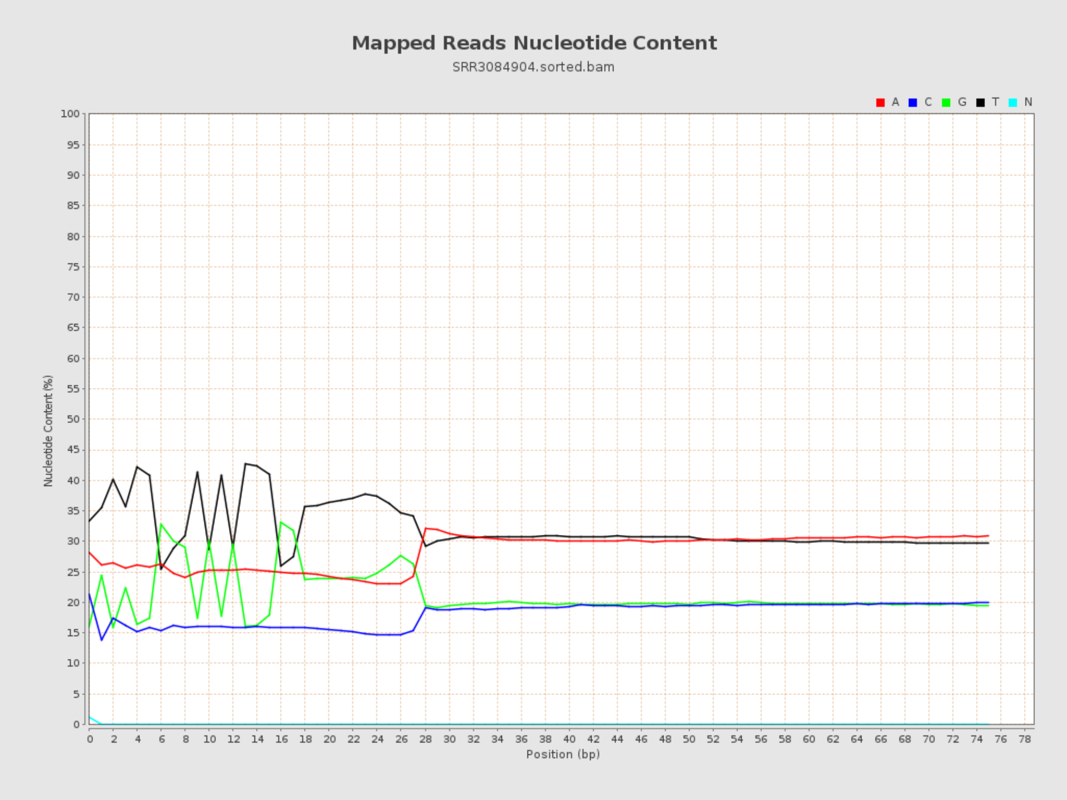
6. Results : Genome Fraction Coverage



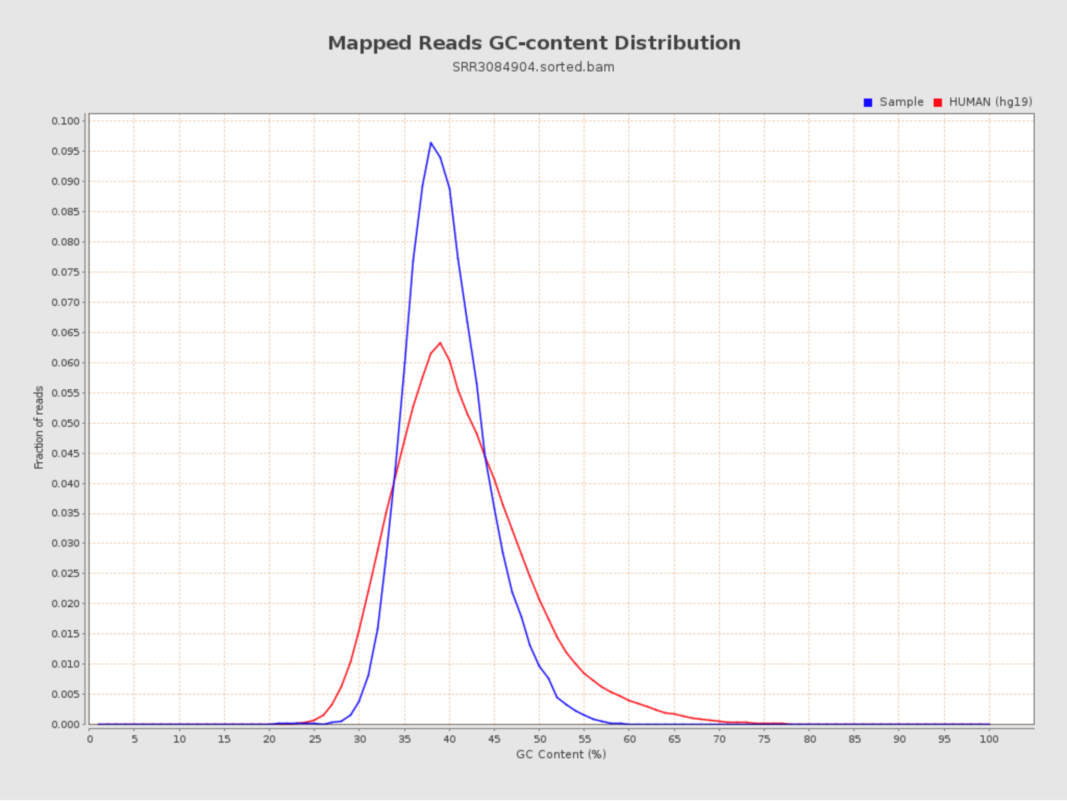
7. Results : Duplication Rate Histogram



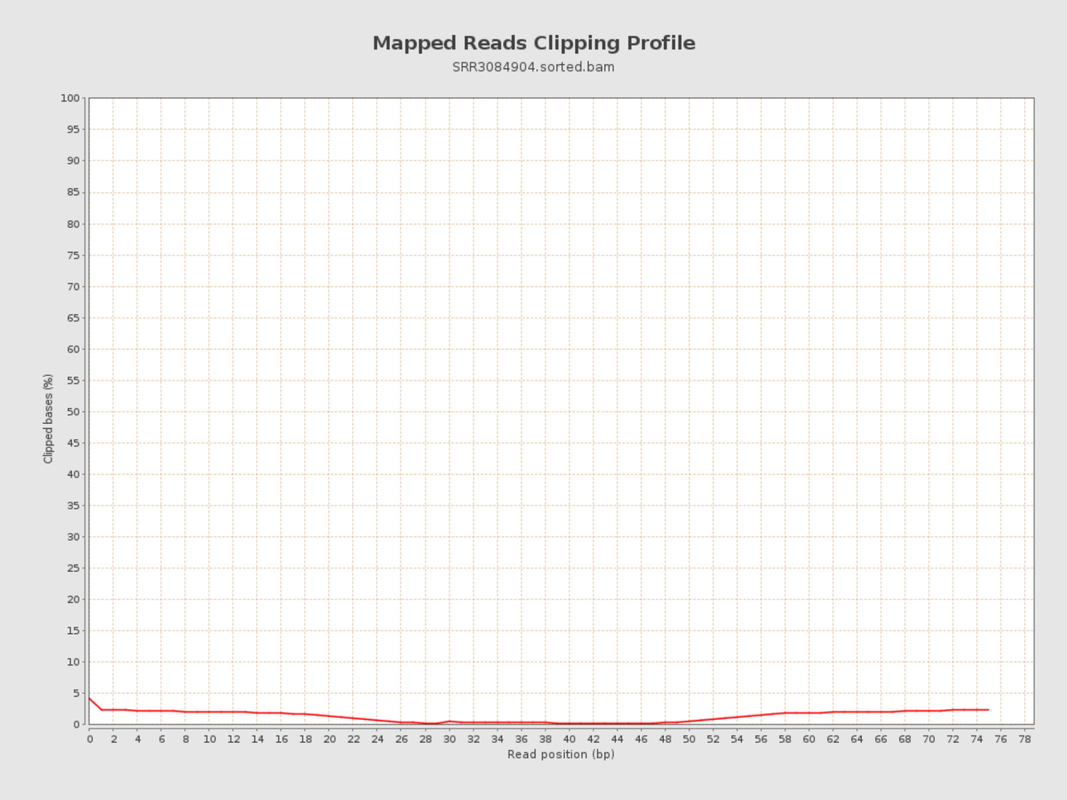
8. Results : Mapped Reads Nucleotide Content



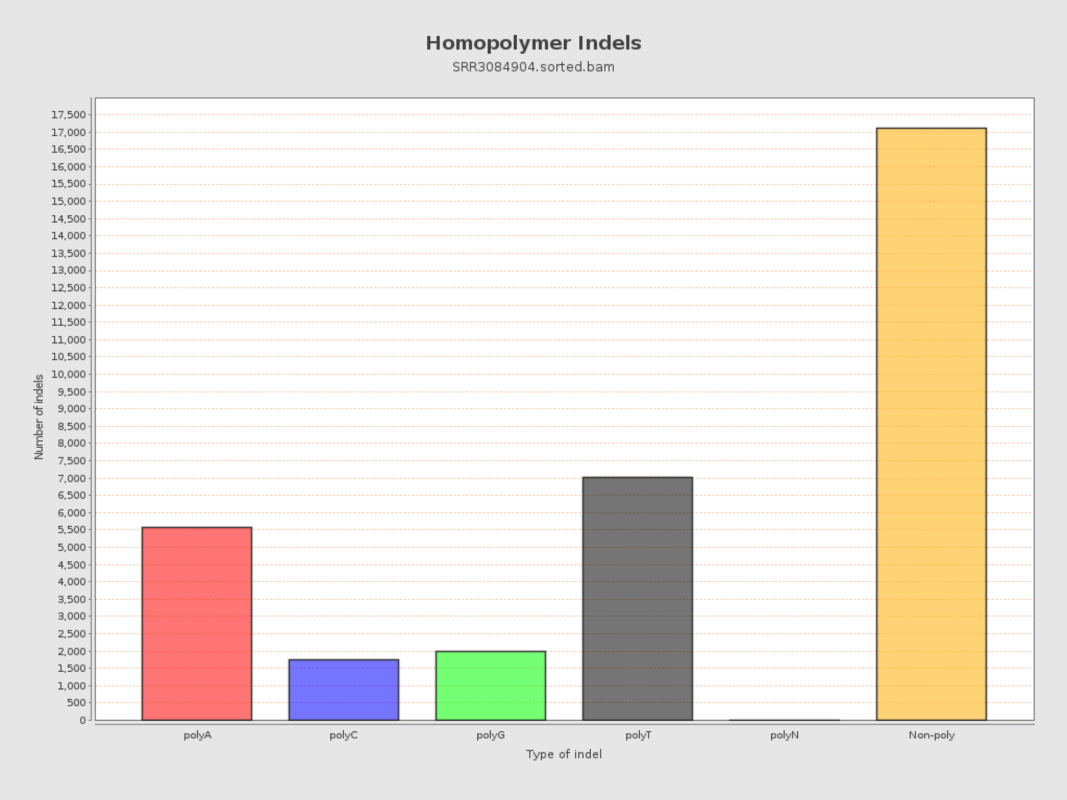
9. Results : Mapped Reads GC-content Distribution



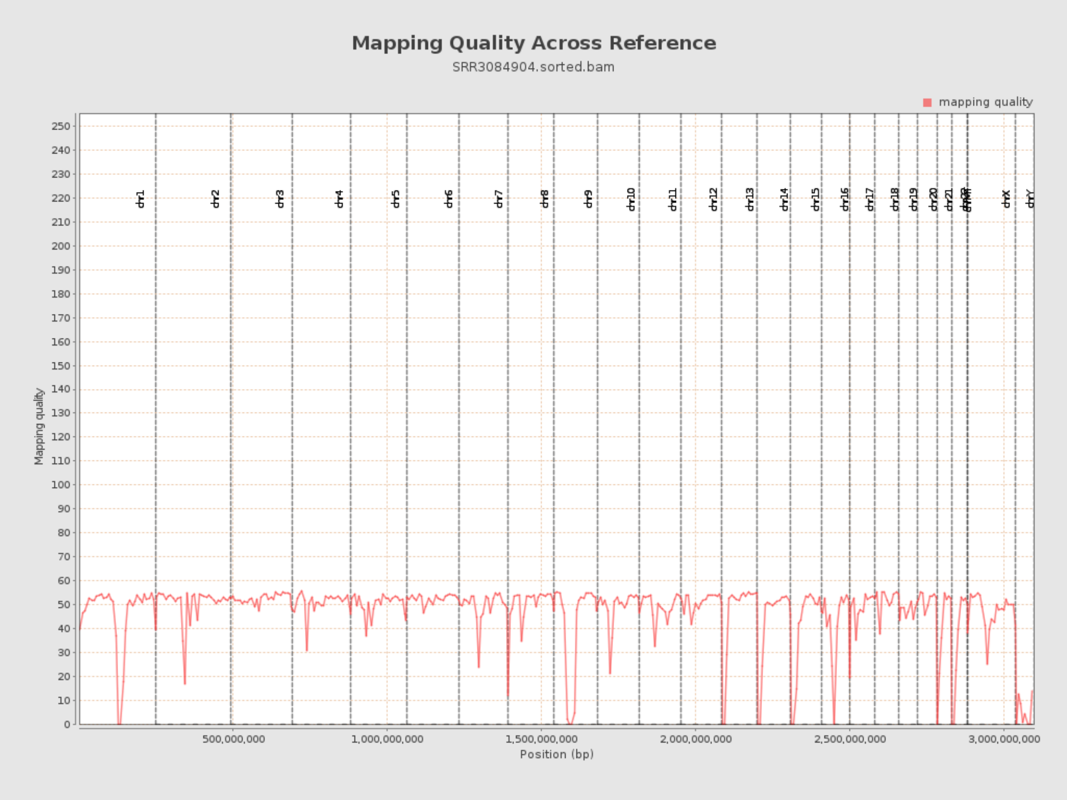
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram