Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:53:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082947.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_SRR3082947 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082947.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:53:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082947.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,736,141
Mapped reads	1,588,385 / 91.49%
Unmapped reads	147,756 / 8.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,243 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	74,211 / 4.27%
Duplication rate	3.75%
Clipped reads	669,548 / 38.57%

2.2. ACGT Content

Number/percentage of A's	29,586,058 / 27.75%
Number/percentage of C's	19,347,548 / 18.15%
Number/percentage of T's	34,304,013 / 32.18%
Number/percentage of G's	23,374,357 / 21.92%
Number/percentage of N's	4,971 / 0%
GC Percentage	40.07%

2.3. Coverage

Mean	0.0345

Standard Deviation	0.3318

2.4. Mapping Quality

Mean Mapping Quality	45.96

2.5. Mismatches and indels

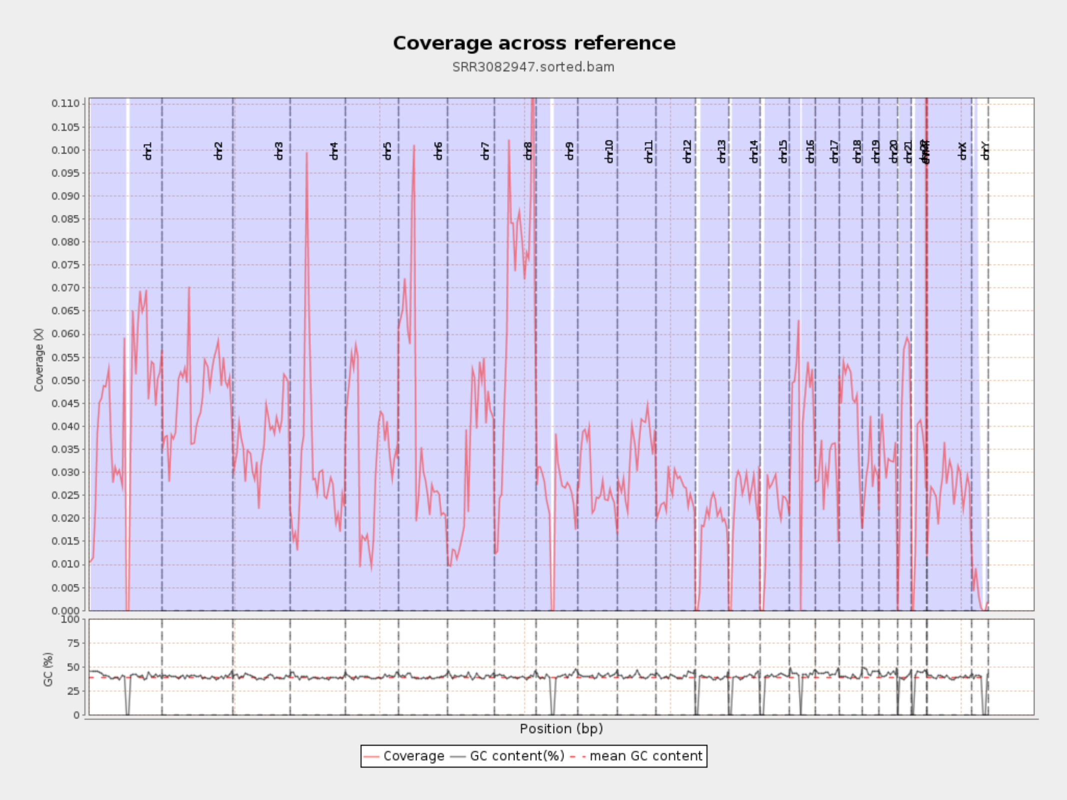
General error rate	0.75%
Mismatches	785,606
Insertions	8,712
Mapped reads with at least one insertion	0.54%
Deletions	25,685
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.24%

2.6. Chromosome stats

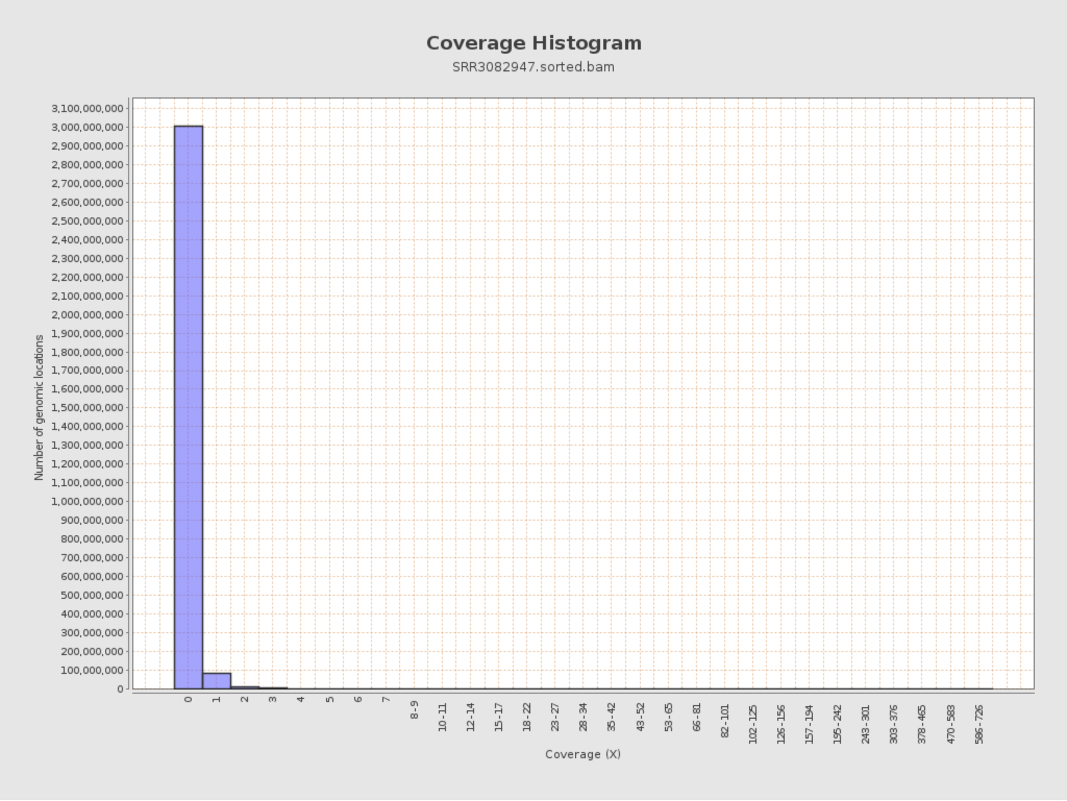
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10551210	0.0423	0.6574
chr2	243199373	11388965	0.0468	0.4343
chr3	198022430	7371981	0.0372	0.2162
chr4	191154276	5791289	0.0303	0.2021
chr5	180915260	6102546	0.0337	0.2079
chr6	171115067	7022850	0.041	0.301
chr7	159138663	5202305	0.0327	0.2848

chr8	146364022	9848021	0.0673	0.4736
chr9	141213431	3459440	0.0245	0.2804
chr10	135534747	3814840	0.0281	0.2268
chr11	135006516	4567984	0.0338	0.2797
chr12	133851895	3404010	0.0254	0.1866
chr13	115169878	2013353	0.0175	0.1518
chr14	107349540	2431285	0.0226	0.192
chr15	102531392	2114999	0.0206	0.1684
chr16	90354753	4014927	0.0444	0.2512
chr17	81195210	2417043	0.0298	0.2251
chr18	78077248	3569012	0.0457	0.5734
chr19	59128983	1757528	0.0297	0.3675
chr20	63025520	2119499	0.0336	0.2164
chr21	48129895	2019729	0.042	0.2352
chr22	51304566	1345426	0.0262	0.1804
chrMT	16571	56370	3.4017	2.5231
chrX	155270560	4088269	0.0263	0.2054
chrY	59373566	185720	0.0031	0.0737

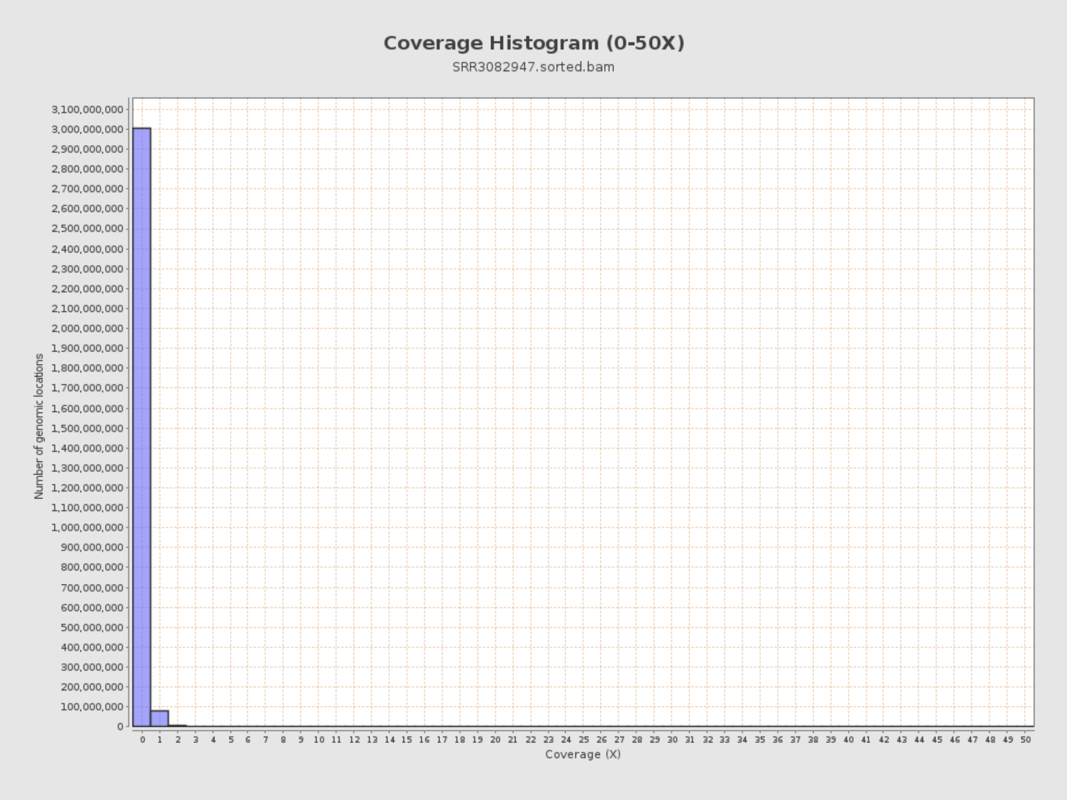
3. Results : Coverage across reference



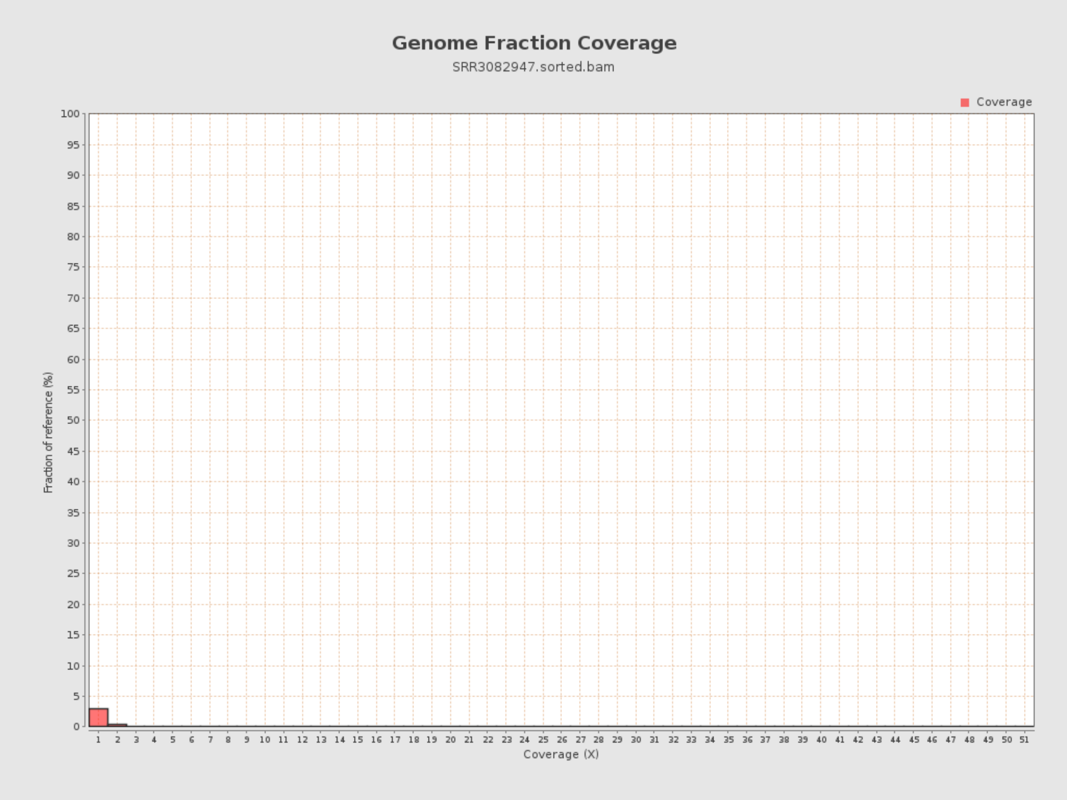
4. Results : Coverage Histogram



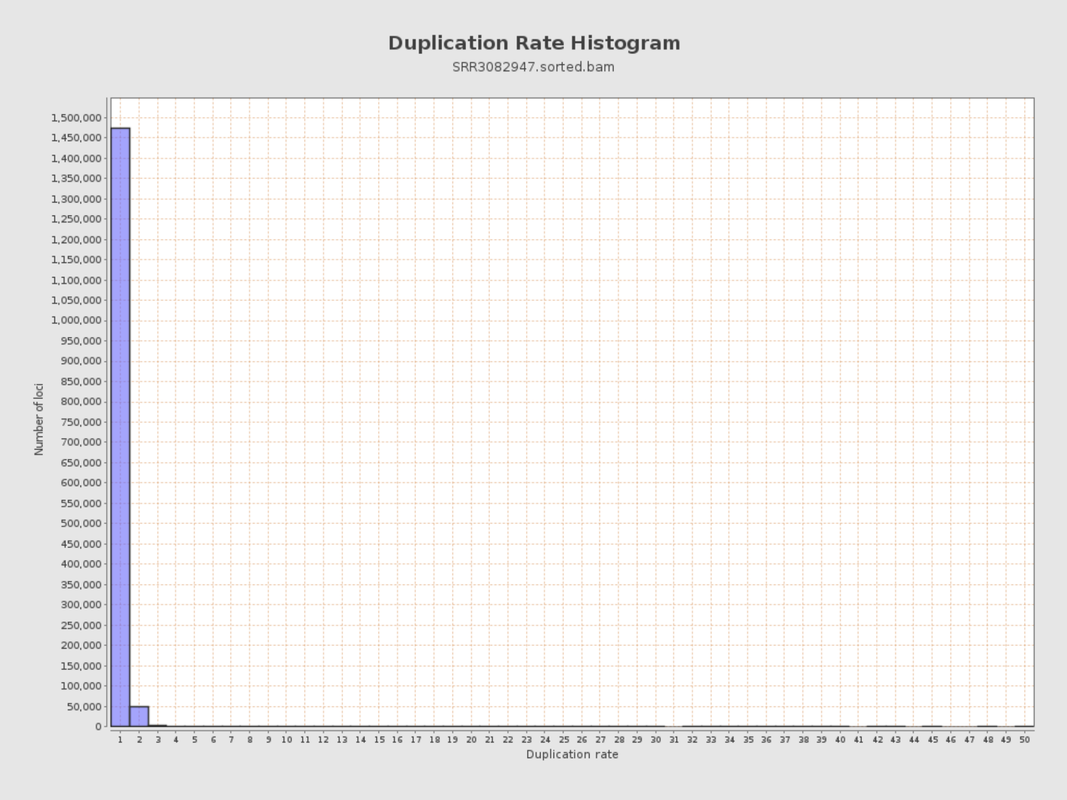
5. Results : Coverage Histogram (0-50X)



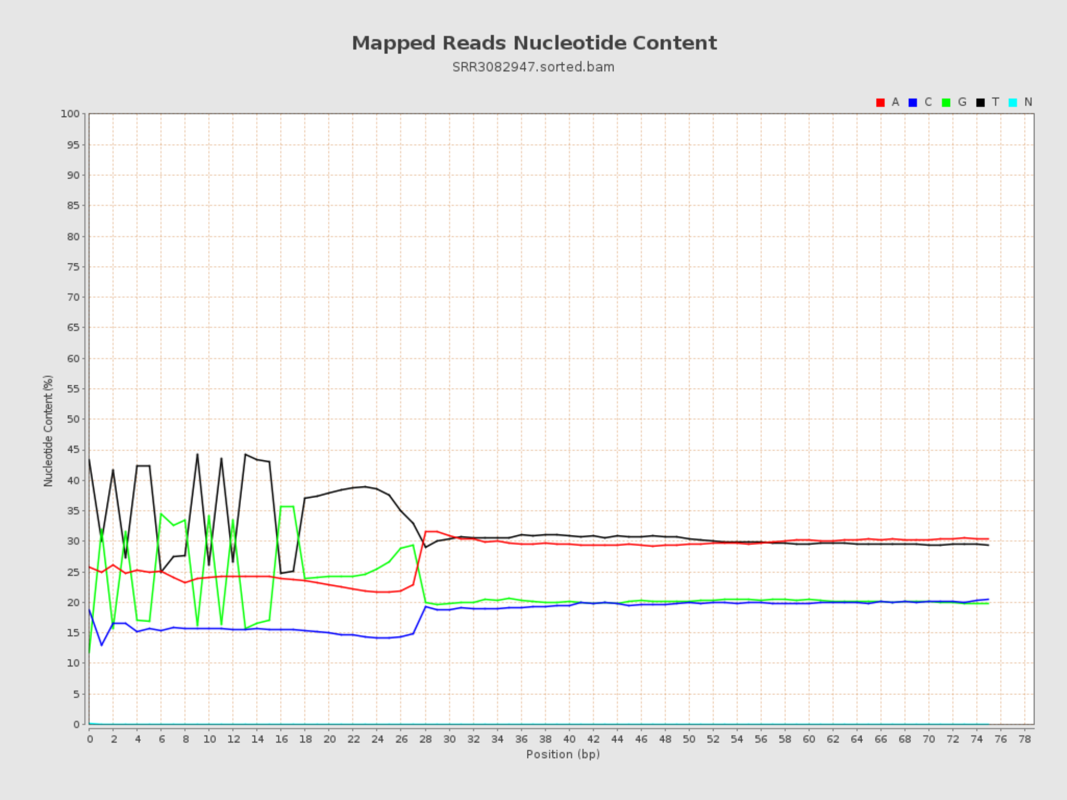
6. Results : Genome Fraction Coverage



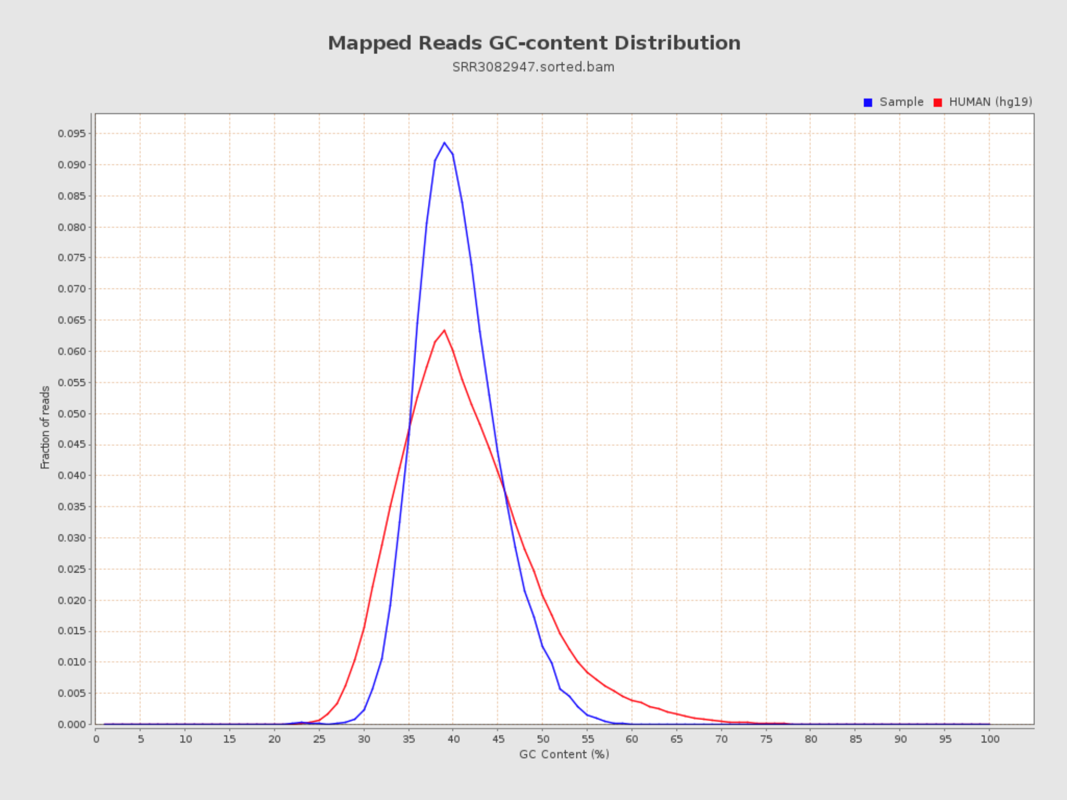
7. Results : Duplication Rate Histogram



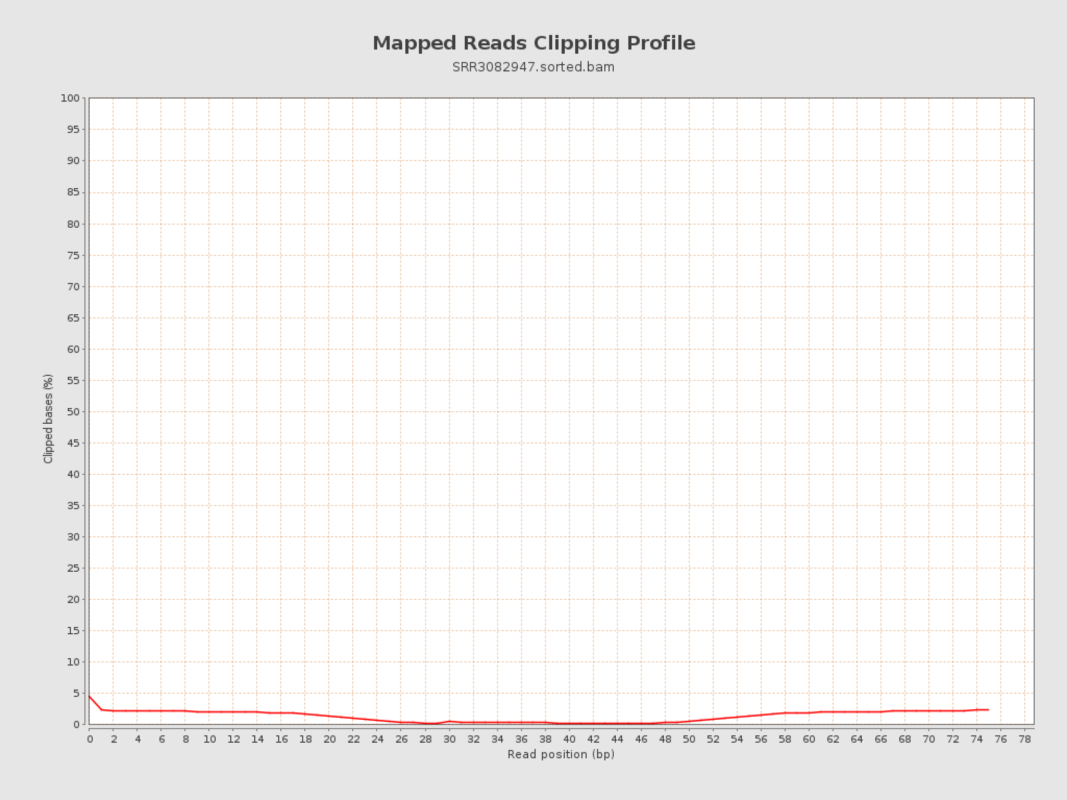
8. Results : Mapped Reads Nucleotide Content



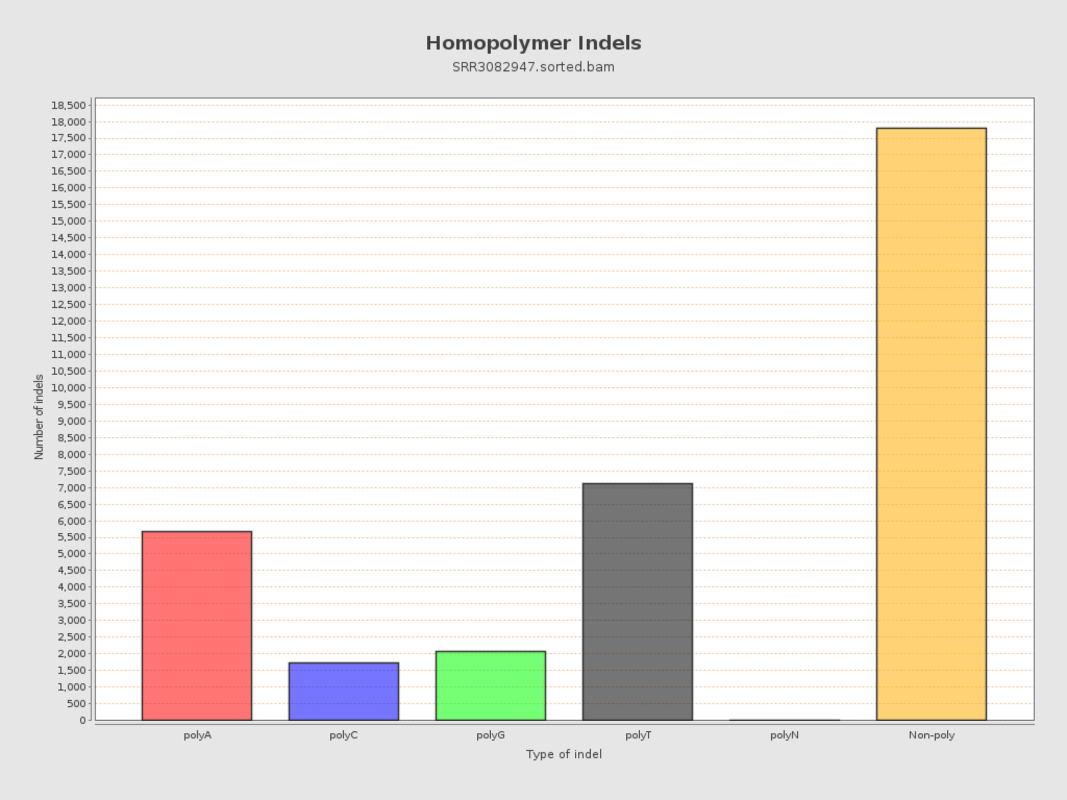
9. Results : Mapped Reads GC-content Distribution



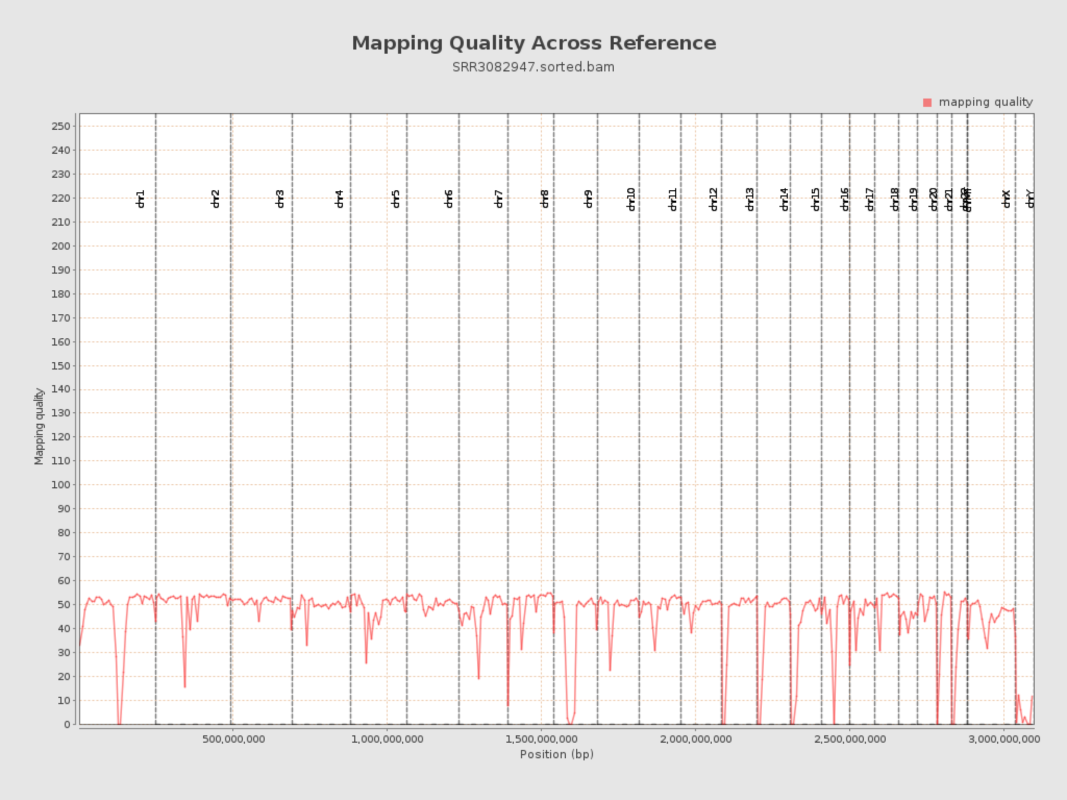
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram