Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:57:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081027.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_SRR3081027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081027.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:57:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081027.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,595,399
Mapped reads	1,987,020 / 76.56%
Unmapped reads	608,379 / 23.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,669 / 0.33%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	59,255 / 2.28%
Duplication rate	2.17%
Clipped reads	1,198,726 / 46.19%

2.2. ACGT Content

Number/percentage of A's	35,627,010 / 28.88%
Number/percentage of C's	24,706,186 / 20.03%
Number/percentage of T's	35,631,712 / 28.89%
Number/percentage of G's	27,386,611 / 22.2%
Number/percentage of N's	1,663 / 0%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0399

Standard Deviation	0.3402

2.4. Mapping Quality

Mean Mapping Quality	44.32

2.5. Mismatches and indels

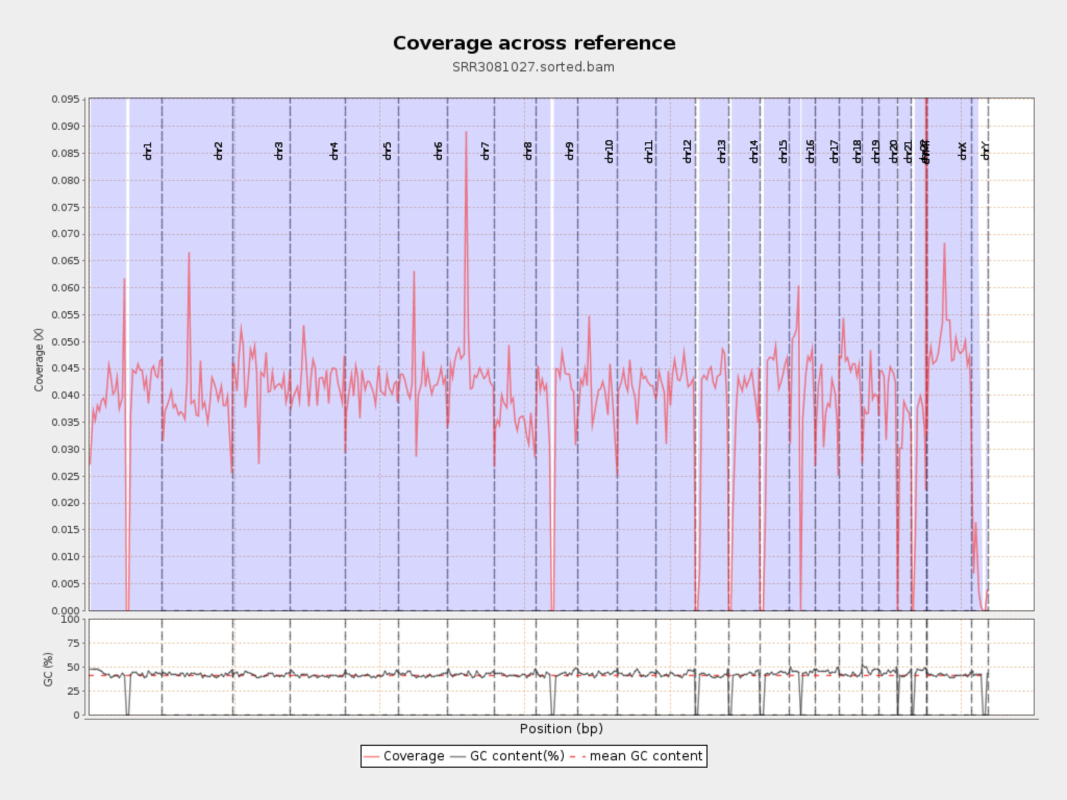
General error rate	0.81%
Mismatches	986,979
Insertions	8,592
Mapped reads with at least one insertion	0.43%
Deletions	24,743
Mapped reads with at least one deletion	1.23%
Homopolymer indels	45.05%

2.6. Chromosome stats

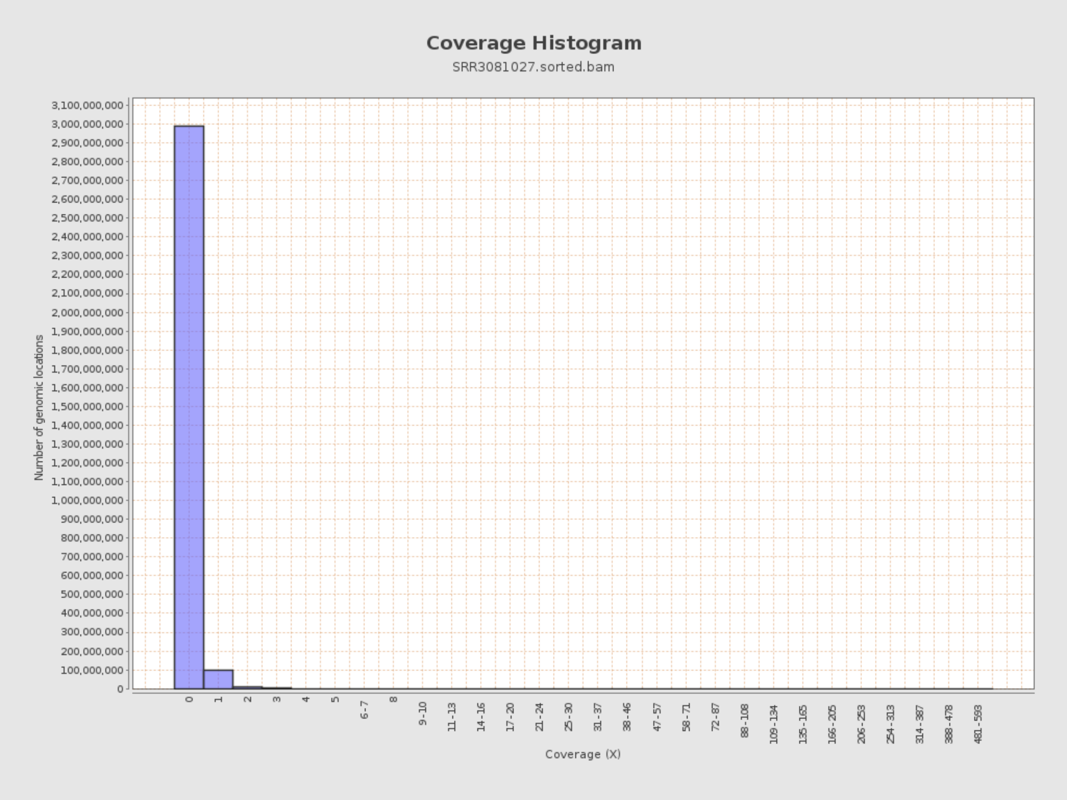
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9764277	0.0392	0.51
chr2	243199373	9519234	0.0391	0.3652
chr3	198022430	8576691	0.0433	0.2279
chr4	191154276	8156965	0.0427	0.2399
chr5	180915260	7494668	0.0414	0.2251
chr6	171115067	7309720	0.0427	0.3112
chr7	159138663	7442888	0.0468	0.6728

chr8	146364022	5278125	0.0361	0.3148
chr9	141213431	5254573	0.0372	0.3122
chr10	135534747	5492761	0.0405	0.2893
chr11	135006516	5612136	0.0416	0.3137
chr12	133851895	5646533	0.0422	0.2286
chr13	115169878	4195906	0.0364	0.2096
chr14	107349540	3680411	0.0343	0.2208
chr15	102531392	3778035	0.0368	0.2244
chr16	90354753	3829891	0.0424	0.2471
chr17	81195210	3063063	0.0377	0.2433
chr18	78077248	3607854	0.0462	0.5786
chr19	59128983	2310932	0.0391	0.4014
chr20	63025520	2604999	0.0413	0.2312
chr21	48129895	1507529	0.0313	0.2091
chr22	51304566	1301576	0.0254	0.1742
chrMT	16571	11360	0.6855	0.9777
chrX	155270560	7621685	0.0491	0.2853
chrY	59373566	333261	0.0056	0.1251

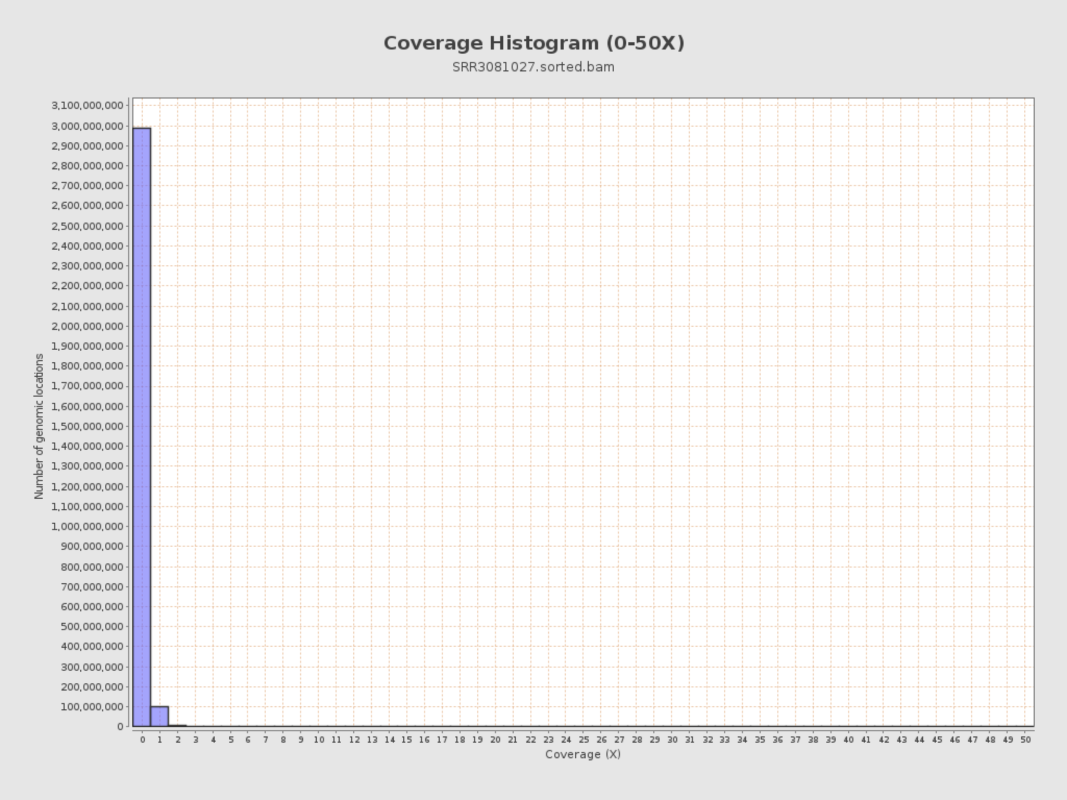
3. Results : Coverage across reference



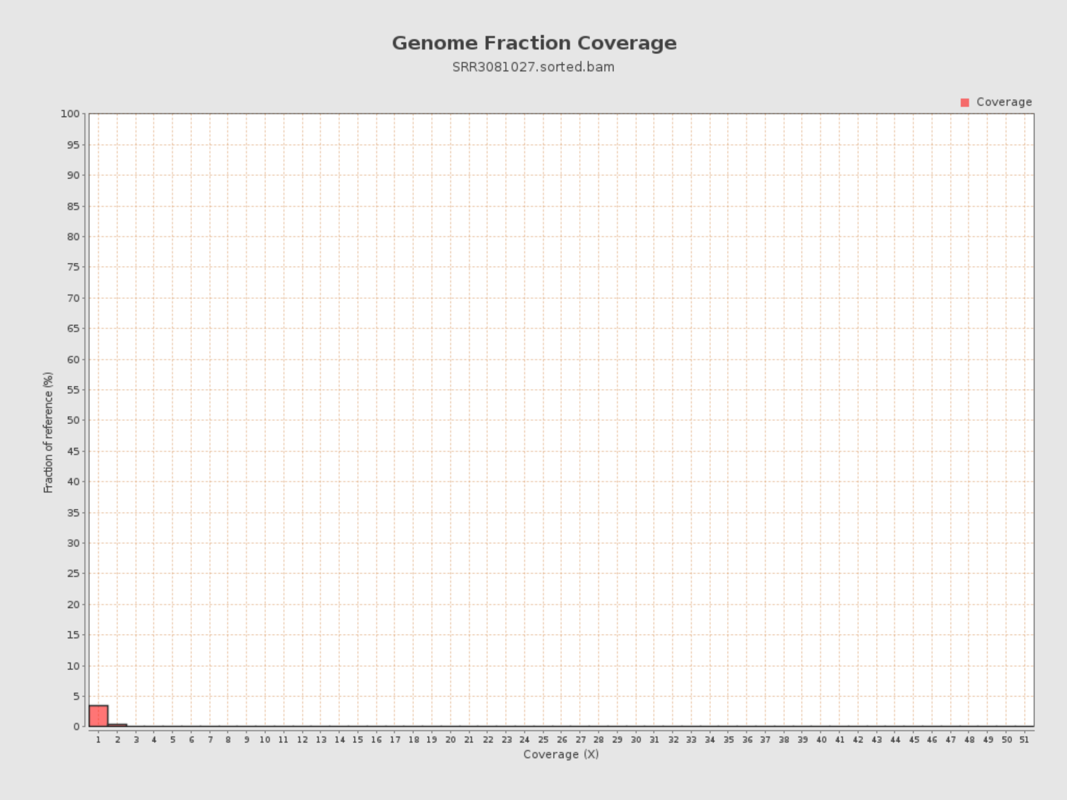
4. Results : Coverage Histogram



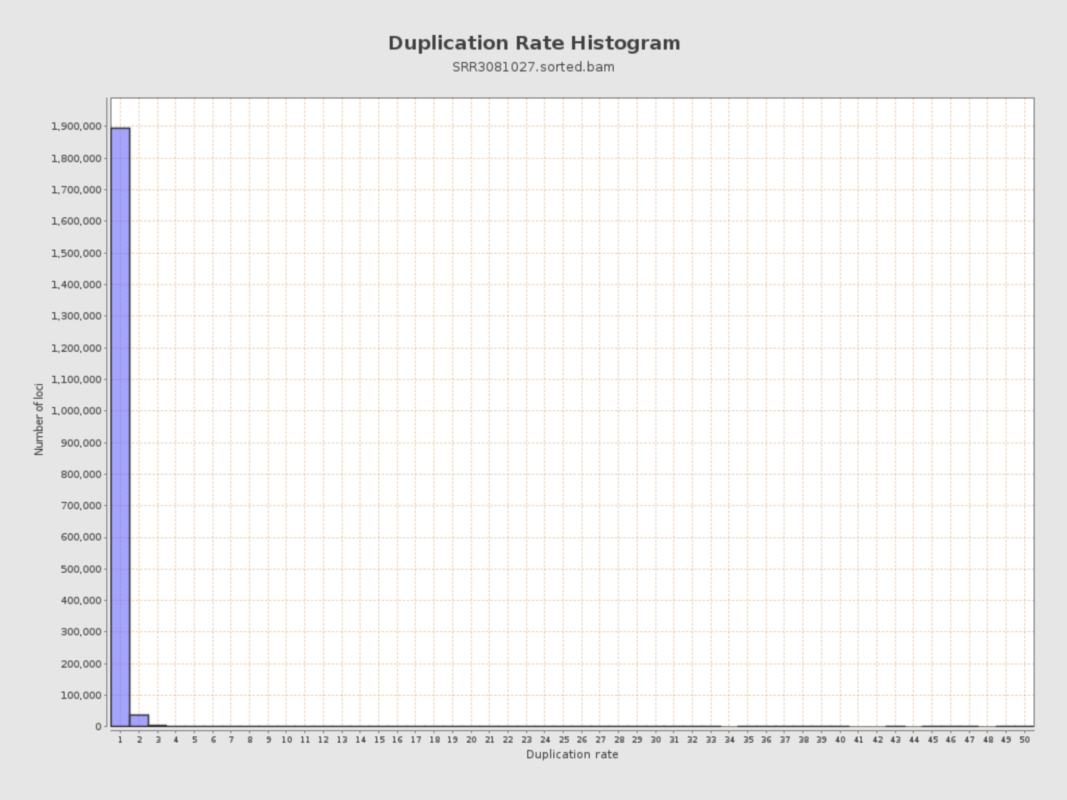
5. Results : Coverage Histogram (0-50X)



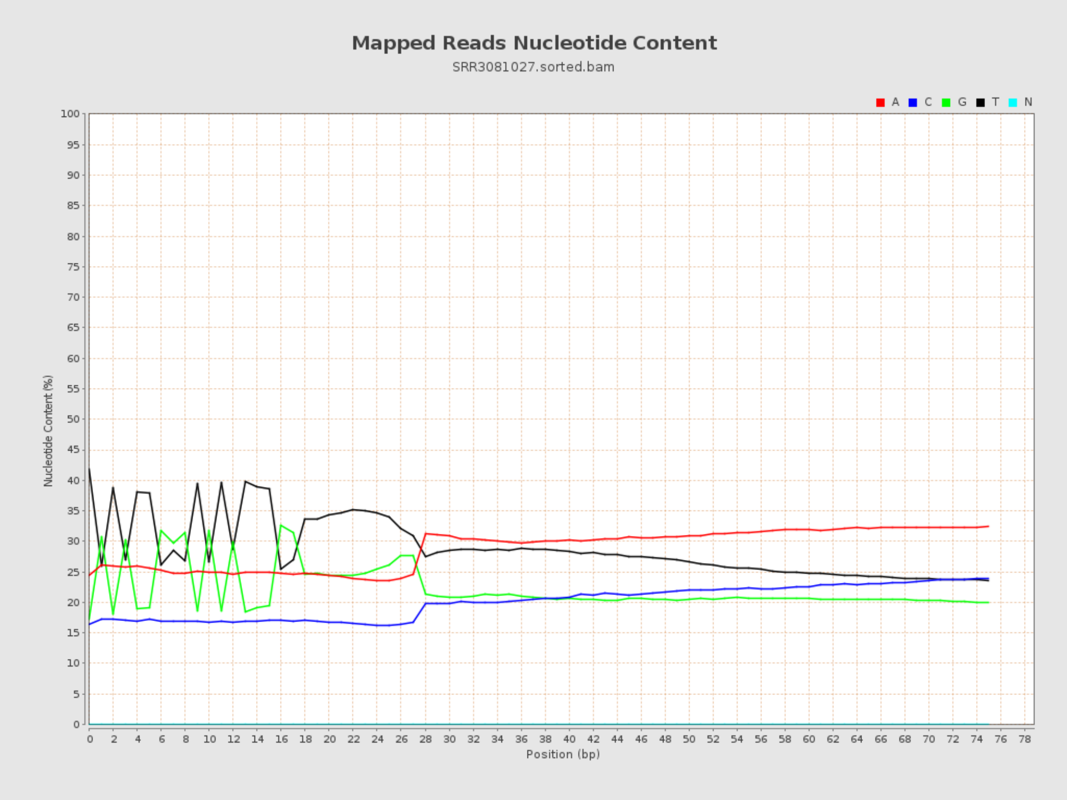
6. Results : Genome Fraction Coverage



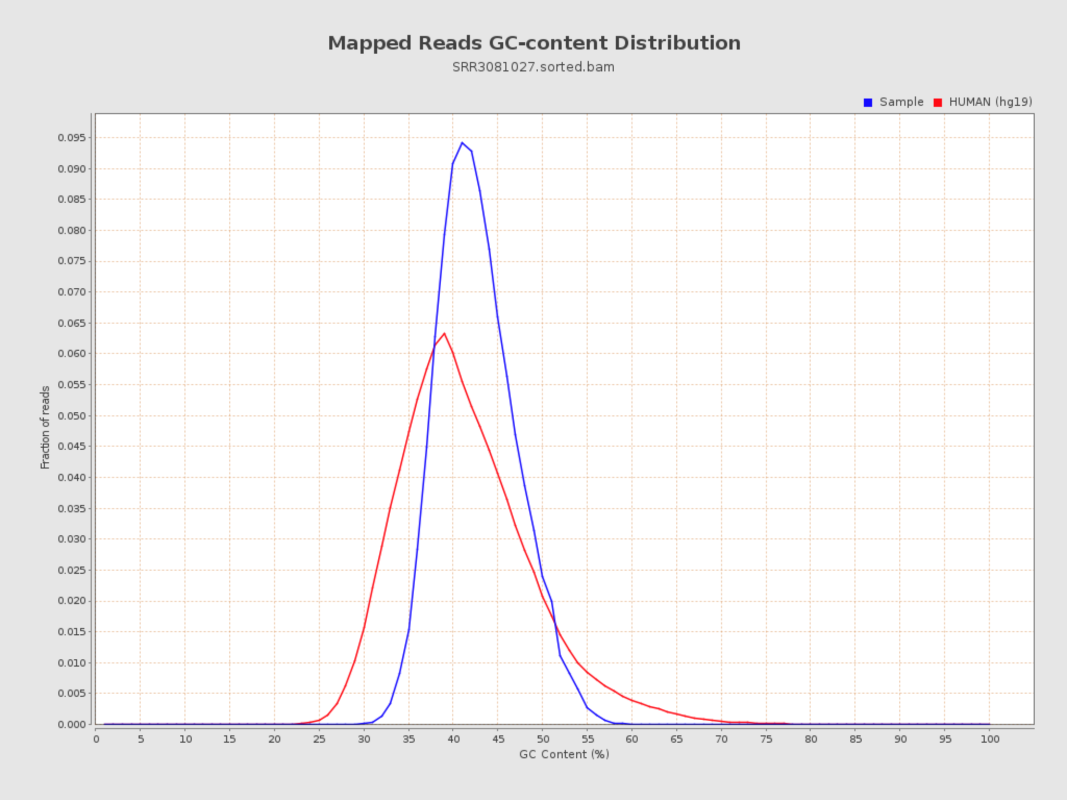
7. Results : Duplication Rate Histogram



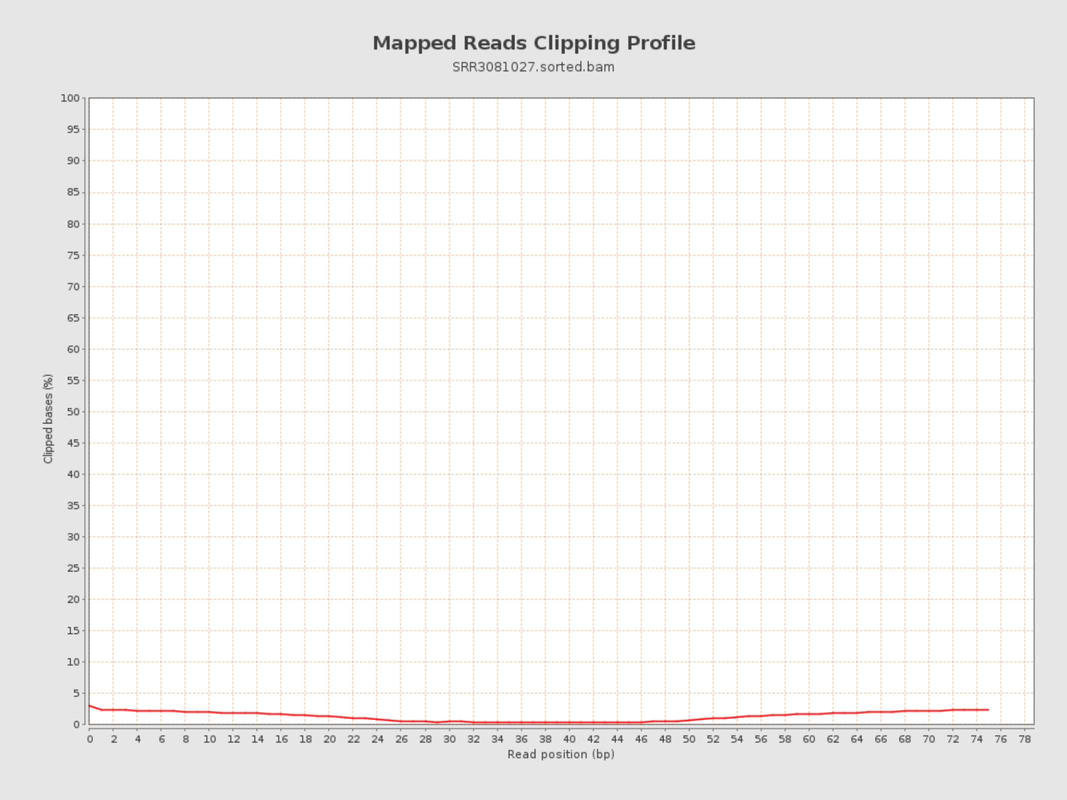
8. Results : Mapped Reads Nucleotide Content



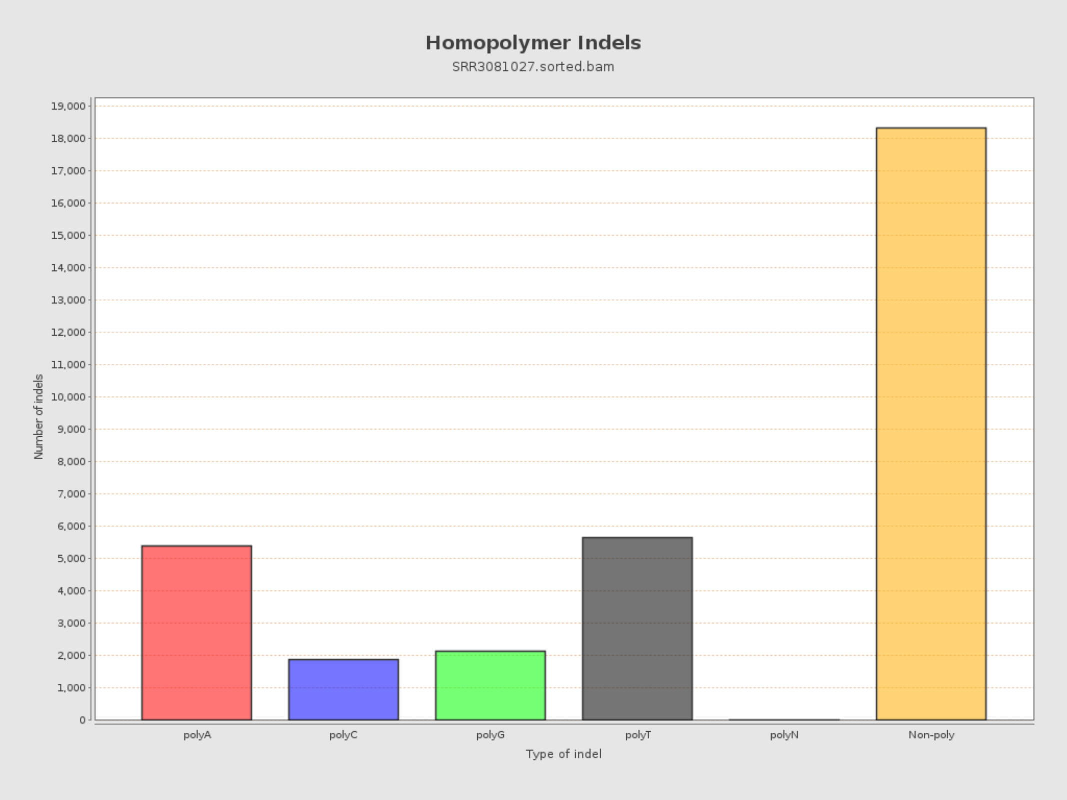
9. Results : Mapped Reads GC-content Distribution



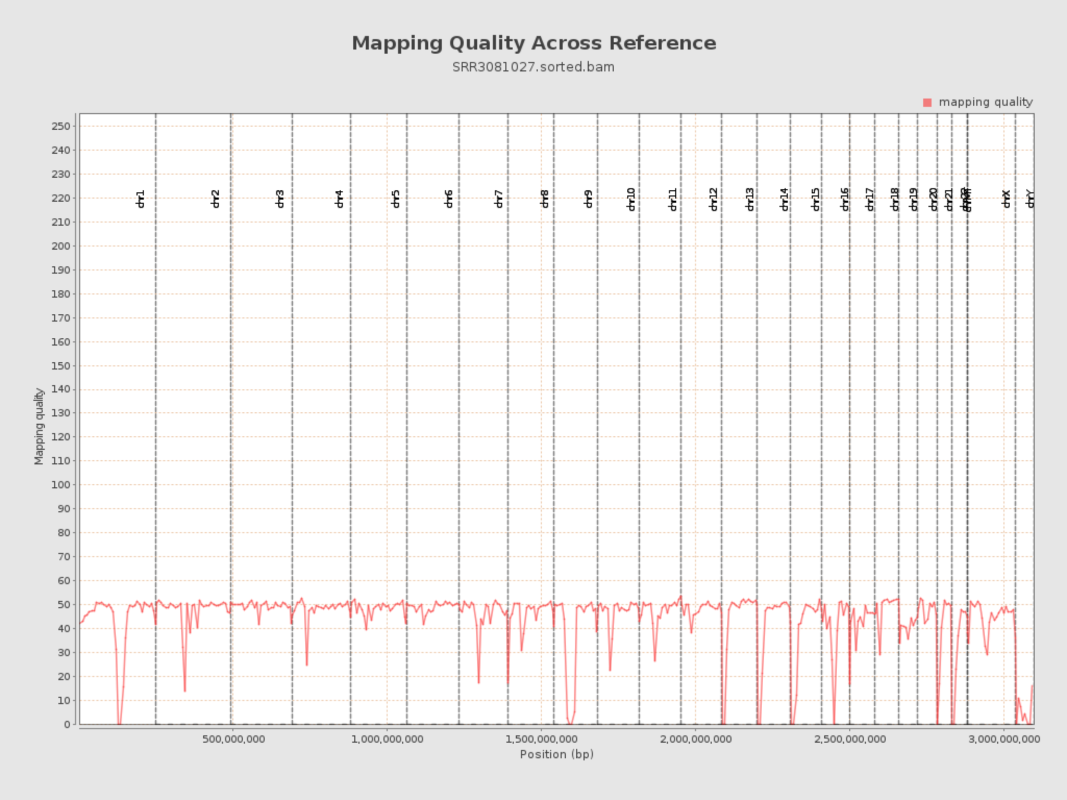
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram