Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:33:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081023.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_SRR3081023 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081023.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:33:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081023.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,302,150
Mapped reads	1,713,924 / 74.45%
Unmapped reads	588,226 / 25.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,254 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	46,868 / 2.04%
Duplication rate	2.09%
Clipped reads	1,114,514 / 48.41%

2.2. ACGT Content

Number/percentage of A's	29,384,578 / 28.48%
Number/percentage of C's	21,123,386 / 20.47%
Number/percentage of T's	29,500,965 / 28.59%
Number/percentage of G's	23,164,622 / 22.45%
Number/percentage of N's	1,234 / 0%
GC Percentage	42.93%

2.3. Coverage

Mean	0.0333

Standard Deviation	0.2737

2.4. Mapping Quality

Mean Mapping Quality	44.28

2.5. Mismatches and indels

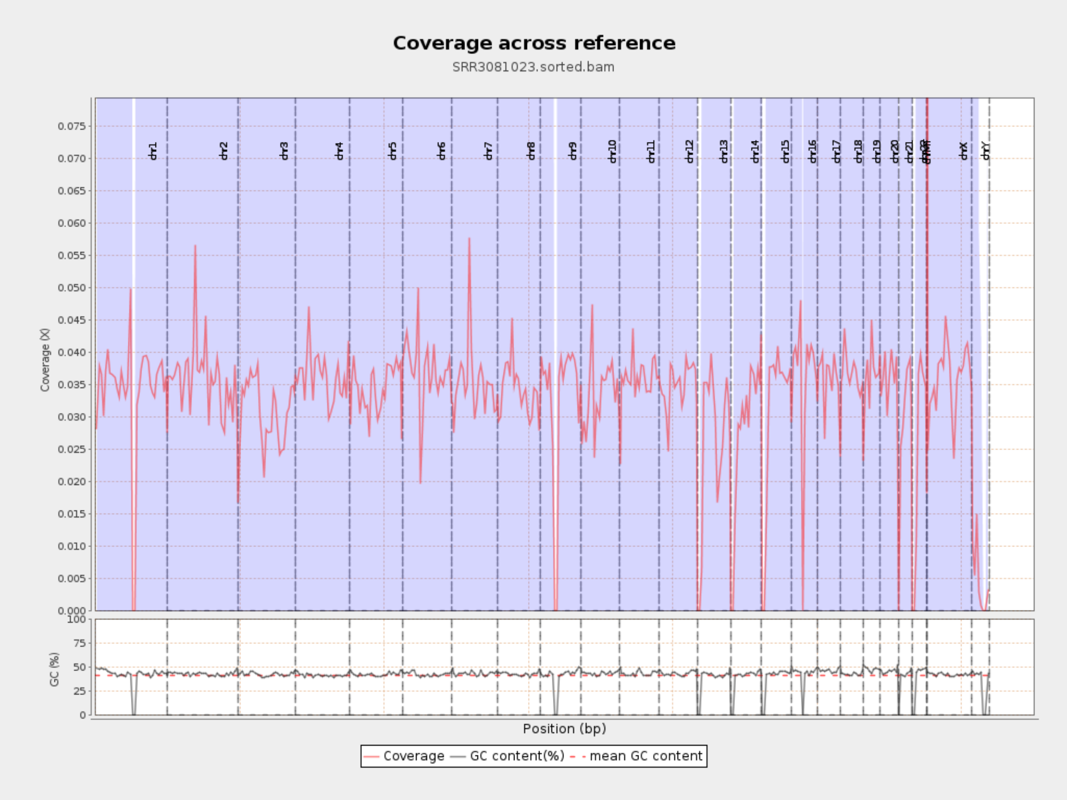
General error rate	0.74%
Mismatches	753,096
Insertions	6,877
Mapped reads with at least one insertion	0.4%
Deletions	20,347
Mapped reads with at least one deletion	1.18%
Homopolymer indels	44.8%

2.6. Chromosome stats

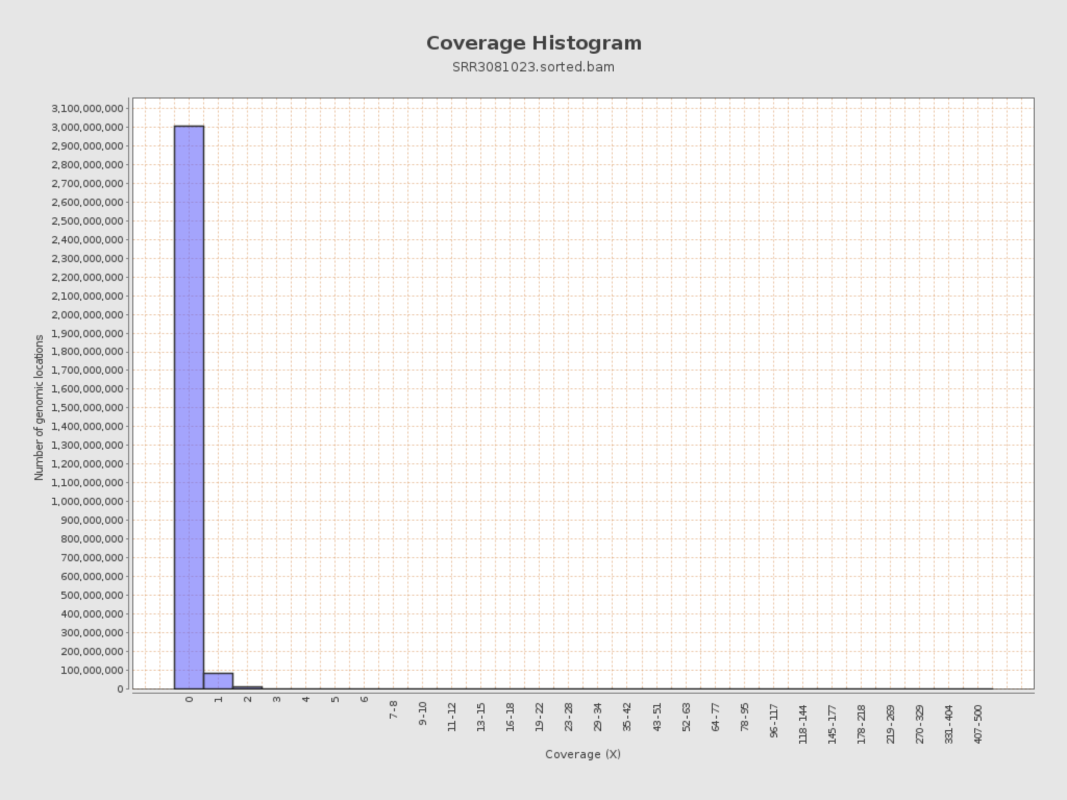
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8424968	0.0338	0.4348
chr2	243199373	8795908	0.0362	0.3049
chr3	198022430	6102321	0.0308	0.1915
chr4	191154276	6947526	0.0363	0.2212
chr5	180915260	6277308	0.0347	0.2036
chr6	171115067	6337394	0.037	0.2683
chr7	159138663	5631217	0.0354	0.3682

chr8	146364022	4982484	0.034	0.2628
chr9	141213431	4584961	0.0325	0.2606
chr10	135534747	4550441	0.0336	0.2564
chr11	135006516	4883272	0.0362	0.2788
chr12	133851895	4669026	0.0349	0.2065
chr13	115169878	2982605	0.0259	0.1748
chr14	107349540	2944542	0.0274	0.1913
chr15	102531392	3100676	0.0302	0.1975
chr16	90354753	3203730	0.0355	0.2247
chr17	81195210	2903423	0.0358	0.2256
chr18	78077248	2869308	0.0367	0.4625
chr19	59128983	2170996	0.0367	0.3497
chr20	63025520	2261804	0.0359	0.2123
chr21	48129895	1423251	0.0296	0.2037
chr22	51304566	1269591	0.0247	0.172
chrMT	16571	17319	1.0451	1.1572
chrX	155270560	5610907	0.0361	0.2269
chrY	59373566	265385	0.0045	0.1141

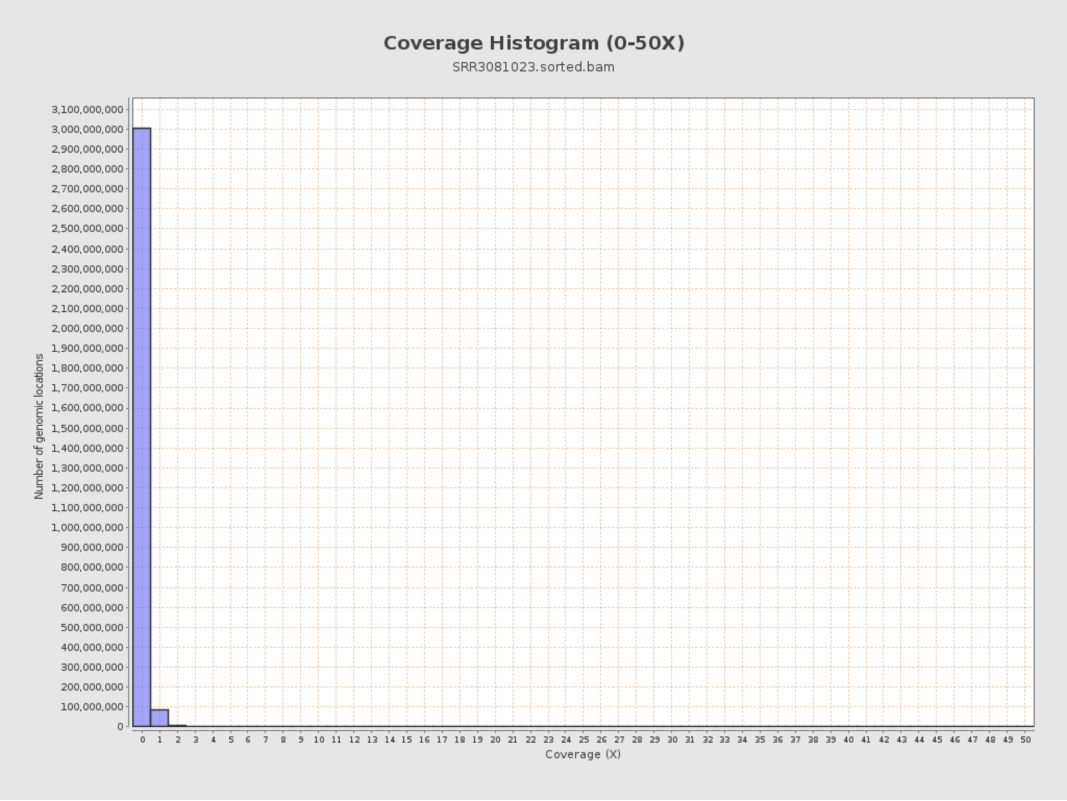
3. Results : Coverage across reference



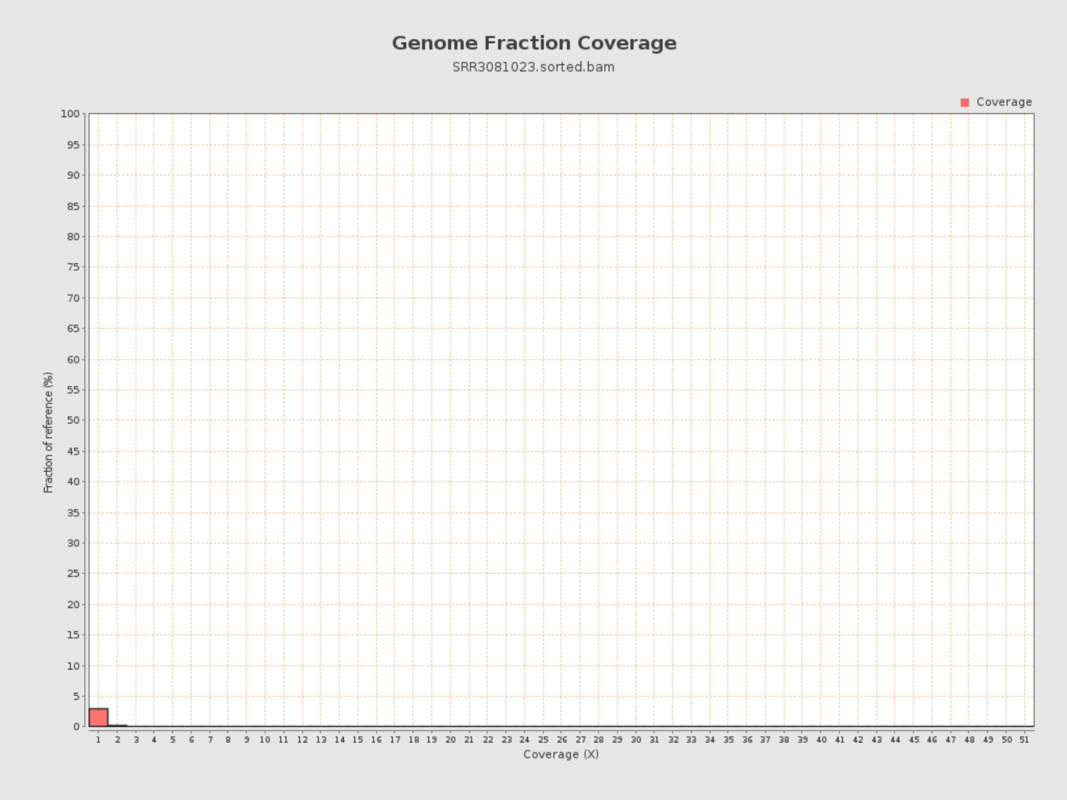
4. Results : Coverage Histogram



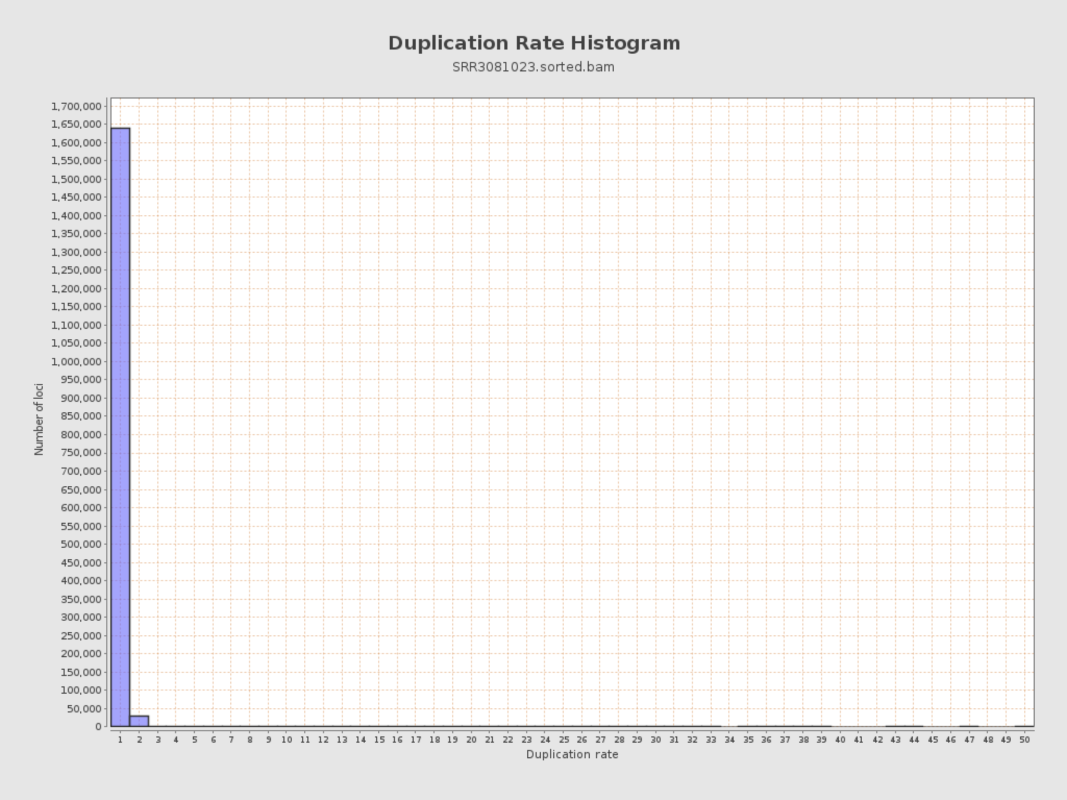
5. Results : Coverage Histogram (0-50X)



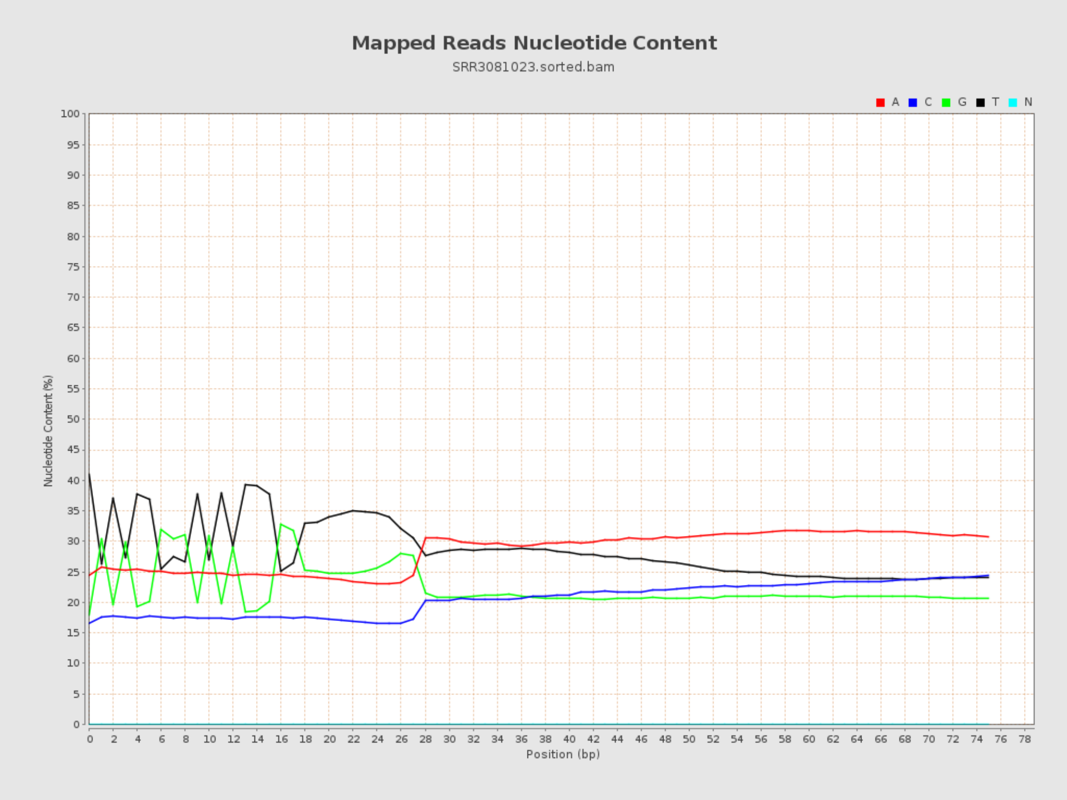
6. Results : Genome Fraction Coverage



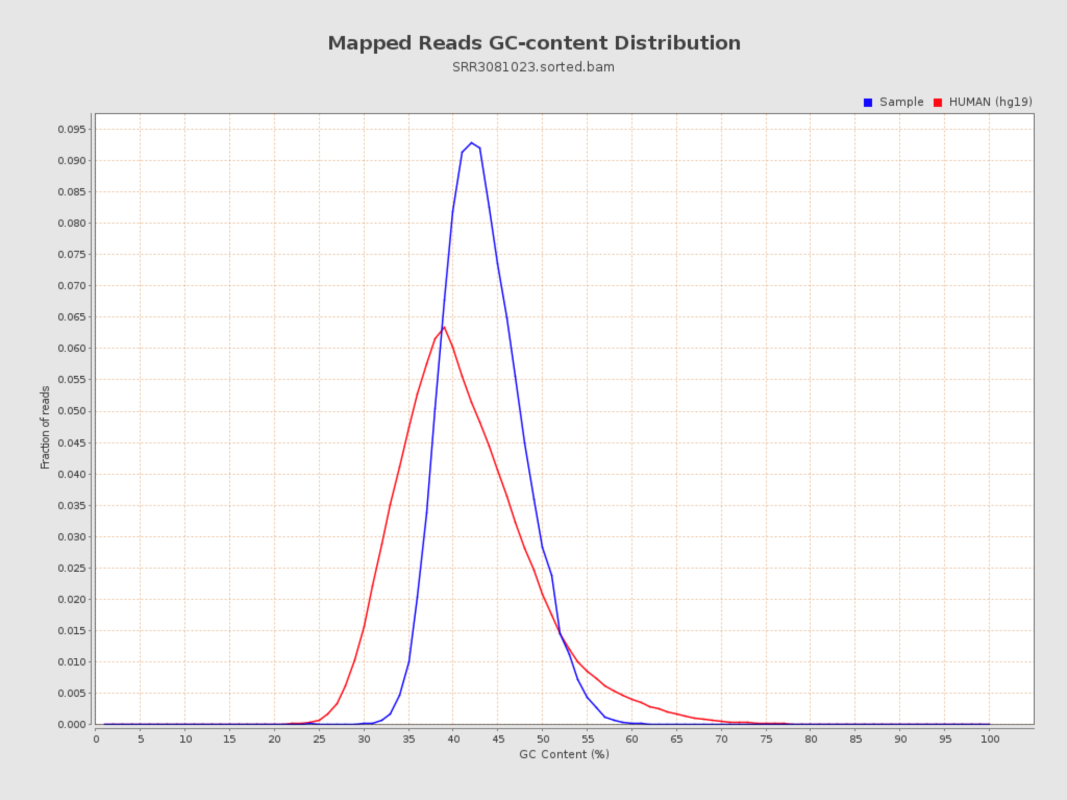
7. Results : Duplication Rate Histogram



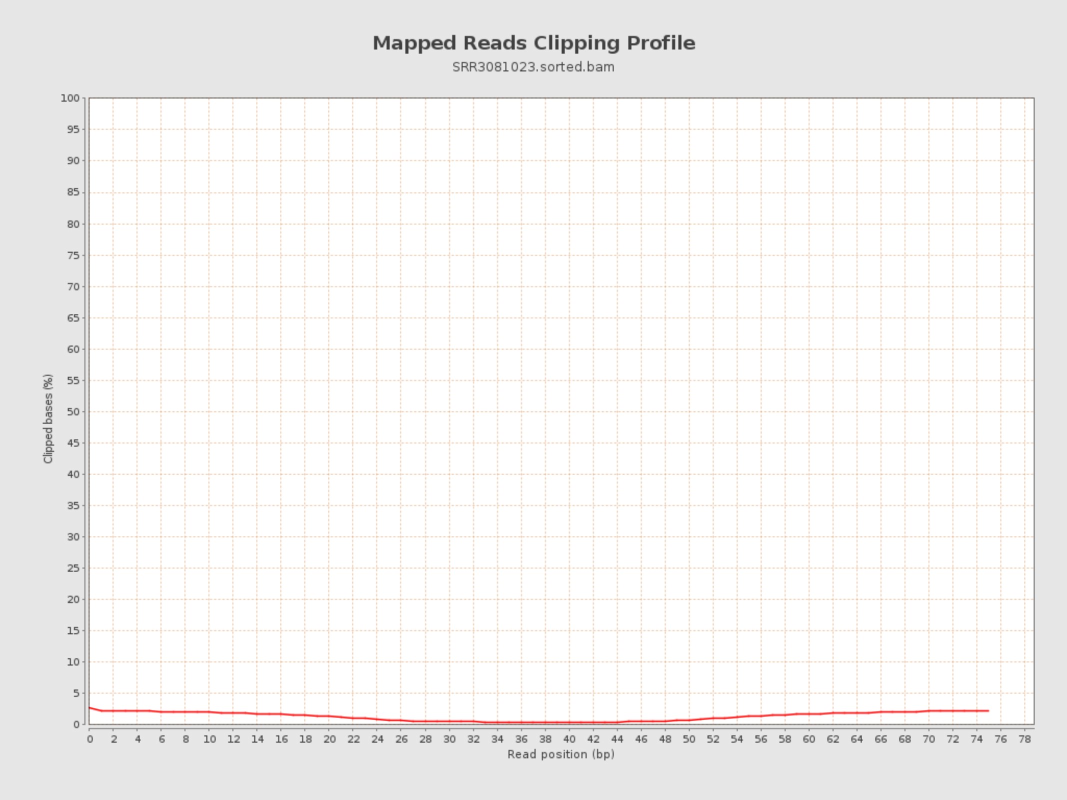
8. Results : Mapped Reads Nucleotide Content



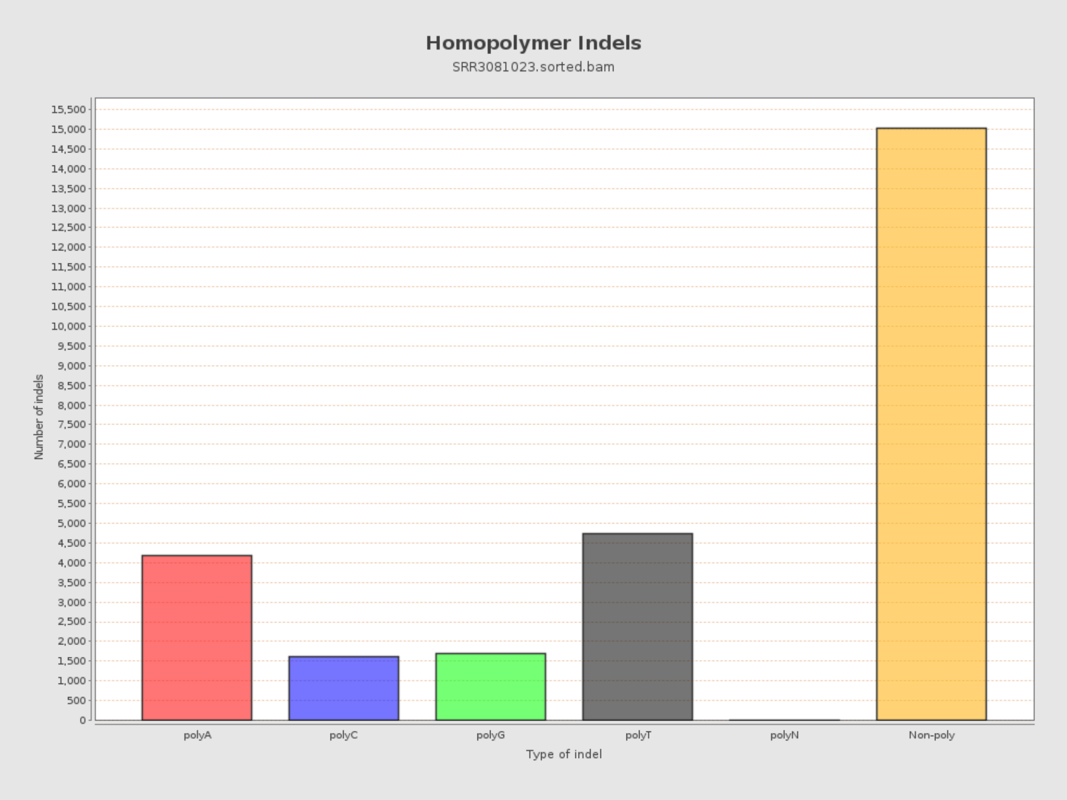
9. Results : Mapped Reads GC-content Distribution



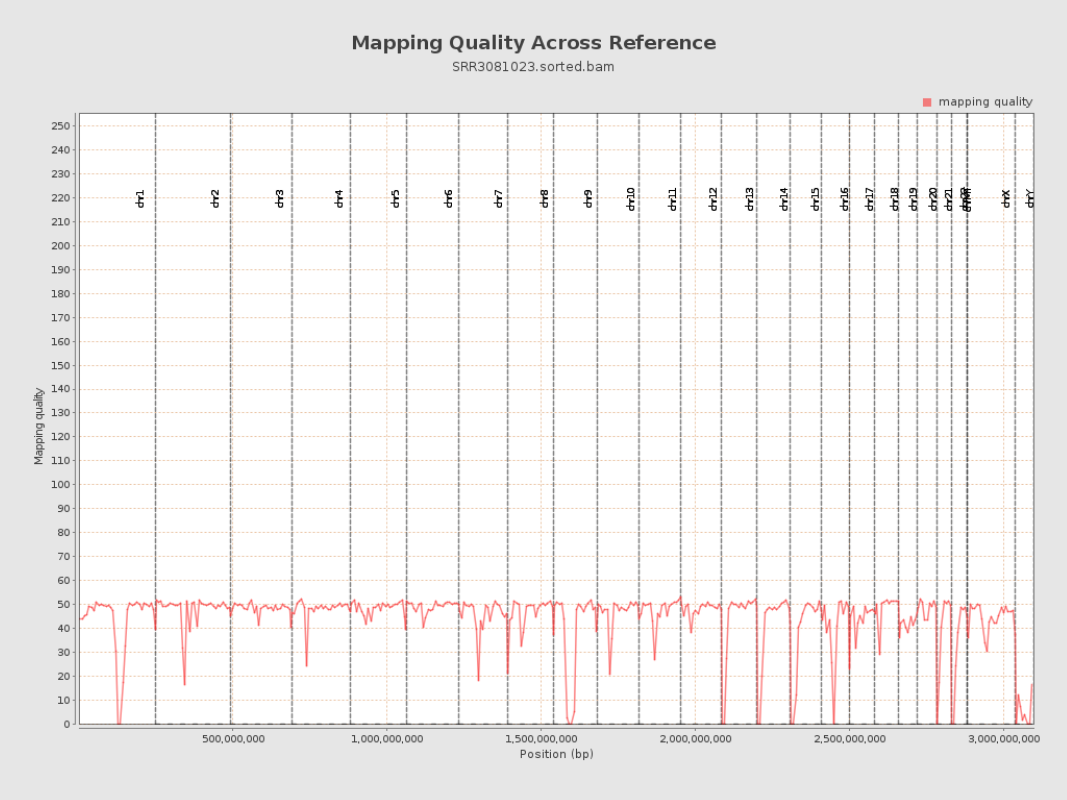
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram