Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:17:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004023.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_SRR6004023 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004023.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:17:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004023.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,265,577
Mapped reads	1,785,878 / 78.83%
Unmapped reads	479,699 / 21.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,028 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	149,324 / 6.59%
Duplication rate	6.99%
Clipped reads	996,837 / 44%

2.2. ACGT Content

Number/percentage of A's	30,696,328 / 26.8%
Number/percentage of C's	21,710,369 / 18.95%
Number/percentage of T's	35,553,582 / 31.04%
Number/percentage of G's	26,554,700 / 23.18%
Number/percentage of N's	22,840 / 0.02%
GC Percentage	42.14%

2.3. Coverage

Mean	0.037

Standard Deviation	0.324

2.4. Mapping Quality

Mean Mapping Quality	45.51

2.5. Mismatches and indels

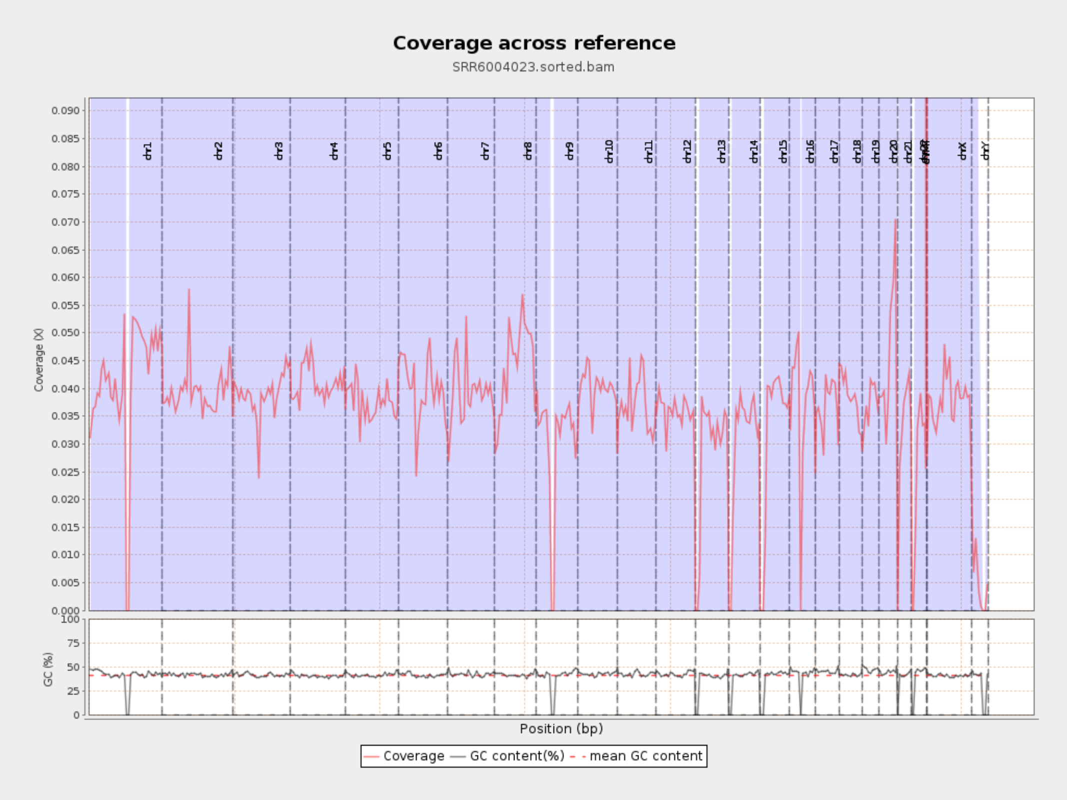
General error rate	0.92%
Mismatches	1,036,430
Insertions	8,723
Mapped reads with at least one insertion	0.48%
Deletions	33,420
Mapped reads with at least one deletion	1.85%
Homopolymer indels	47.7%

2.6. Chromosome stats

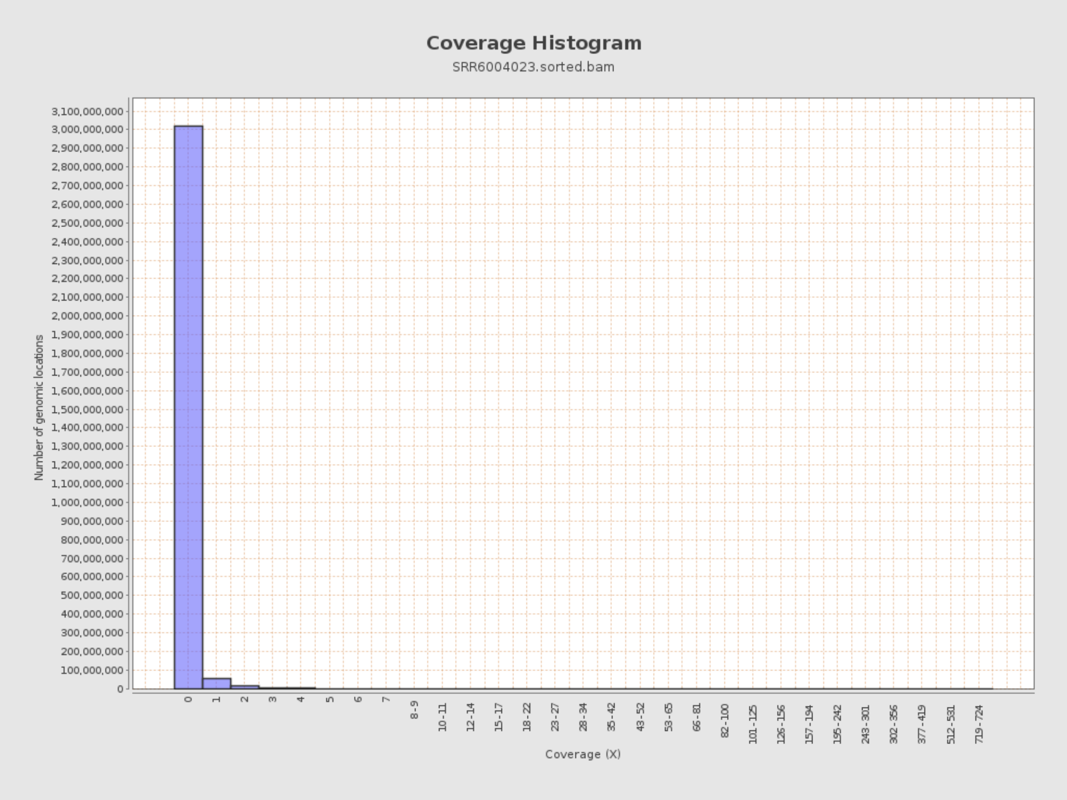
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10261257	0.0412	0.4306
chr2	243199373	9625929	0.0396	0.4453
chr3	198022430	7673091	0.0387	0.2686
chr4	191154276	7848167	0.0411	0.2814
chr5	180915260	6783959	0.0375	0.2649
chr6	171115067	6860187	0.0401	0.3089
chr7	159138663	6302732	0.0396	0.4096

chr8	146364022	6483134	0.0443	0.3395
chr9	141213431	4224568	0.0299	0.2817
chr10	135534747	5479272	0.0404	0.3092
chr11	135006516	5002281	0.0371	0.3223
chr12	133851895	4793069	0.0358	0.2616
chr13	115169878	3231799	0.0281	0.2321
chr14	107349540	3201154	0.0298	0.2532
chr15	102531392	3270439	0.0319	0.252
chr16	90354753	3387852	0.0375	0.275
chr17	81195210	2995264	0.0369	0.279
chr18	78077248	3026545	0.0388	0.4439
chr19	59128983	2198290	0.0372	0.3577
chr20	63025520	2884374	0.0458	0.3044
chr21	48129895	1543078	0.0321	0.2572
chr22	51304566	1229445	0.024	0.2117
chrMT	16571	95569	5.7672	5.2272
chrX	155270560	5903214	0.038	0.2822
chrY	59373566	287422	0.0048	0.1115

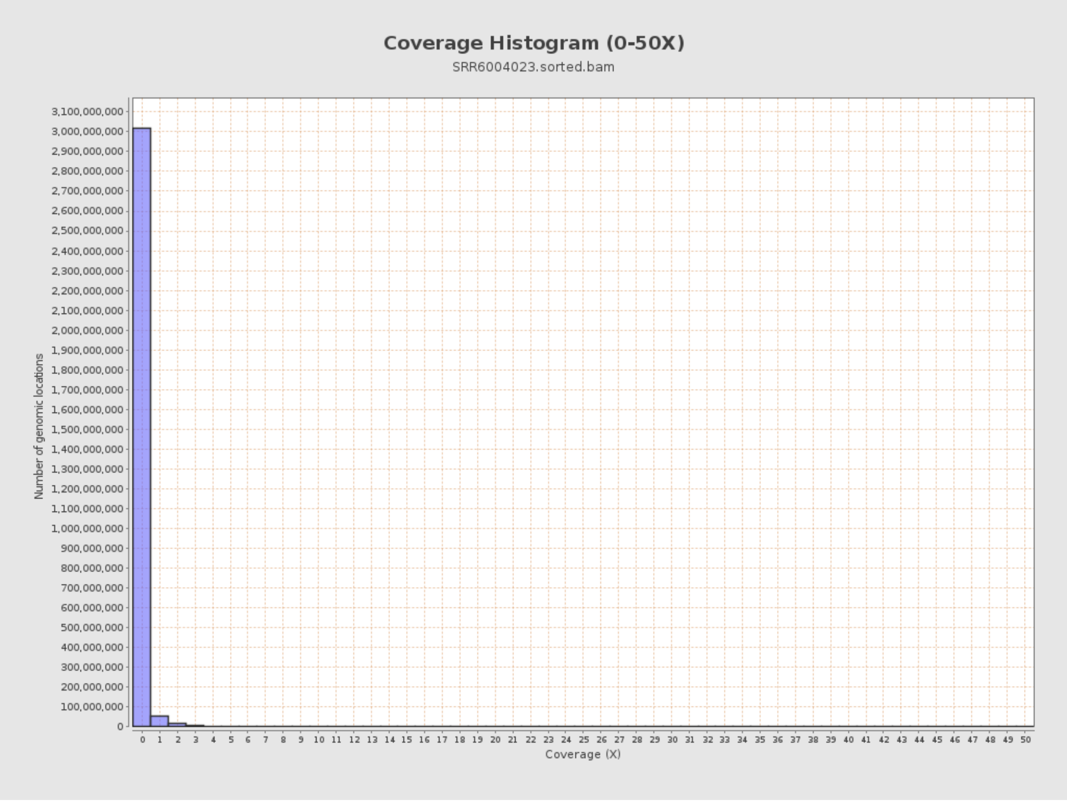
3. Results : Coverage across reference



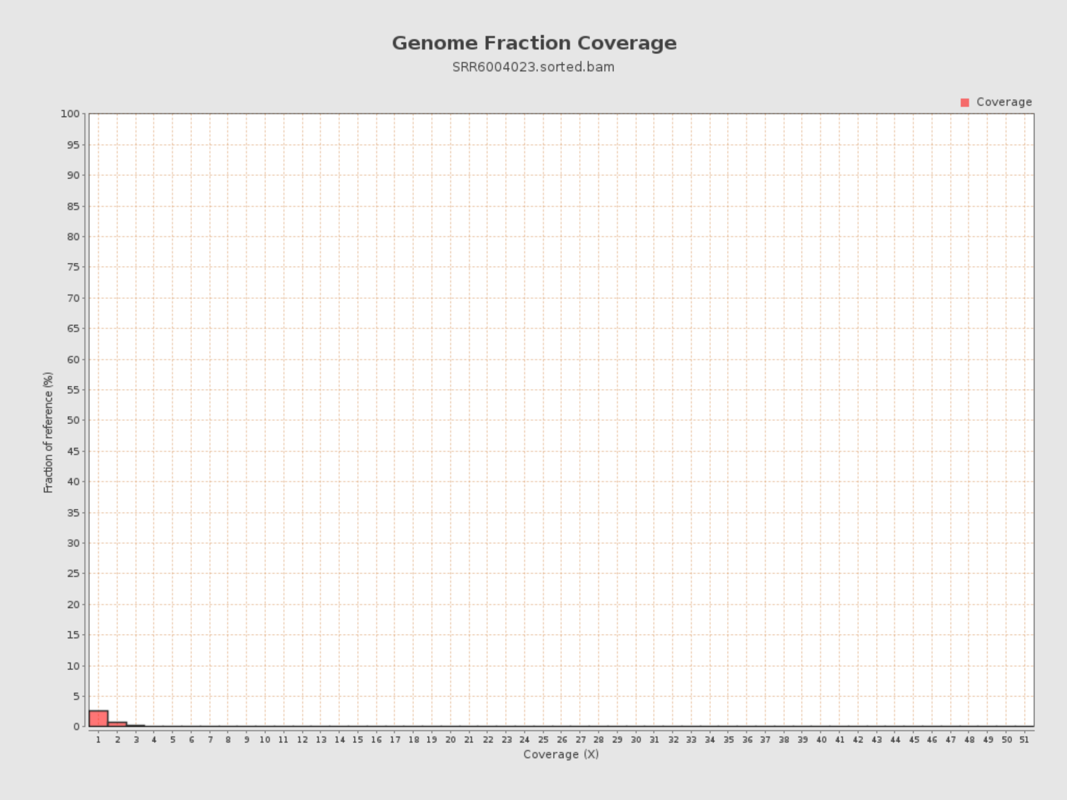
4. Results : Coverage Histogram



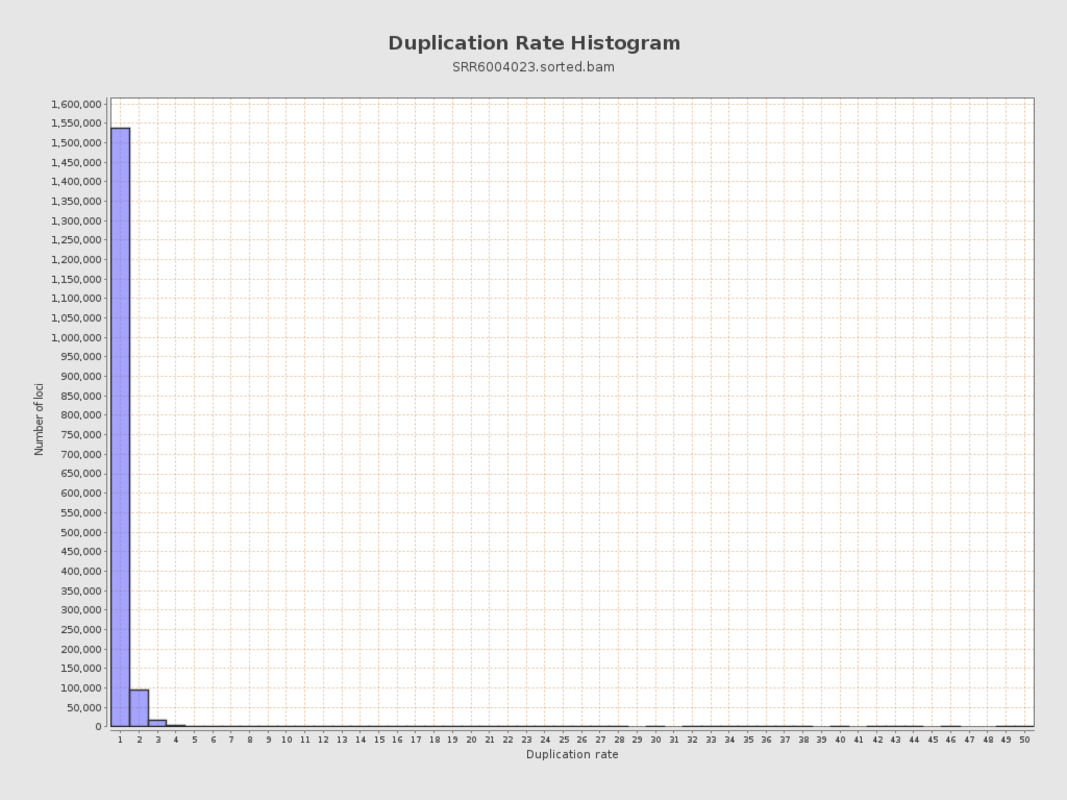
5. Results : Coverage Histogram (0-50X)



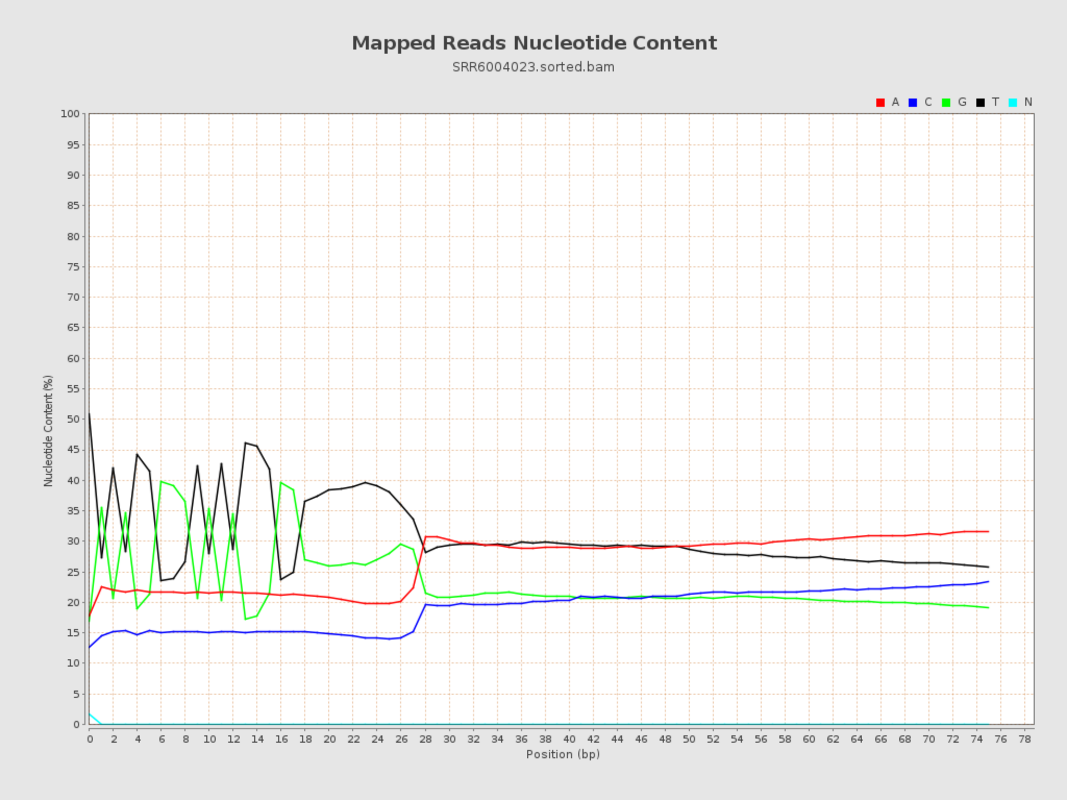
6. Results : Genome Fraction Coverage



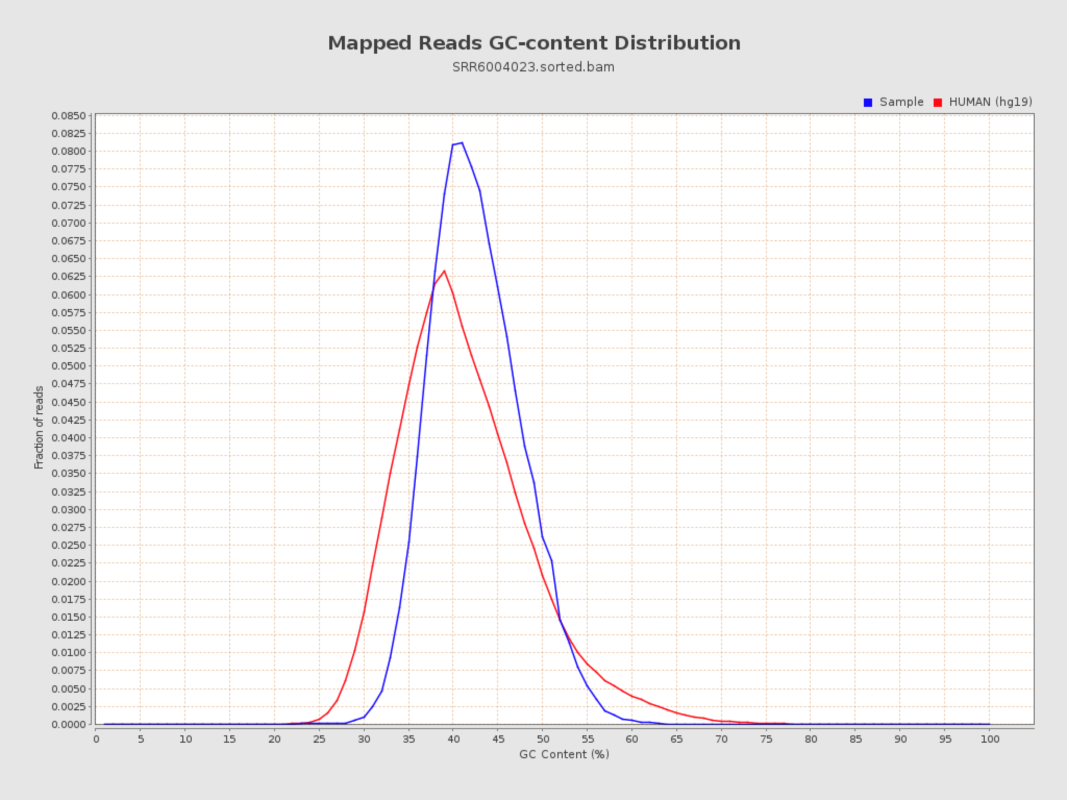
7. Results : Duplication Rate Histogram



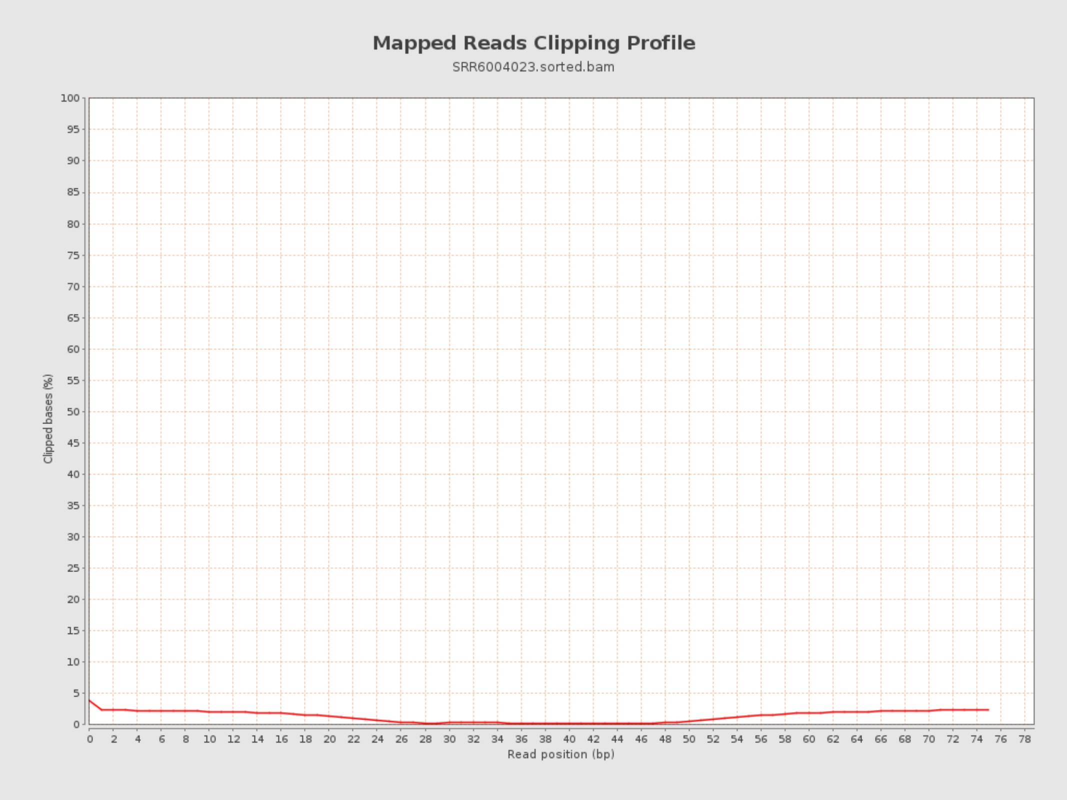
8. Results : Mapped Reads Nucleotide Content



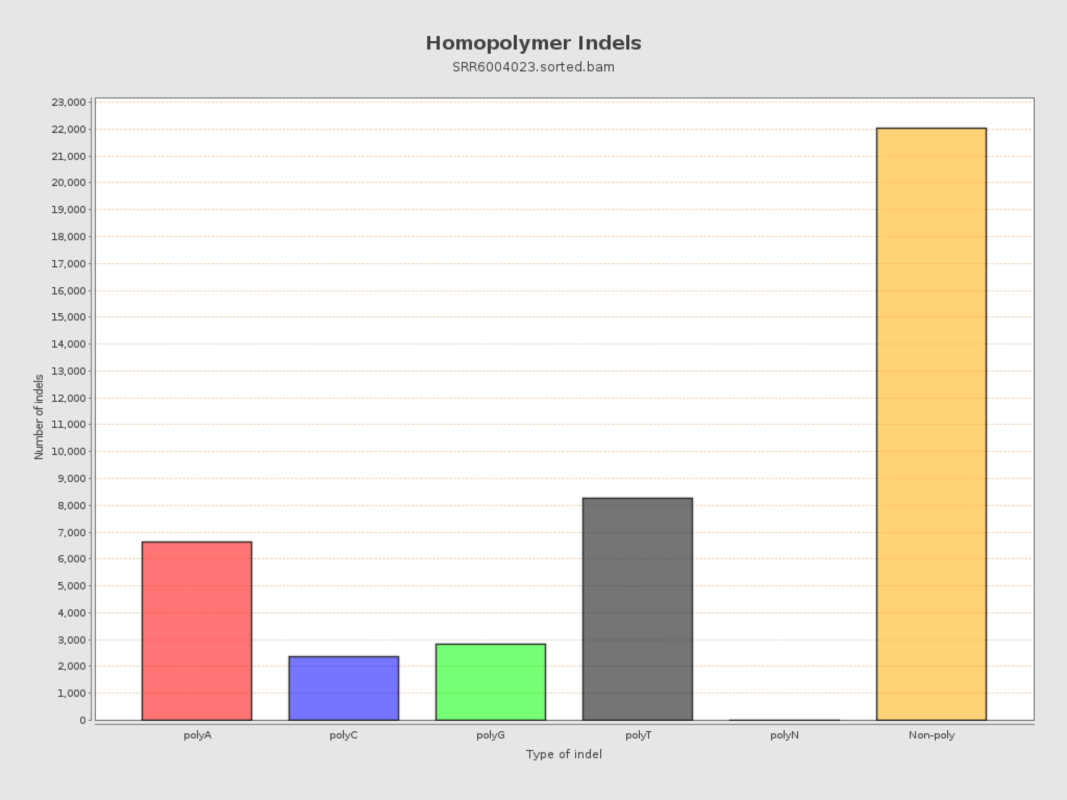
9. Results : Mapped Reads GC-content Distribution



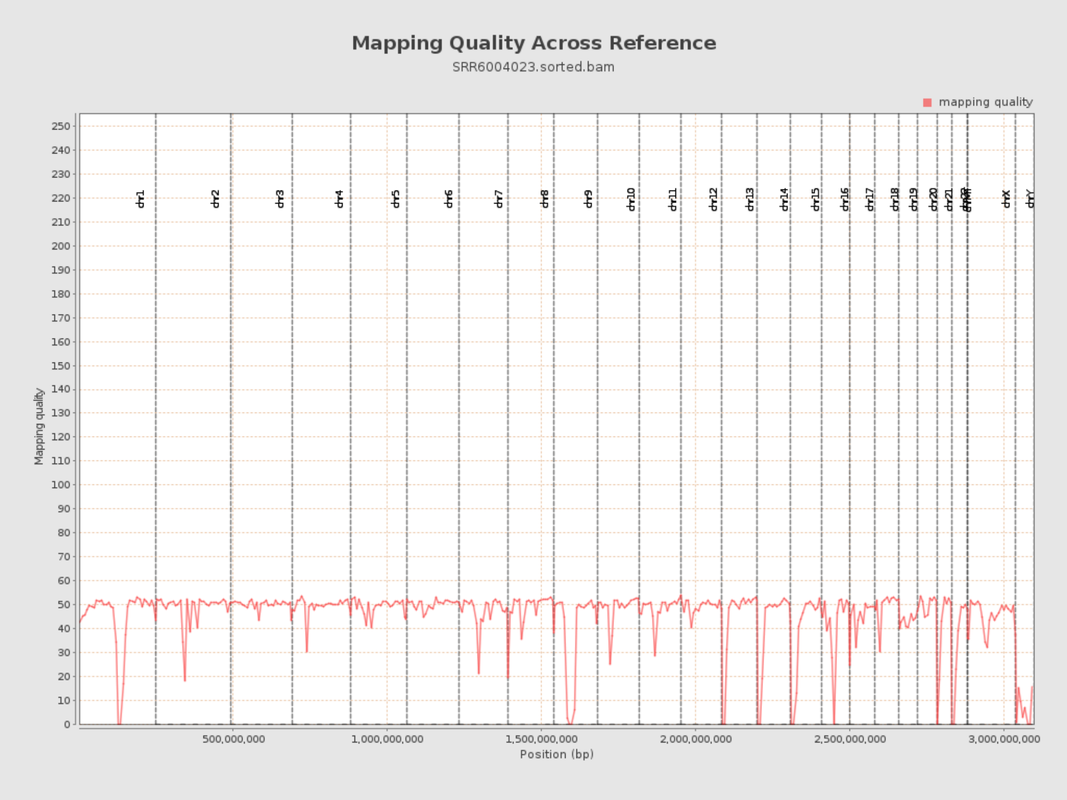
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram