Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:33:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004028.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_SRR6004028 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004028.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:33:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004028.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,744,429
Mapped reads	1,508,440 / 86.47%
Unmapped reads	235,989 / 13.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,116 / 1.1%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	101,114 / 5.8%
Duplication rate	5.2%
Clipped reads	703,915 / 40.35%

2.2. ACGT Content

Number/percentage of A's	28,308,900 / 28.31%
Number/percentage of C's	18,175,537 / 18.18%
Number/percentage of T's	32,192,715 / 32.2%
Number/percentage of G's	21,292,425 / 21.3%
Number/percentage of N's	16,566 / 0.02%
GC Percentage	39.47%

2.3. Coverage

Mean	0.0323

Standard Deviation	0.3896

2.4. Mapping Quality

Mean Mapping Quality	43.73

2.5. Mismatches and indels

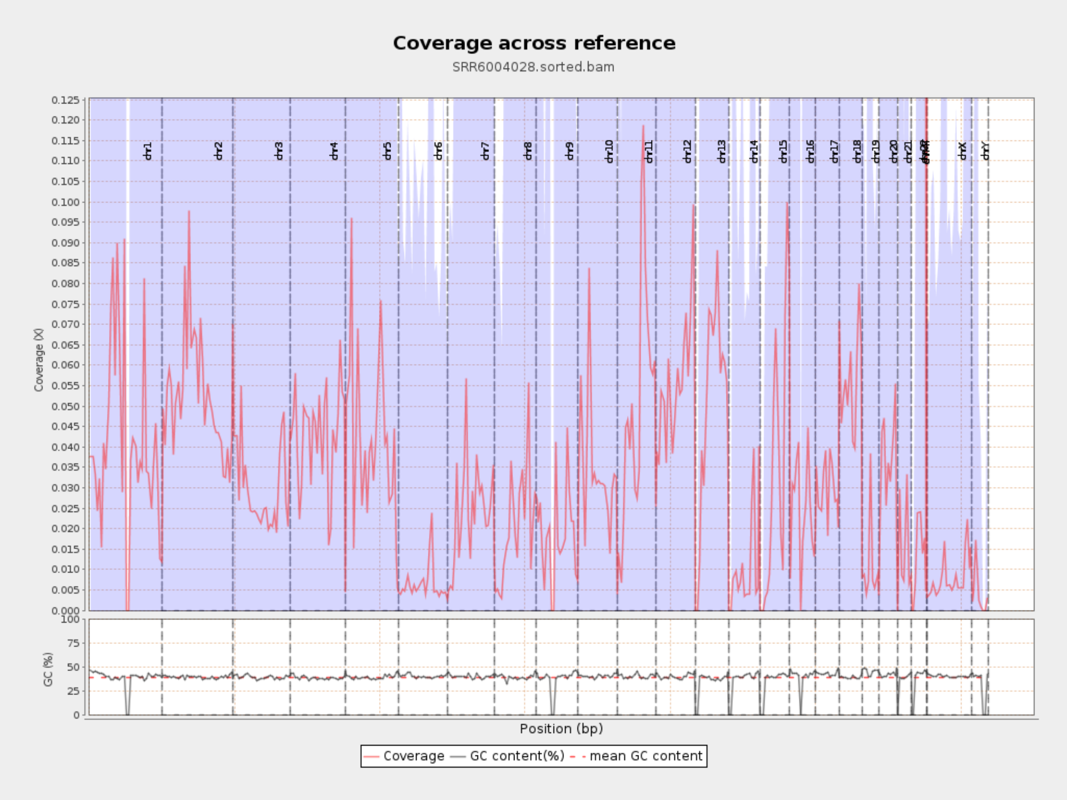
General error rate	0.99%
Mismatches	972,502
Insertions	7,989
Mapped reads with at least one insertion	0.52%
Deletions	34,969
Mapped reads with at least one deletion	2.28%
Homopolymer indels	44.63%

2.6. Chromosome stats

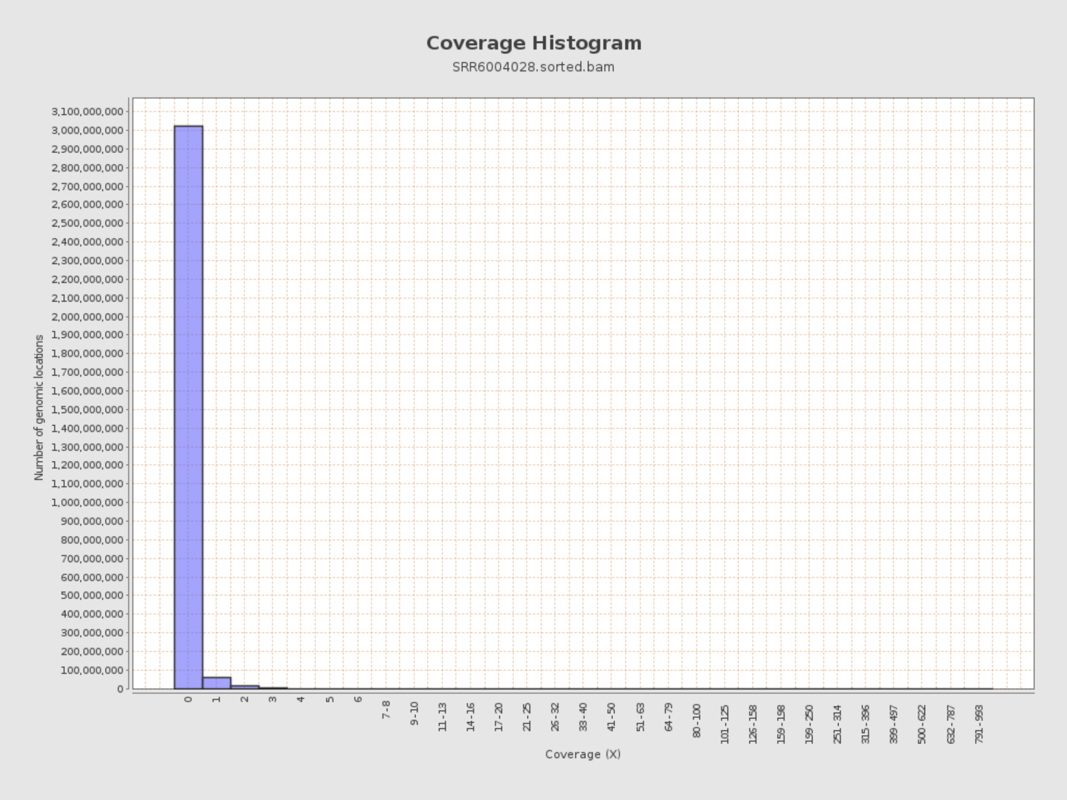
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10290623	0.0413	0.8414
chr2	243199373	12820595	0.0527	0.4482
chr3	198022430	5985520	0.0302	0.2242
chr4	191154276	8245837	0.0431	0.2829
chr5	180915260	7790698	0.0431	0.2658
chr6	171115067	1144056	0.0067	0.1069
chr7	159138663	3860216	0.0243	0.3716

chr8	146364022	3030568	0.0207	0.3445
chr9	141213431	2623899	0.0186	0.2932
chr10	135534747	4719367	0.0348	0.4477
chr11	135006516	6780520	0.0502	0.4476
chr12	133851895	7472019	0.0558	0.3048
chr13	115169878	5874801	0.051	0.2868
chr14	107349540	1035838	0.0096	0.1487
chr15	102531392	3366196	0.0328	0.2313
chr16	90354753	2243505	0.0248	0.2261
chr17	81195210	2444528	0.0301	0.265
chr18	78077248	4373102	0.056	0.5708
chr19	59128983	650635	0.011	0.5788
chr20	63025520	2369606	0.0376	0.2501
chr21	48129895	704702	0.0146	0.1946
chr22	51304566	679890	0.0133	0.1414
chrMT	16571	53064	3.2022	2.9854
chrX	155270560	1255563	0.0081	0.1709
chrY	59373566	230311	0.0039	0.1376

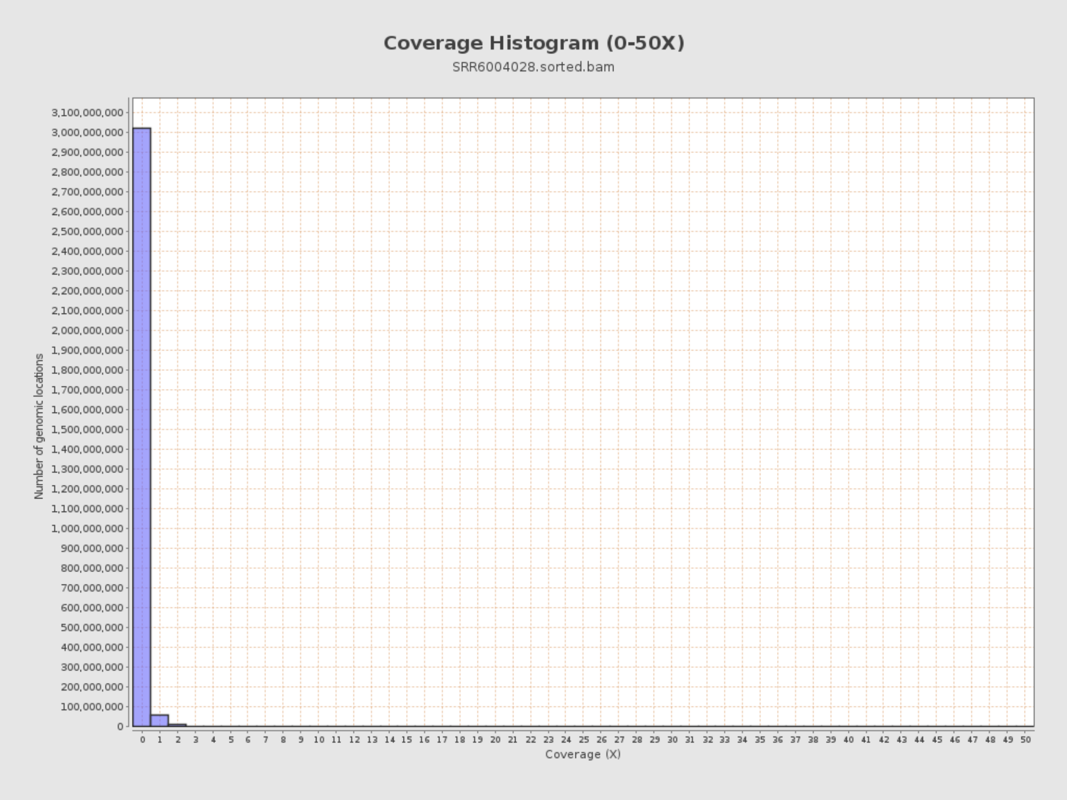
3. Results : Coverage across reference



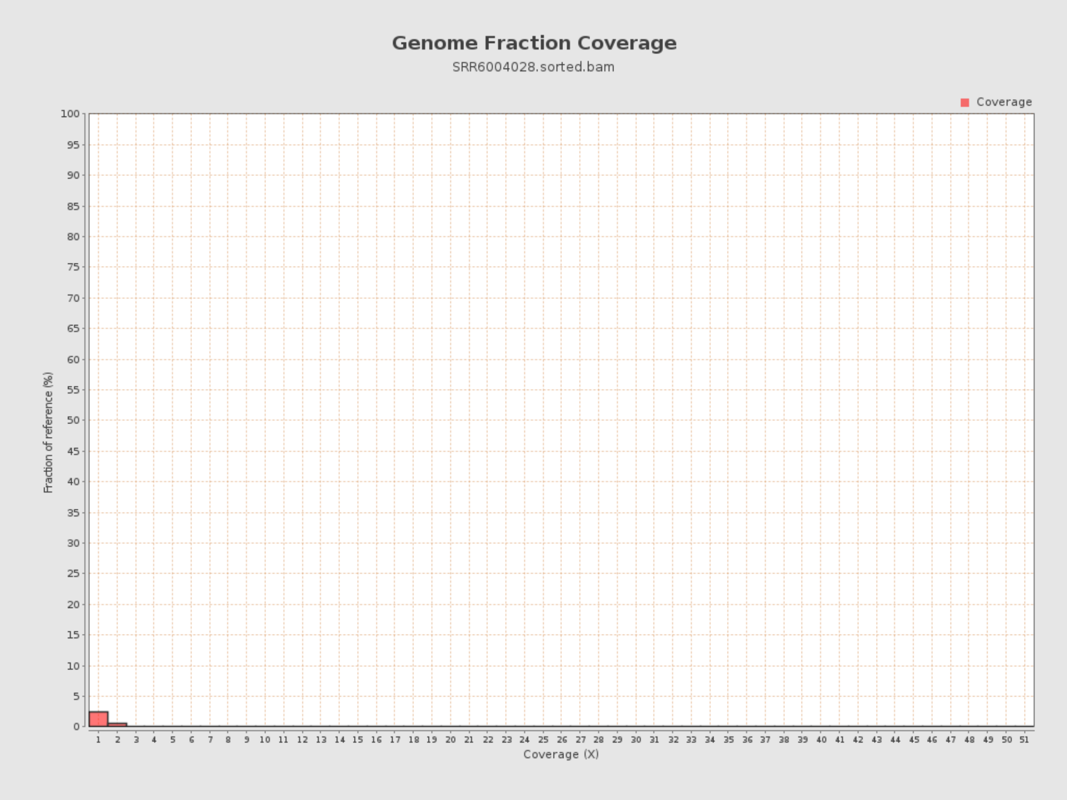
4. Results : Coverage Histogram



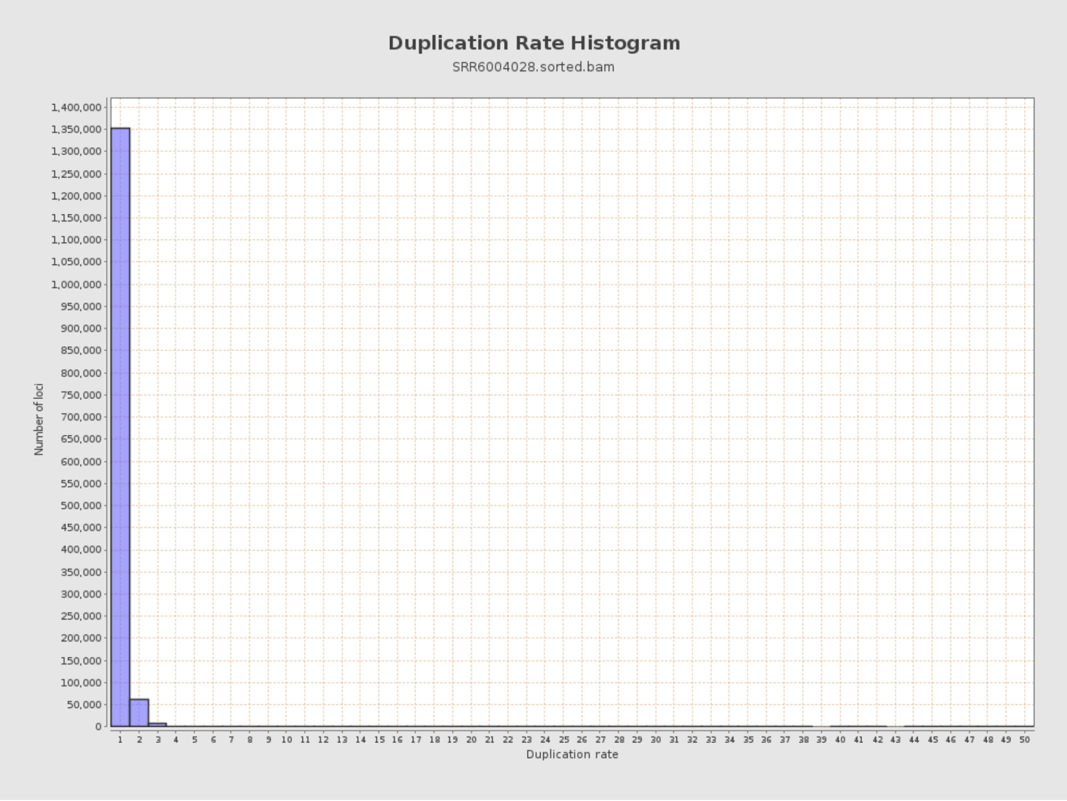
5. Results : Coverage Histogram (0-50X)



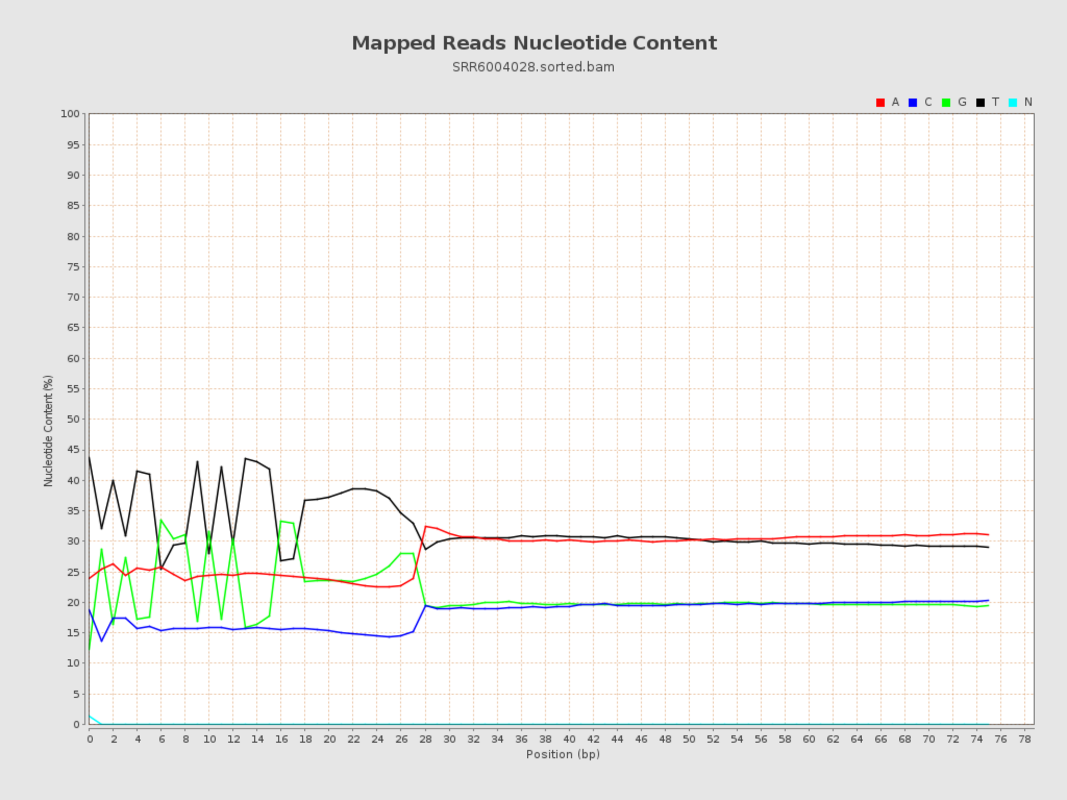
6. Results : Genome Fraction Coverage



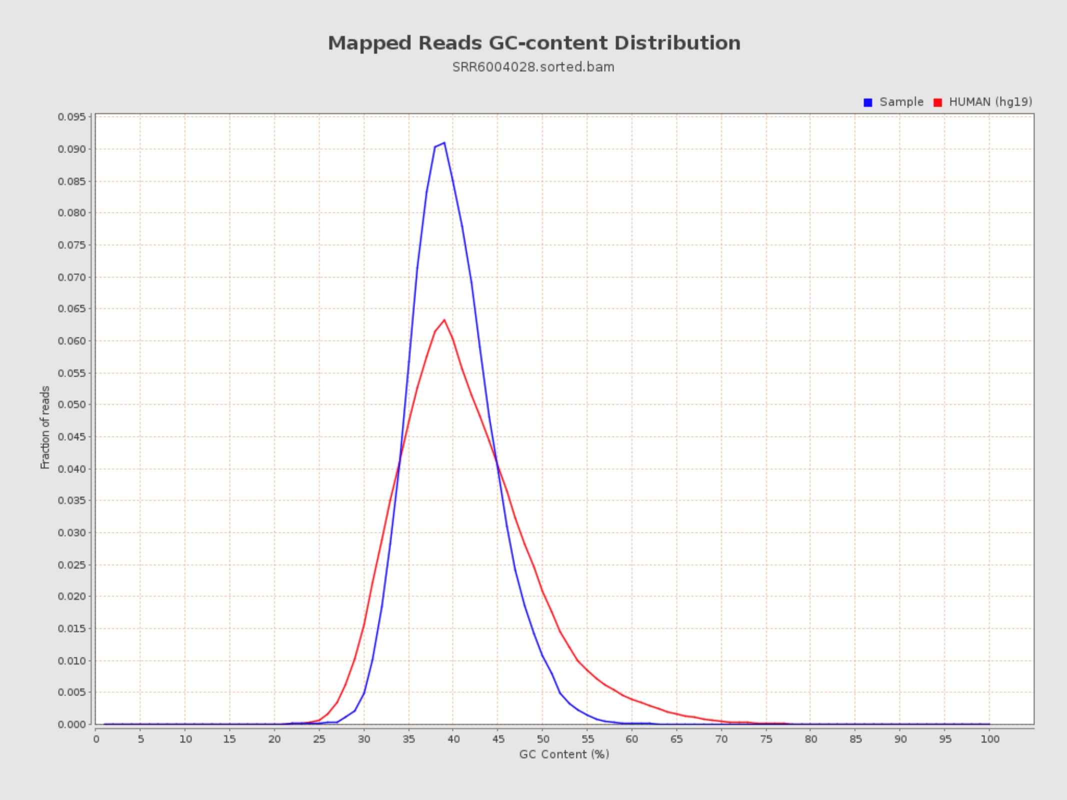
7. Results : Duplication Rate Histogram



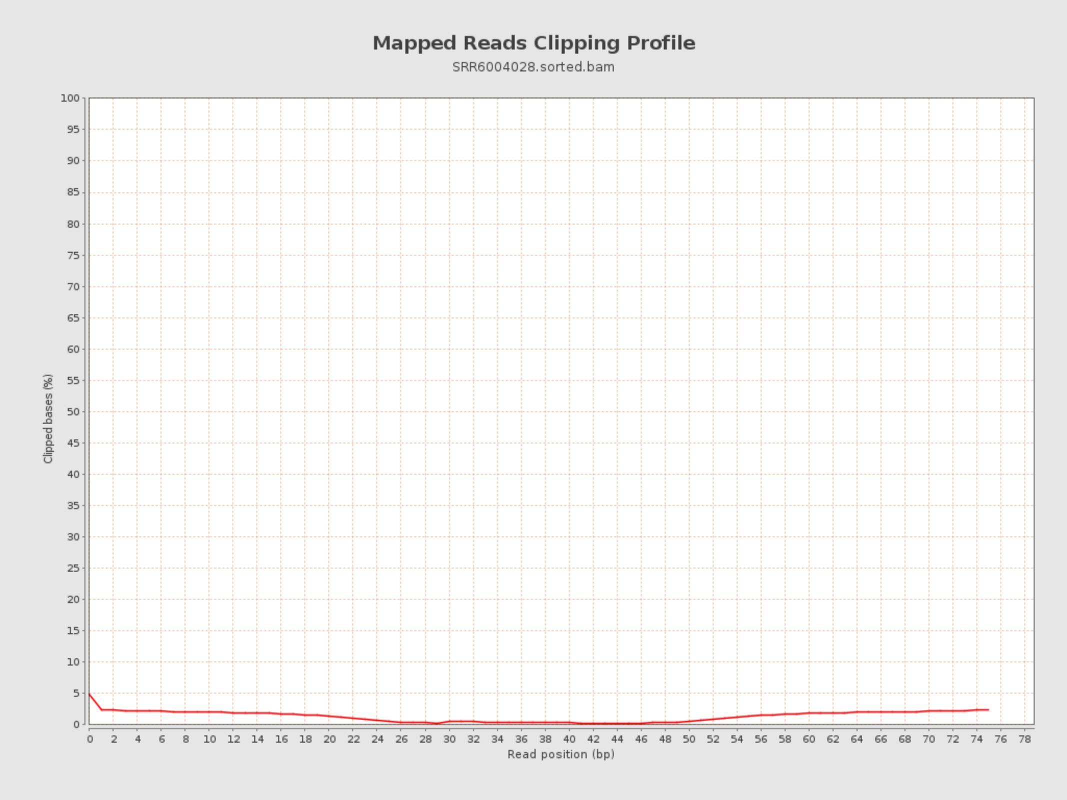
8. Results : Mapped Reads Nucleotide Content



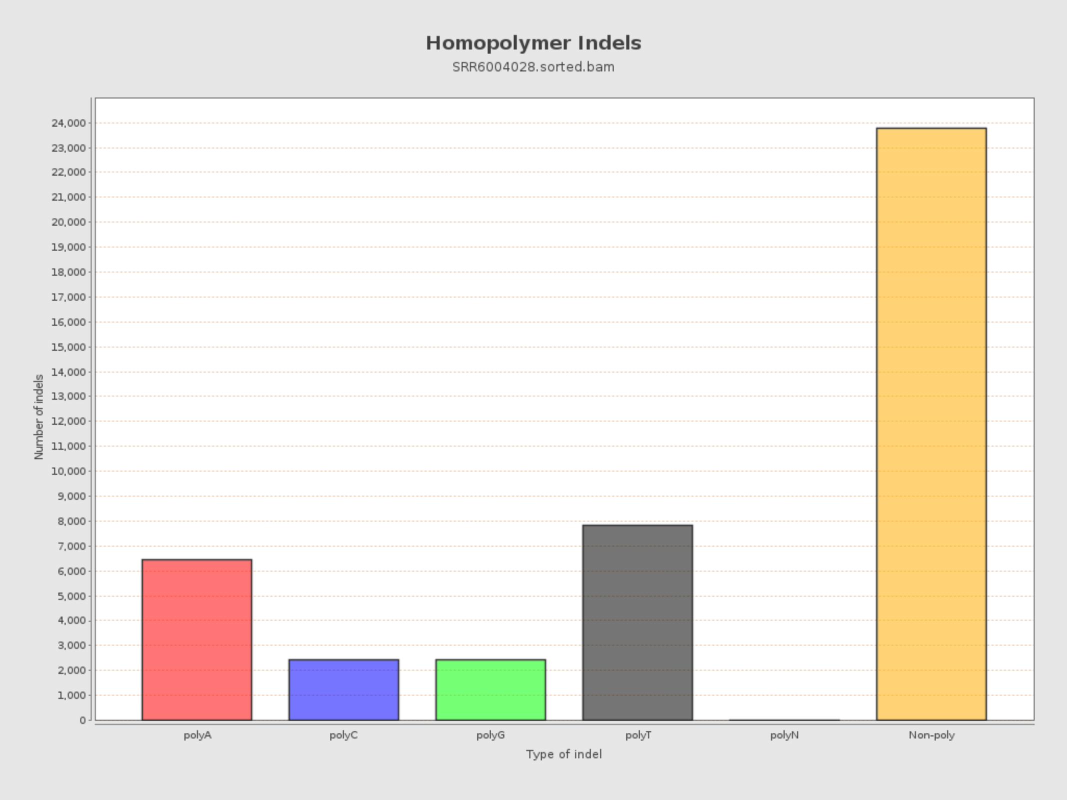
9. Results : Mapped Reads GC-content Distribution



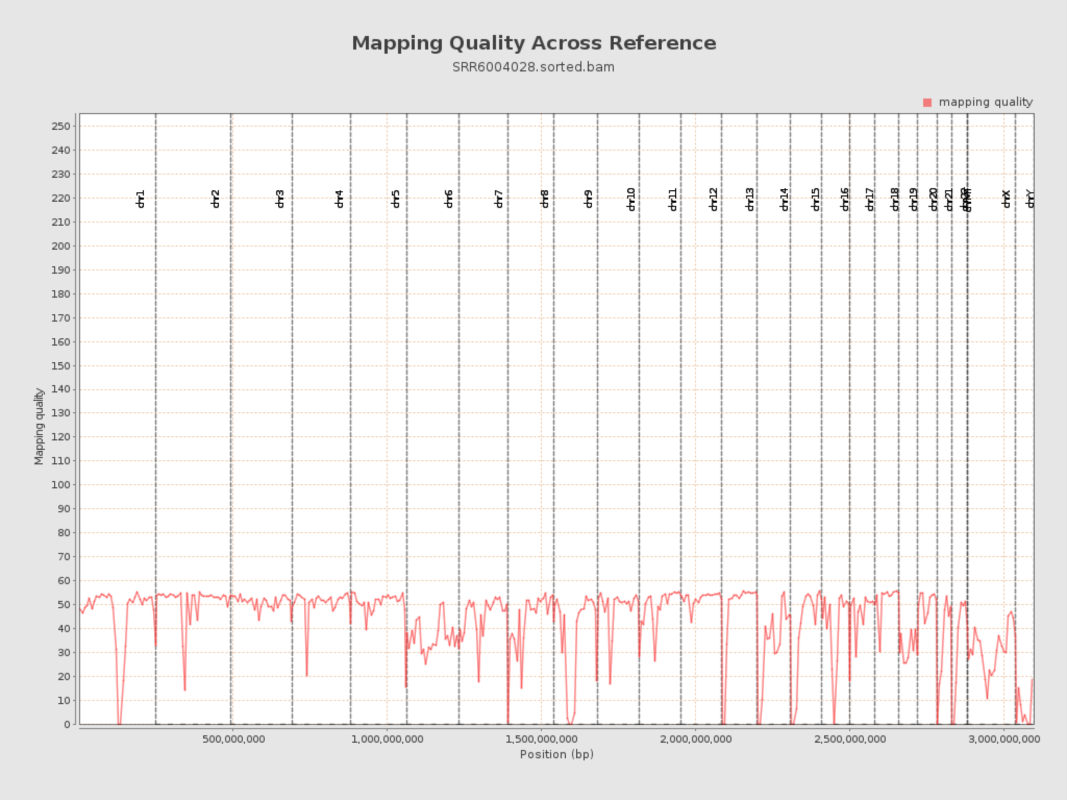
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram