Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:19:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004024.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_SRR6004024 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004024.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:19:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004024.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,015,664
Mapped reads	789,442 / 39.17%
Unmapped reads	1,226,222 / 60.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,771 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	133,379 / 6.62%
Duplication rate	12.04%
Clipped reads	467,419 / 23.19%

2.2. ACGT Content

Number/percentage of A's	13,437,634 / 26.93%
Number/percentage of C's	9,282,437 / 18.6%
Number/percentage of T's	15,684,165 / 31.43%
Number/percentage of G's	11,485,648 / 23.02%
Number/percentage of N's	9,612 / 0.02%
GC Percentage	41.62%

2.3. Coverage

Mean	0.0161

Standard Deviation	0.2633

2.4. Mapping Quality

Mean Mapping Quality	44.42

2.5. Mismatches and indels

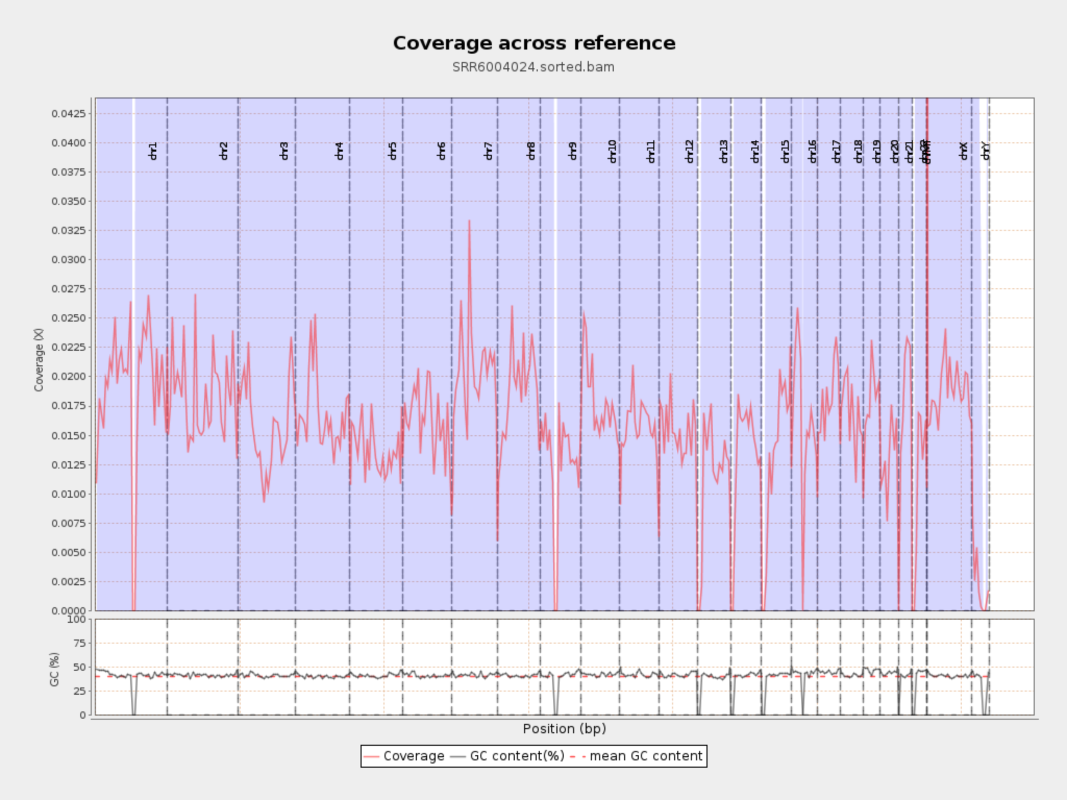
General error rate	1.06%
Mismatches	523,504
Insertions	3,995
Mapped reads with at least one insertion	0.5%
Deletions	16,812
Mapped reads with at least one deletion	2.1%
Homopolymer indels	47%

2.6. Chromosome stats

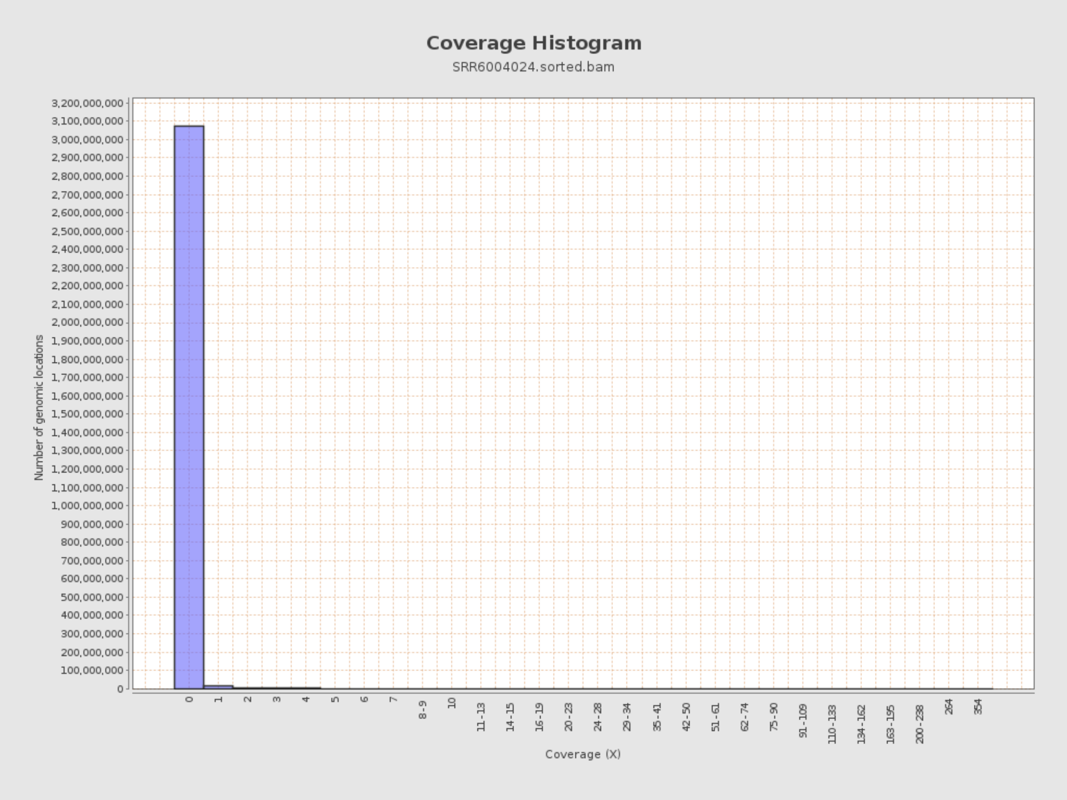
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4743182	0.019	0.3165
chr2	243199373	4487228	0.0185	0.3172
chr3	198022430	3163175	0.016	0.2405
chr4	191154276	3214833	0.0168	0.2564
chr5	180915260	2483177	0.0137	0.2162
chr6	171115067	2781449	0.0163	0.2503
chr7	159138663	3268030	0.0205	0.3374

chr8	146364022	2755172	0.0188	0.2966
chr9	141213431	1771732	0.0125	0.2197
chr10	135534747	2442683	0.018	0.2623
chr11	135006516	2134520	0.0158	0.2559
chr12	133851895	2061273	0.0154	0.2319
chr13	115169878	1301771	0.0113	0.1967
chr14	107349540	1408016	0.0131	0.2382
chr15	102531392	1325344	0.0129	0.231
chr16	90354753	1434059	0.0159	0.2428
chr17	81195210	1477056	0.0182	0.248
chr18	78077248	1319414	0.0169	0.3114
chr19	59128983	1071547	0.0181	0.2901
chr20	63025520	812422	0.0129	0.2121
chr21	48129895	843950	0.0175	0.2982
chr22	51304566	548462	0.0107	0.1909
chrMT	16571	15288	0.9226	1.616
chrX	155270560	2932447	0.0189	0.2605
chrY	59373566	131229	0.0022	0.0746

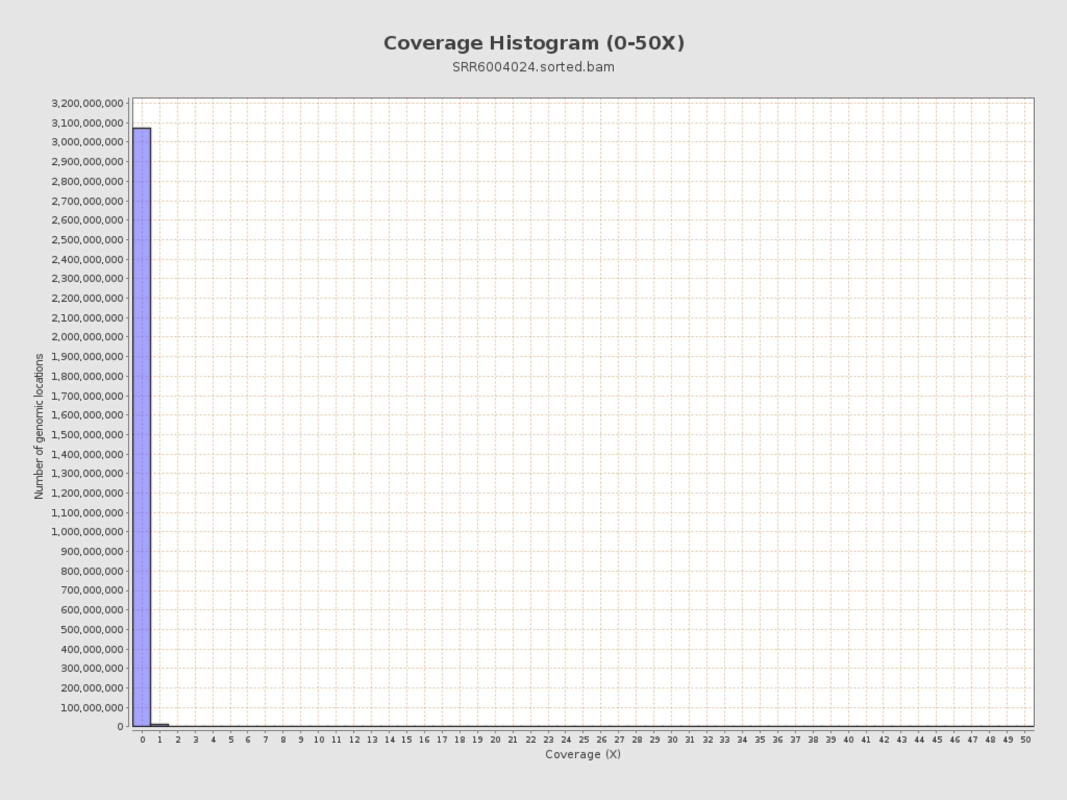
3. Results : Coverage across reference



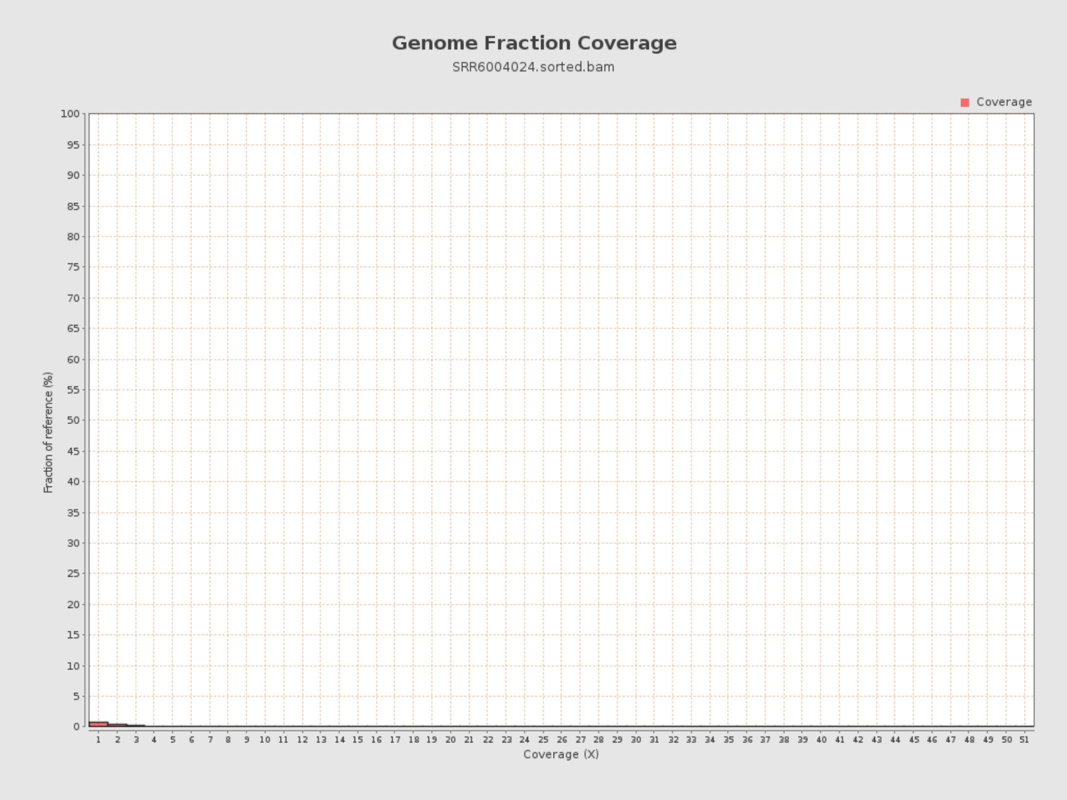
4. Results : Coverage Histogram



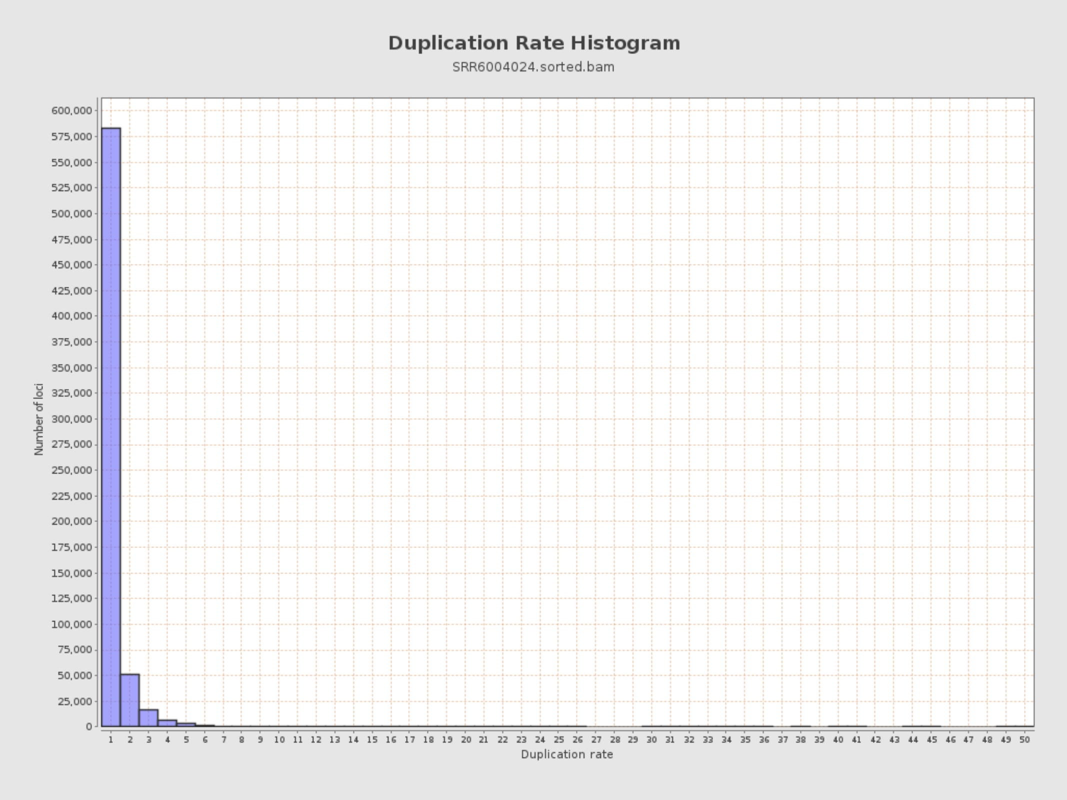
5. Results : Coverage Histogram (0-50X)



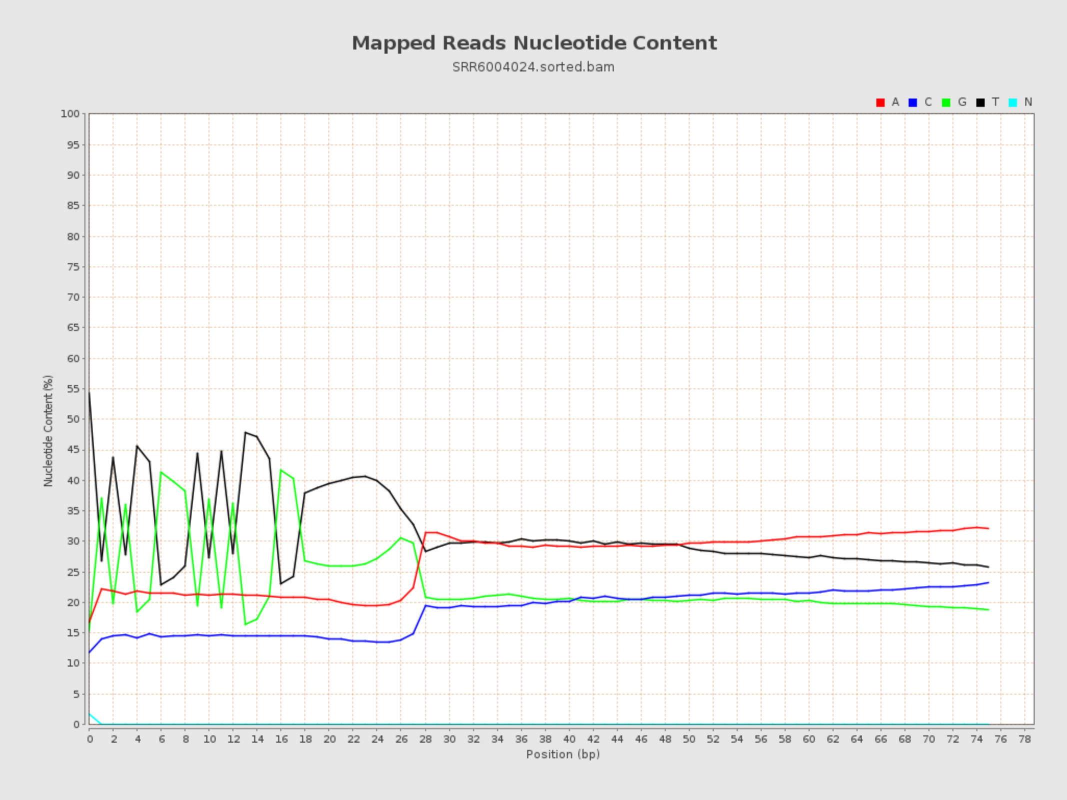
6. Results : Genome Fraction Coverage



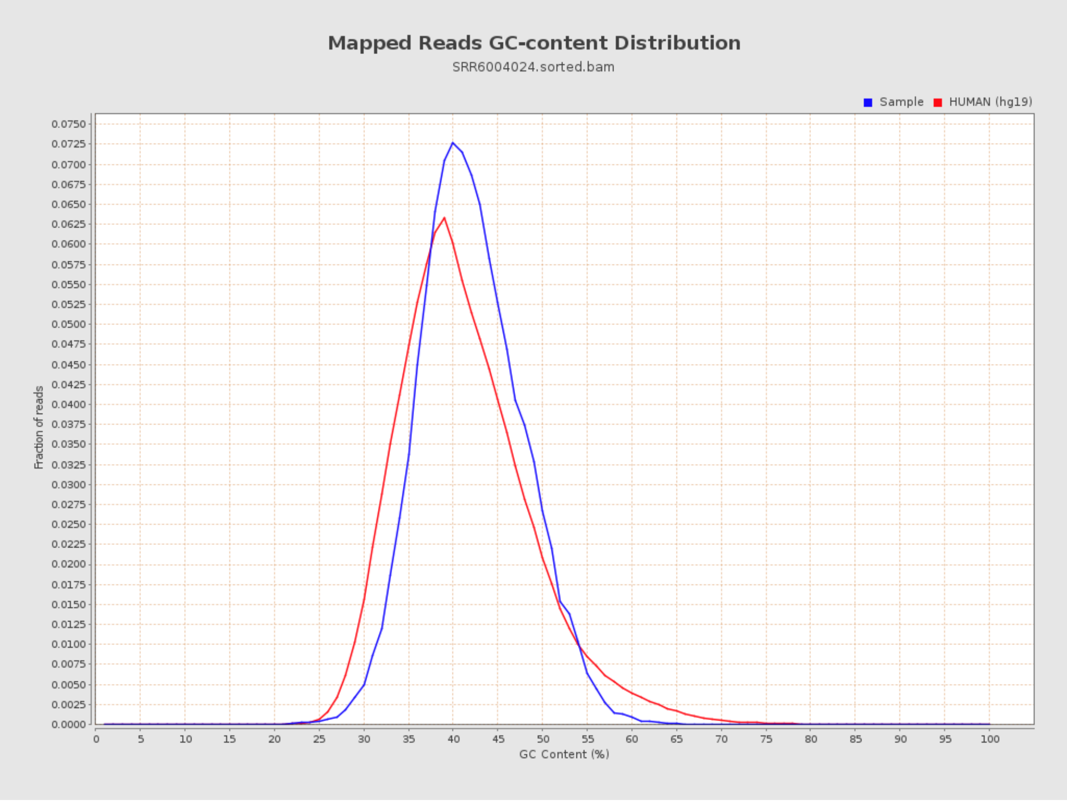
7. Results : Duplication Rate Histogram



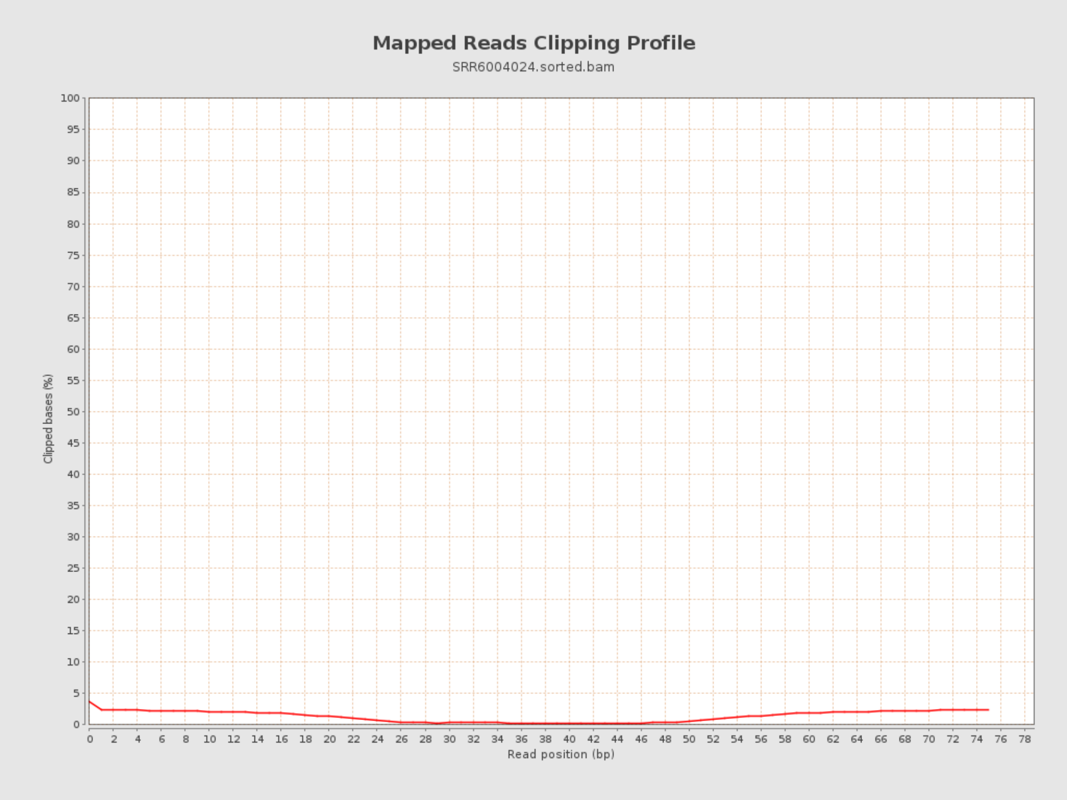
8. Results : Mapped Reads Nucleotide Content



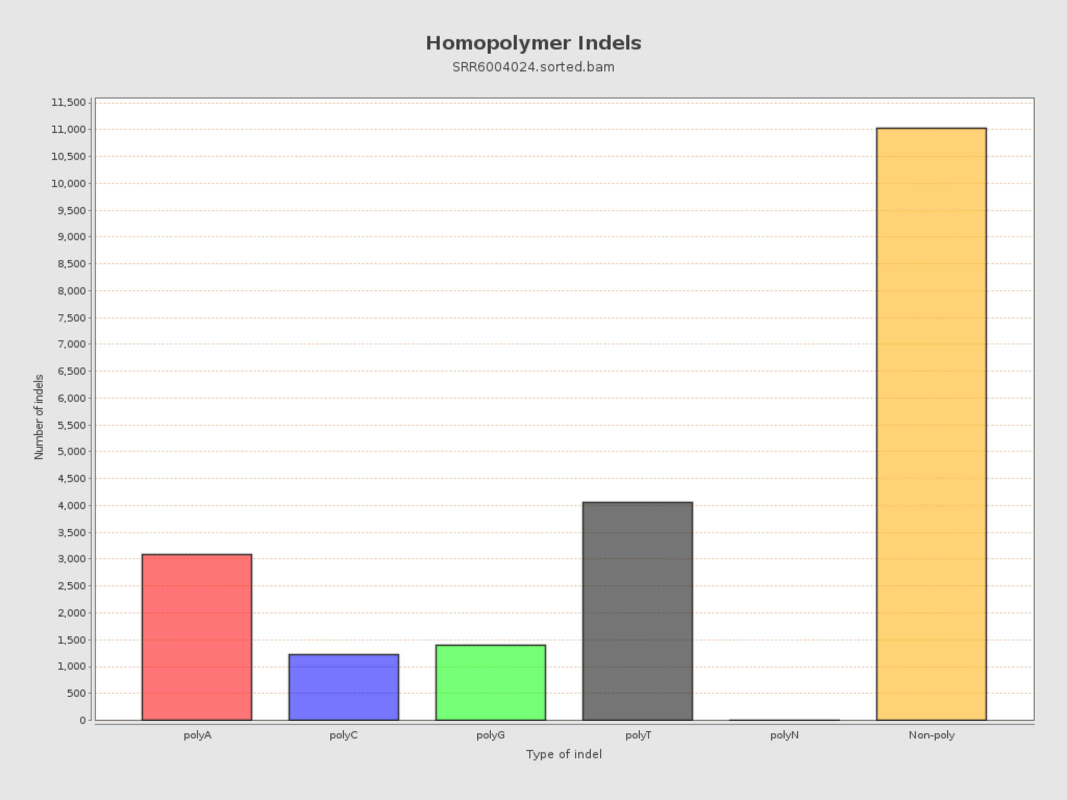
9. Results : Mapped Reads GC-content Distribution



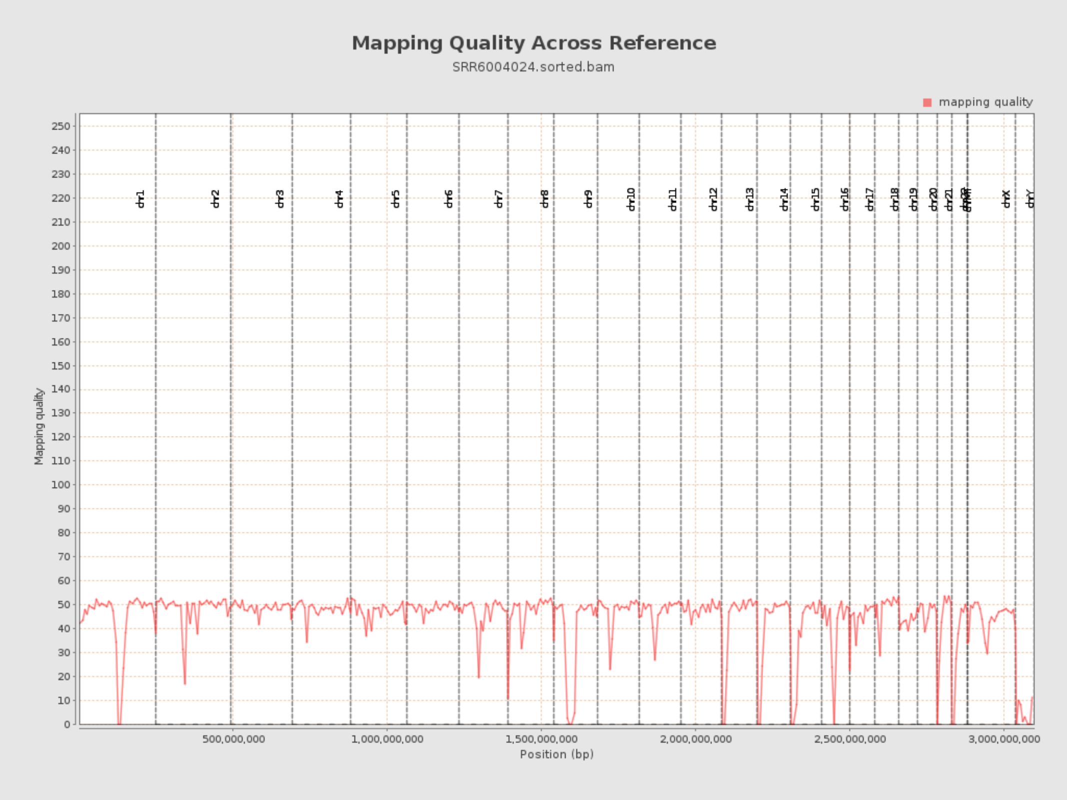
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram