Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:53:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004071.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_SRR6004071 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004071.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:53:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004071.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,102,706
Mapped reads	1,914,923 / 91.07%
Unmapped reads	187,783 / 8.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,373 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	66,305 / 3.15%
Duplication rate	2.8%
Clipped reads	744,531 / 35.41%

2.2. ACGT Content

Number/percentage of A's	37,074,078 / 28.43%
Number/percentage of C's	24,355,068 / 18.67%
Number/percentage of T's	40,892,876 / 31.35%
Number/percentage of G's	28,073,958 / 21.53%
Number/percentage of N's	24,037 / 0.02%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0421

Standard Deviation	0.3346

2.4. Mapping Quality

Mean Mapping Quality	46.4

2.5. Mismatches and indels

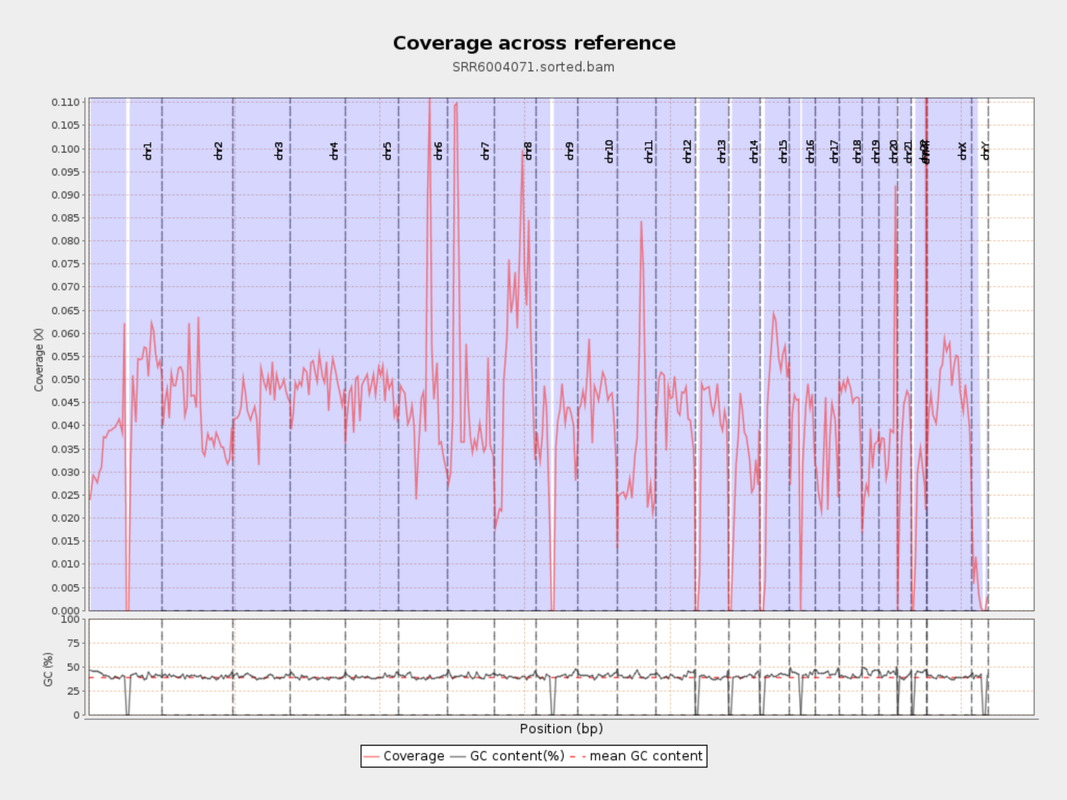
General error rate	0.85%
Mismatches	1,089,090
Insertions	9,116
Mapped reads with at least one insertion	0.47%
Deletions	32,291
Mapped reads with at least one deletion	1.67%
Homopolymer indels	46.85%

2.6. Chromosome stats

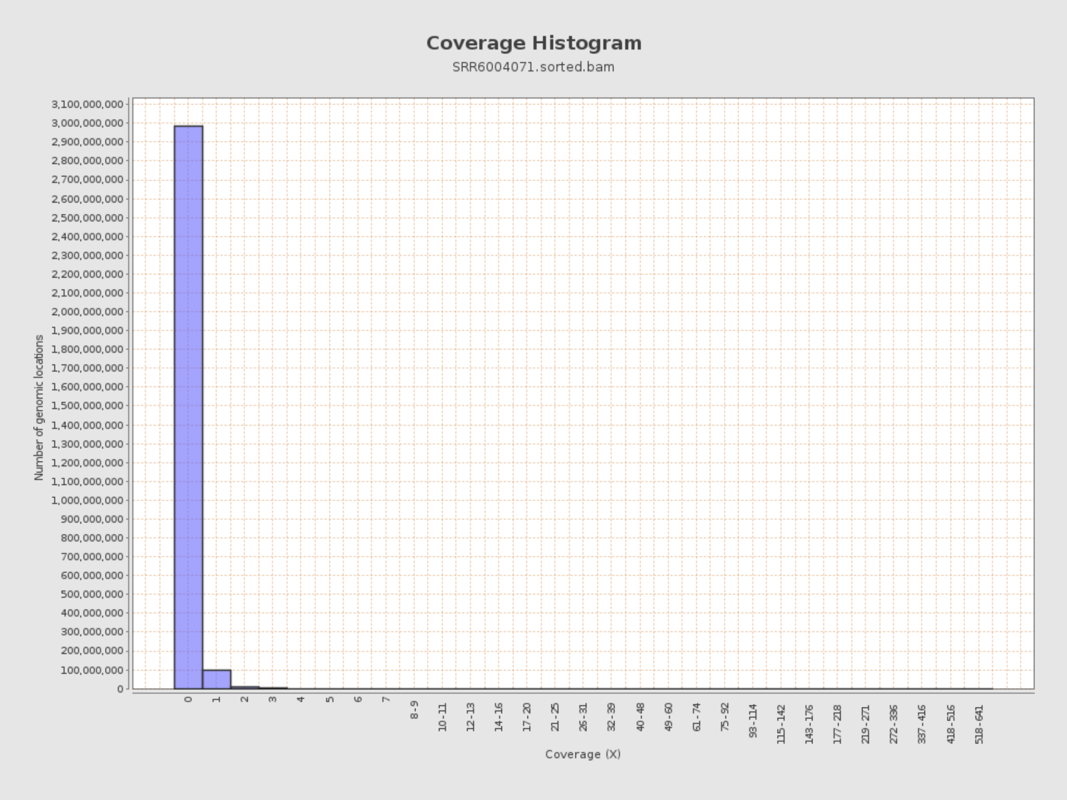
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10323033	0.0414	0.6042
chr2	243199373	10462311	0.043	0.3546
chr3	198022430	9067289	0.0458	0.2388
chr4	191154276	9461855	0.0495	0.2576
chr5	180915260	8605575	0.0476	0.244
chr6	171115067	8019790	0.0469	0.2608
chr7	159138663	7533269	0.0473	0.4261

chr8	146364022	8249959	0.0564	0.474
chr9	141213431	4923741	0.0349	0.2961
chr10	135534747	6286486	0.0464	0.3208
chr11	135006516	4732320	0.0351	0.2509
chr12	133851895	6003085	0.0448	0.2407
chr13	115169878	4287147	0.0372	0.2203
chr14	107349540	3081199	0.0287	0.2028
chr15	102531392	4467802	0.0436	0.2368
chr16	90354753	3487293	0.0386	0.2366
chr17	81195210	2690732	0.0331	0.2109
chr18	78077248	3626281	0.0464	0.5106
chr19	59128983	1830707	0.031	0.4244
chr20	63025520	2771469	0.044	0.2393
chr21	48129895	1717168	0.0357	0.2216
chr22	51304566	1071225	0.0209	0.1592
chrMT	16571	30148	1.8193	1.7241
chrX	155270560	7477445	0.0482	0.2633
chrY	59373566	268965	0.0045	0.0913

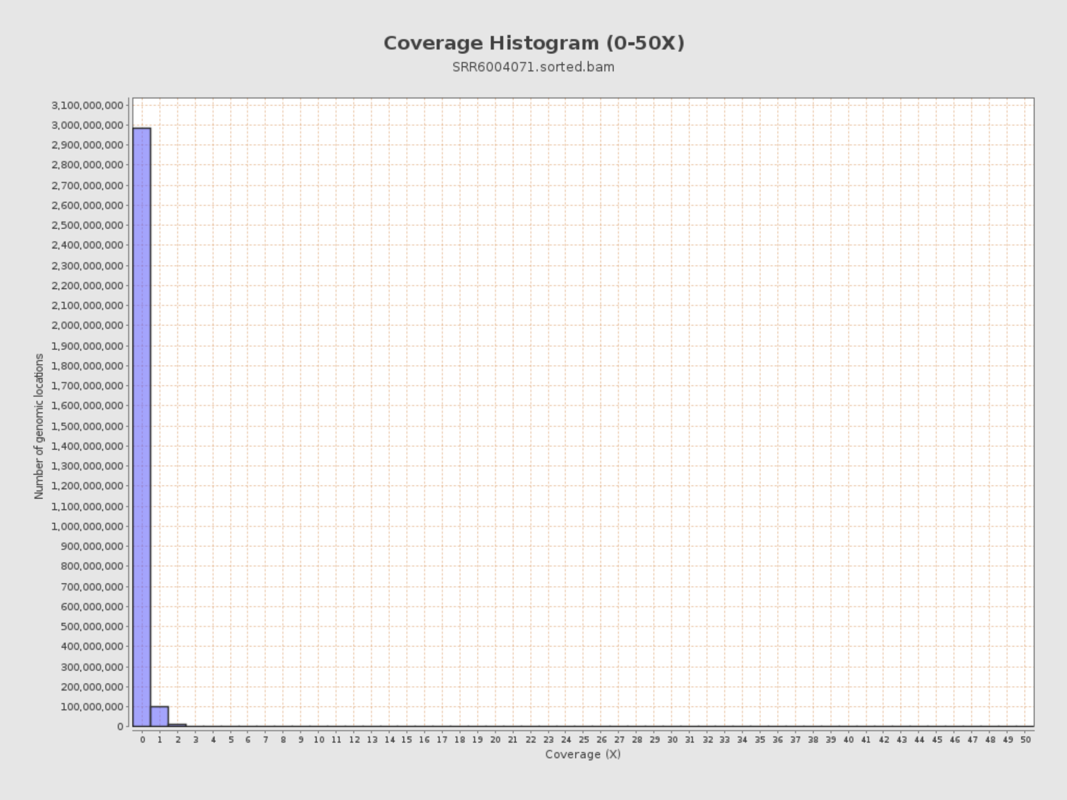
3. Results : Coverage across reference



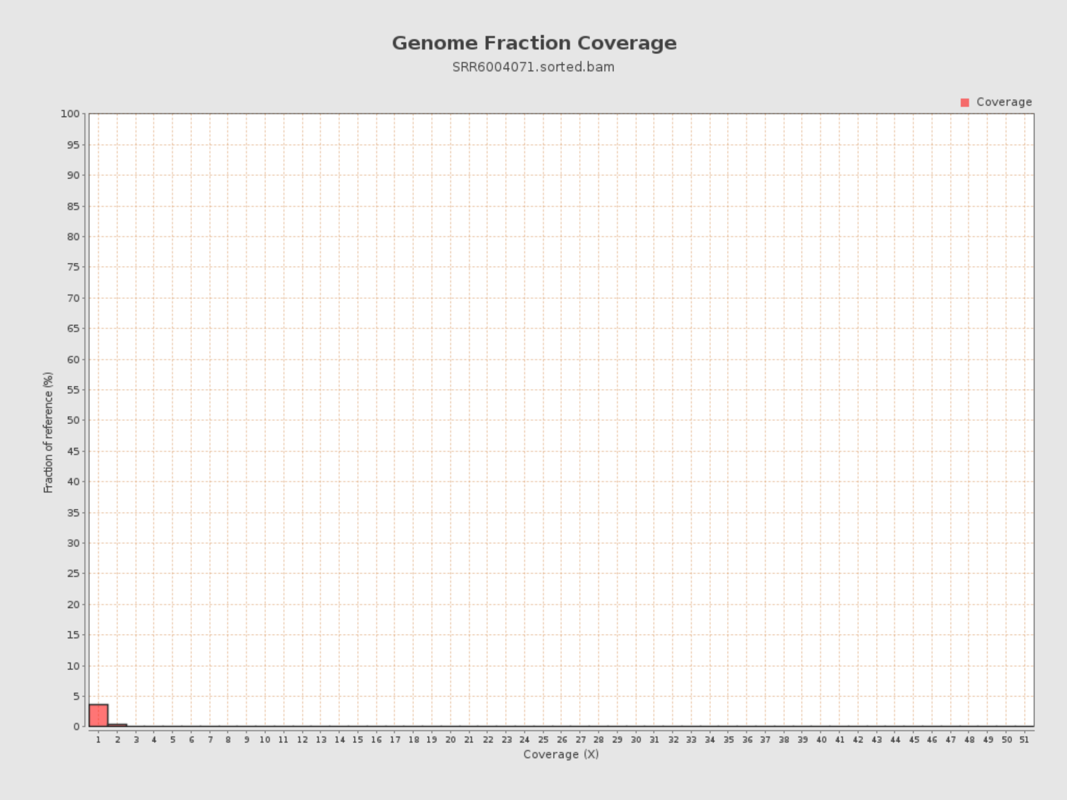
4. Results : Coverage Histogram



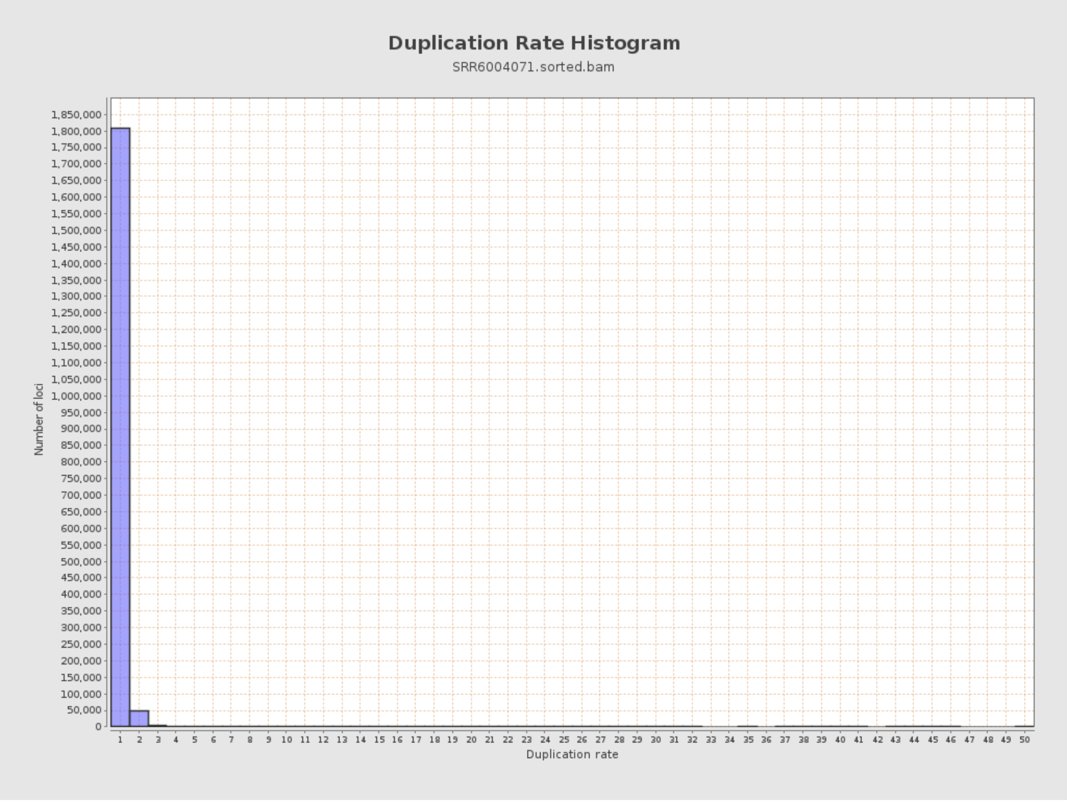
5. Results : Coverage Histogram (0-50X)



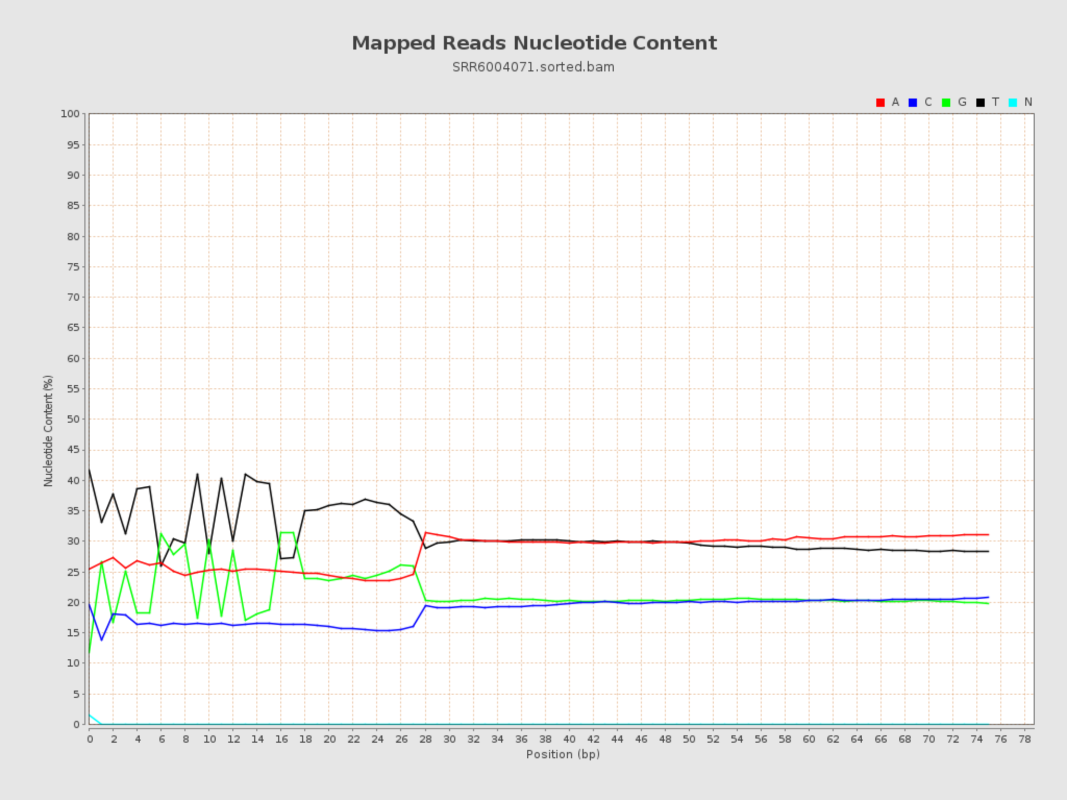
6. Results : Genome Fraction Coverage



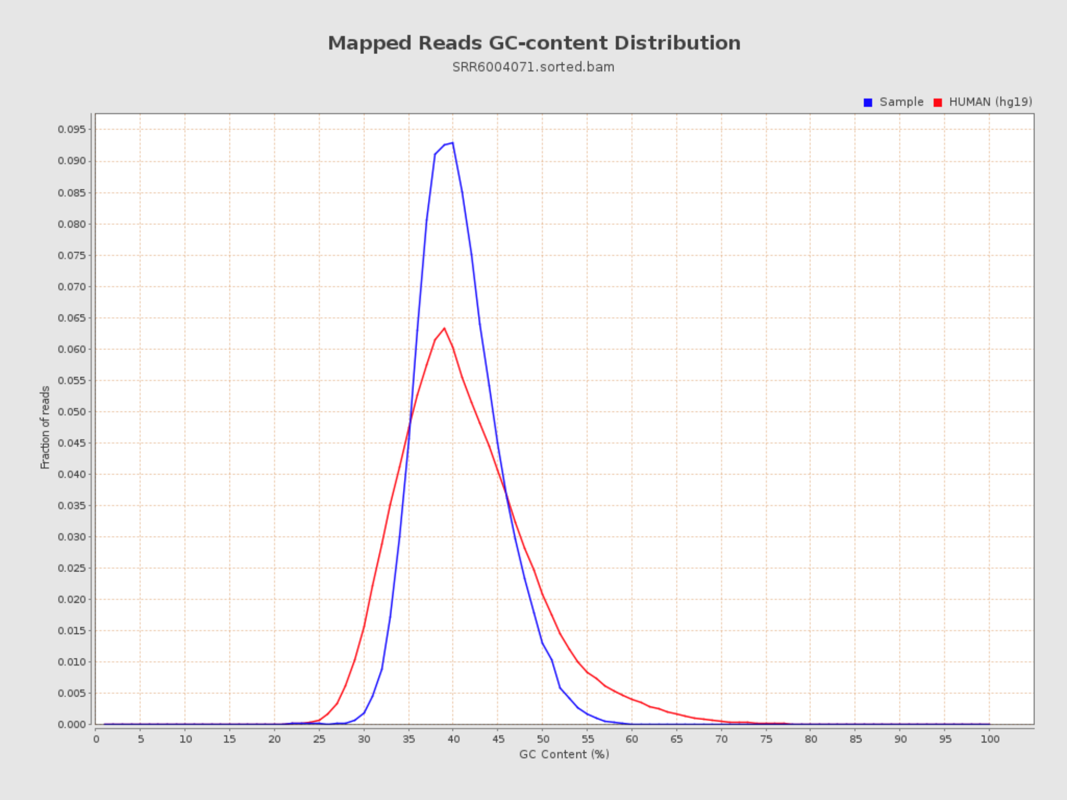
7. Results : Duplication Rate Histogram



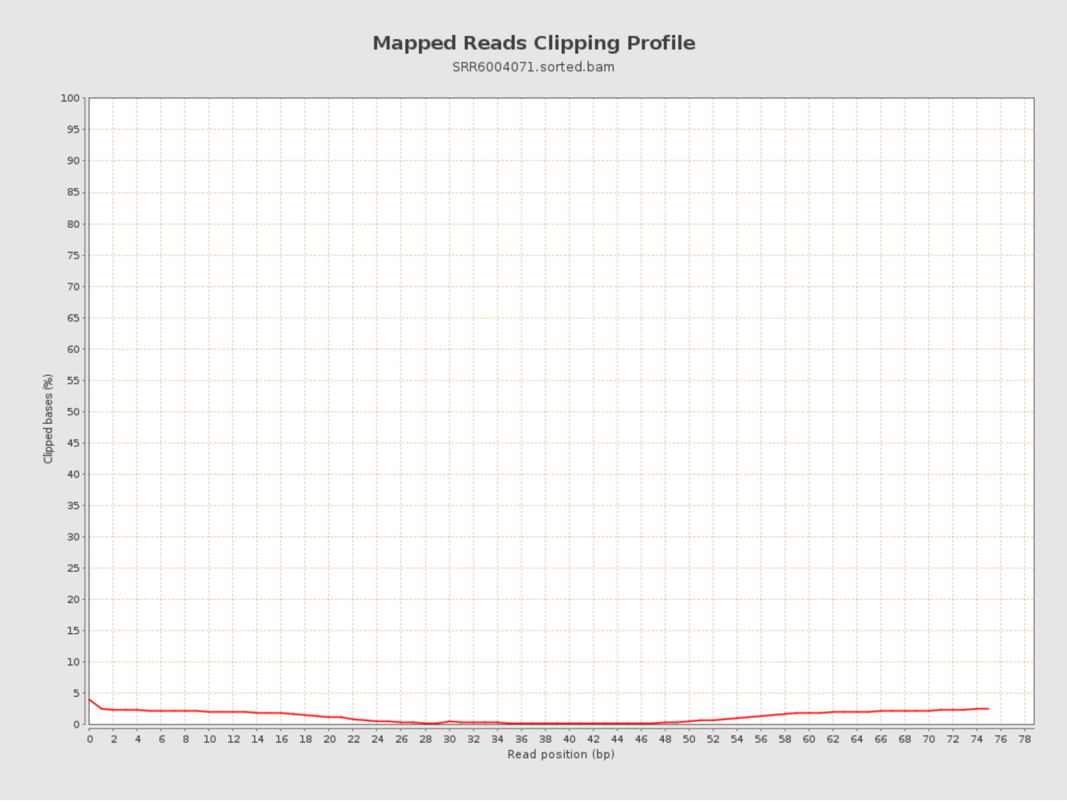
8. Results : Mapped Reads Nucleotide Content



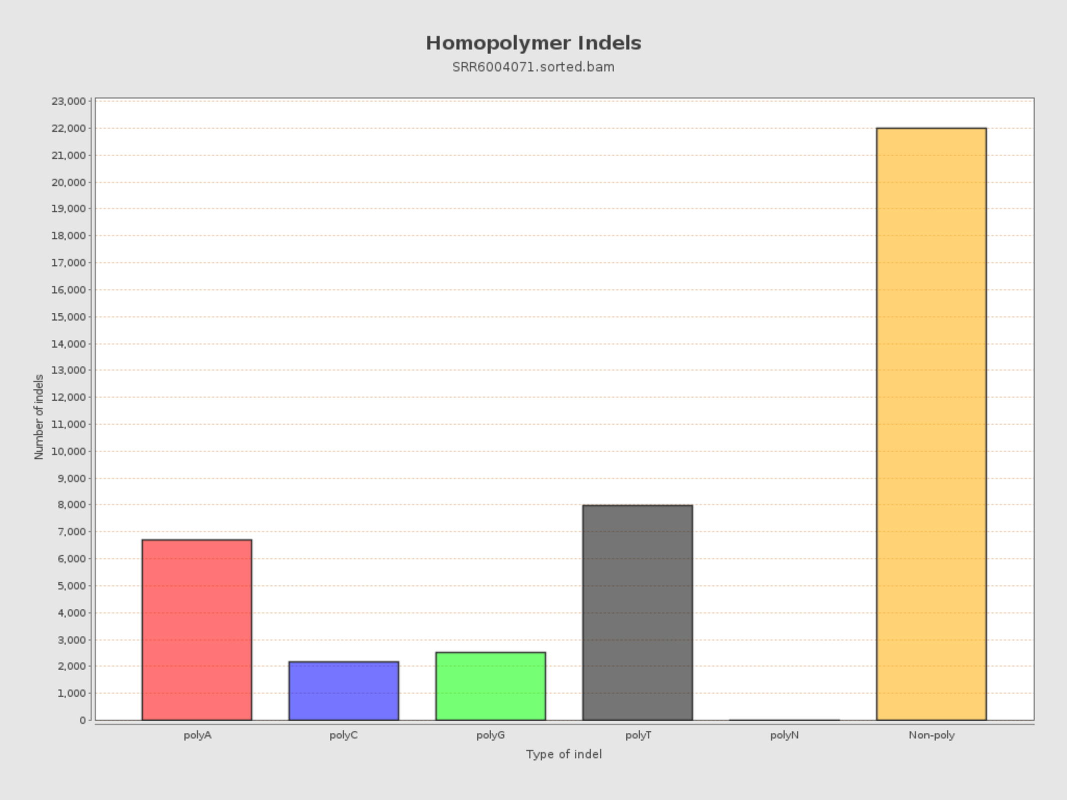
9. Results : Mapped Reads GC-content Distribution



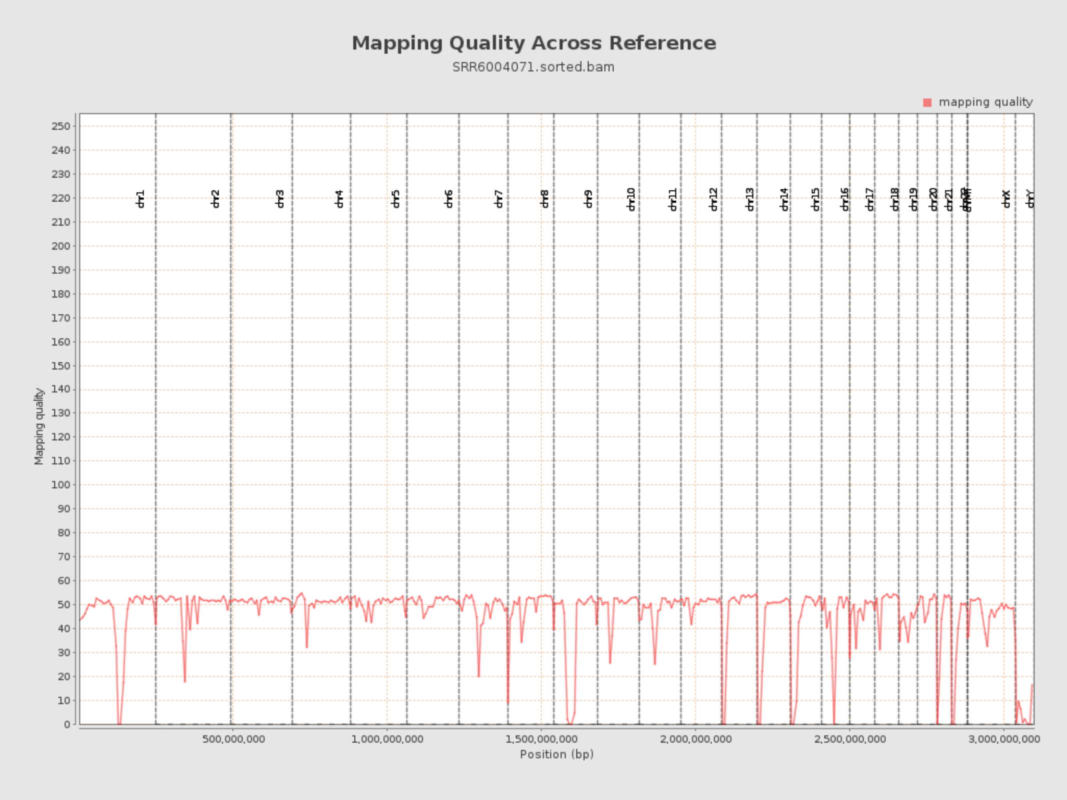
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram