Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:39:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004131.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_SRR6004131 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004131.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:39:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004131.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,354,880
Mapped reads	2,151,289 / 91.35%
Unmapped reads	203,591 / 8.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,203 / 1.11%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	62,625 / 2.66%
Duplication rate	1.64%
Clipped reads	973,445 / 41.34%

2.2. ACGT Content

Number/percentage of A's	41,143,081 / 28.53%
Number/percentage of C's	27,252,986 / 18.9%
Number/percentage of T's	43,200,314 / 29.95%
Number/percentage of G's	32,591,610 / 22.6%
Number/percentage of N's	29,793 / 0.02%
GC Percentage	41.5%

2.3. Coverage

Mean	0.0466

Standard Deviation	0.519

2.4. Mapping Quality

Mean Mapping Quality	43.11

2.5. Mismatches and indels

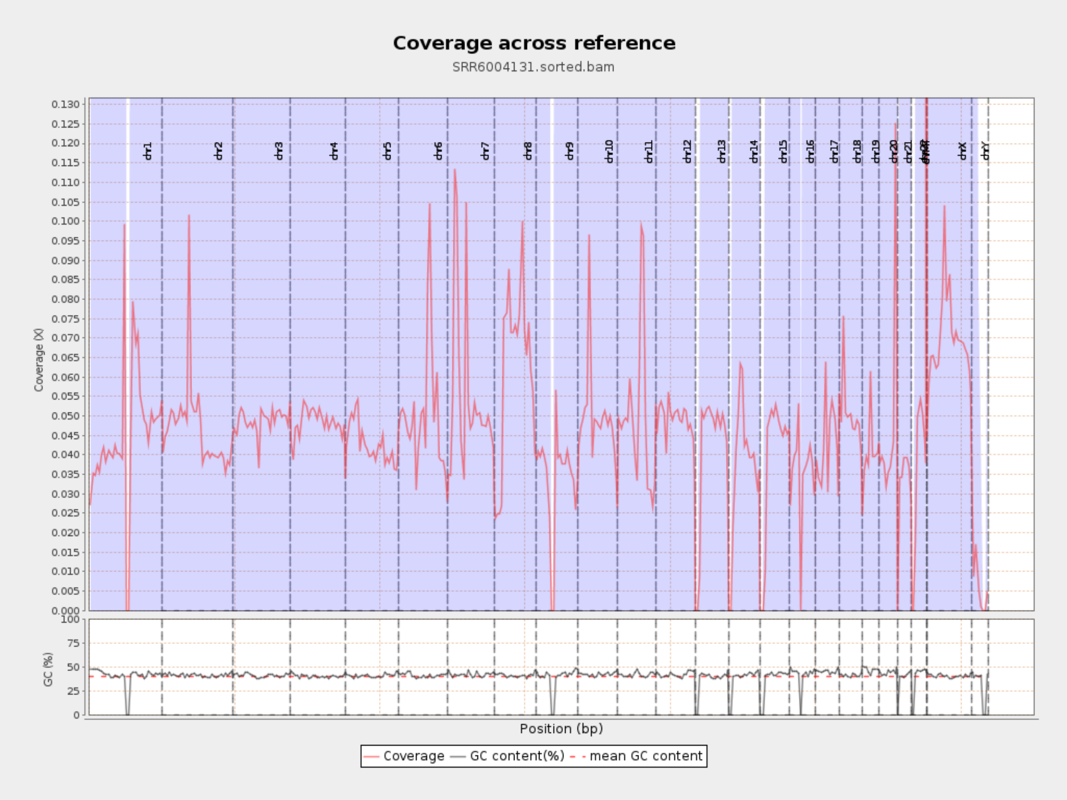
General error rate	0.86%
Mismatches	1,215,146
Insertions	12,807
Mapped reads with at least one insertion	0.59%
Deletions	38,968
Mapped reads with at least one deletion	1.79%
Homopolymer indels	43.75%

2.6. Chromosome stats

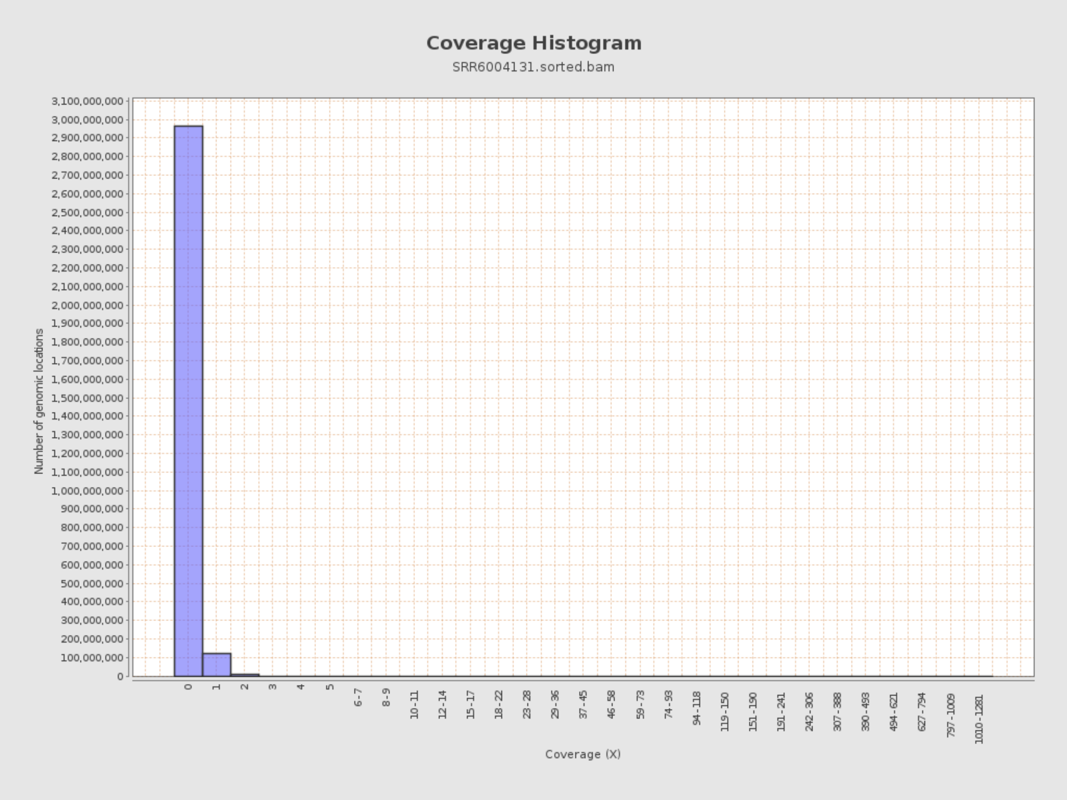
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11162713	0.0448	1.1159
chr2	243199373	11379994	0.0468	0.501
chr3	198022430	9624256	0.0486	0.2393
chr4	191154276	9226147	0.0483	0.2417
chr5	180915260	7733784	0.0427	0.2267
chr6	171115067	8702121	0.0509	0.2849
chr7	159138663	8973919	0.0564	0.7895

chr8	146364022	9043527	0.0618	0.5726
chr9	141213431	4771201	0.0338	0.4301
chr10	135534747	6777590	0.05	0.5067
chr11	135006516	6718877	0.0498	0.4374
chr12	133851895	6571411	0.0491	0.2427
chr13	115169878	4705791	0.0409	0.2139
chr14	107349540	3976355	0.037	0.2487
chr15	102531392	3953956	0.0386	0.2157
chr16	90354753	3180837	0.0352	0.2787
chr17	81195210	3464657	0.0427	0.2558
chr18	78077248	3995196	0.0512	1.0092
chr19	59128983	2437326	0.0412	0.7753
chr20	63025520	3172222	0.0503	0.2567
chr21	48129895	1560487	0.0324	0.2251
chr22	51304566	1746775	0.034	0.1939
chrMT	16571	156204	9.4263	6.6022
chrX	155270560	10845488	0.0698	0.3498
chrY	59373566	401924	0.0068	0.118

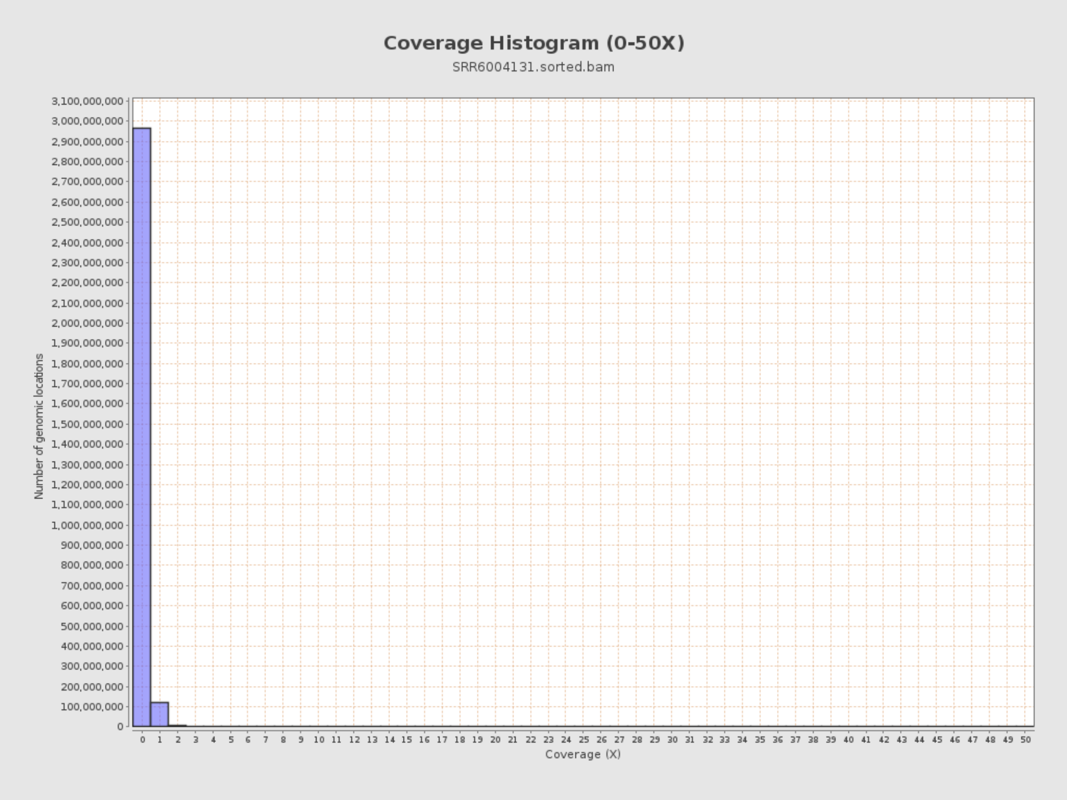
3. Results : Coverage across reference



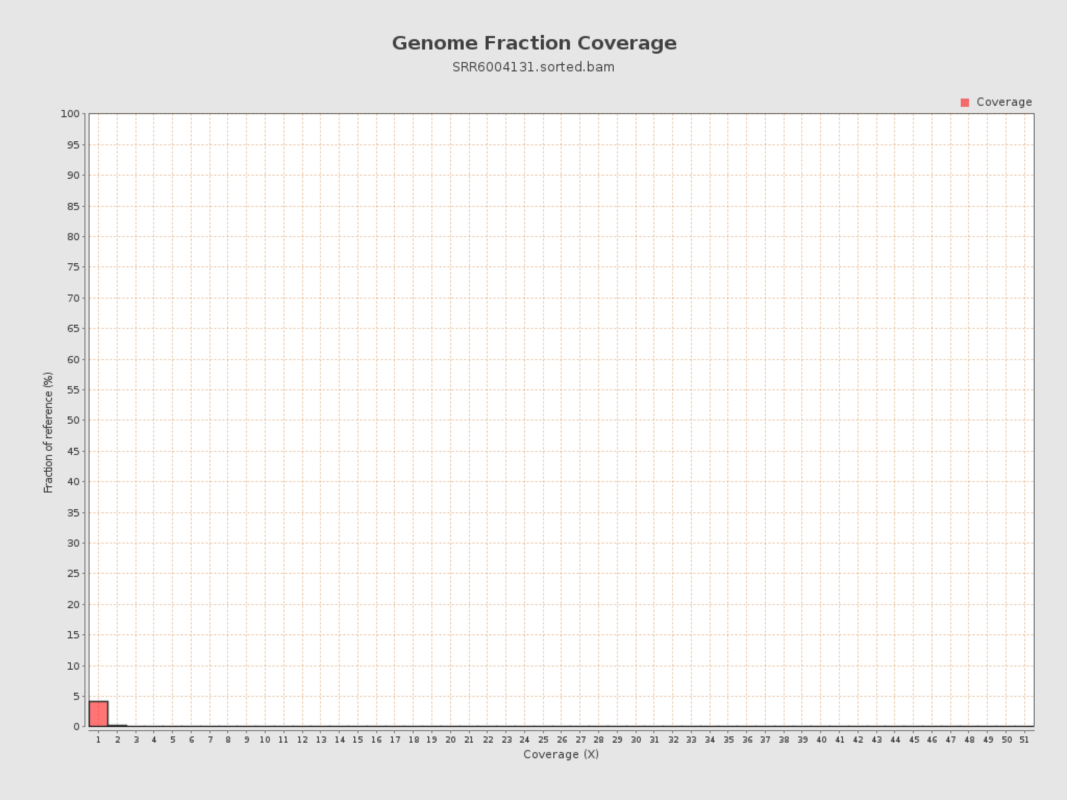
4. Results : Coverage Histogram



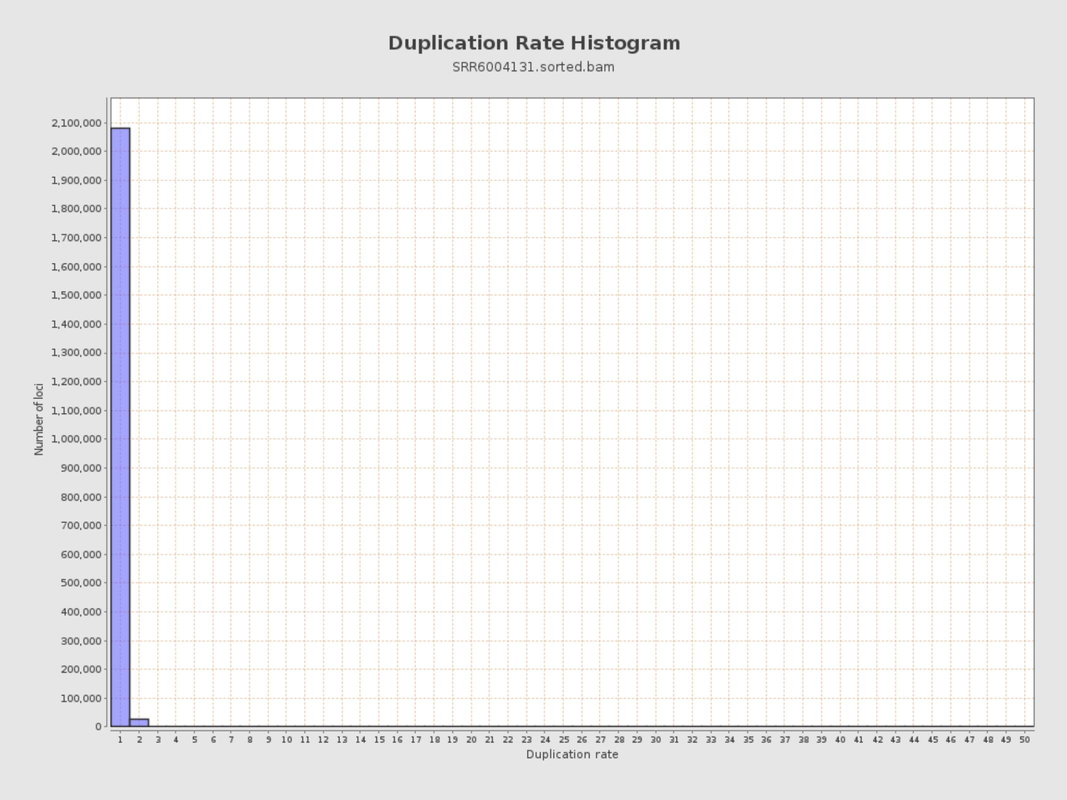
5. Results : Coverage Histogram (0-50X)



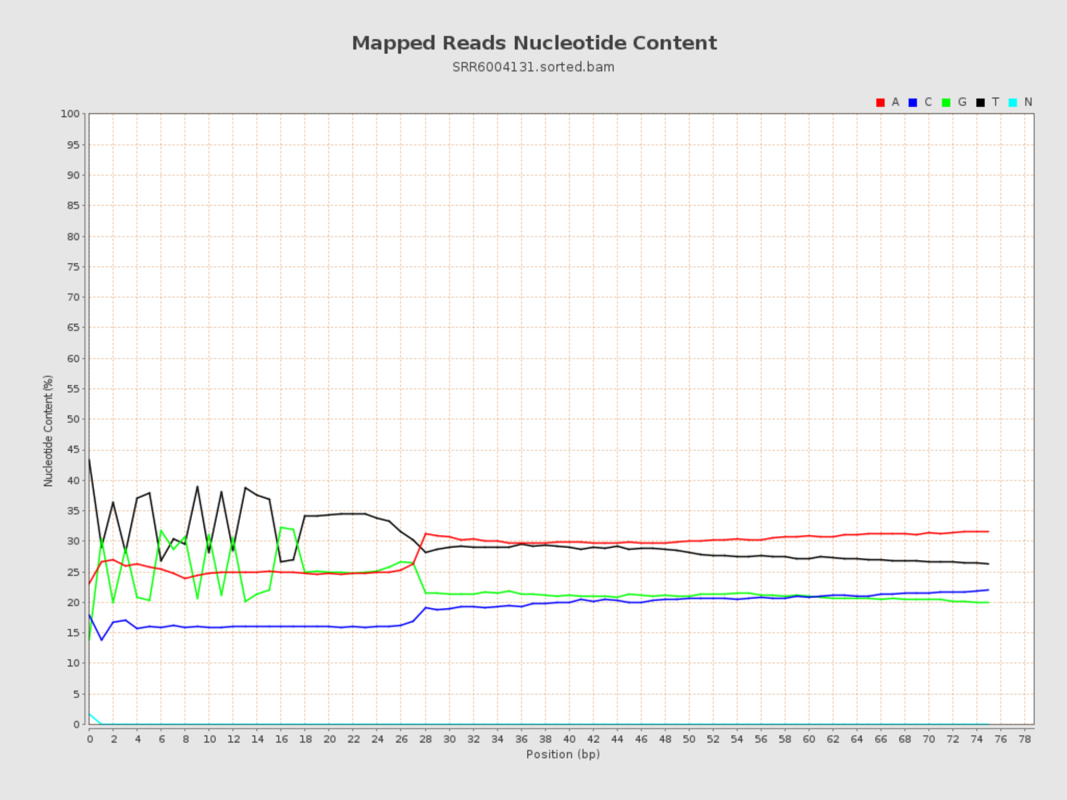
6. Results : Genome Fraction Coverage



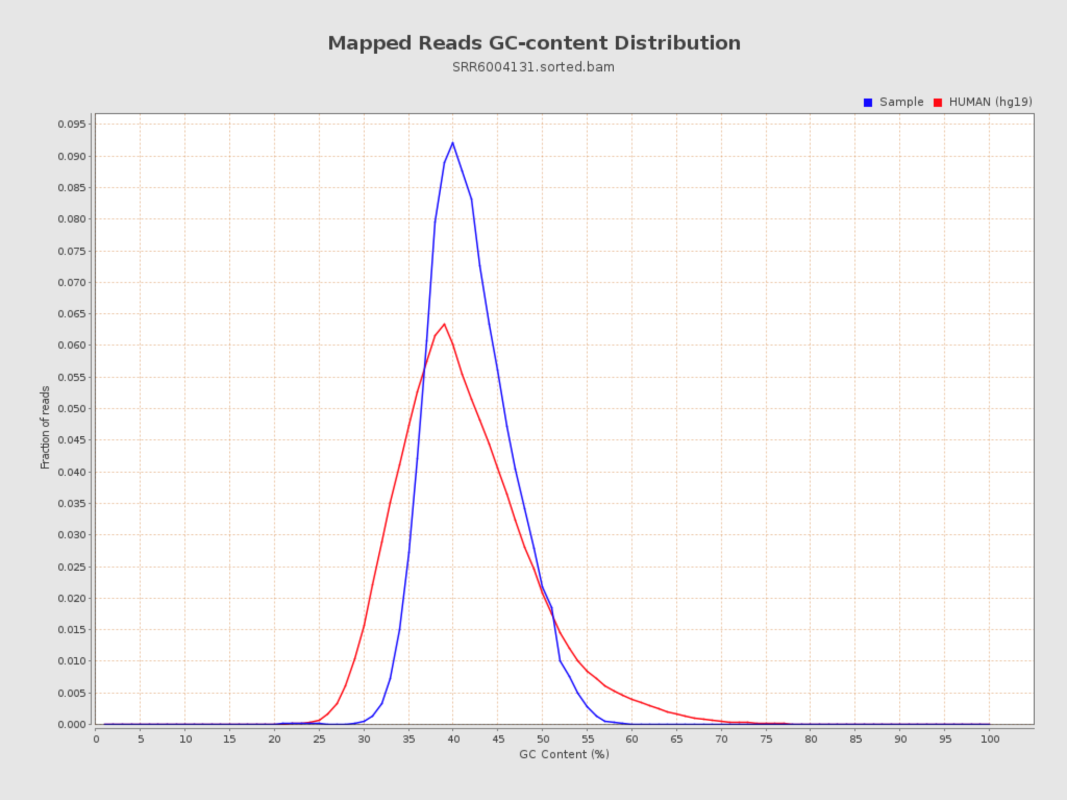
7. Results : Duplication Rate Histogram



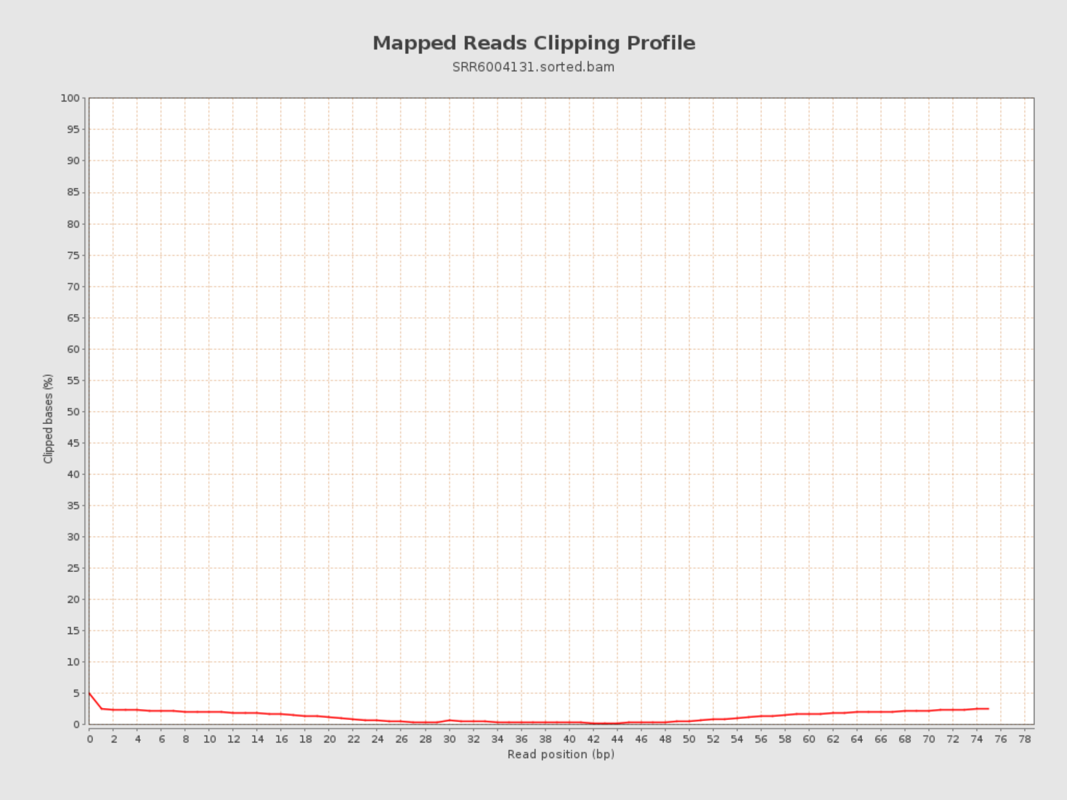
8. Results : Mapped Reads Nucleotide Content



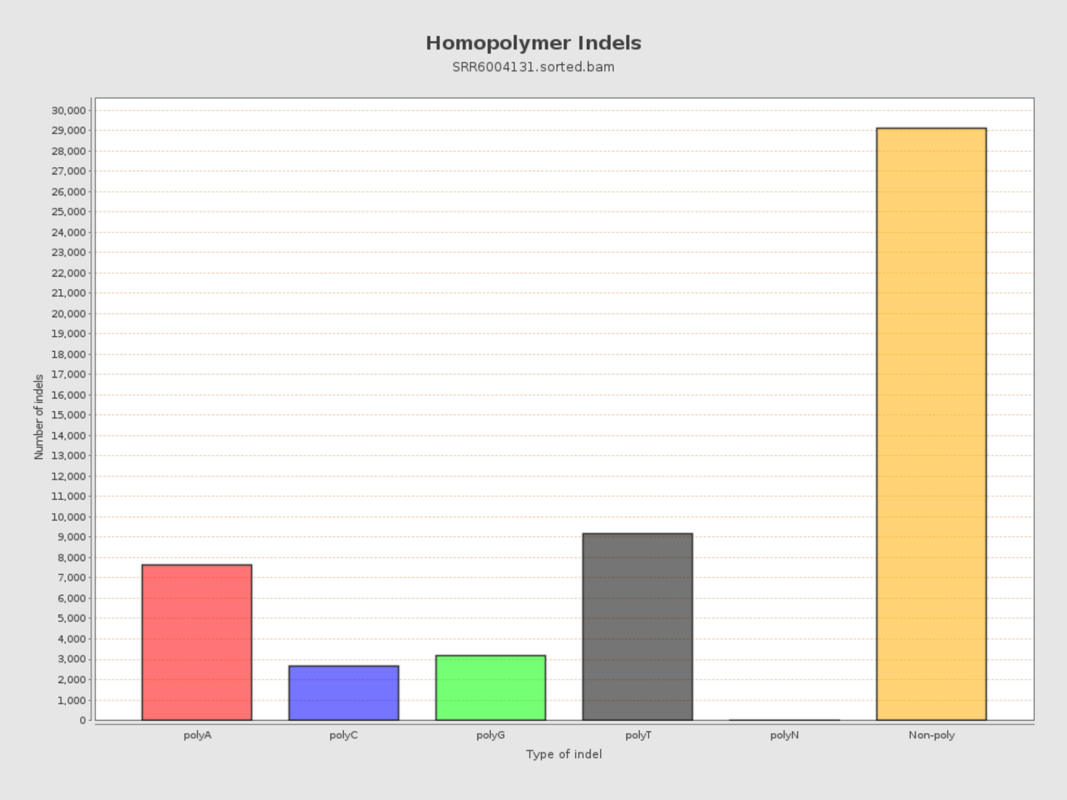
9. Results : Mapped Reads GC-content Distribution



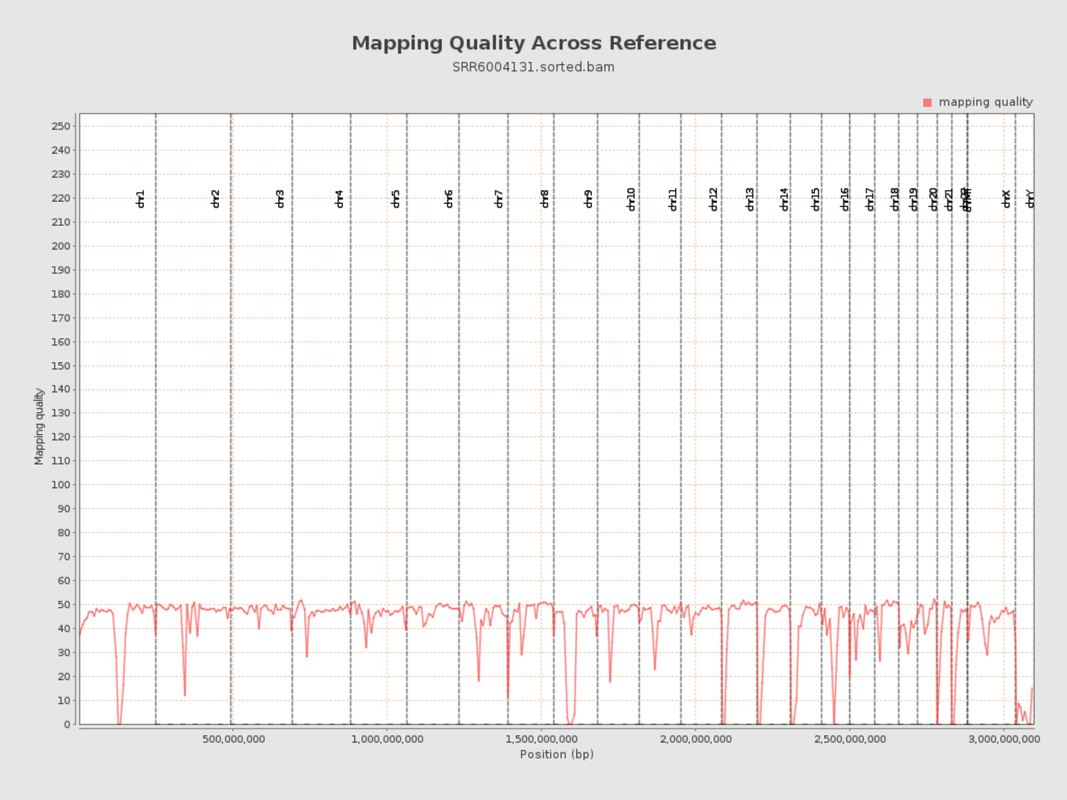
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram