Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:56:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013311.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_SRR6013311 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013311.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:56:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013311.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,091,726
Mapped reads	1,808,828 / 86.48%
Unmapped reads	282,898 / 13.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,182 / 1.16%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	165,261 / 7.9%
Duplication rate	7.29%
Clipped reads	895,562 / 42.81%

2.2. ACGT Content

Number/percentage of A's	32,607,299 / 27.36%
Number/percentage of C's	22,459,635 / 18.84%
Number/percentage of T's	37,376,024 / 31.36%
Number/percentage of G's	26,720,092 / 22.42%
Number/percentage of N's	27,806 / 0.02%
GC Percentage	41.26%

2.3. Coverage

Mean	0.0385

Standard Deviation	0.3924

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

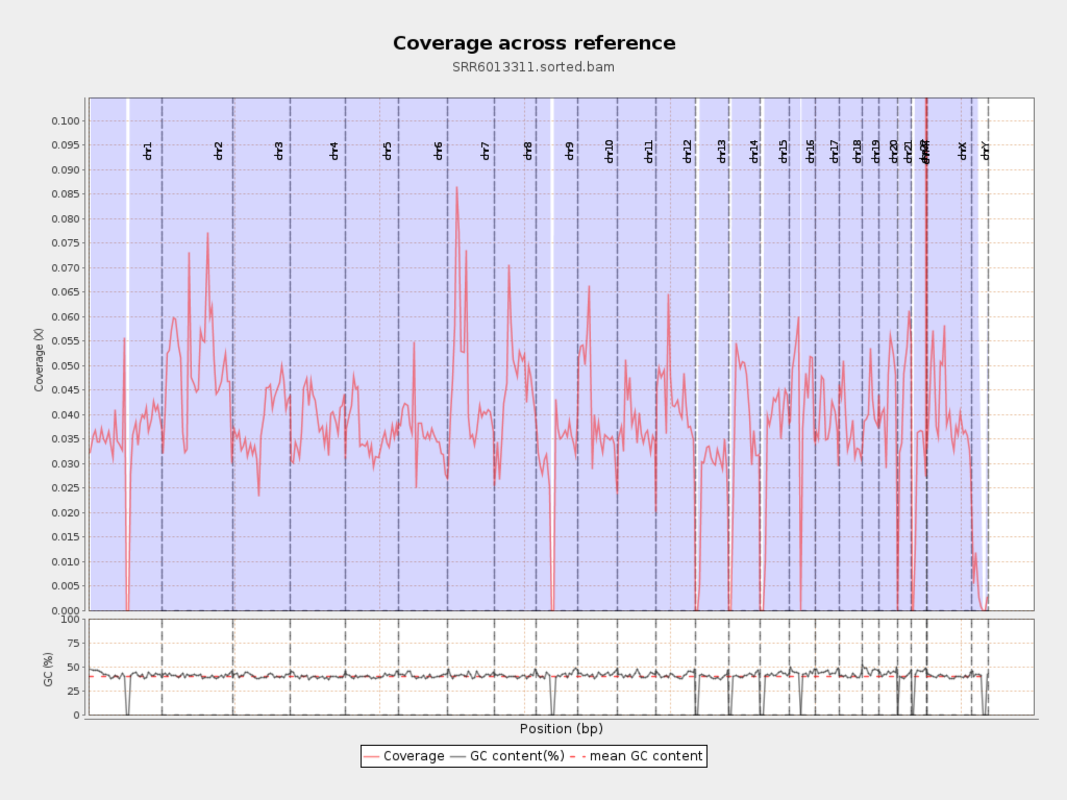
General error rate	0.84%
Mismatches	990,132
Insertions	7,837
Mapped reads with at least one insertion	0.43%
Deletions	29,209
Mapped reads with at least one deletion	1.6%
Homopolymer indels	45.27%

2.6. Chromosome stats

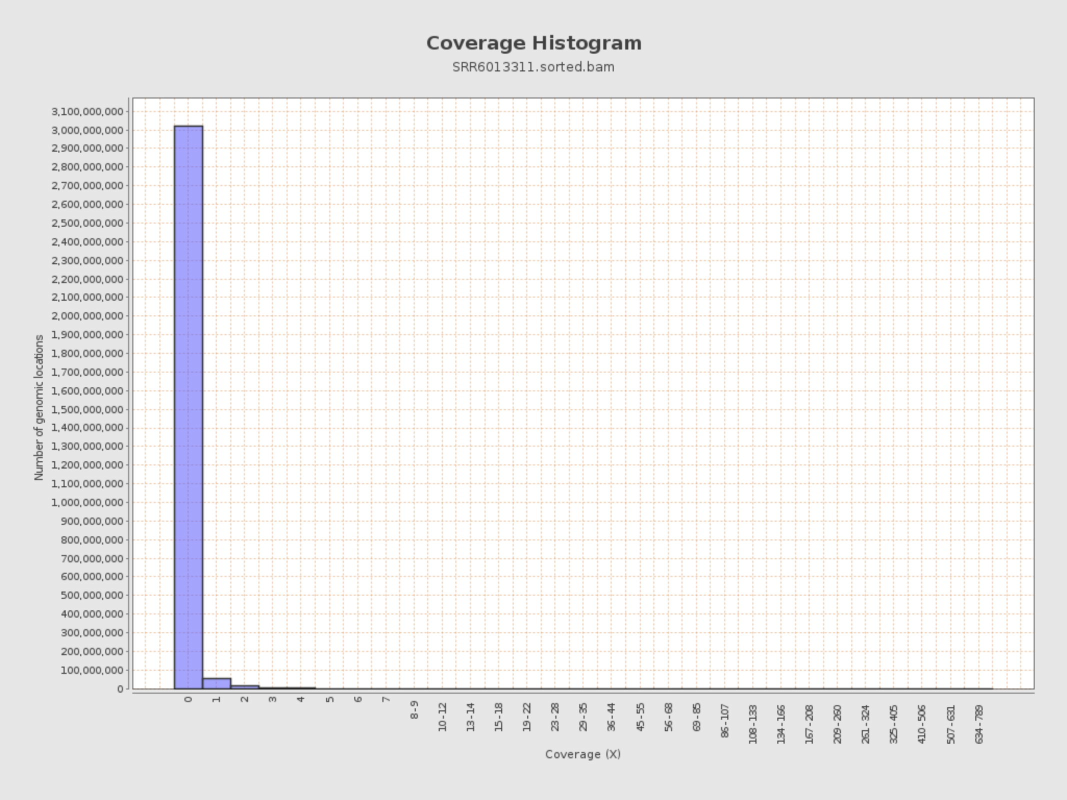
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8683746	0.0348	0.6625
chr2	243199373	12231377	0.0503	0.4857
chr3	198022430	7642268	0.0386	0.2819
chr4	191154276	7375240	0.0386	0.2843
chr5	180915260	6554752	0.0362	0.2816
chr6	171115067	6244681	0.0365	0.325
chr7	159138663	7474694	0.047	0.5393

chr8	146364022	6706007	0.0458	0.3879
chr9	141213431	4259117	0.0302	0.3357
chr10	135534747	5635088	0.0416	0.3897
chr11	135006516	5075965	0.0376	0.3253
chr12	133851895	5822389	0.0435	0.3011
chr13	115169878	2979503	0.0259	0.2309
chr14	107349540	3870714	0.0361	0.2825
chr15	102531392	3386889	0.033	0.2621
chr16	90354753	3952346	0.0437	0.3125
chr17	81195210	3153344	0.0388	0.3205
chr18	78077248	2942035	0.0377	0.5552
chr19	59128983	2439026	0.0412	0.5692
chr20	63025520	2752367	0.0437	0.3064
chr21	48129895	2049575	0.0426	0.3056
chr22	51304566	1246876	0.0243	0.2193
chrMT	16571	209864	12.6645	9.2496
chrX	155270560	6301048	0.0406	0.3137
chrY	59373566	251904	0.0042	0.1

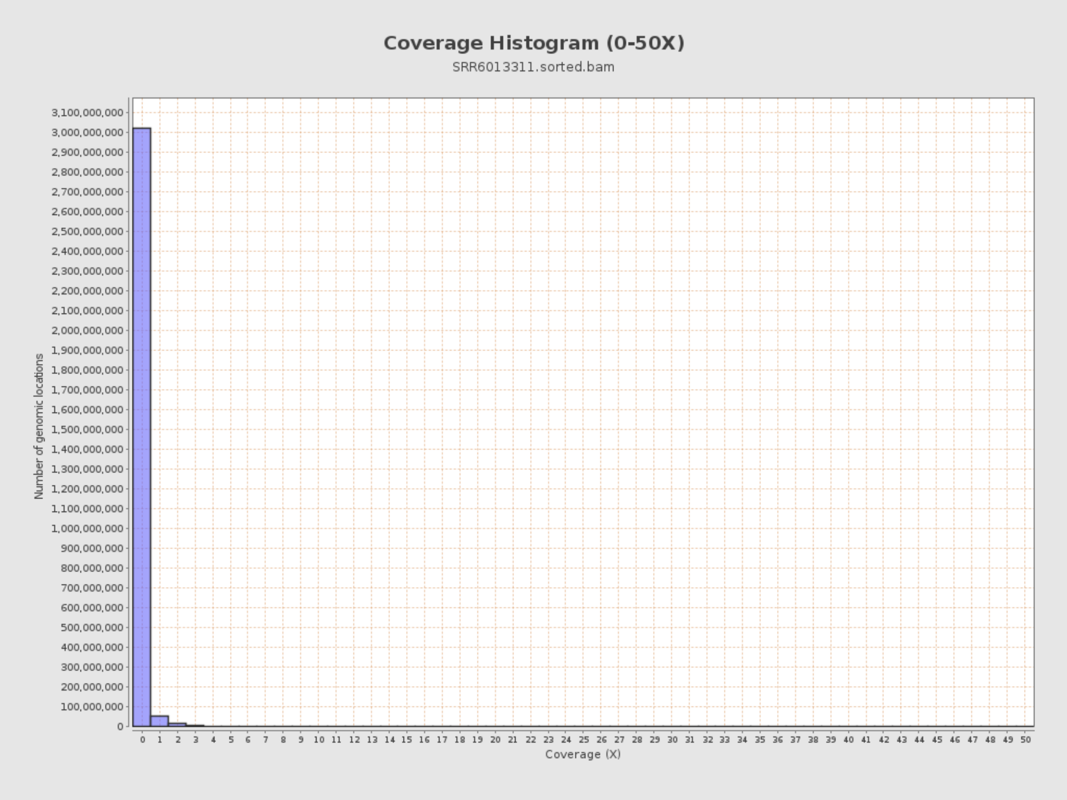
3. Results : Coverage across reference



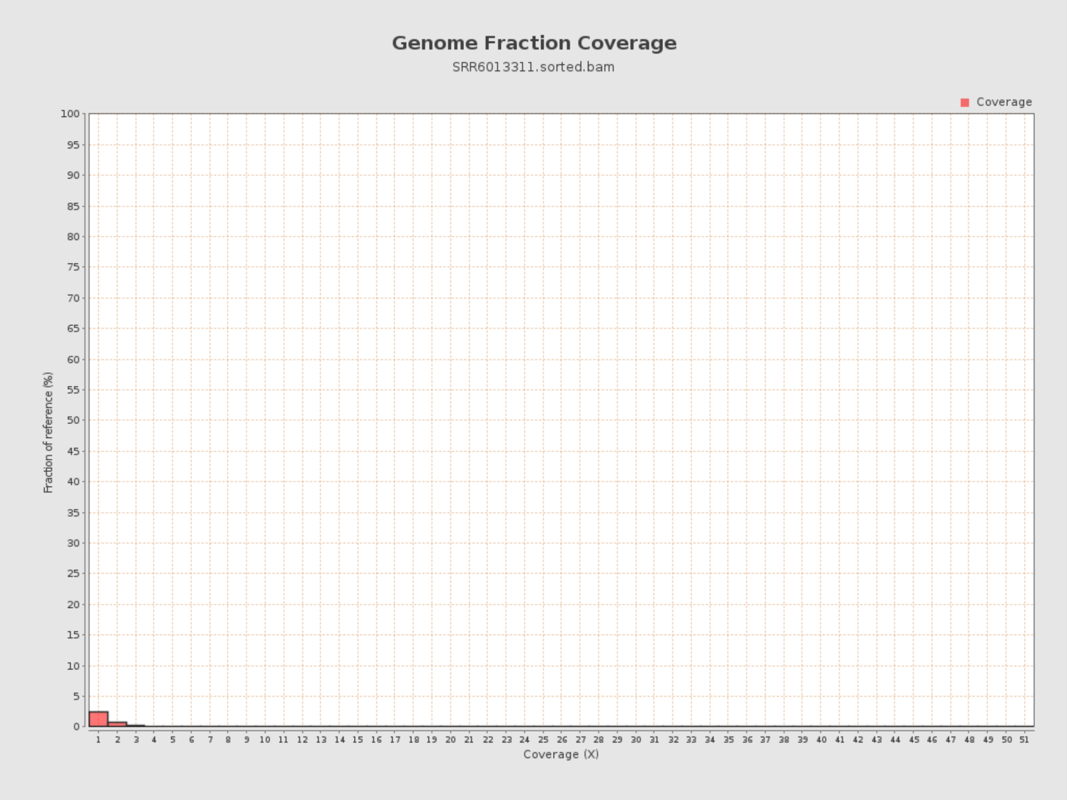
4. Results : Coverage Histogram



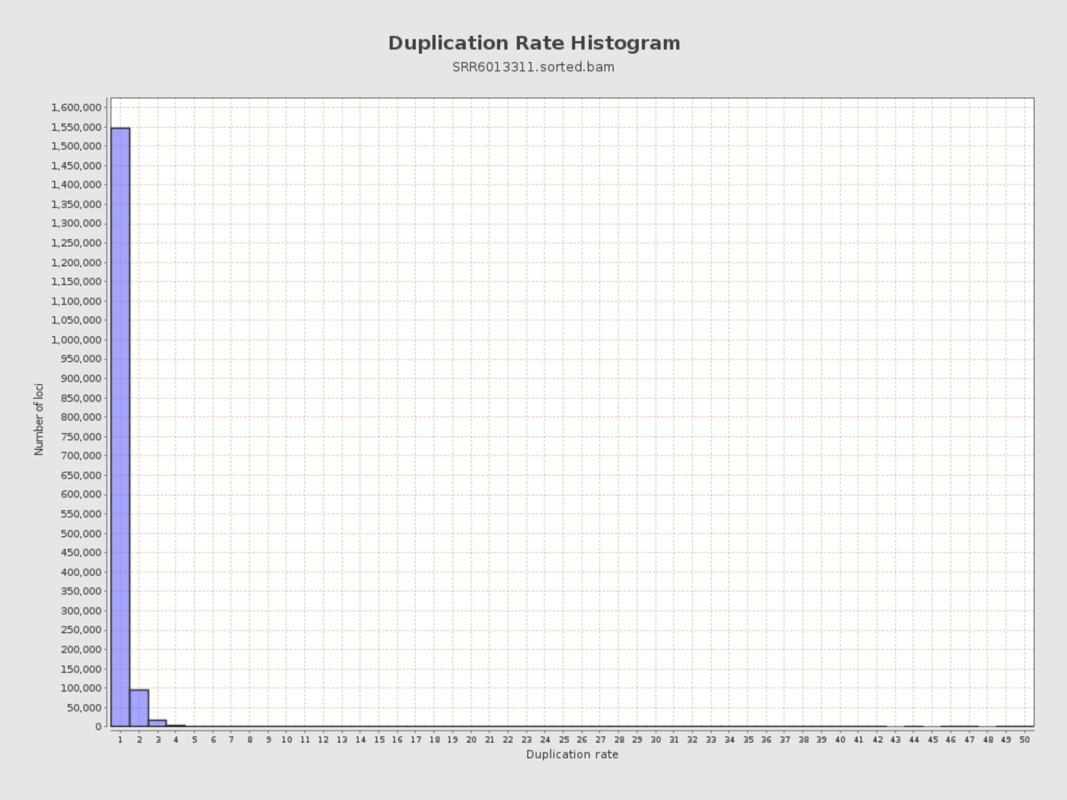
5. Results : Coverage Histogram (0-50X)



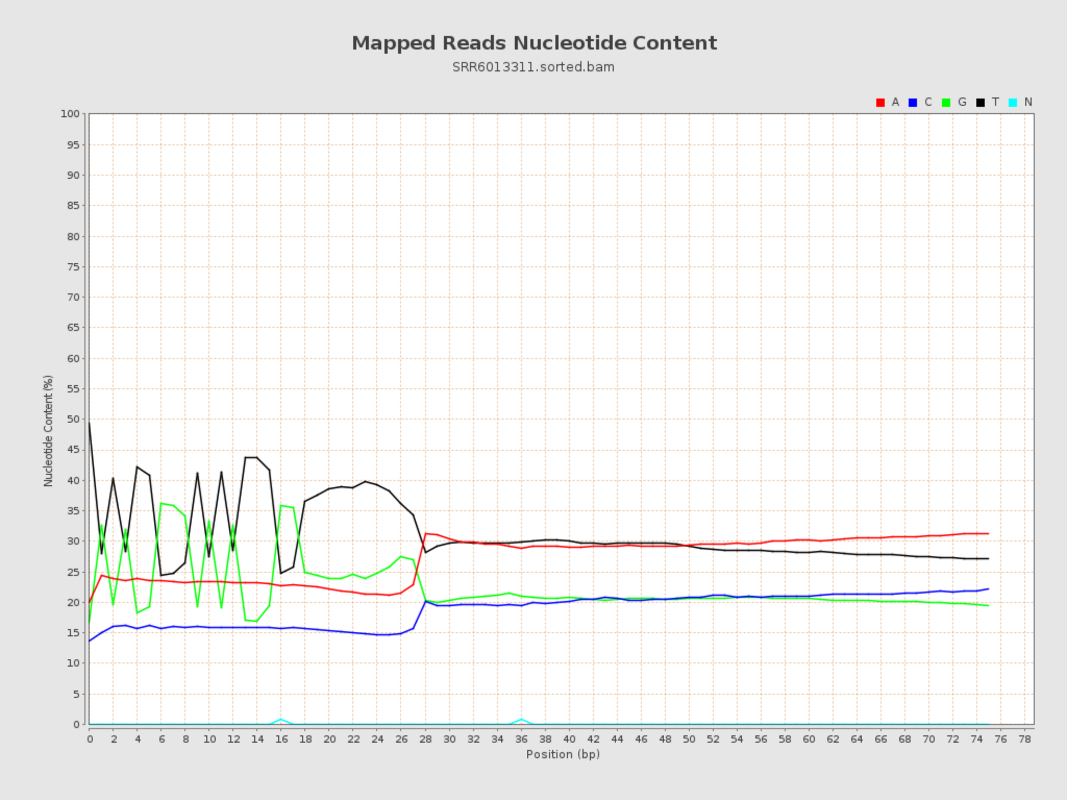
6. Results : Genome Fraction Coverage



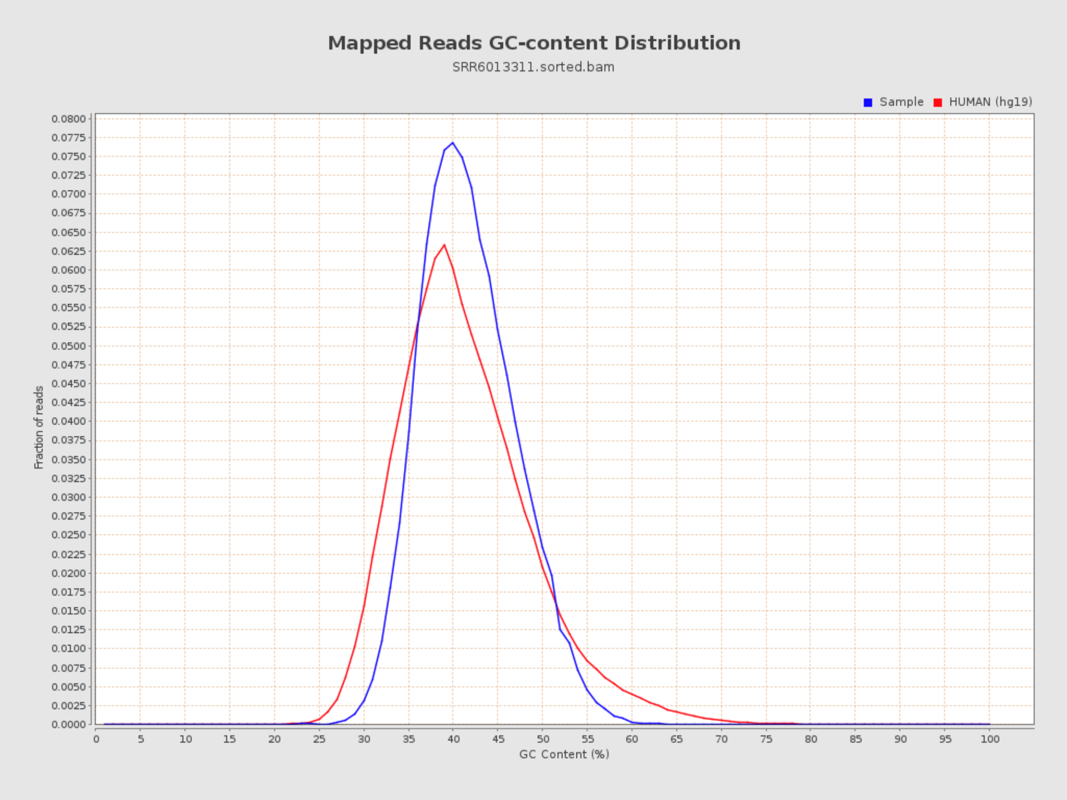
7. Results : Duplication Rate Histogram



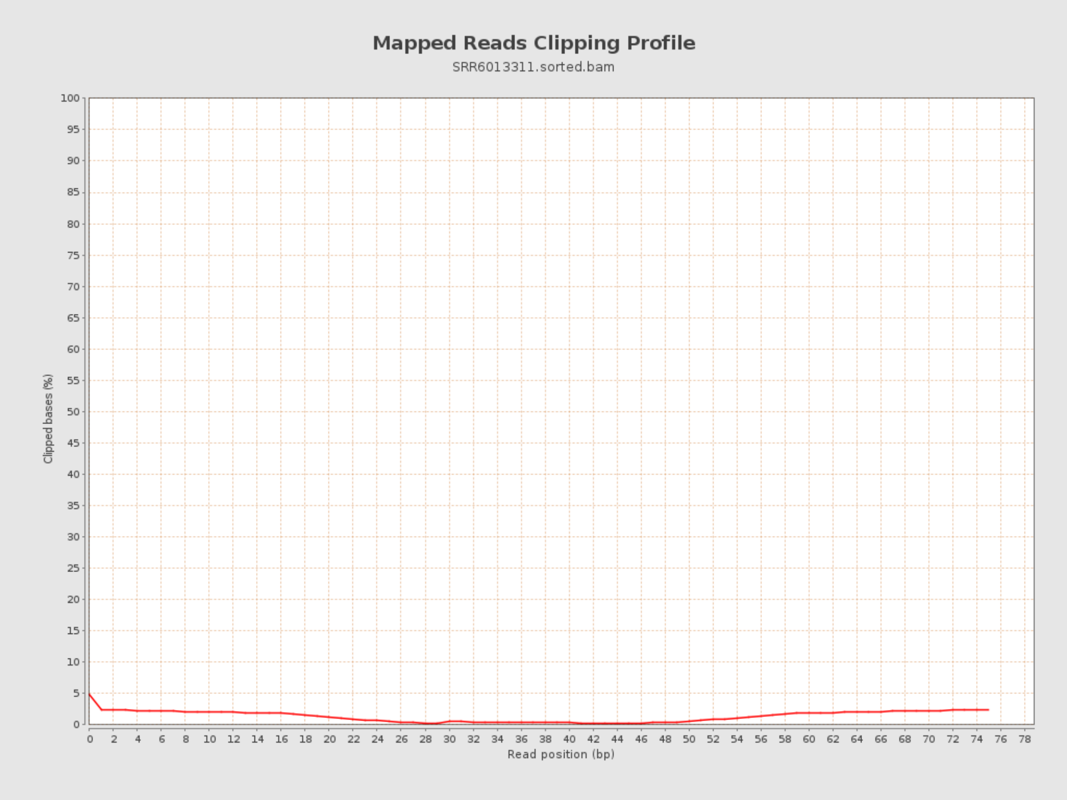
8. Results : Mapped Reads Nucleotide Content



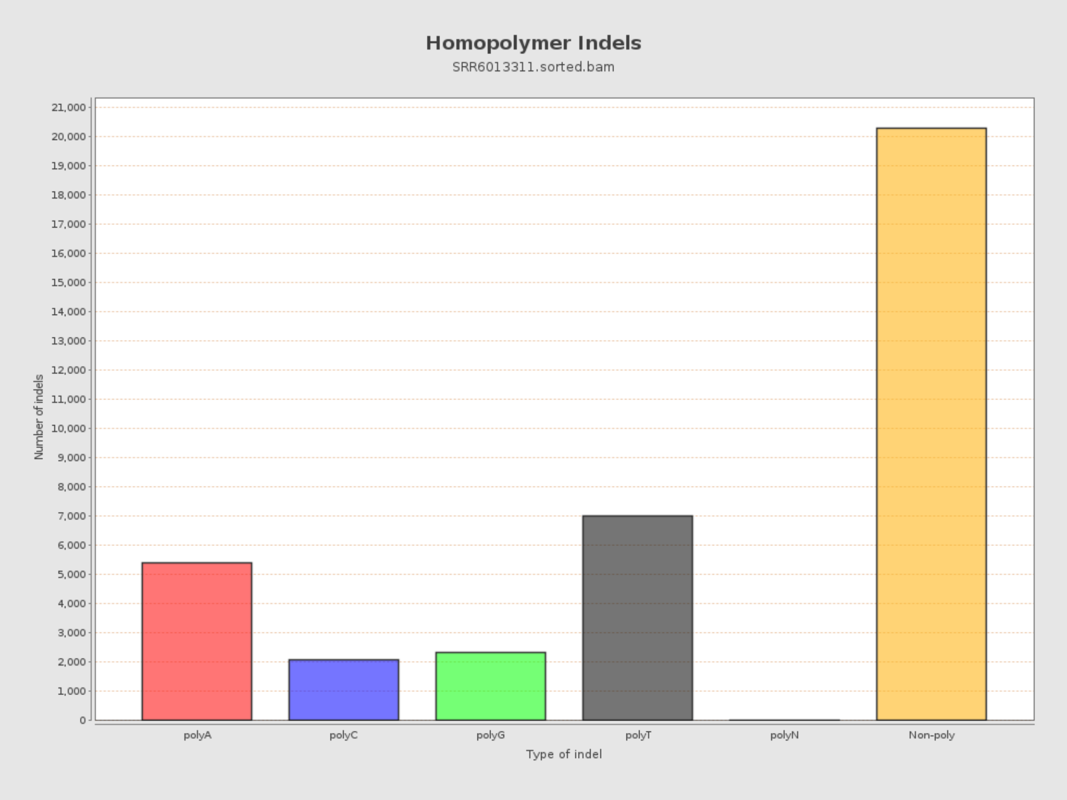
9. Results : Mapped Reads GC-content Distribution



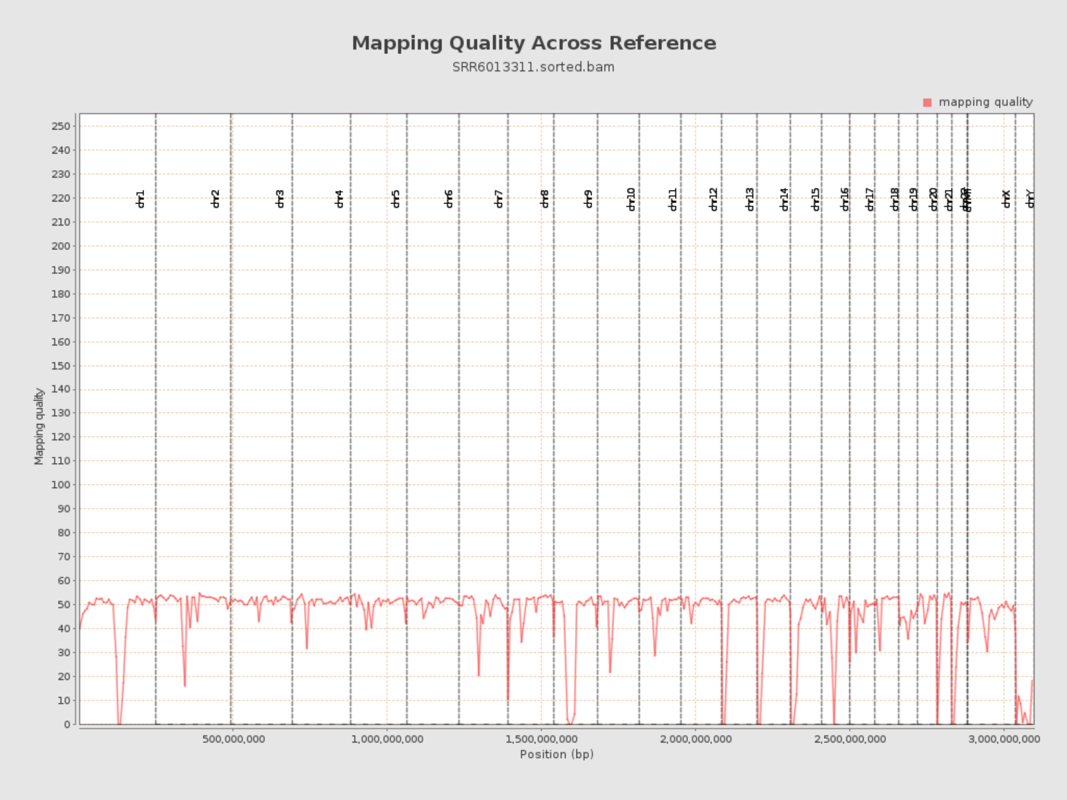
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram