Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 19:47:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003996.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_SRR6003996 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003996.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 19:47:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003996.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,037,076
Mapped reads	3,715,720 / 92.04%
Unmapped reads	321,356 / 7.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,145 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	182,005 / 4.51%
Duplication rate	3.64%
Clipped reads	1,687,293 / 41.79%

2.2. ACGT Content

Number/percentage of A's	66,722,748 / 27.01%
Number/percentage of C's	47,821,941 / 19.36%
Number/percentage of T's	75,168,612 / 30.43%
Number/percentage of G's	57,228,702 / 23.17%
Number/percentage of N's	51,371 / 0.02%
GC Percentage	42.53%

2.3. Coverage

Mean	0.0798

Standard Deviation	0.6125

2.4. Mapping Quality

Mean Mapping Quality	41.4

2.5. Mismatches and indels

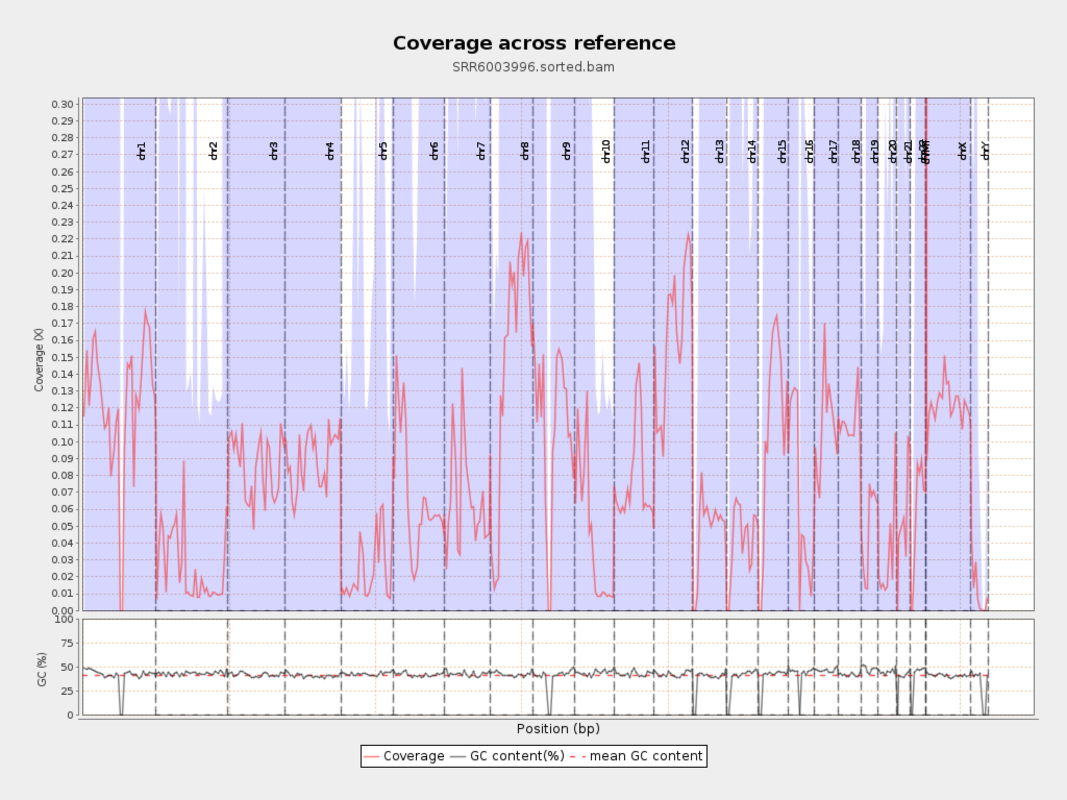
General error rate	0.83%
Mismatches	2,003,137
Insertions	19,142
Mapped reads with at least one insertion	0.51%
Deletions	61,960
Mapped reads with at least one deletion	1.65%
Homopolymer indels	45.93%

2.6. Chromosome stats

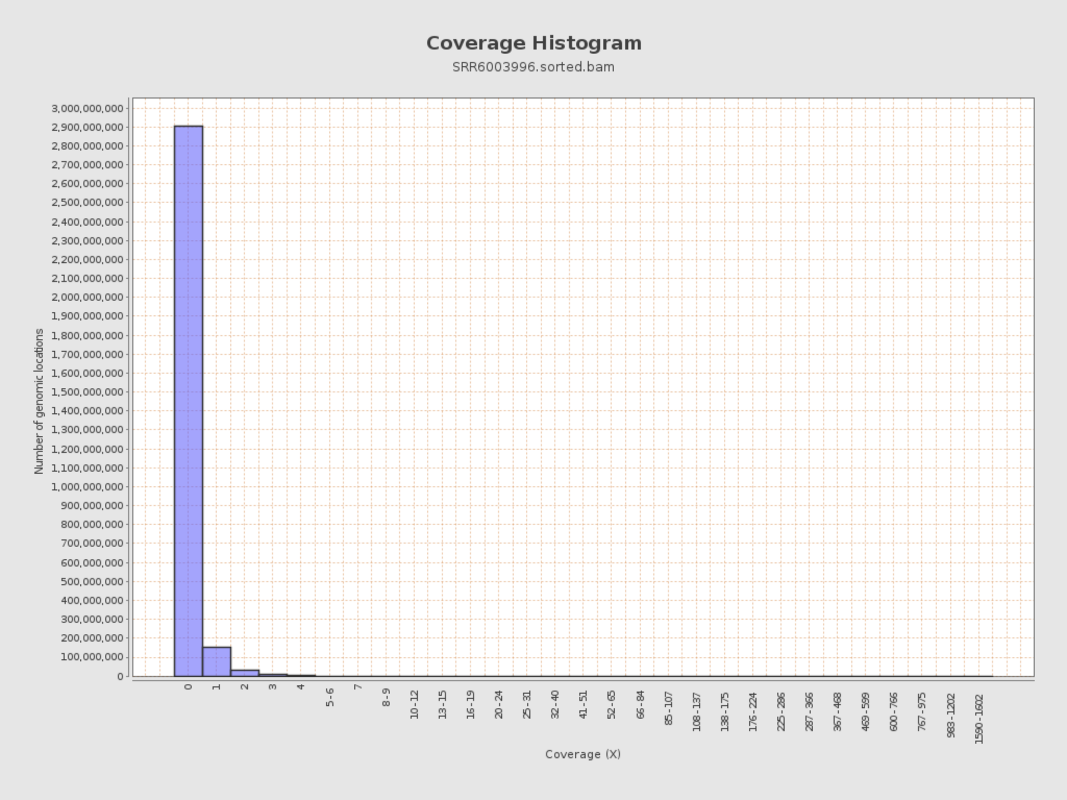
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30586625	0.1227	0.9401
chr2	243199373	6160440	0.0253	0.8126
chr3	198022430	16668325	0.0842	0.3573
chr4	191154276	17071459	0.0893	0.4065
chr5	180915260	4474646	0.0247	0.2052
chr6	171115067	11570202	0.0676	0.3658
chr7	159138663	10348308	0.065	0.9643

chr8	146364022	21720584	0.1484	0.6416
chr9	141213431	15269223	0.1081	0.7115
chr10	135534747	5798712	0.0428	0.6273
chr11	135006516	10471693	0.0776	0.5426
chr12	133851895	22131939	0.1653	0.5227
chr13	115169878	5536103	0.0481	0.2657
chr14	107349540	4548552	0.0424	0.4097
chr15	102531392	11135174	0.1086	0.4185
chr16	90354753	5883101	0.0651	0.4133
chr17	81195210	8922549	0.1099	0.4697
chr18	78077248	8773830	0.1124	1.2193
chr19	59128983	2830229	0.0479	0.6758
chr20	63025520	2004381	0.0318	0.2472
chr21	48129895	2644358	0.0549	0.3762
chr22	51304566	2908417	0.0567	0.2887
chrMT	16571	45141	2.7241	2.5945
chrX	155270560	18929956	0.1219	0.5045
chrY	59373566	661948	0.0111	0.2327

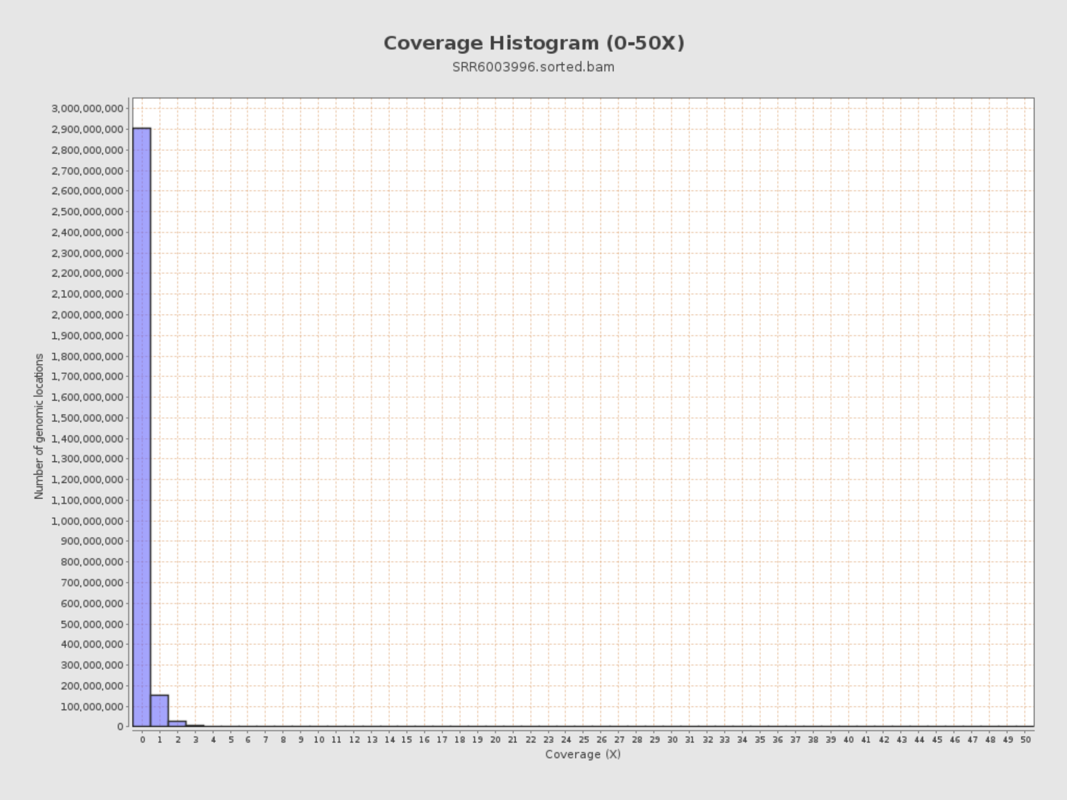
3. Results : Coverage across reference



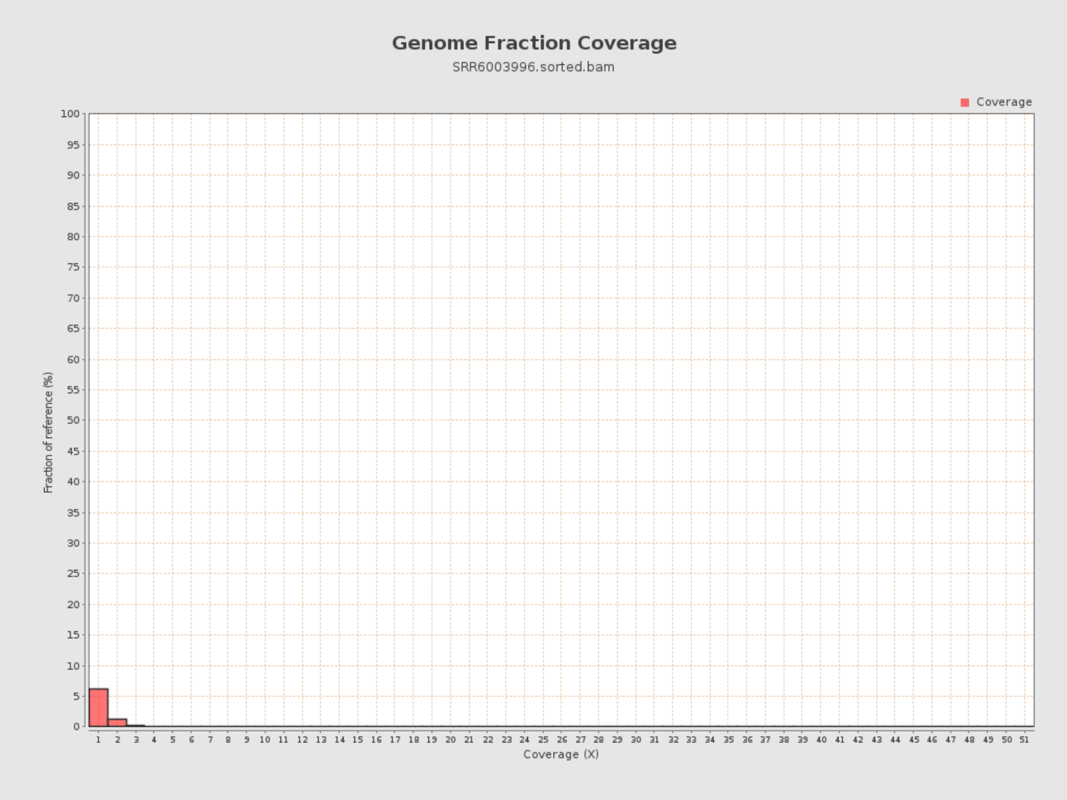
4. Results : Coverage Histogram



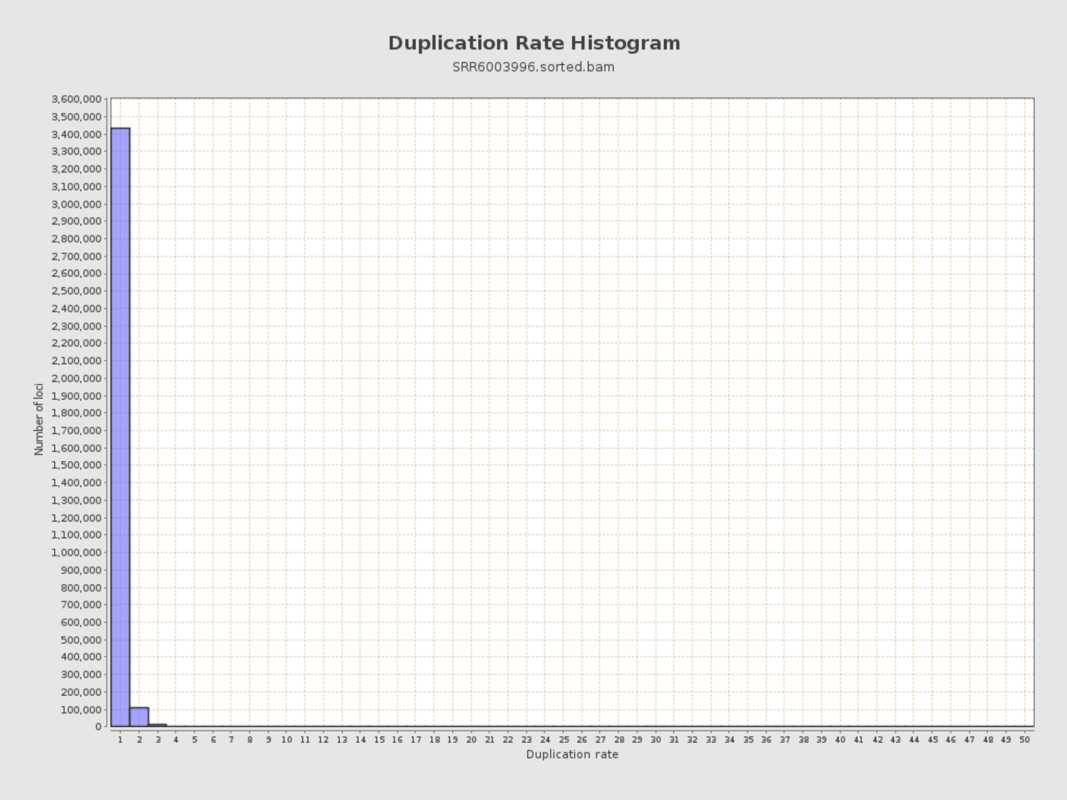
5. Results : Coverage Histogram (0-50X)



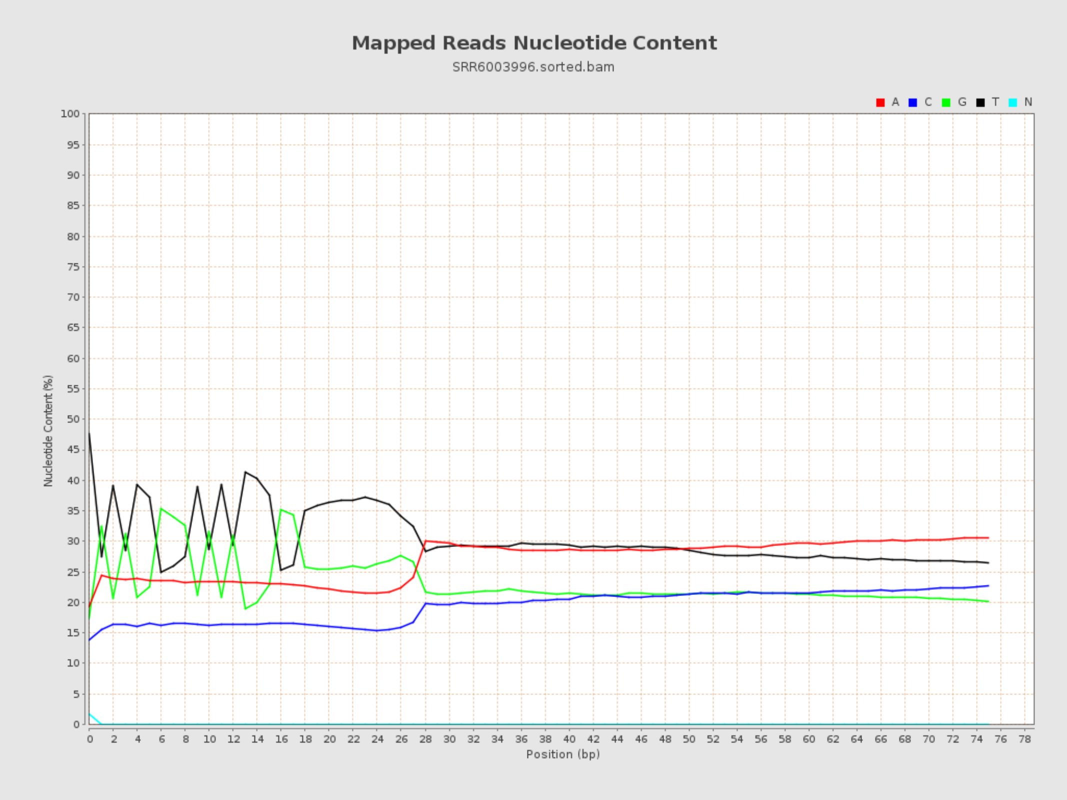
6. Results : Genome Fraction Coverage



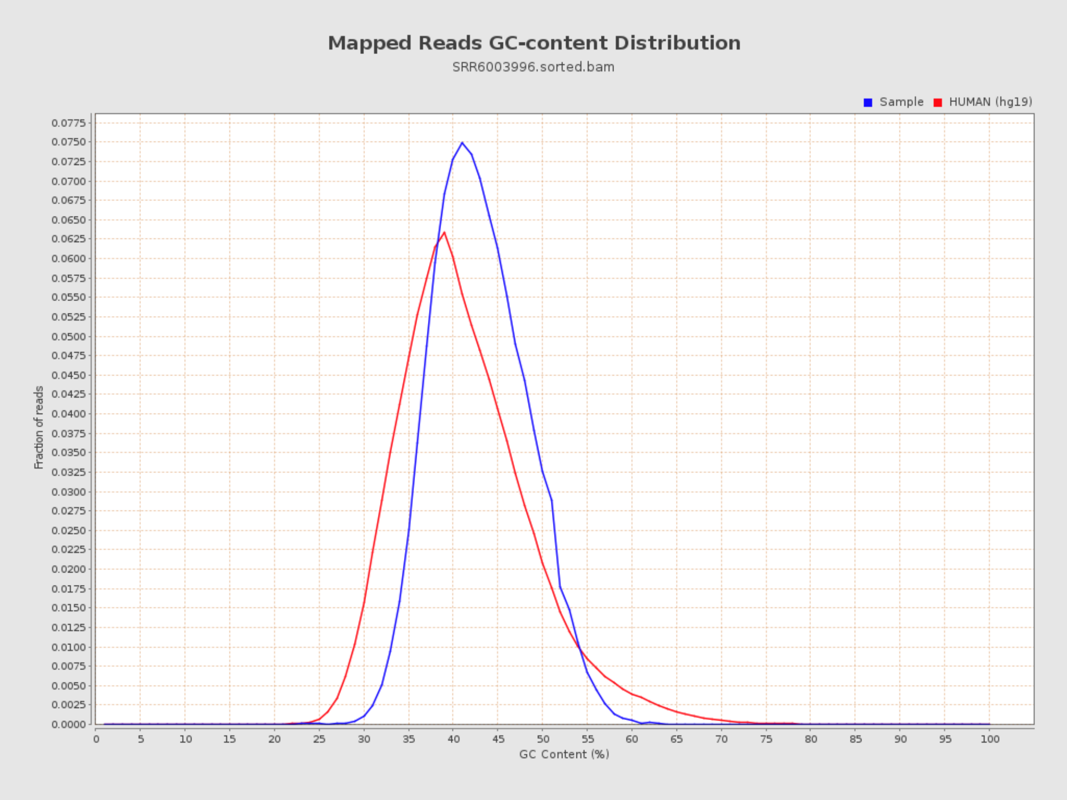
7. Results : Duplication Rate Histogram



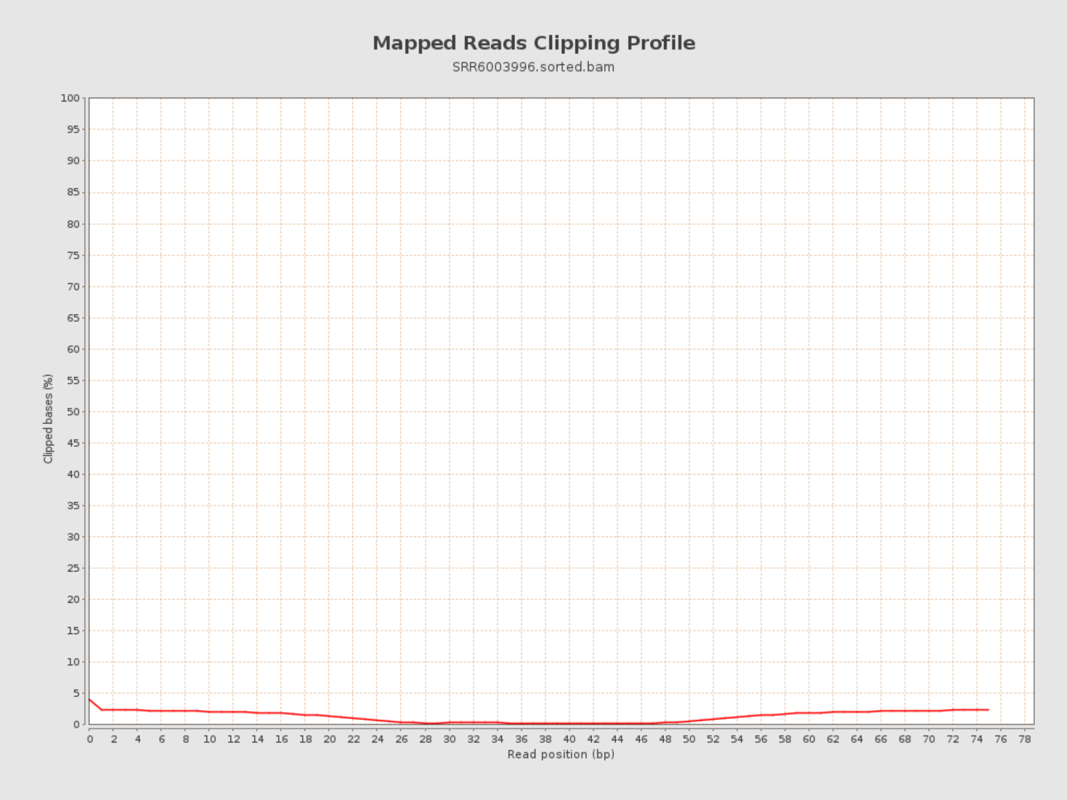
8. Results : Mapped Reads Nucleotide Content



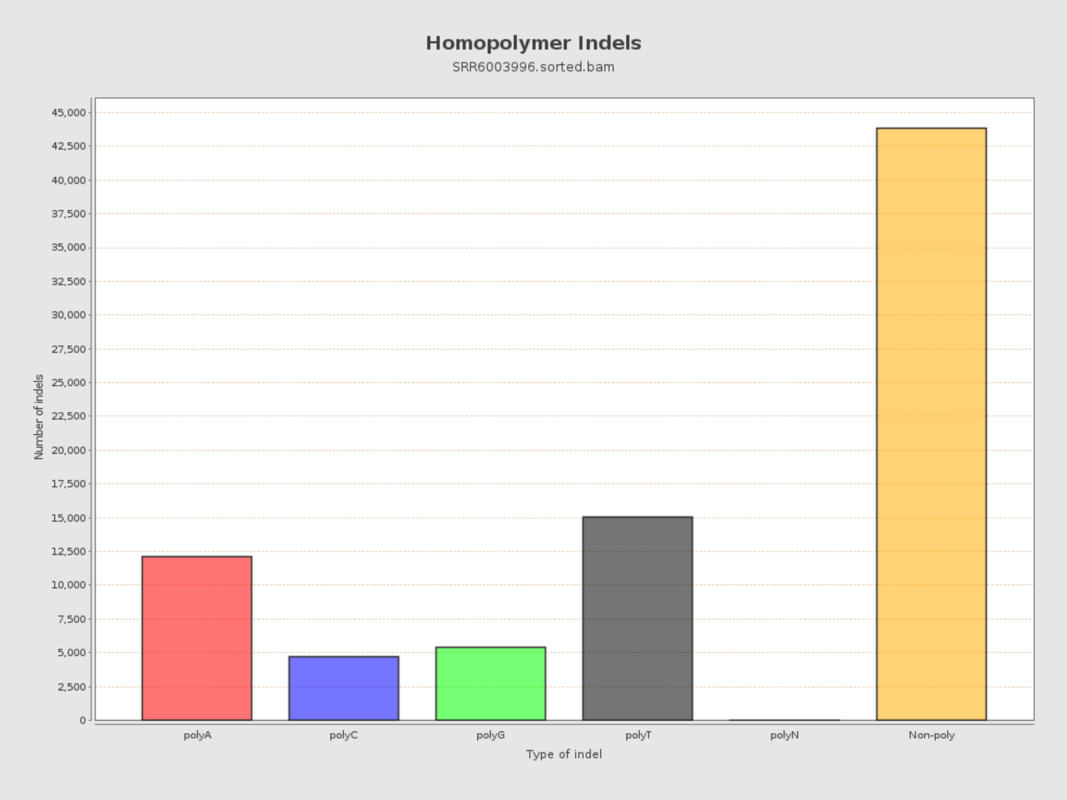
9. Results : Mapped Reads GC-content Distribution



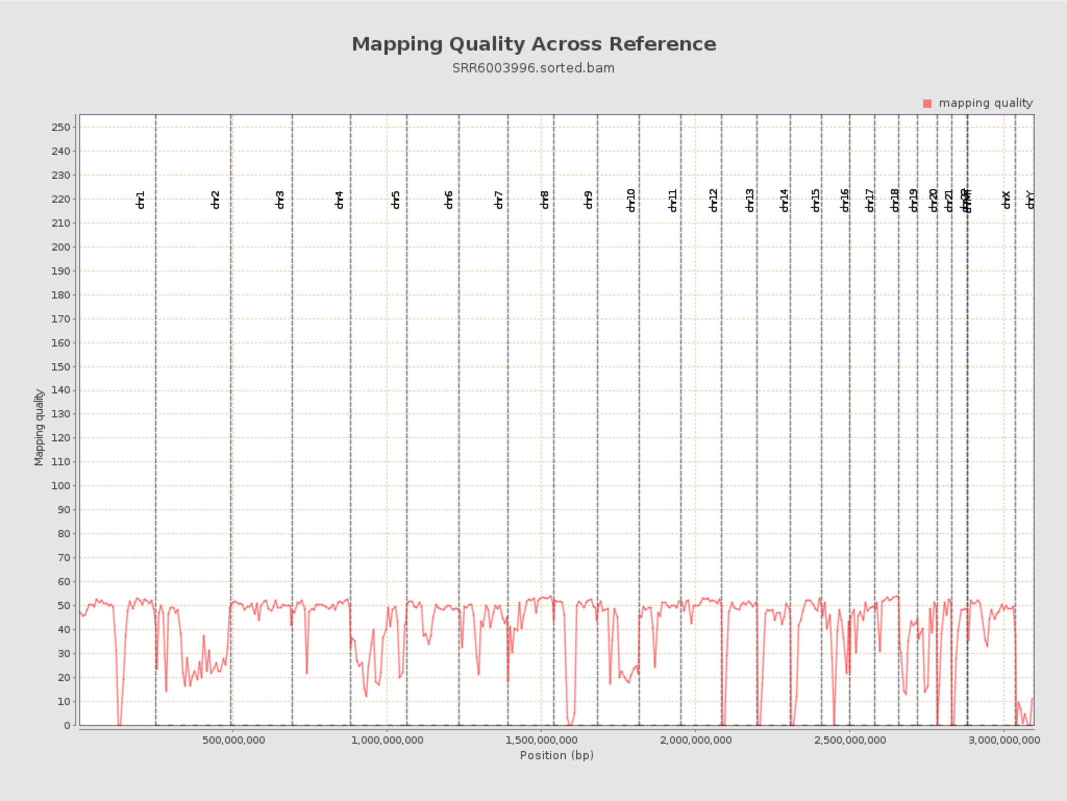
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram