Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:14:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004095.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_SRR6004095 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004095.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:14:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004095.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,532,792
Mapped reads	1,864,227 / 73.6%
Unmapped reads	668,565 / 26.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,034 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	164,164 / 6.48%
Duplication rate	7.25%
Clipped reads	962,677 / 38.01%

2.2. ACGT Content

Number/percentage of A's	32,368,164 / 26.61%
Number/percentage of C's	22,215,335 / 18.26%
Number/percentage of T's	39,654,141 / 32.6%
Number/percentage of G's	27,389,040 / 22.52%
Number/percentage of N's	15,504 / 0.01%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0393

Standard Deviation	0.3557

2.4. Mapping Quality

Mean Mapping Quality	45.73

2.5. Mismatches and indels

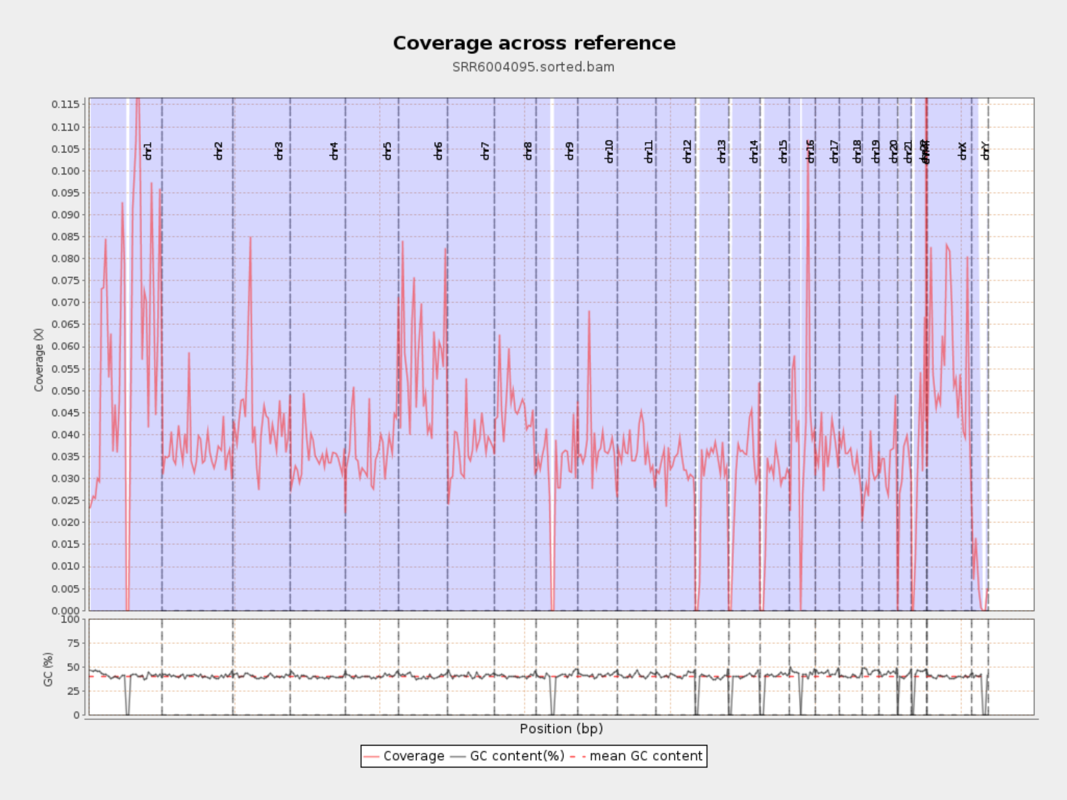
General error rate	1.01%
Mismatches	1,213,771
Insertions	10,065
Mapped reads with at least one insertion	0.54%
Deletions	34,308
Mapped reads with at least one deletion	1.82%
Homopolymer indels	47.55%

2.6. Chromosome stats

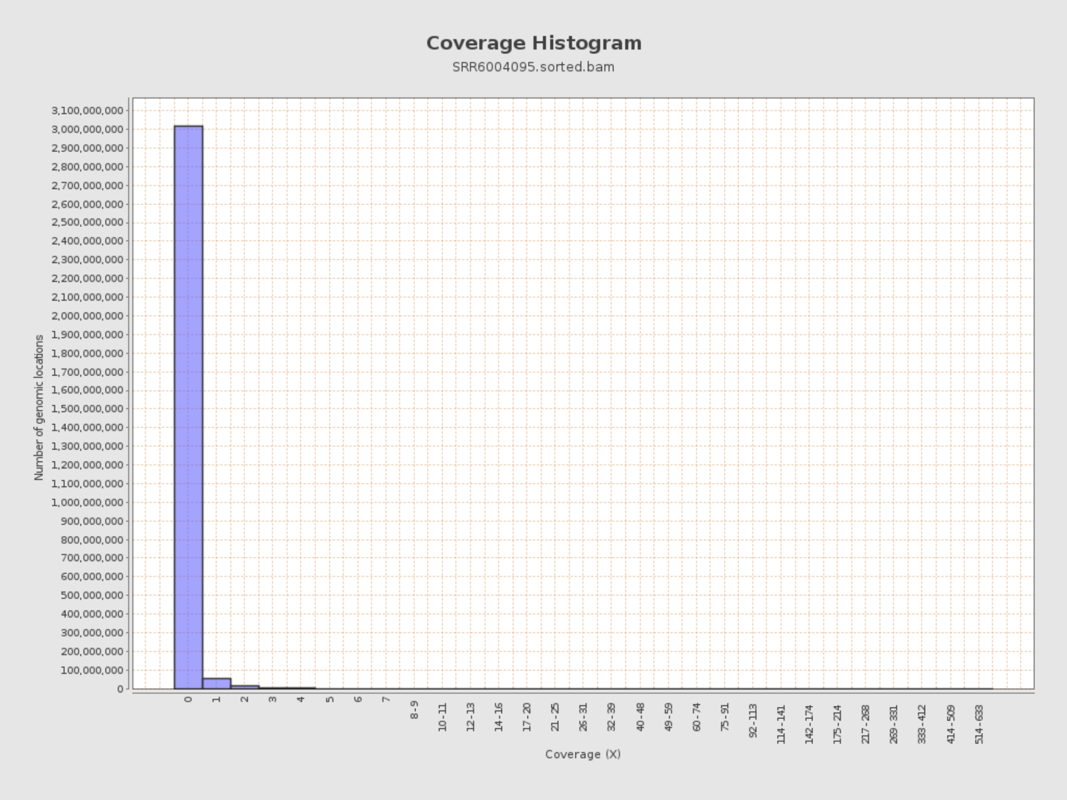
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14879805	0.0597	0.5619
chr2	243199373	8899498	0.0366	0.4105
chr3	198022430	8588548	0.0434	0.3005
chr4	191154276	6630445	0.0347	0.2711
chr5	180915260	6653796	0.0368	0.2736
chr6	171115067	9673624	0.0565	0.3902
chr7	159138663	5936830	0.0373	0.4078

chr8	146364022	6736055	0.046	0.412
chr9	141213431	4318249	0.0306	0.2984
chr10	135534747	5095183	0.0376	0.3936
chr11	135006516	4890957	0.0362	0.3174
chr12	133851895	4379834	0.0327	0.2559
chr13	115169878	3318323	0.0288	0.2399
chr14	107349540	3242399	0.0302	0.2514
chr15	102531392	2674942	0.0261	0.2299
chr16	90354753	3962187	0.0439	0.3109
chr17	81195210	2964329	0.0365	0.2817
chr18	78077248	2729481	0.035	0.485
chr19	59128983	1789241	0.0303	0.3659
chr20	63025520	2177991	0.0346	0.2693
chr21	48129895	1448326	0.0301	0.2609
chr22	51304566	1592681	0.031	0.2561
chrMT	16571	78428	4.7328	3.6946
chrX	155270560	8689493	0.056	0.3577
chrY	59373566	348362	0.0059	0.1257

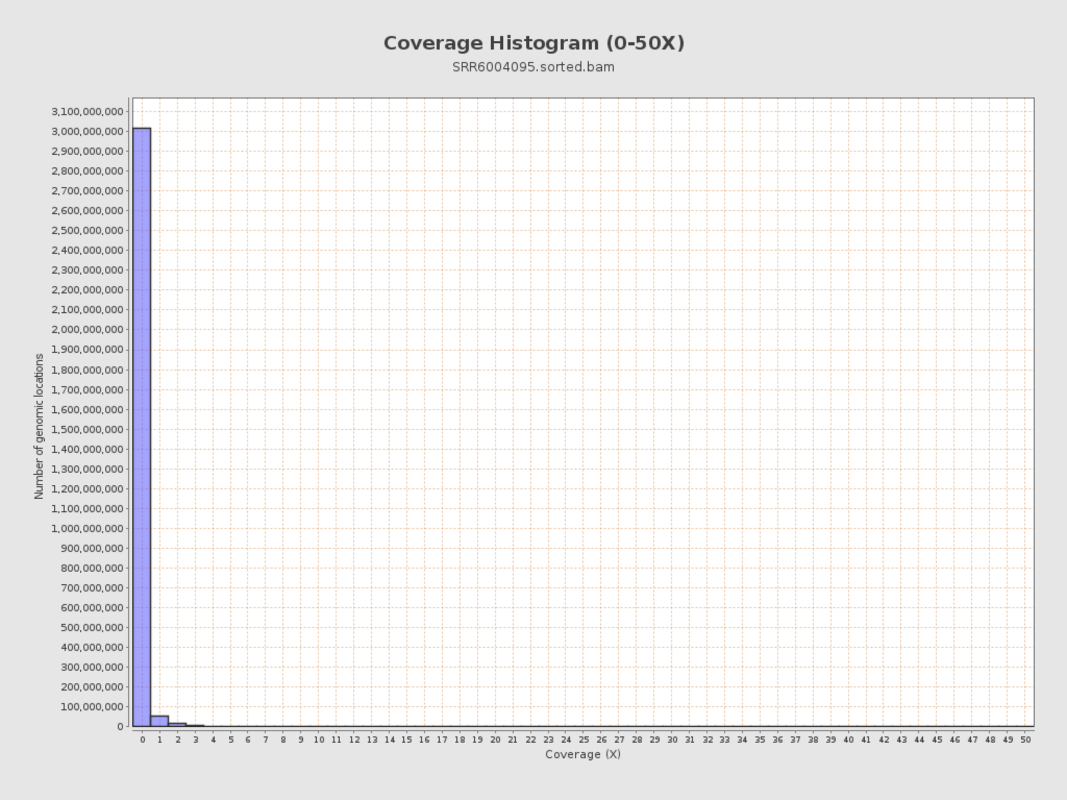
3. Results : Coverage across reference



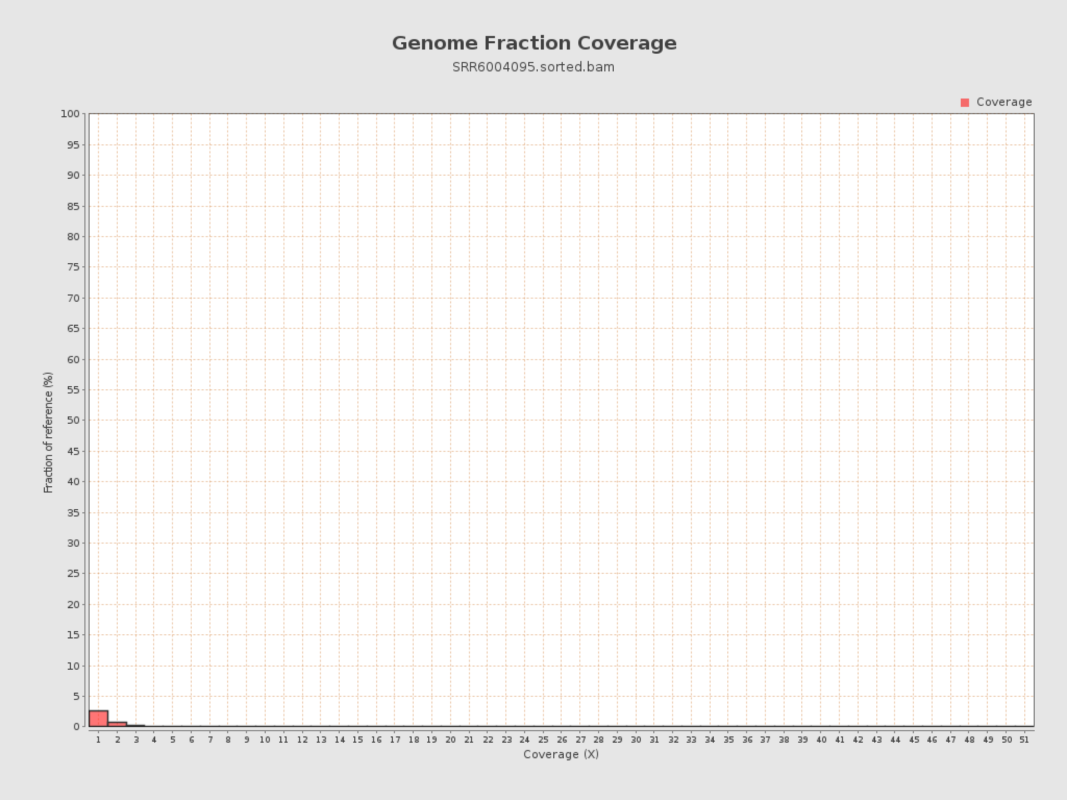
4. Results : Coverage Histogram



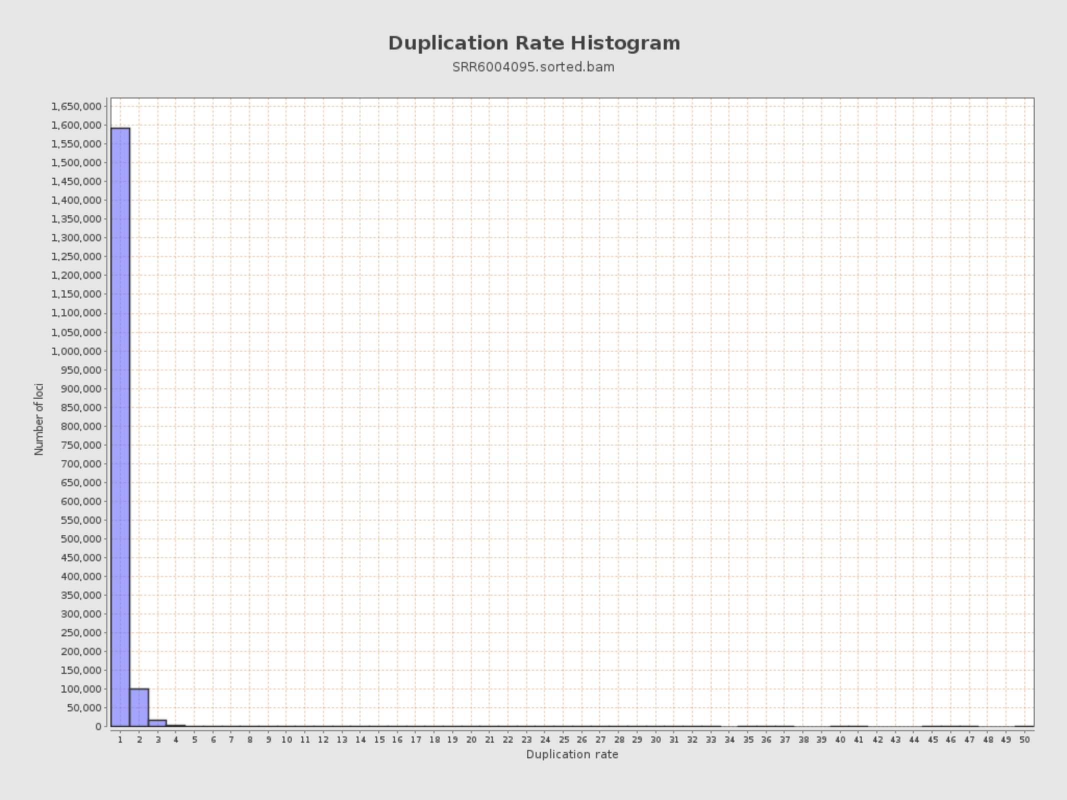
5. Results : Coverage Histogram (0-50X)



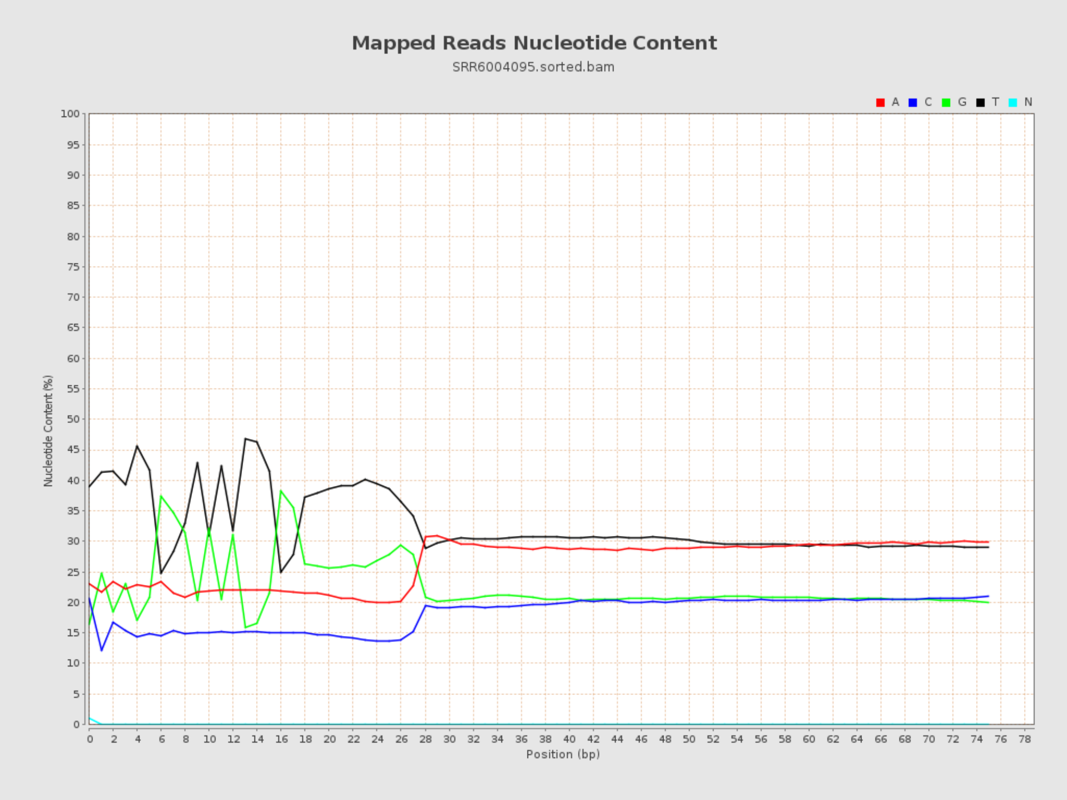
6. Results : Genome Fraction Coverage



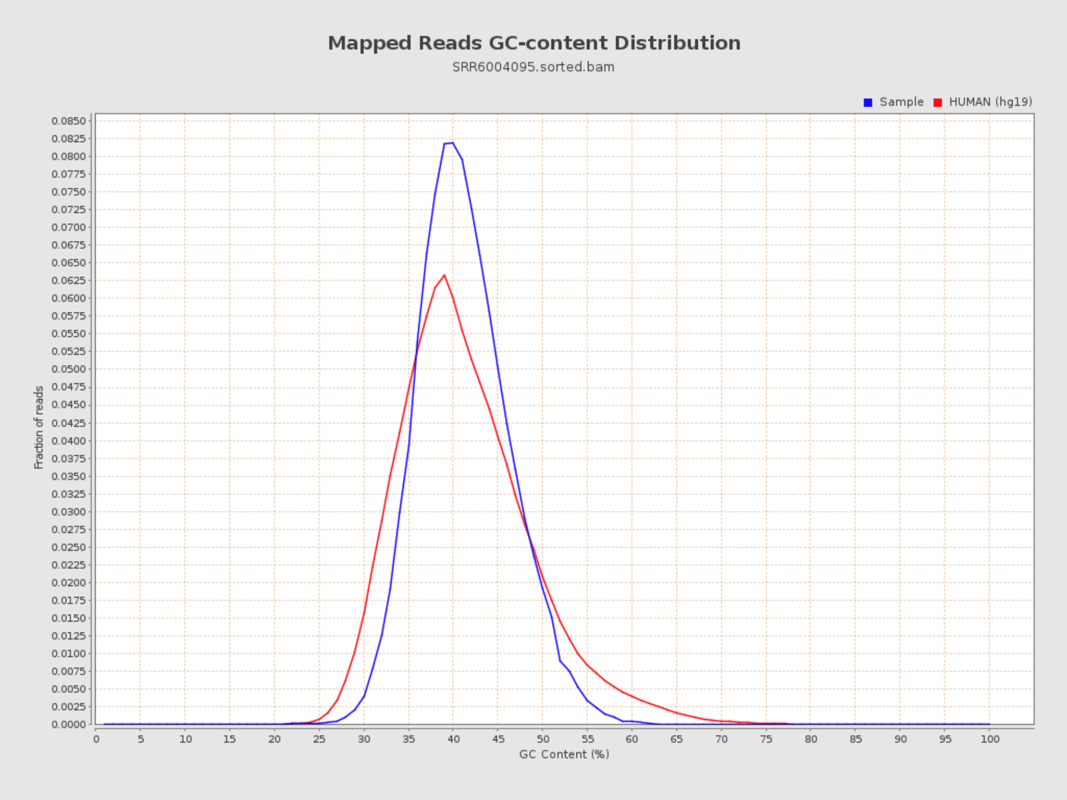
7. Results : Duplication Rate Histogram



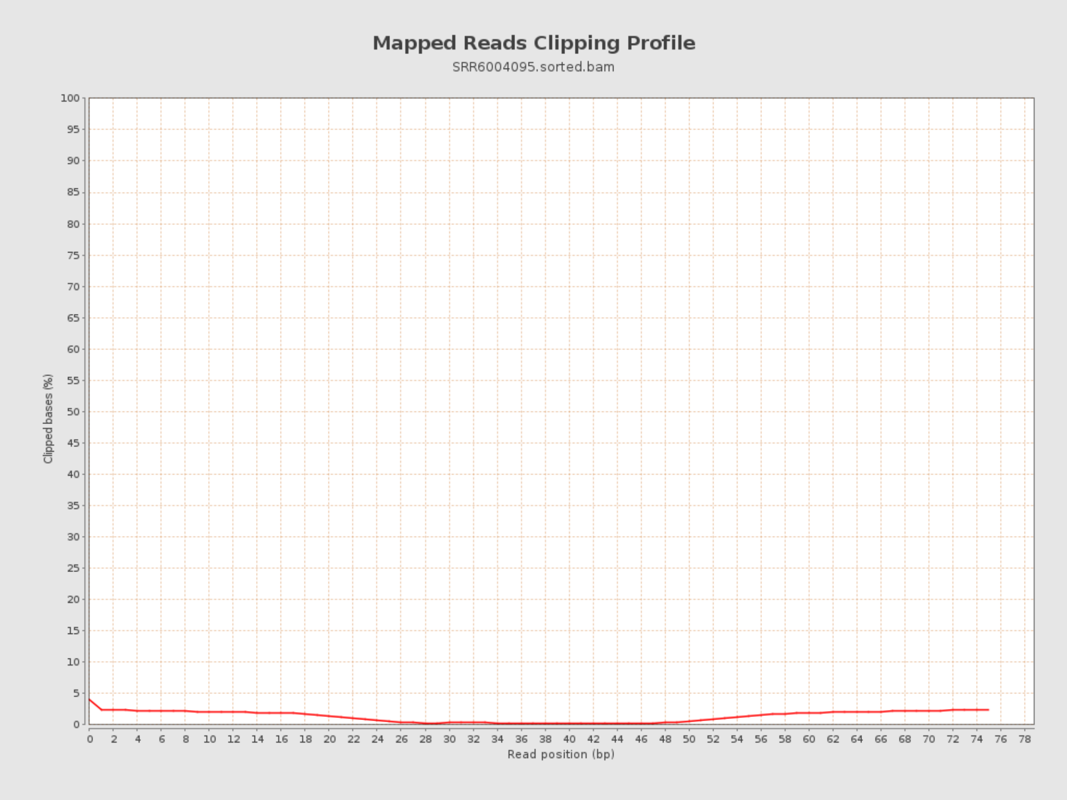
8. Results : Mapped Reads Nucleotide Content



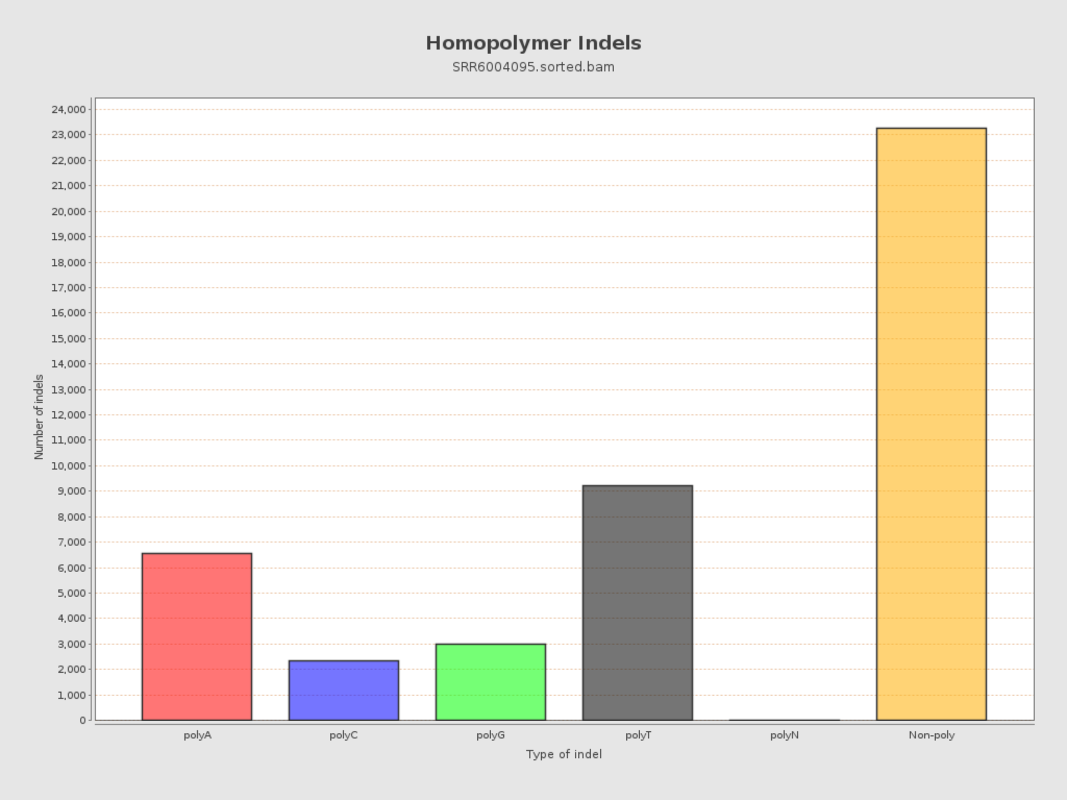
9. Results : Mapped Reads GC-content Distribution



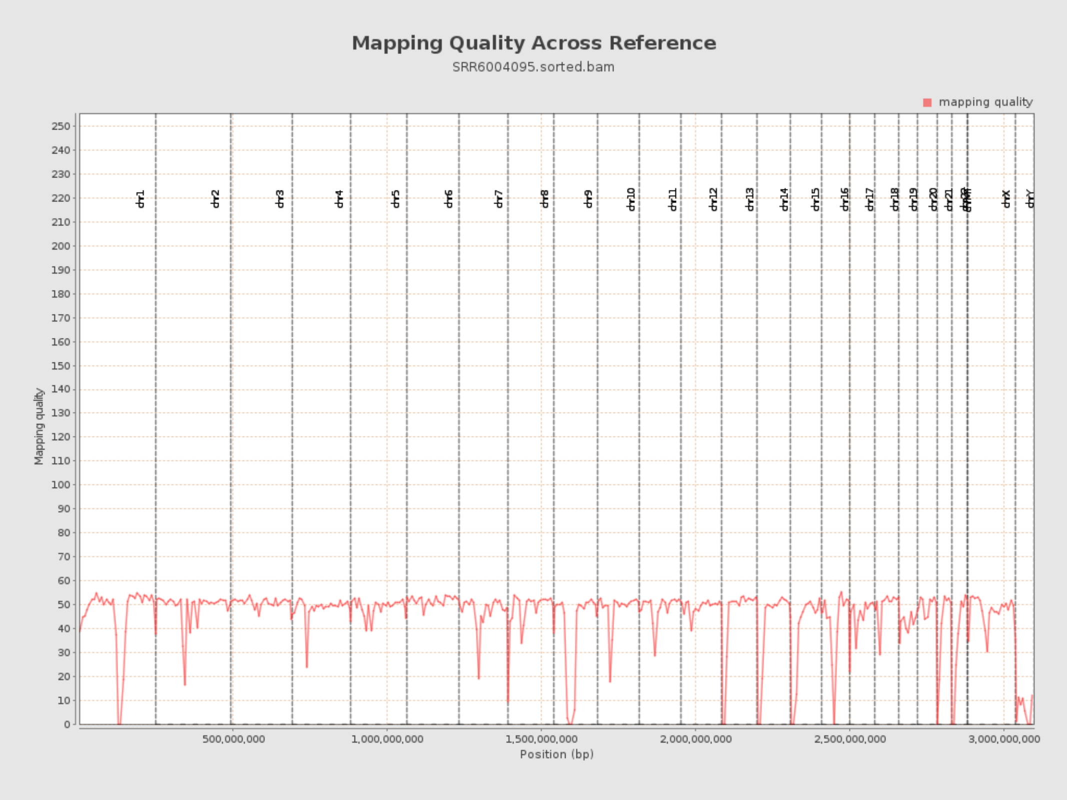
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram