Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 02:16:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004110.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_SRR6004110 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004110.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 02:16:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004110.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,159,493
Mapped reads	3,452,768 / 83.01%
Unmapped reads	706,725 / 16.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,027 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	207,693 / 4.99%
Duplication rate	4.2%
Clipped reads	1,819,209 / 43.74%

2.2. ACGT Content

Number/percentage of A's	62,671,029 / 27.78%
Number/percentage of C's	41,318,166 / 18.31%
Number/percentage of T's	71,498,407 / 31.69%
Number/percentage of G's	50,094,053 / 22.2%
Number/percentage of N's	28,558 / 0.01%
GC Percentage	40.52%

2.3. Coverage

Mean	0.0729

Standard Deviation	0.7916

2.4. Mapping Quality

Mean Mapping Quality	43.17

2.5. Mismatches and indels

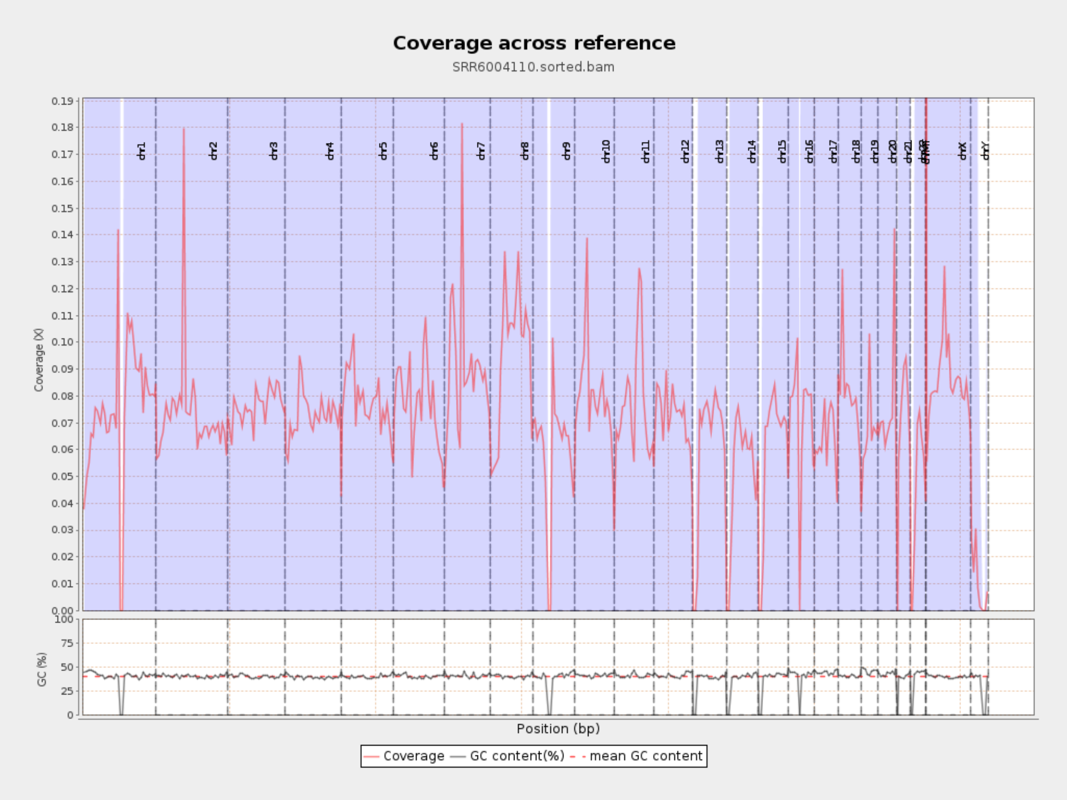
General error rate	1.11%
Mismatches	2,457,625
Insertions	21,798
Mapped reads with at least one insertion	0.63%
Deletions	77,970
Mapped reads with at least one deletion	2.23%
Homopolymer indels	46.86%

2.6. Chromosome stats

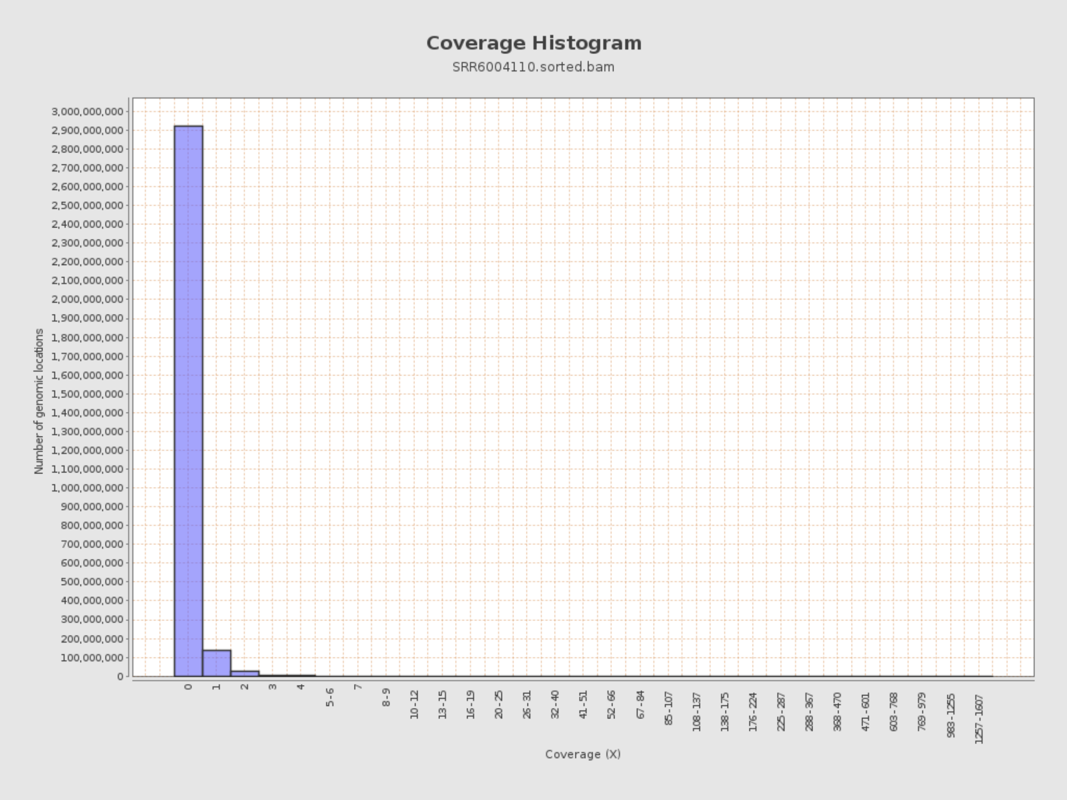
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18681261	0.0749	1.4122
chr2	243199373	17851566	0.0734	0.9711
chr3	198022430	15083549	0.0762	0.3541
chr4	191154276	13986698	0.0732	0.3681
chr5	180915260	14086501	0.0779	0.3562
chr6	171115067	13281091	0.0776	0.459
chr7	159138663	14326319	0.09	1.4904

chr8	146364022	13983669	0.0955	0.8264
chr9	141213431	8330686	0.059	0.7881
chr10	135534747	10965528	0.0809	0.672
chr11	135006516	10324138	0.0765	0.7278
chr12	133851895	9752721	0.0729	0.3554
chr13	115169878	6929934	0.0602	0.3065
chr14	107349540	5602368	0.0522	0.4223
chr15	102531392	5999835	0.0585	0.3248
chr16	90354753	6332427	0.0701	0.4266
chr17	81195210	5239611	0.0645	0.4046
chr18	78077248	6450338	0.0826	1.6959
chr19	59128983	3976779	0.0673	0.976
chr20	63025520	4891644	0.0776	0.3918
chr21	48129895	3331528	0.0692	0.394
chr22	51304566	2319826	0.0452	0.26
chrMT	16571	106375	6.4193	5.7537
chrX	155270560	13292561	0.0856	0.4851
chrY	59373566	611675	0.0103	0.2097

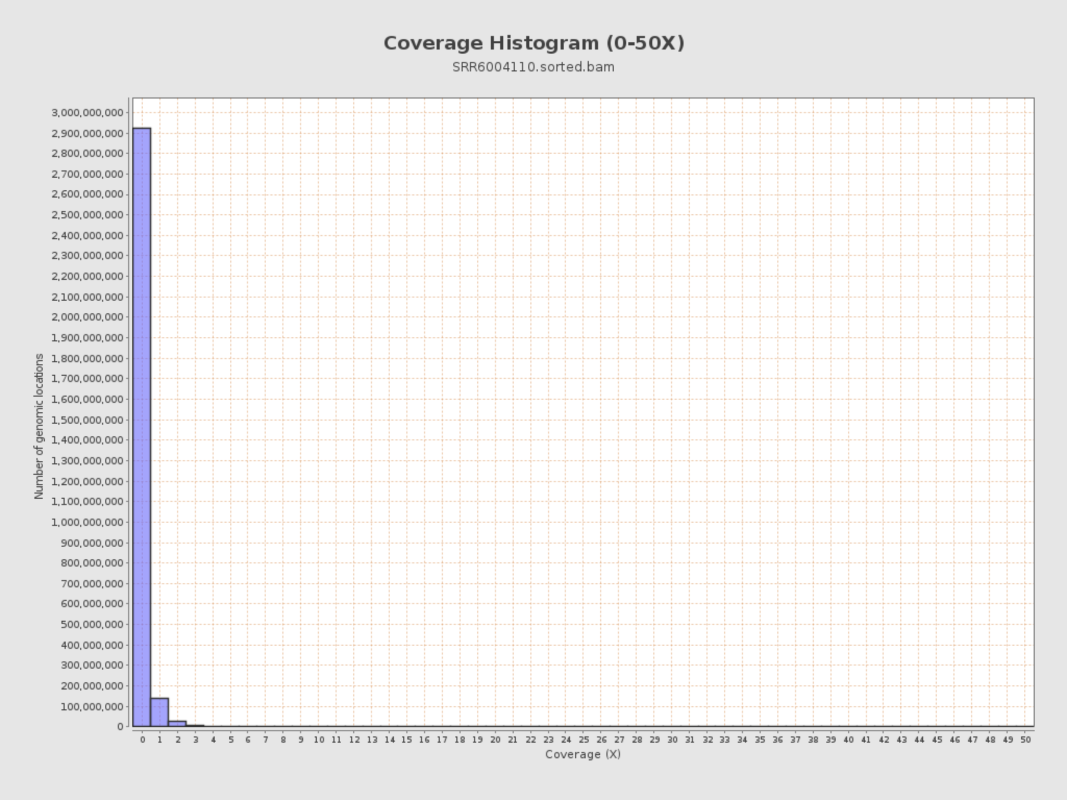
3. Results : Coverage across reference



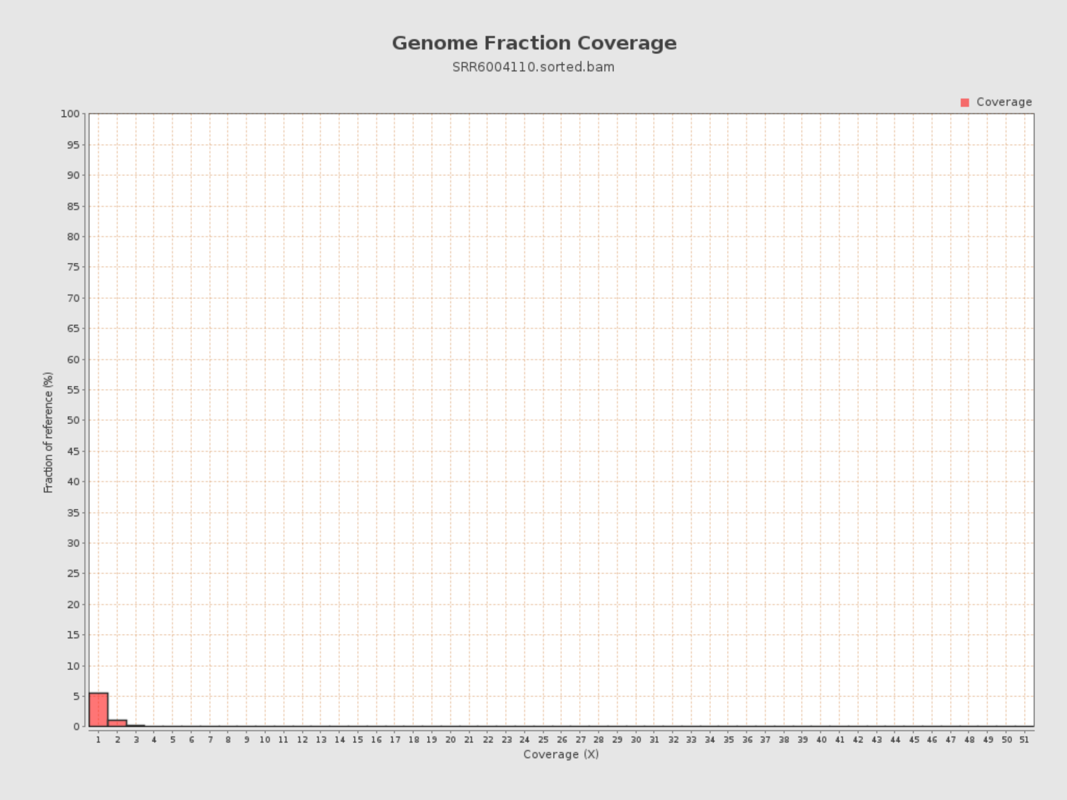
4. Results : Coverage Histogram



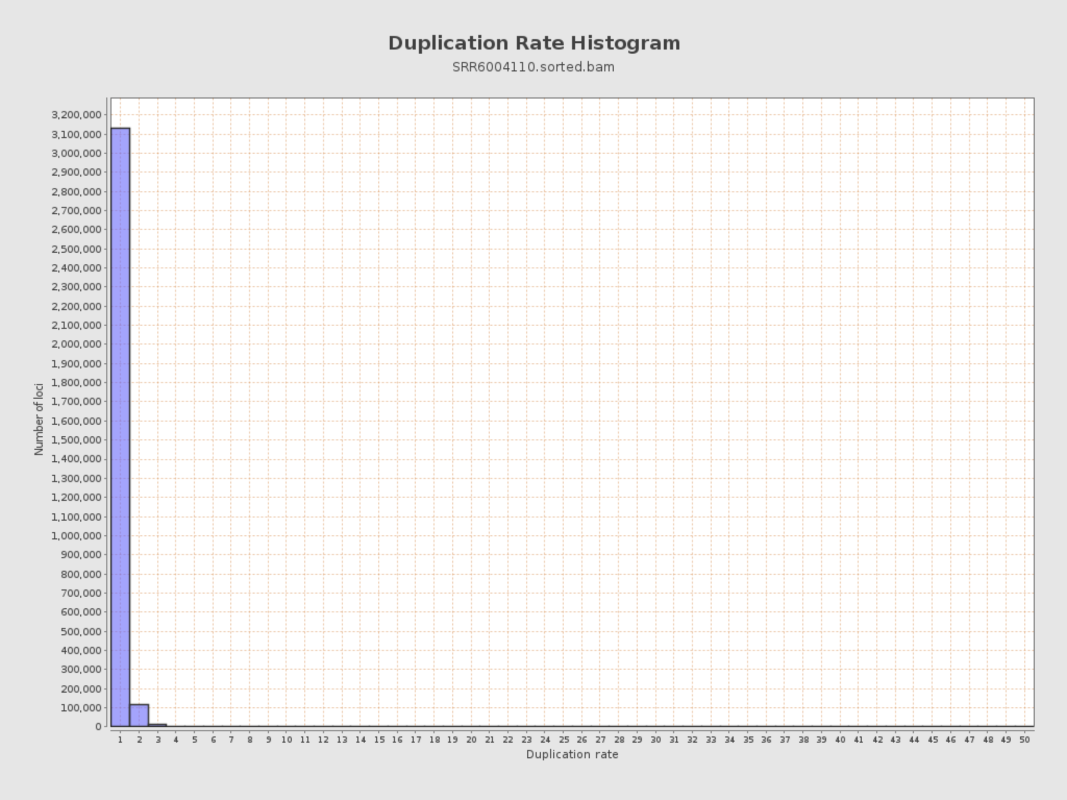
5. Results : Coverage Histogram (0-50X)



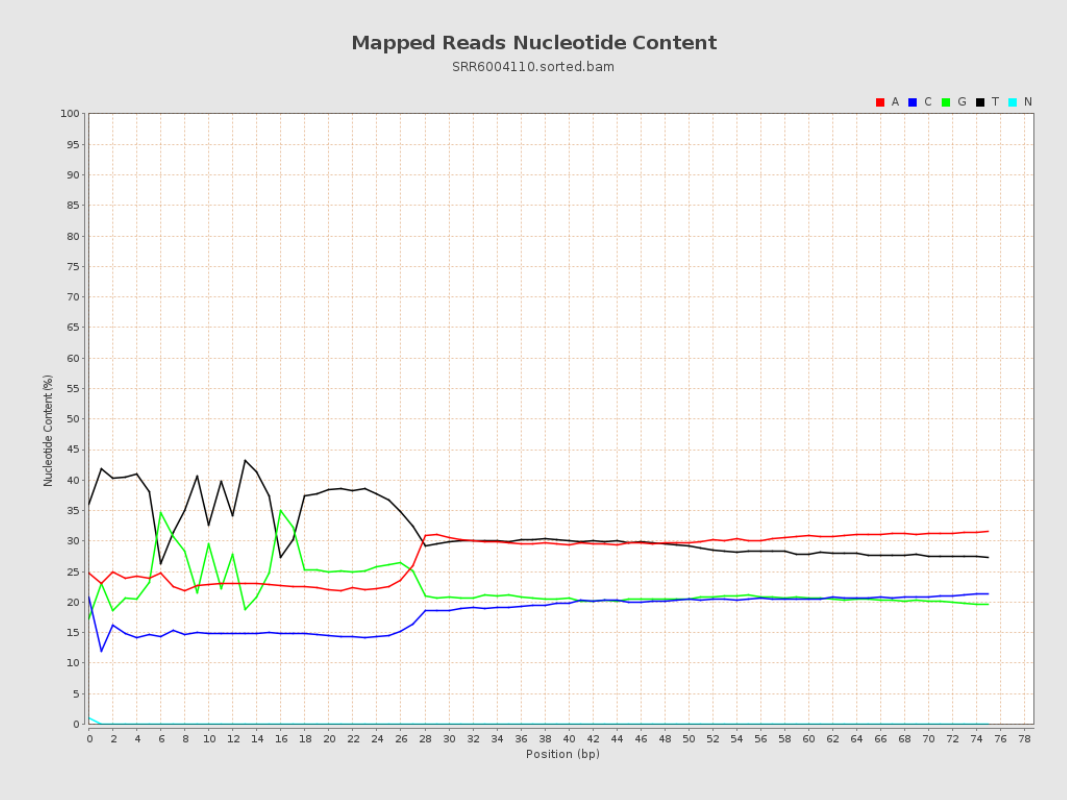
6. Results : Genome Fraction Coverage



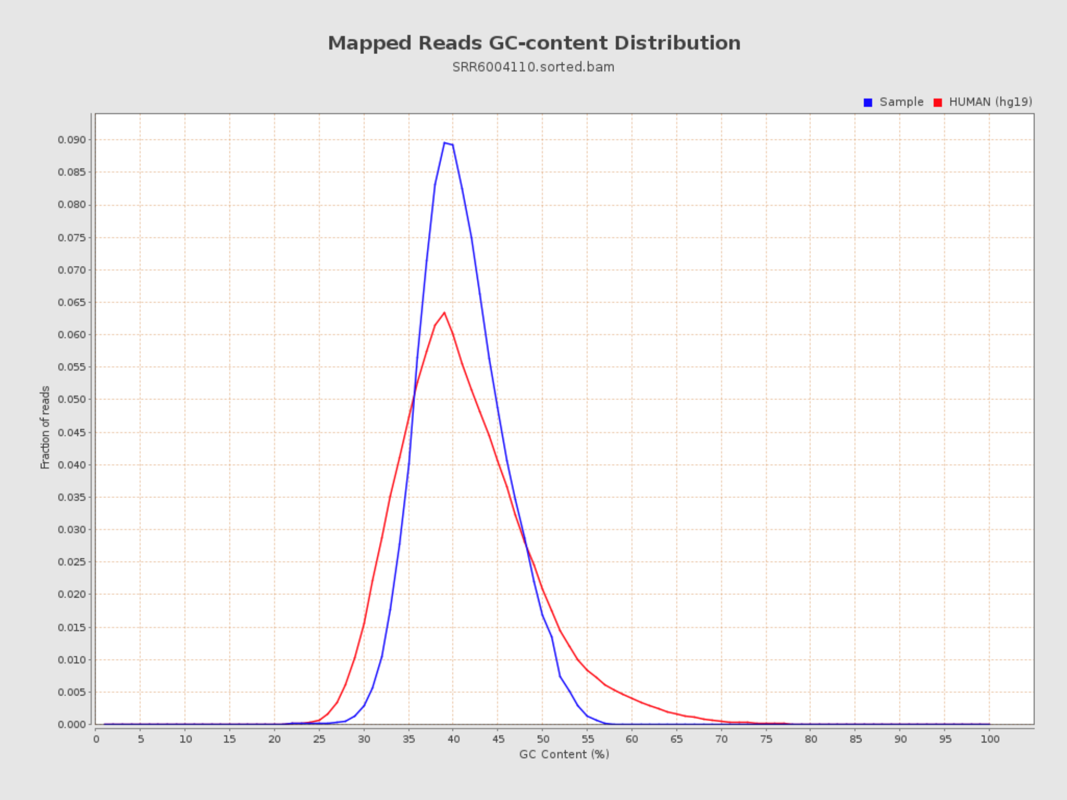
7. Results : Duplication Rate Histogram



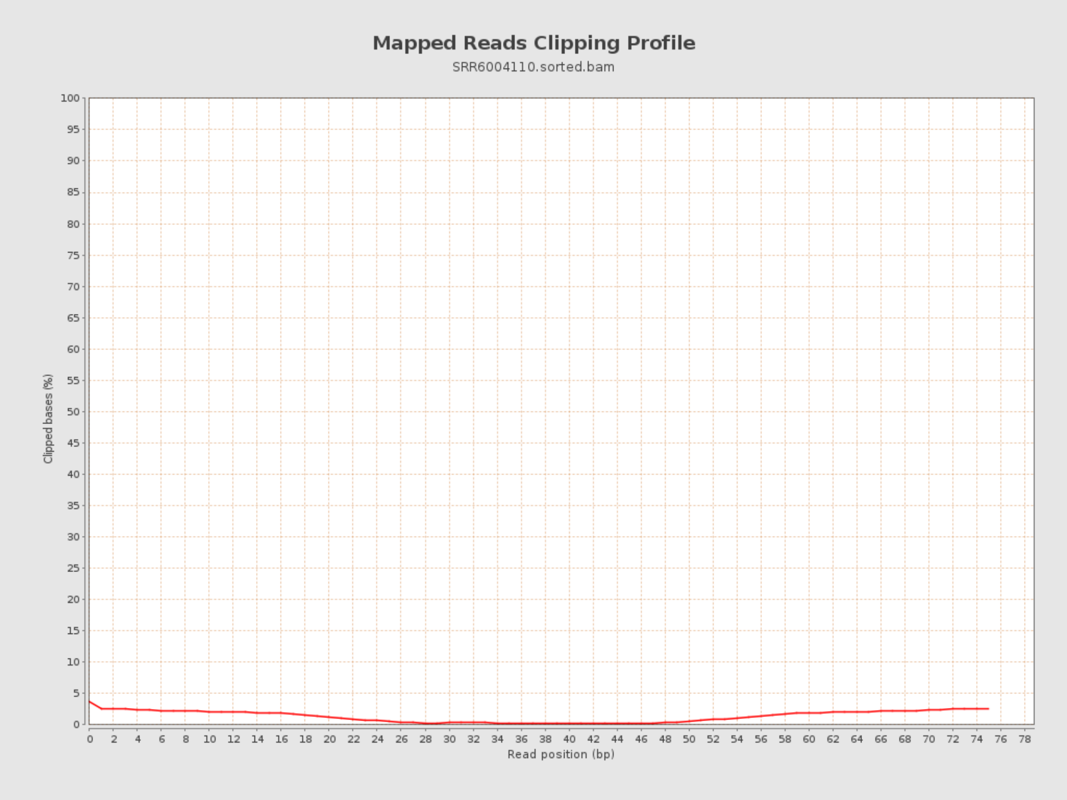
8. Results : Mapped Reads Nucleotide Content



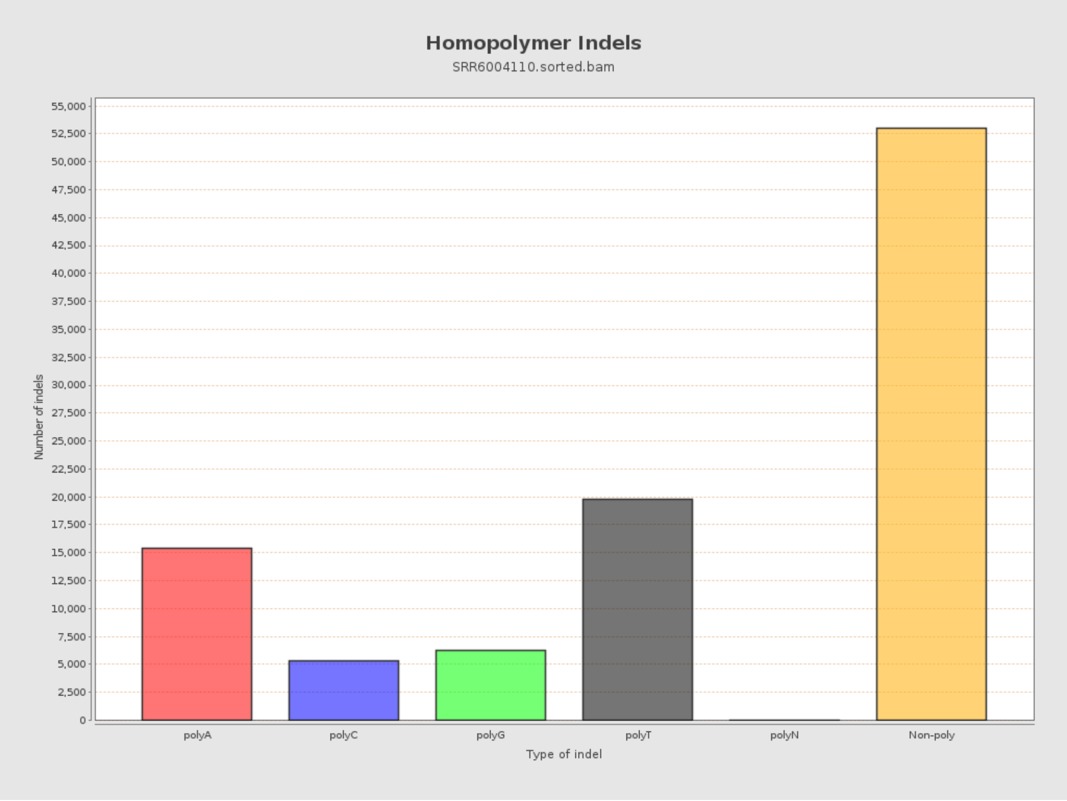
9. Results : Mapped Reads GC-content Distribution



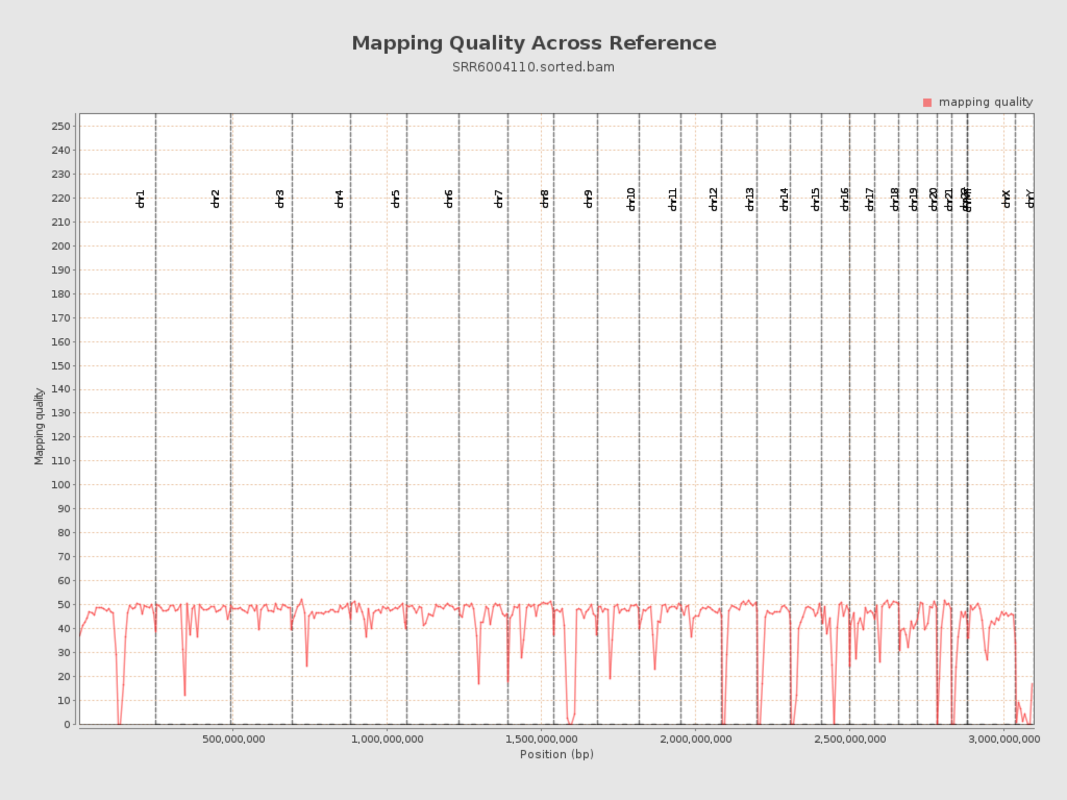
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram