Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:19:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004144.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_SRR6004144 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004144.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:19:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004144.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,027,254
Mapped reads	2,348,777 / 77.59%
Unmapped reads	678,477 / 22.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,600 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	108,121 / 3.57%
Duplication rate	3.35%
Clipped reads	1,187,720 / 39.23%

2.2. ACGT Content

Number/percentage of A's	41,709,018 / 27.12%
Number/percentage of C's	27,362,259 / 17.79%
Number/percentage of T's	49,689,171 / 32.31%
Number/percentage of G's	34,995,189 / 22.76%
Number/percentage of N's	15,477 / 0.01%
GC Percentage	40.55%

2.3. Coverage

Mean	0.0497

Standard Deviation	0.4941

2.4. Mapping Quality

Mean Mapping Quality	43.8

2.5. Mismatches and indels

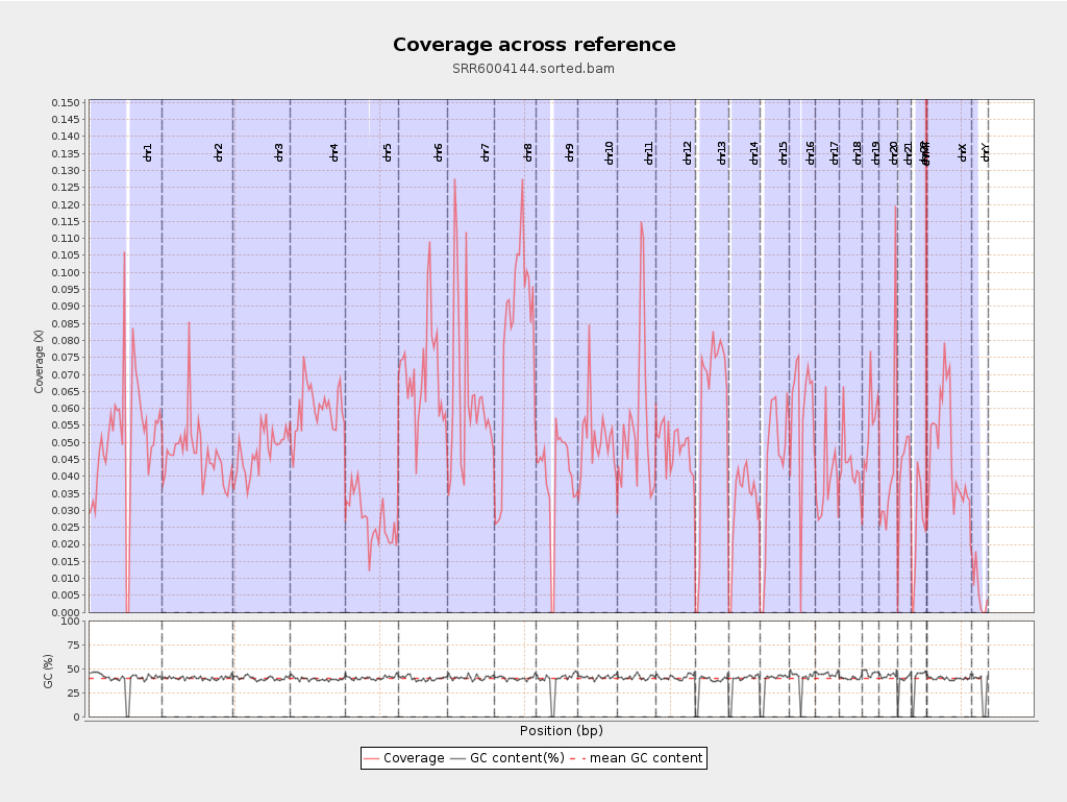
General error rate	1.01%
Mismatches	1,526,496
Insertions	14,212
Mapped reads with at least one insertion	0.6%
Deletions	45,443
Mapped reads with at least one deletion	1.91%
Homopolymer indels	46.54%

2.6. Chromosome stats

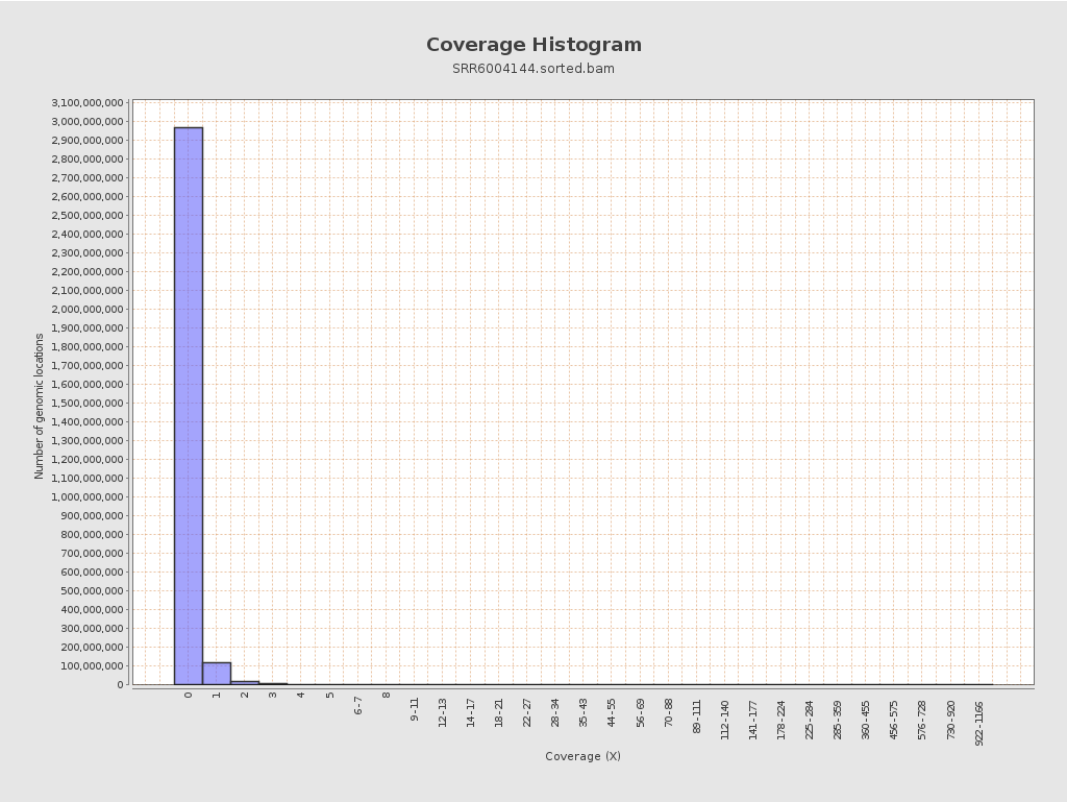
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12680371	0.0509	0.867
chr2	243199373	11292626	0.0464	0.5673
chr3	198022430	9387263	0.0474	0.2477
chr4	191154276	11417366	0.0597	0.295
chr5	180915260	4966299	0.0275	0.1977
chr6	171115067	11971311	0.07	0.3662
chr7	159138663	10300391	0.0647	0.8123

chr8	146364022	11656710	0.0796	0.778
chr9	141213431	5590364	0.0396	0.418
chr10	135534747	6917857	0.051	0.4126
chr11	135006516	7555858	0.056	0.4817
chr12	133851895	6515414	0.0487	0.2607
chr13	115169878	7066223	0.0614	0.2822
chr14	107349540	3396222	0.0316	0.2613
chr15	102531392	4434408	0.0432	0.2448
chr16	90354753	5333590	0.059	0.328
chr17	81195210	3130952	0.0386	0.2706
chr18	78077248	3398800	0.0435	0.8908
chr19	59128983	3222585	0.0545	0.6215
chr20	63025520	2806173	0.0445	0.2706
chr21	48129895	1968326	0.0409	0.2585
chr22	51304566	1204358	0.0235	0.1701
chrMT	16571	36518	2.2037	2.1855
chrX	155270560	7247195	0.0467	0.3115
chrY	59373566	349175	0.0059	0.1394

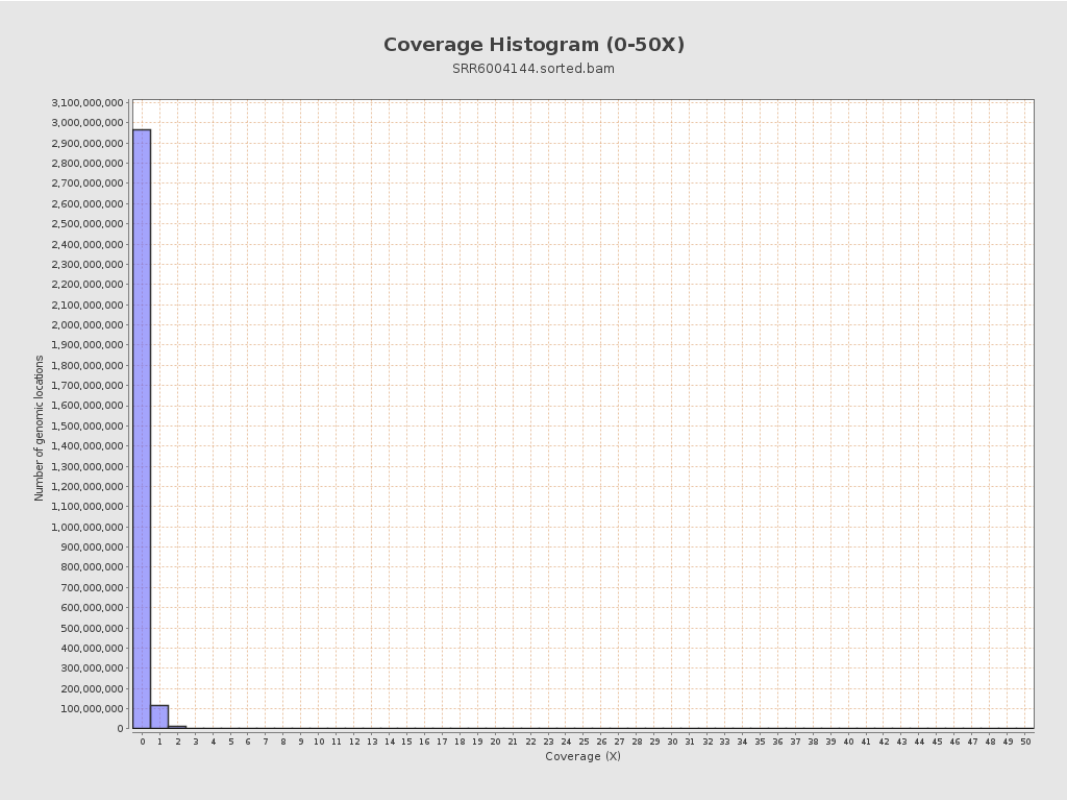
3. Results : Coverage across reference



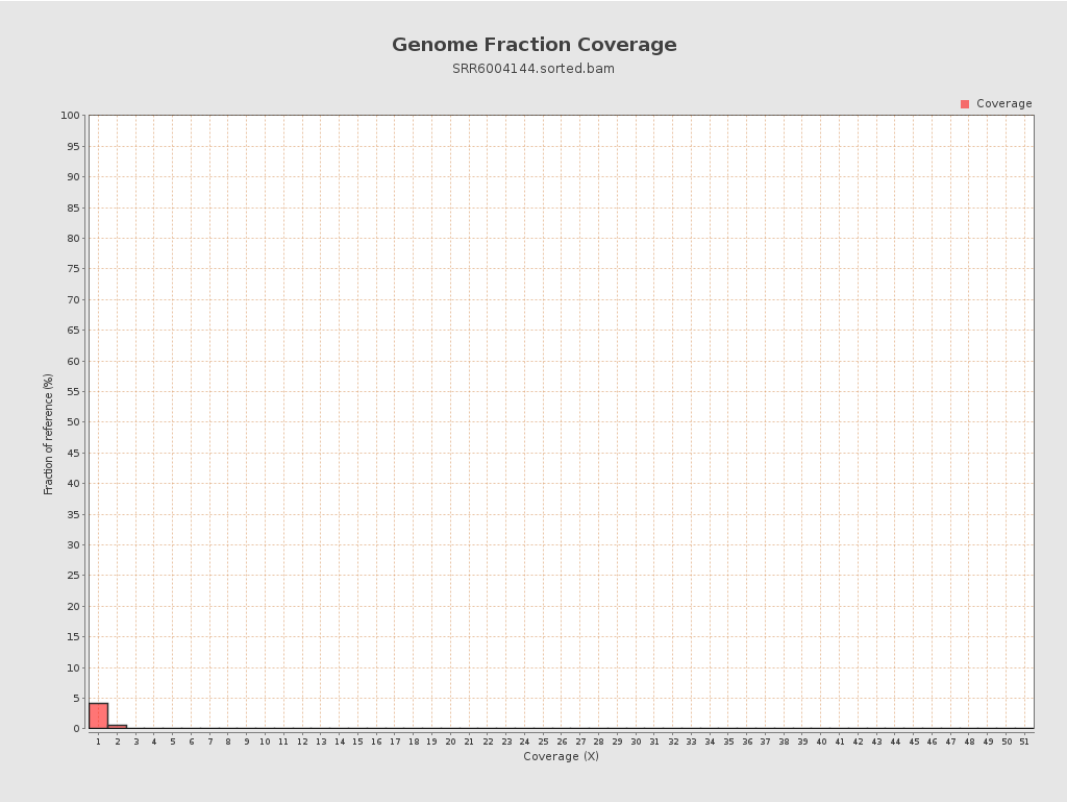
4. Results : Coverage Histogram



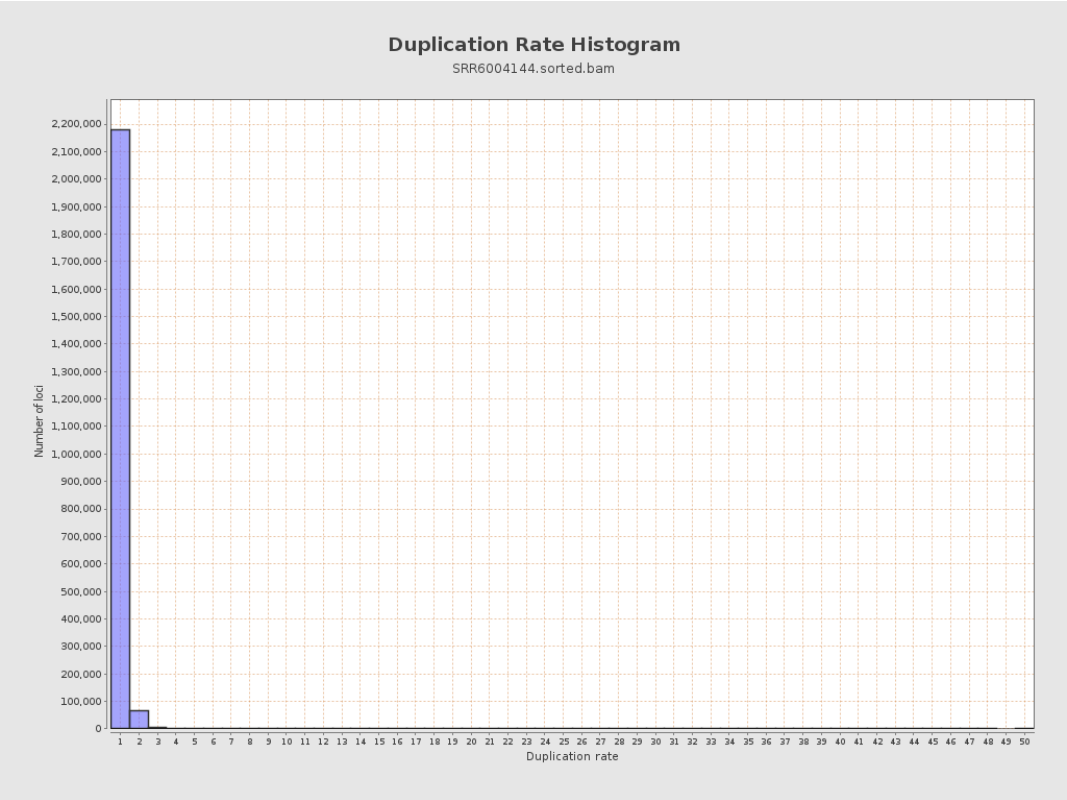
5. Results : Coverage Histogram (0-50X)



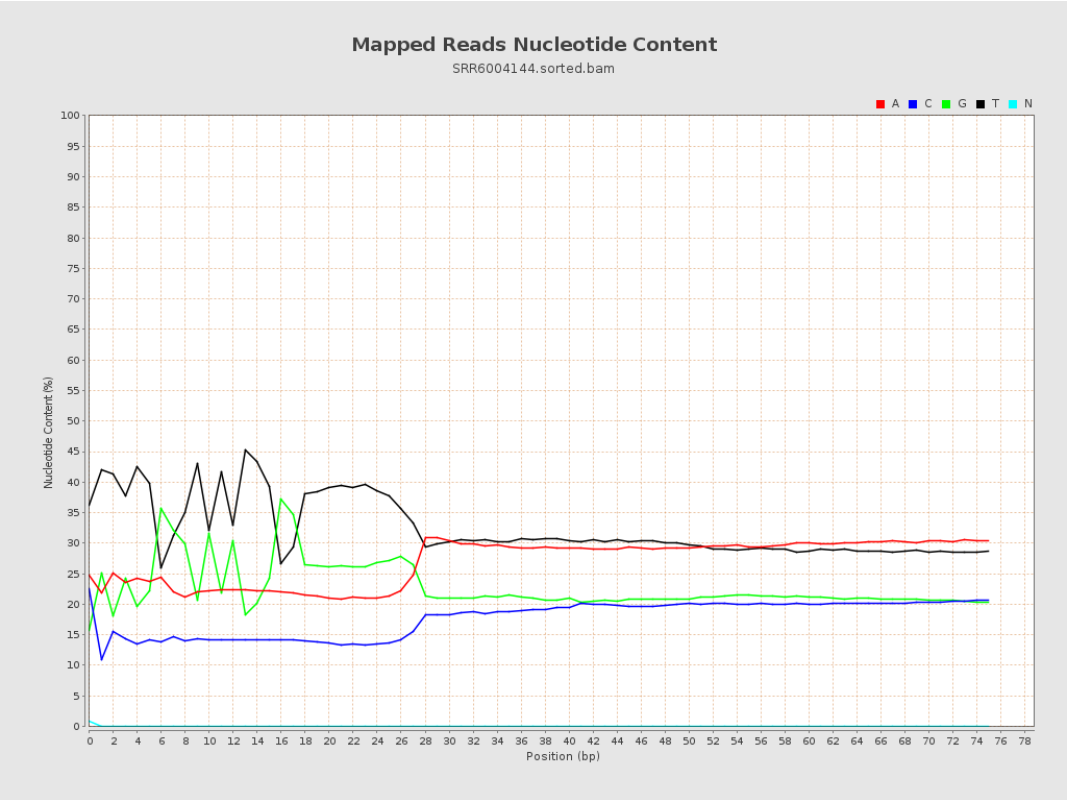
6. Results : Genome Fraction Coverage



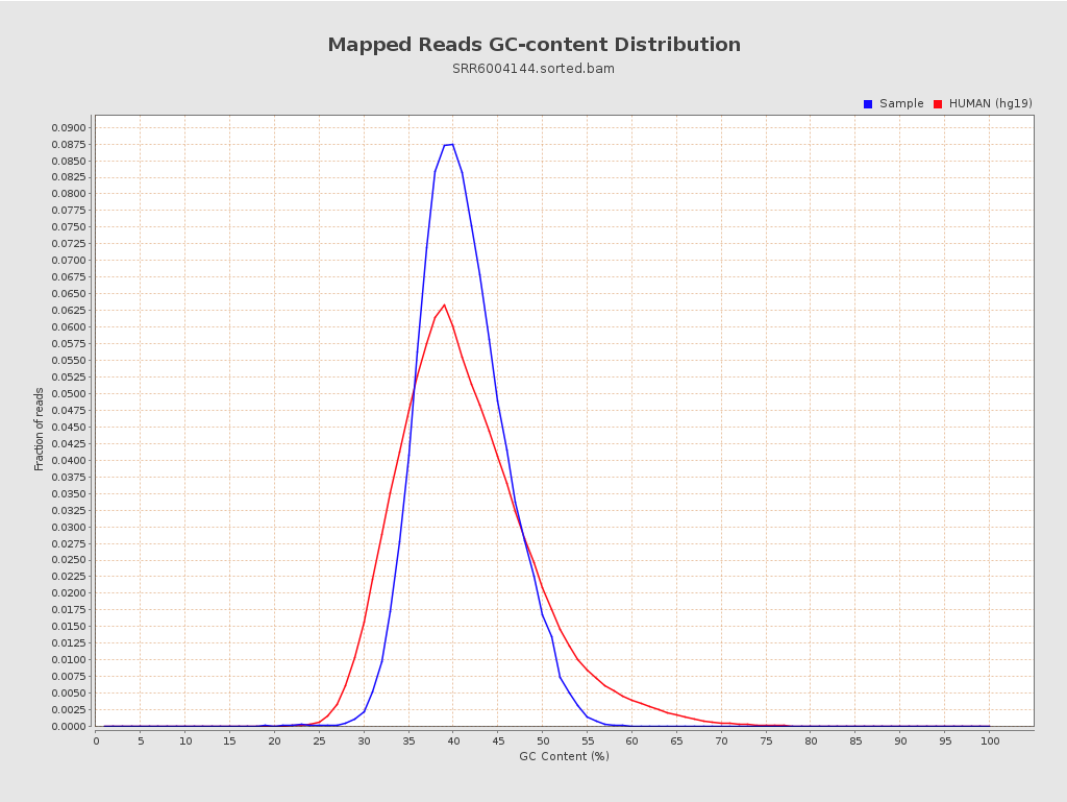
7. Results : Duplication Rate Histogram



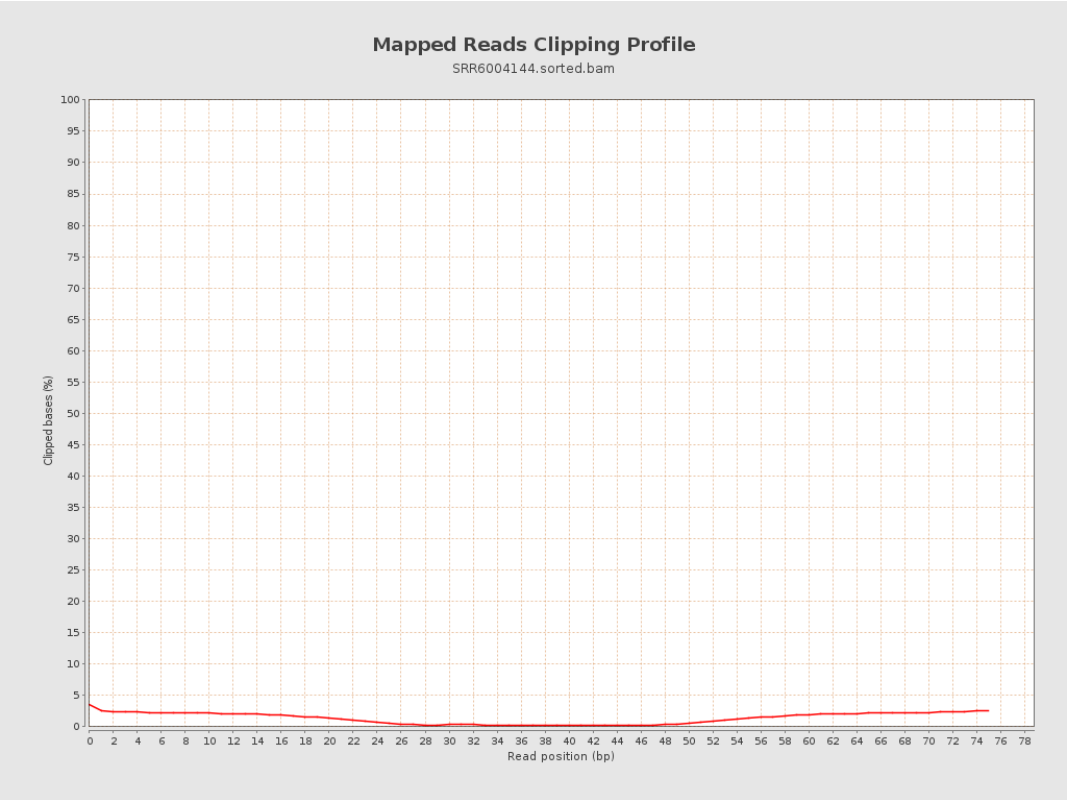
8. Results : Mapped Reads Nucleotide Content



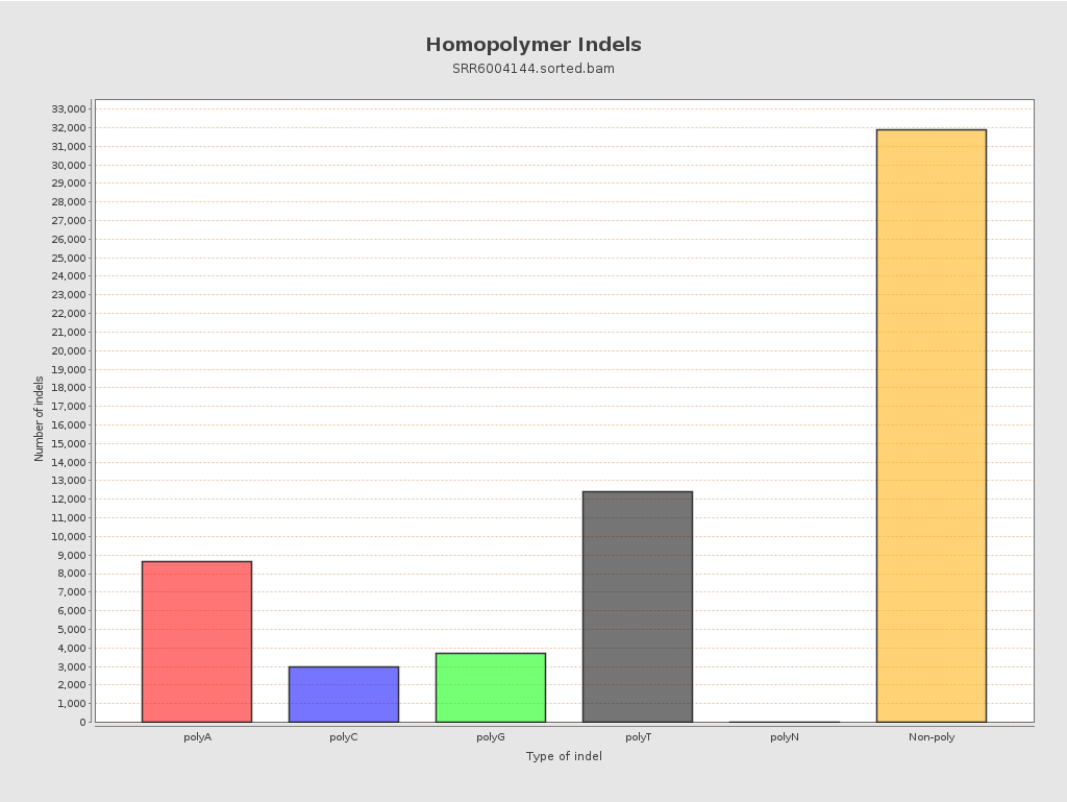
9. Results : Mapped Reads GC-content Distribution



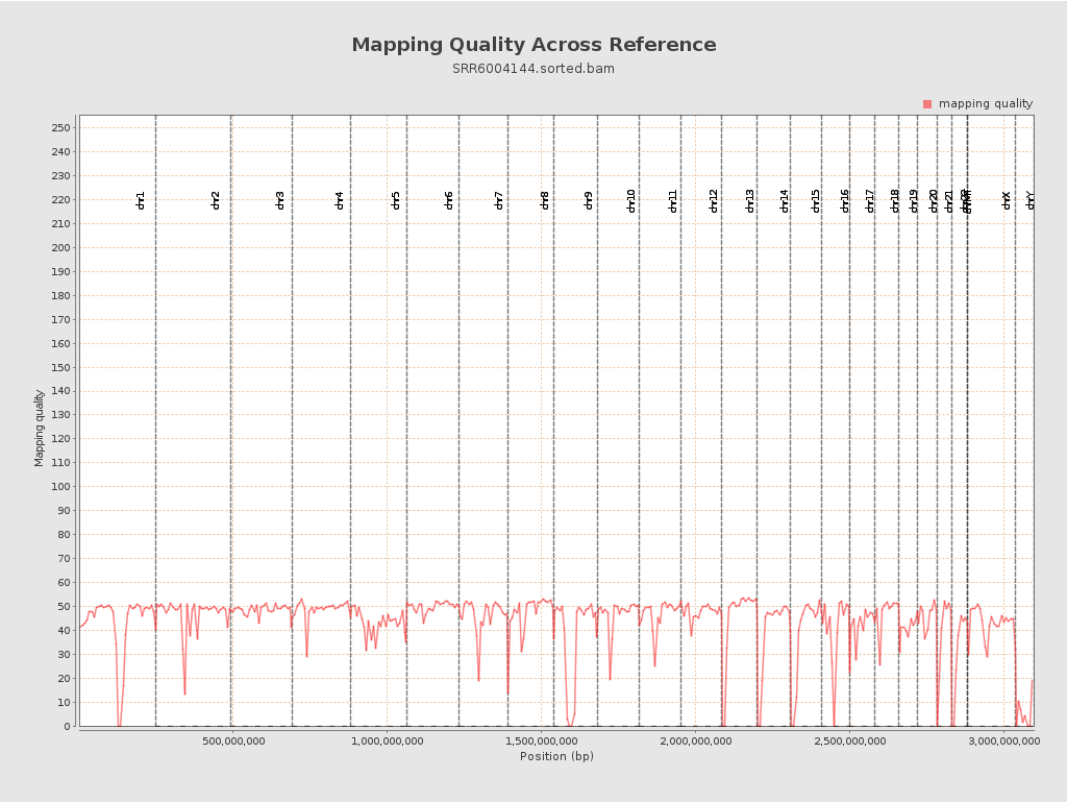
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram