Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:14:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524314.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_SRR10524314 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524314.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:14:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524314.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,918,599
Mapped reads	3,566,937 / 91.03%
Unmapped reads	351,662 / 8.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,103 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	173,290 / 4.42%
Duplication rate	3.35%
Clipped reads	3,578,032 / 91.31%

2.2. ACGT Content

Number/percentage of A's	50,949,399 / 24.54%
Number/percentage of C's	39,094,044 / 18.83%
Number/percentage of T's	66,503,623 / 32.04%
Number/percentage of G's	51,012,370 / 24.57%
Number/percentage of N's	28,267 / 0.01%
GC Percentage	43.41%

2.3. Coverage

Mean	0.0671

Standard Deviation	0.5731

2.4. Mapping Quality

Mean Mapping Quality	43.71

2.5. Mismatches and indels

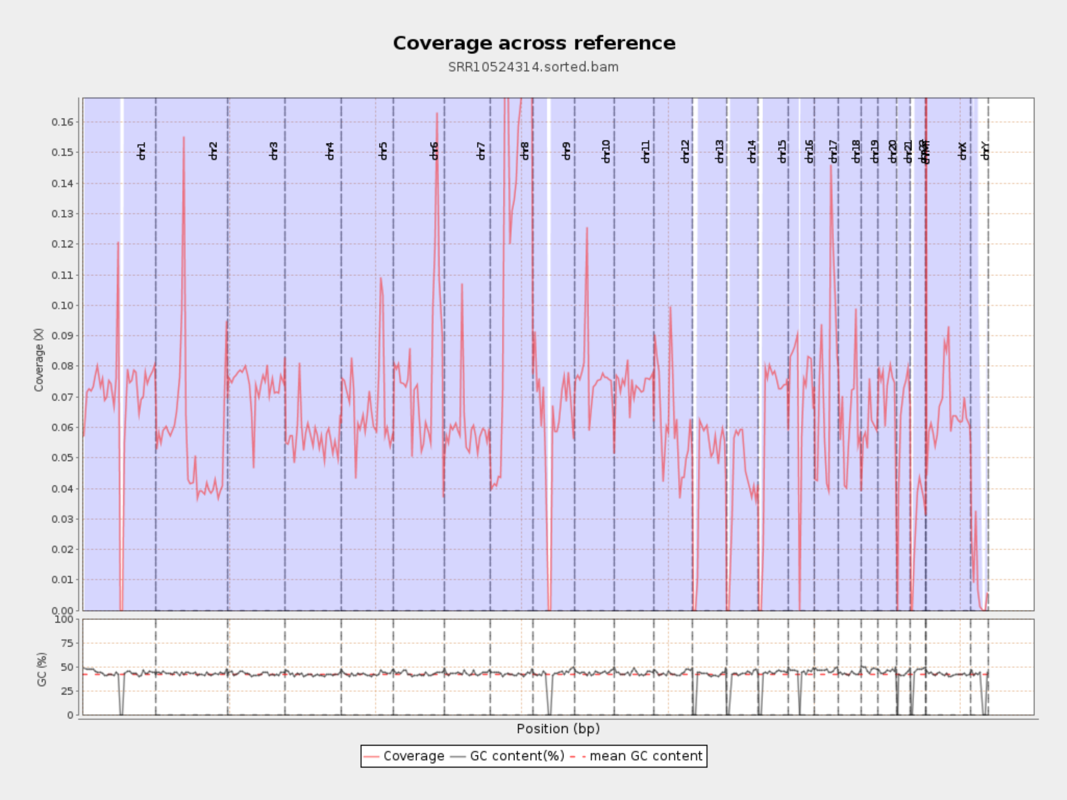
General error rate	0.52%
Mismatches	1,067,001
Insertions	11,632
Mapped reads with at least one insertion	0.32%
Deletions	35,176
Mapped reads with at least one deletion	0.98%
Homopolymer indels	42.53%

2.6. Chromosome stats

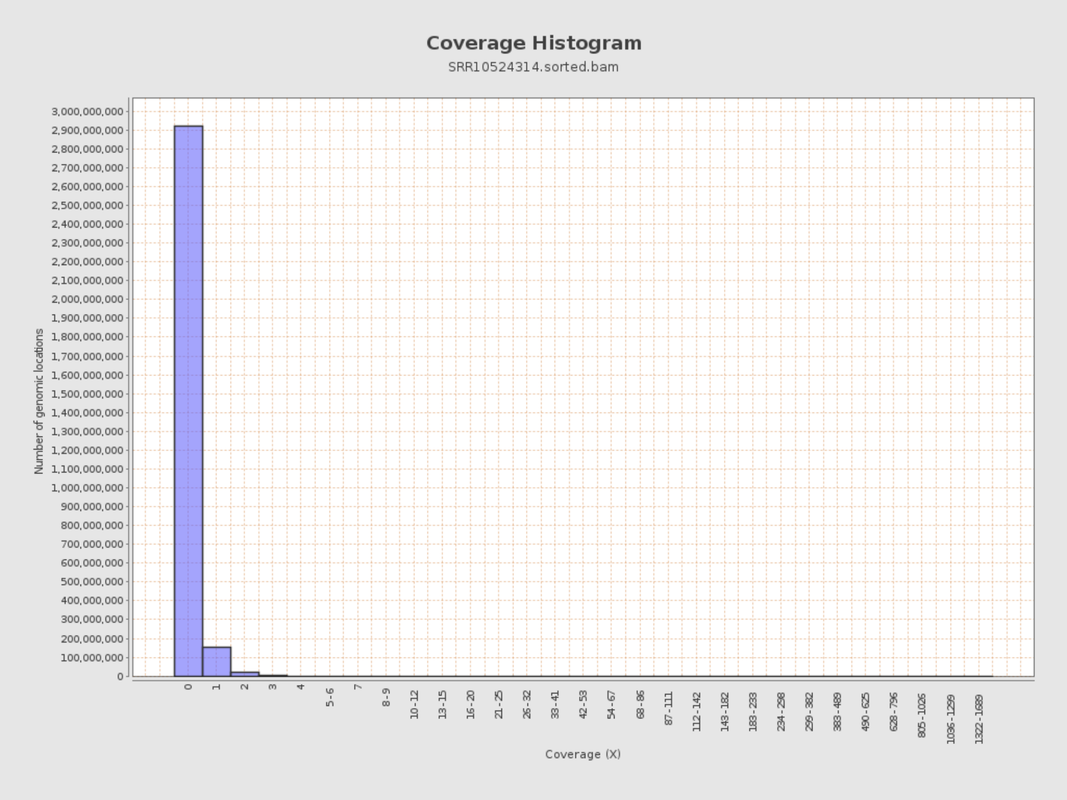
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17444142	0.07	1.1854
chr2	243199373	13539081	0.0557	0.7626
chr3	198022430	14616527	0.0738	0.3199
chr4	191154276	10929378	0.0572	0.322
chr5	180915260	12330756	0.0682	0.3046
chr6	171115067	13445678	0.0786	0.3761
chr7	159138663	9547422	0.06	0.7696

chr8	146364022	21752979	0.1486	0.6732
chr9	141213431	8586521	0.0608	0.4185
chr10	135534747	10444157	0.0771	0.548
chr11	135006516	9936312	0.0736	0.4563
chr12	133851895	8297706	0.062	0.2986
chr13	115169878	5405573	0.0469	0.2553
chr14	107349540	4405749	0.041	0.2689
chr15	102531392	6263983	0.0611	0.3029
chr16	90354753	6373063	0.0705	0.3461
chr17	81195210	6219146	0.0766	0.385
chr18	78077248	4900422	0.0628	0.8403
chr19	59128983	3551616	0.0601	0.7828
chr20	63025520	4625133	0.0734	0.3299
chr21	48129895	2894183	0.0601	0.3212
chr22	51304566	1438066	0.028	0.1934
chrMT	16571	11200	0.6759	0.9675
chrX	155270560	10133286	0.0653	0.365
chrY	59373566	550809	0.0093	0.23

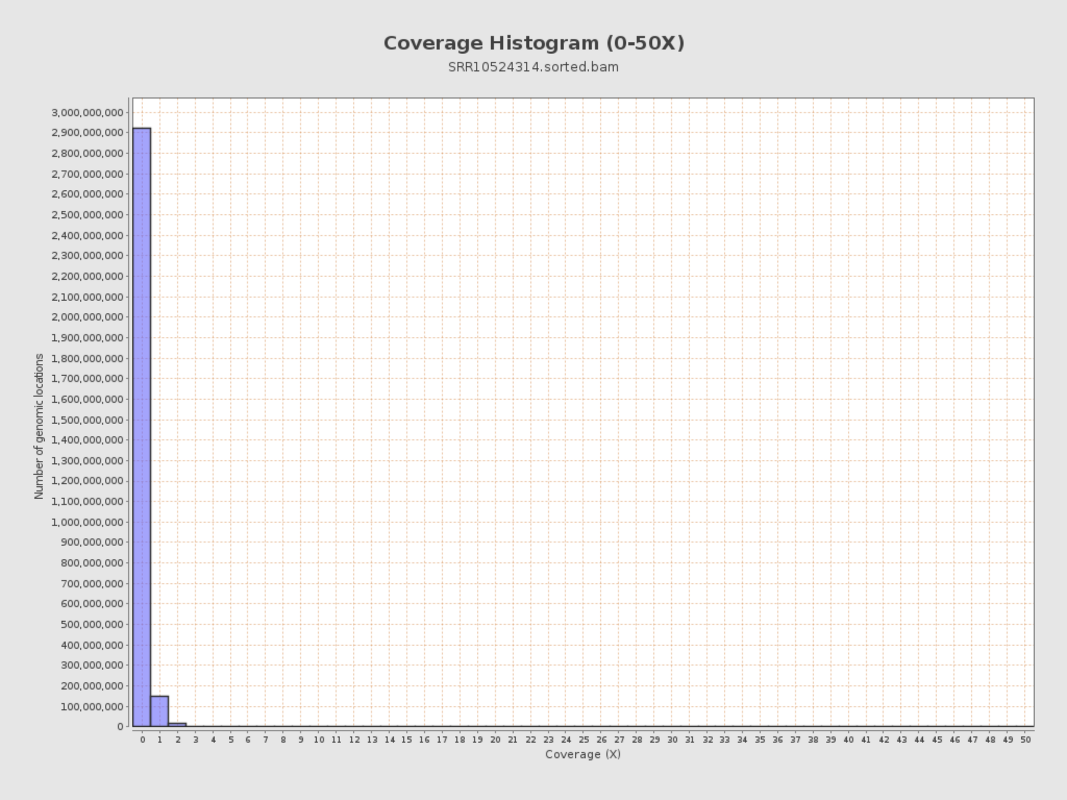
3. Results : Coverage across reference



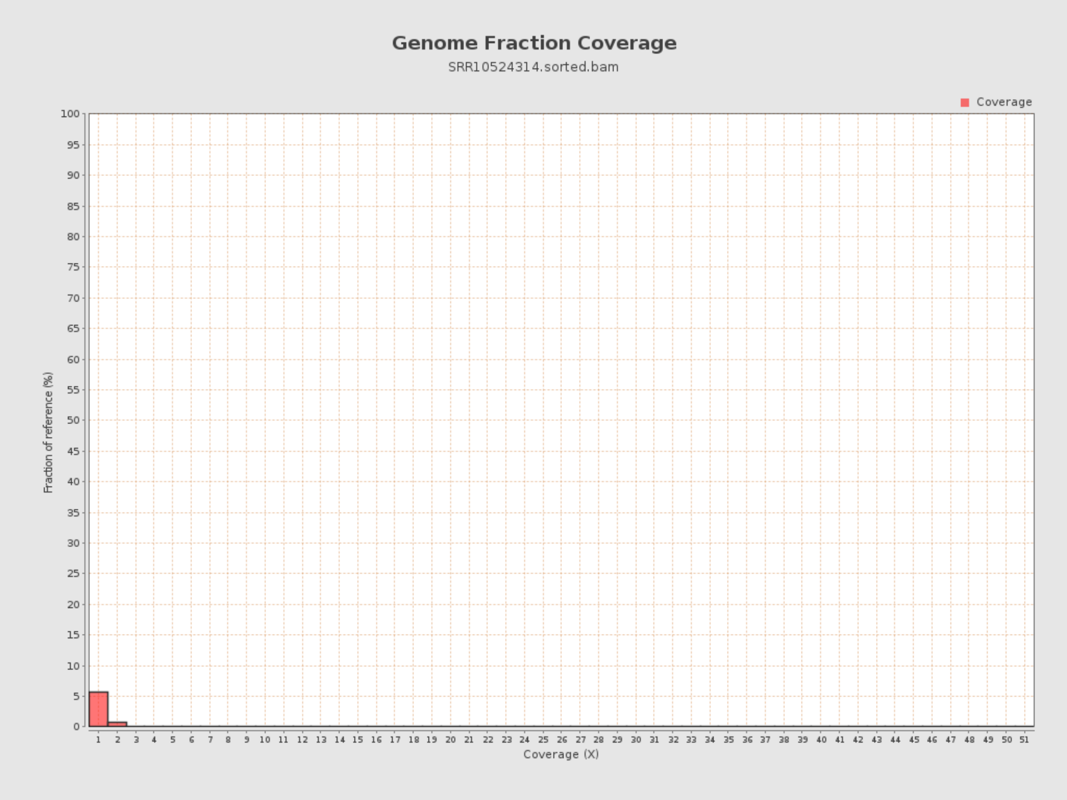
4. Results : Coverage Histogram



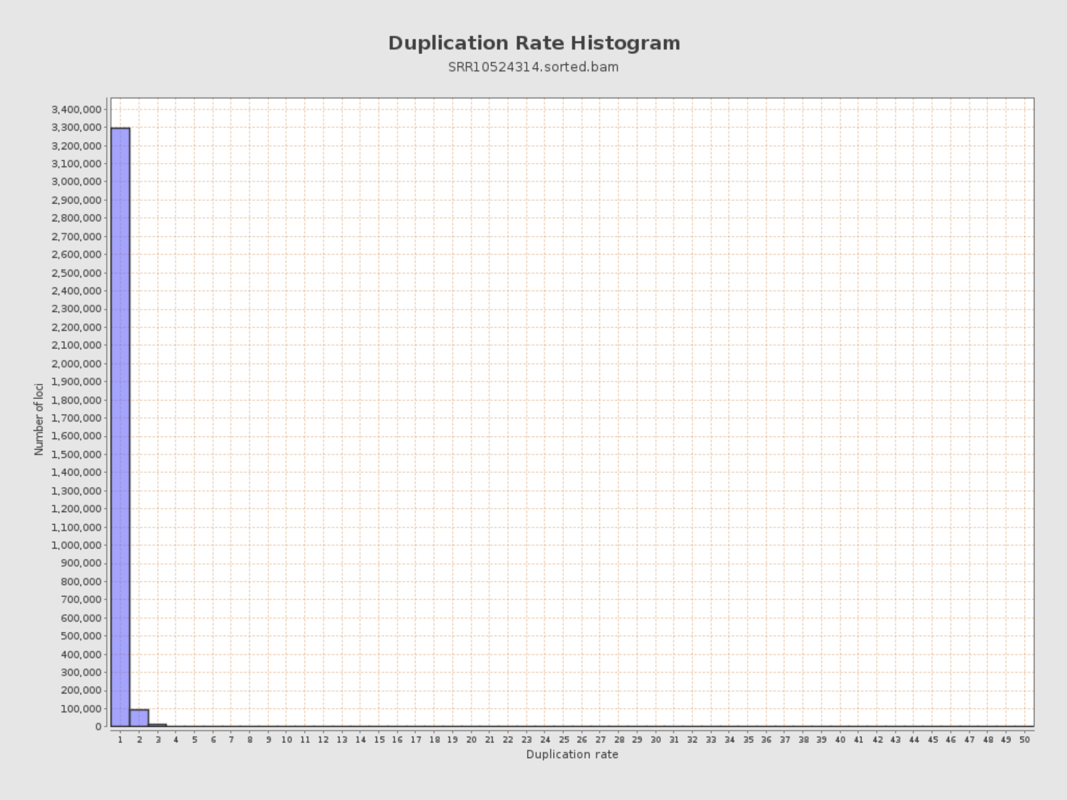
5. Results : Coverage Histogram (0-50X)



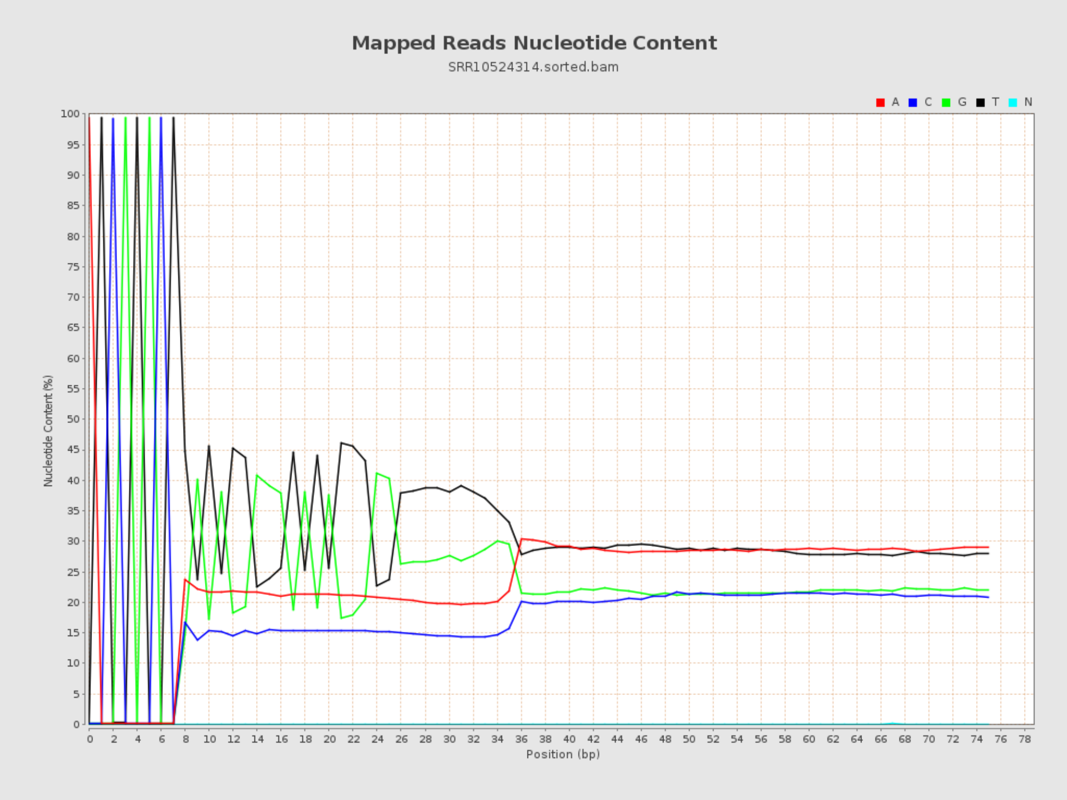
6. Results : Genome Fraction Coverage



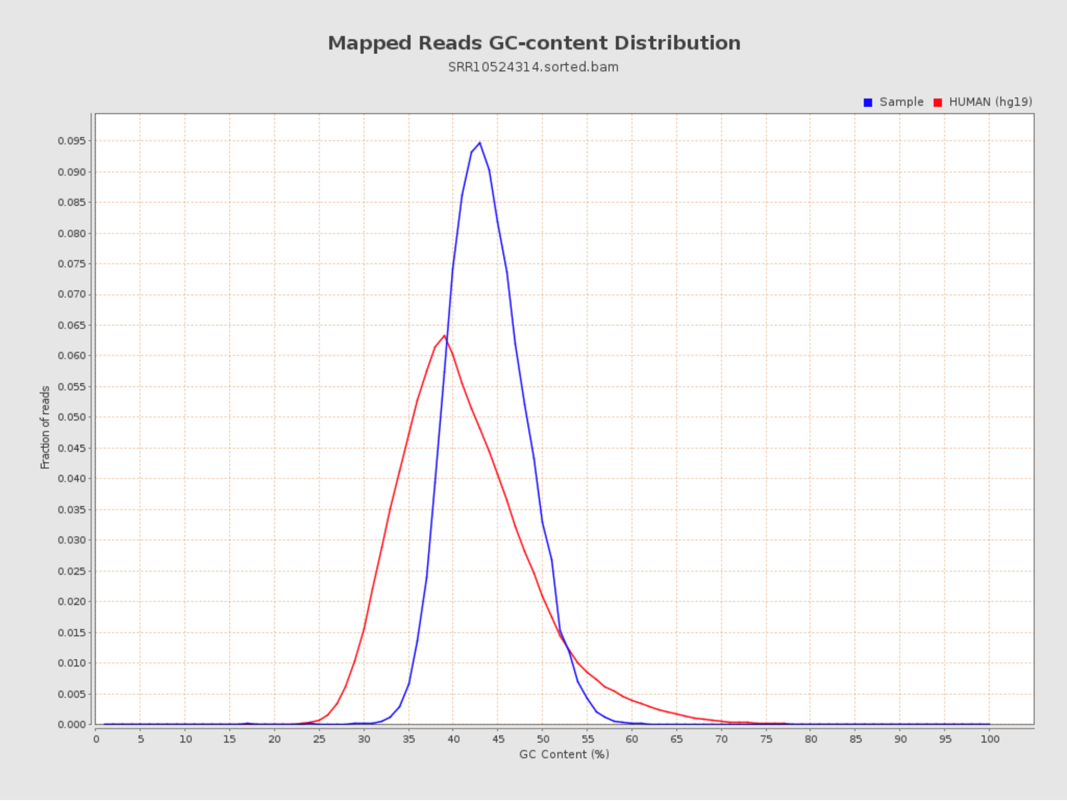
7. Results : Duplication Rate Histogram



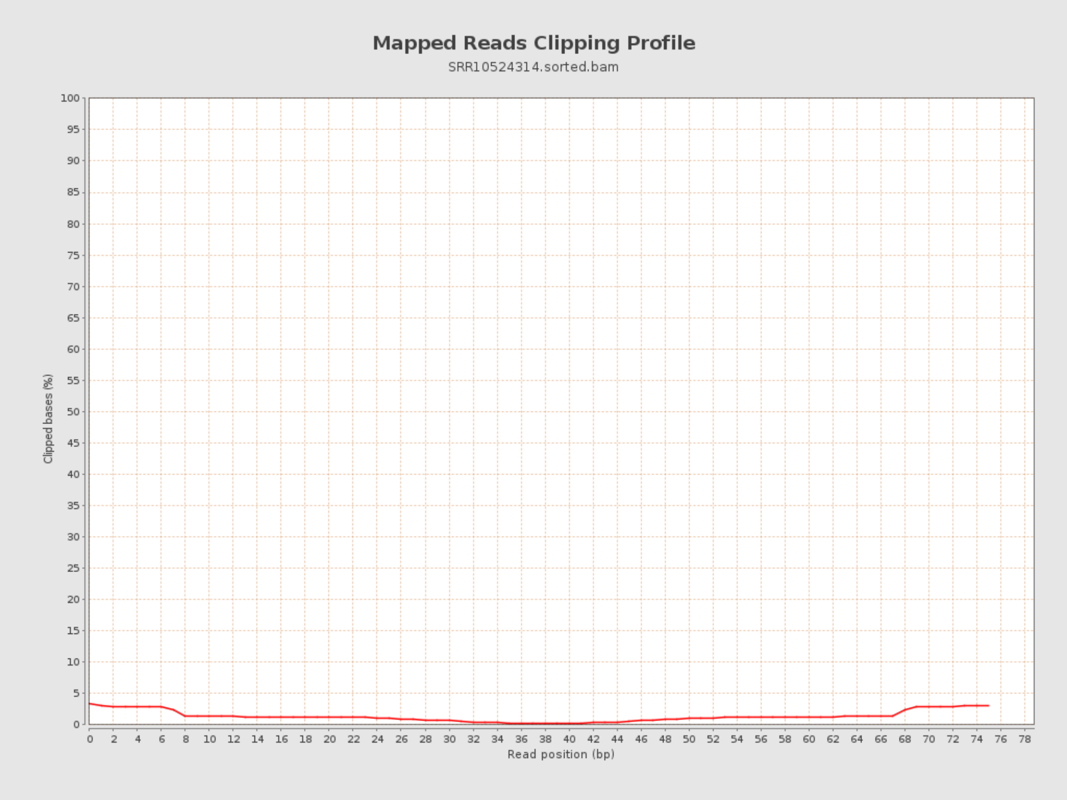
8. Results : Mapped Reads Nucleotide Content



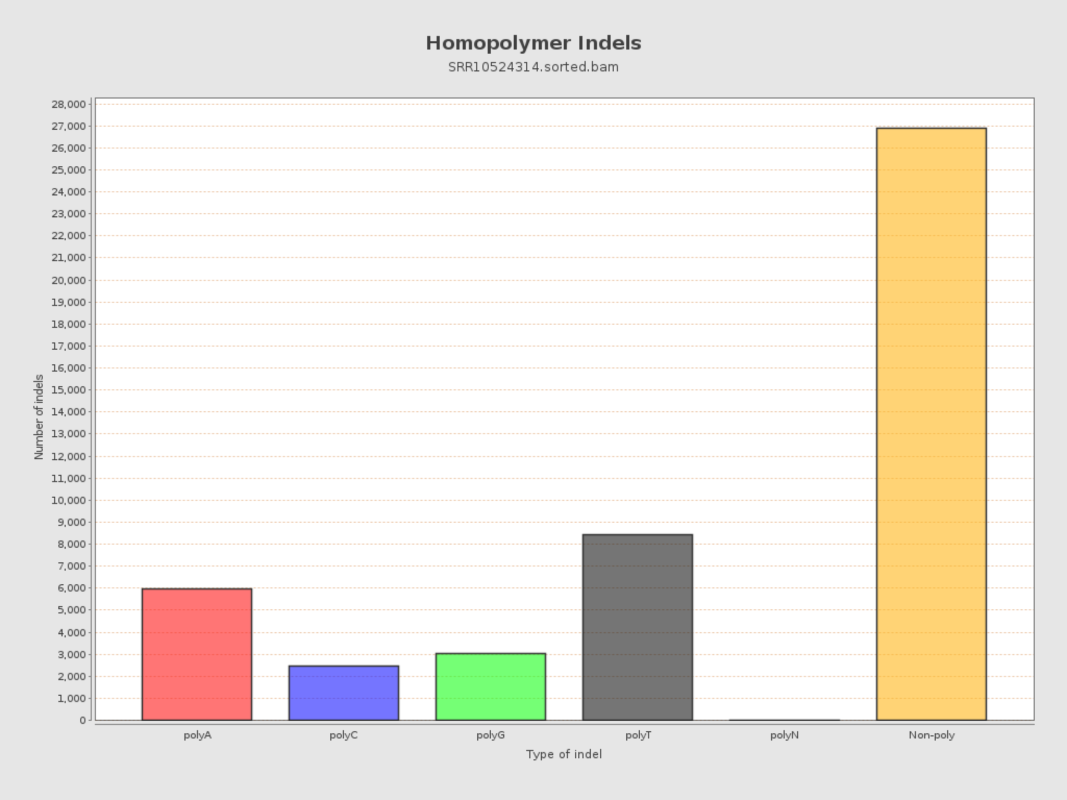
9. Results : Mapped Reads GC-content Distribution



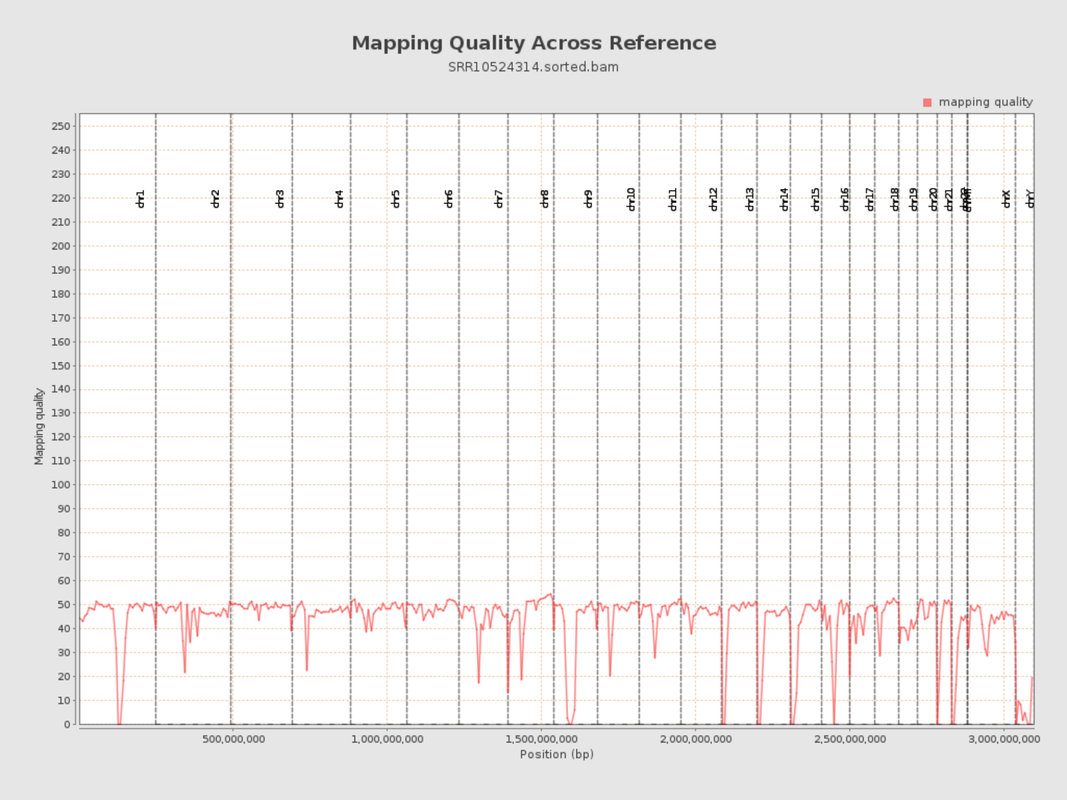
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram