Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:48:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716147.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_SRR9716147 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716147.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:48:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716147.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,699,405
Mapped reads	2,451,662 / 90.82%
Unmapped reads	247,743 / 9.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,438 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	143,514 / 5.32%
Duplication rate	4.58%
Clipped reads	2,457,679 / 91.05%

2.2. ACGT Content

Number/percentage of A's	36,458,540 / 25.59%
Number/percentage of C's	26,365,453 / 18.51%
Number/percentage of T's	43,735,685 / 30.7%
Number/percentage of G's	35,907,666 / 25.2%
Number/percentage of N's	1,038 / 0%
GC Percentage	43.71%

2.3. Coverage

Mean	0.046

Standard Deviation	0.3719

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

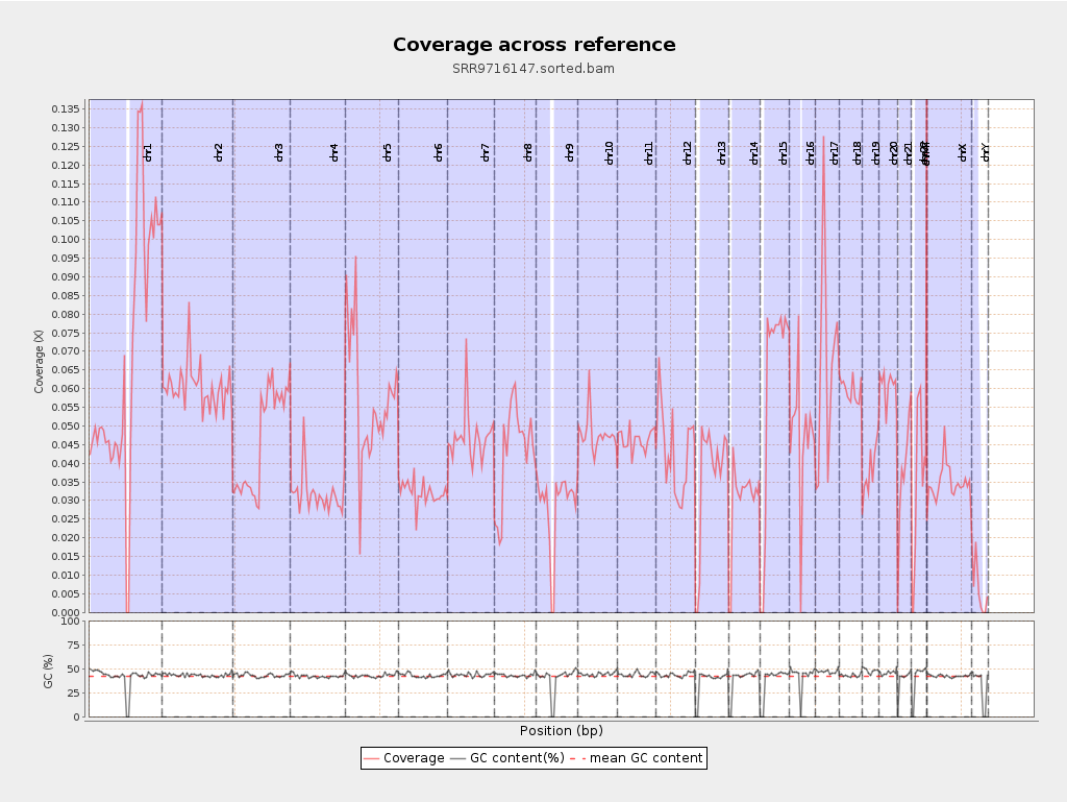
General error rate	0.51%
Mismatches	706,992
Insertions	11,750
Mapped reads with at least one insertion	0.48%
Deletions	26,362
Mapped reads with at least one deletion	1.07%
Homopolymer indels	39.07%

2.6. Chromosome stats

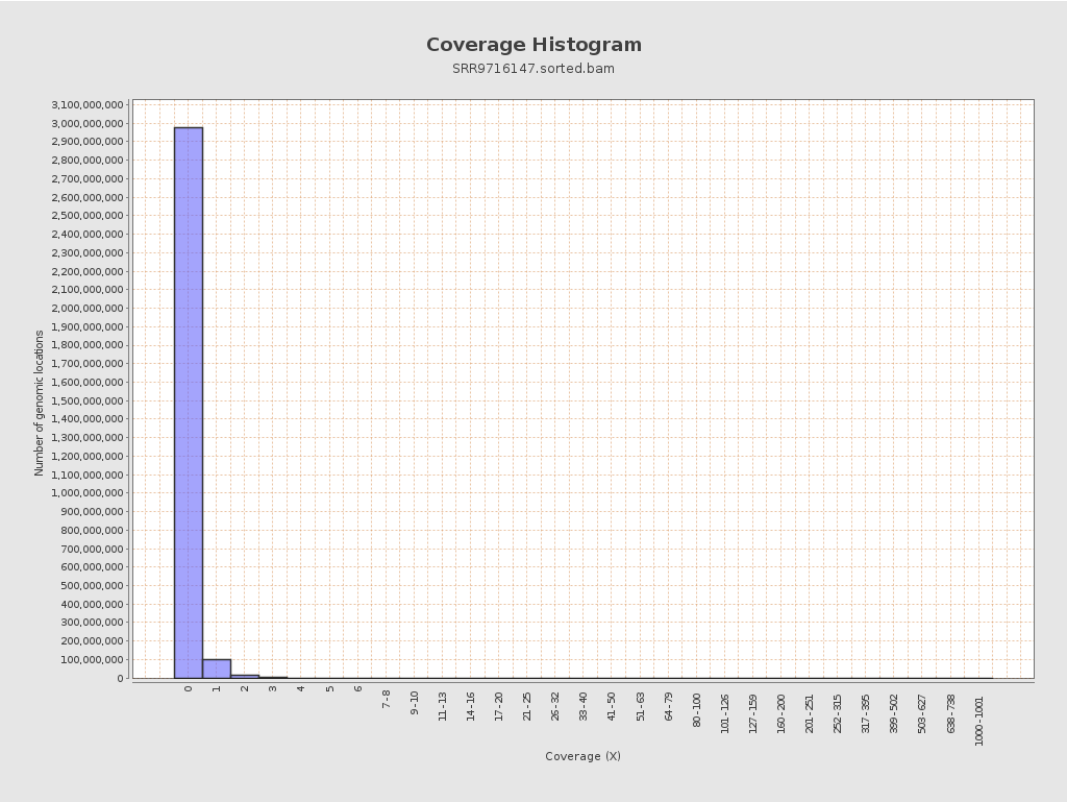
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17011816	0.0683	0.6262
chr2	243199373	14695355	0.0604	0.5426
chr3	198022430	9099584	0.046	0.2501
chr4	191154276	6034390	0.0316	0.2424
chr5	180915260	10346094	0.0572	0.2811
chr6	171115067	5505665	0.0322	0.24
chr7	159138663	7496076	0.0471	0.4912

chr8	146364022	6373312	0.0435	0.3246
chr9	141213431	3968543	0.0281	0.284
chr10	135534747	6469633	0.0477	0.3224
chr11	135006516	6231569	0.0462	0.3763
chr12	133851895	5745120	0.0429	0.2456
chr13	115169878	4200966	0.0365	0.226
chr14	107349540	3165342	0.0295	0.2184
chr15	102531392	6309714	0.0615	0.2945
chr16	90354753	4304197	0.0476	0.2768
chr17	81195210	5493327	0.0677	0.3396
chr18	78077248	4650454	0.0596	0.6525
chr19	59128983	2283381	0.0386	0.4618
chr20	63025520	3821159	0.0606	0.2935
chr21	48129895	1841185	0.0383	0.2442
chr22	51304566	1717030	0.0335	0.213
chrMT	16571	2695	0.1626	0.4732
chrX	155270560	5394507	0.0347	0.2549
chrY	59373566	348767	0.0059	0.14

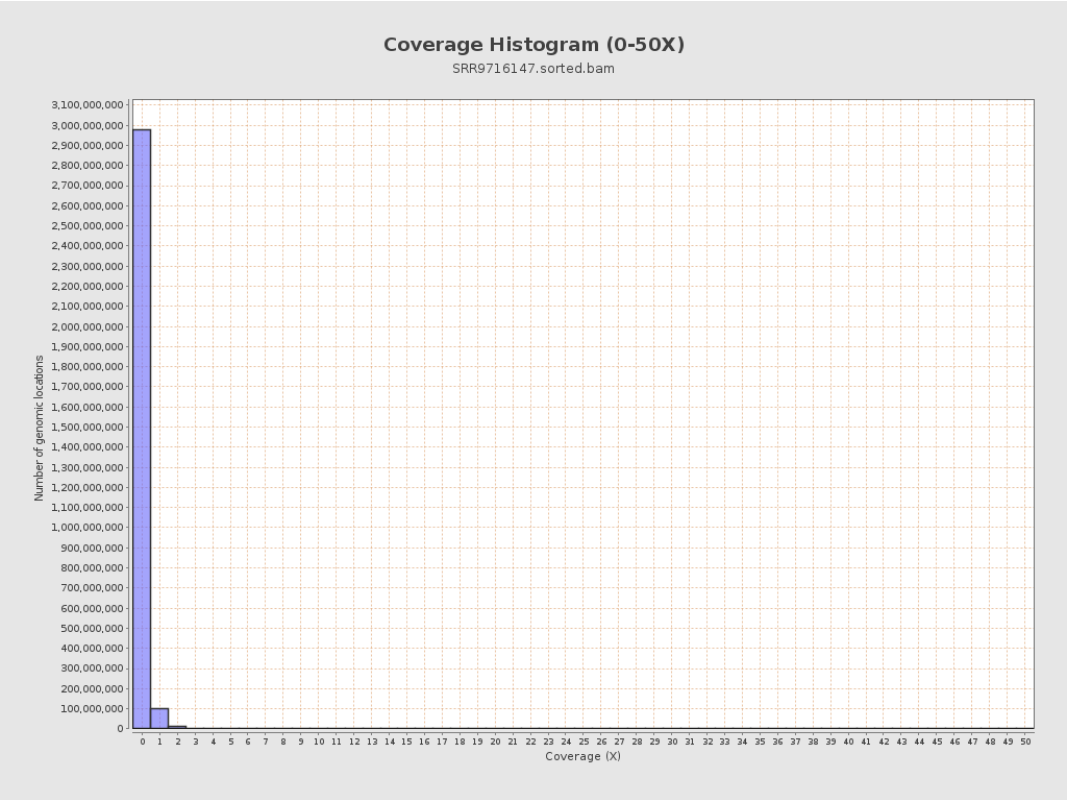
3. Results : Coverage across reference



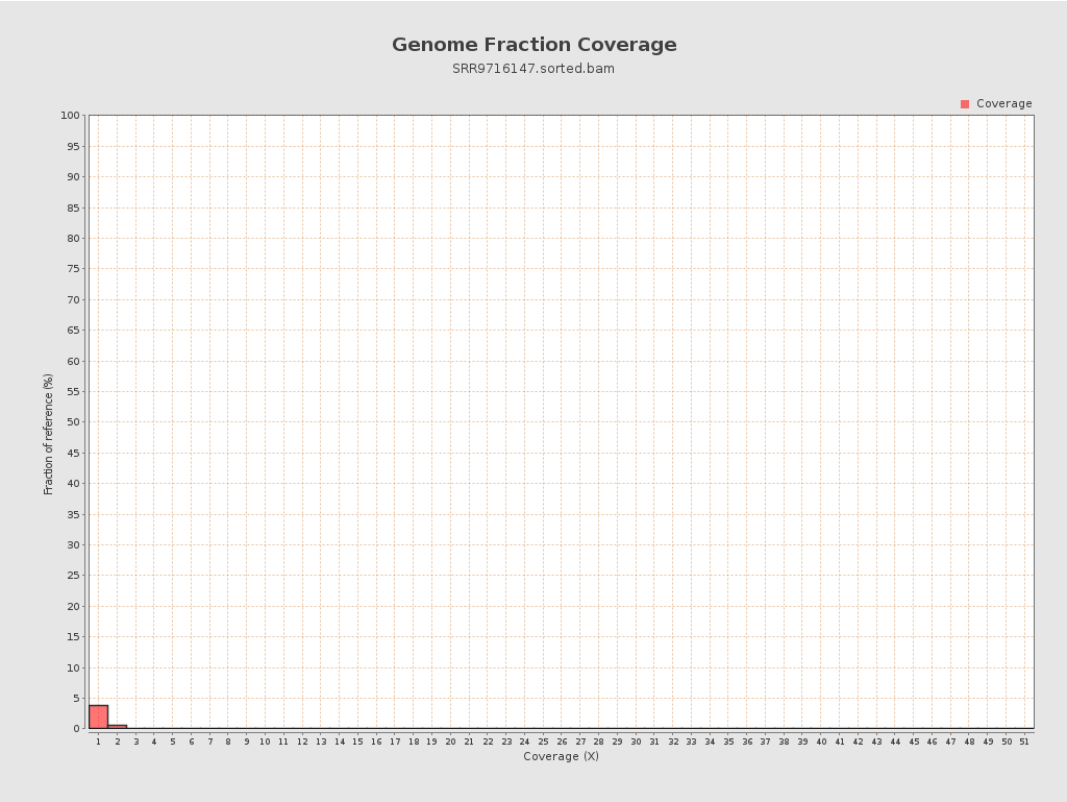
4. Results : Coverage Histogram



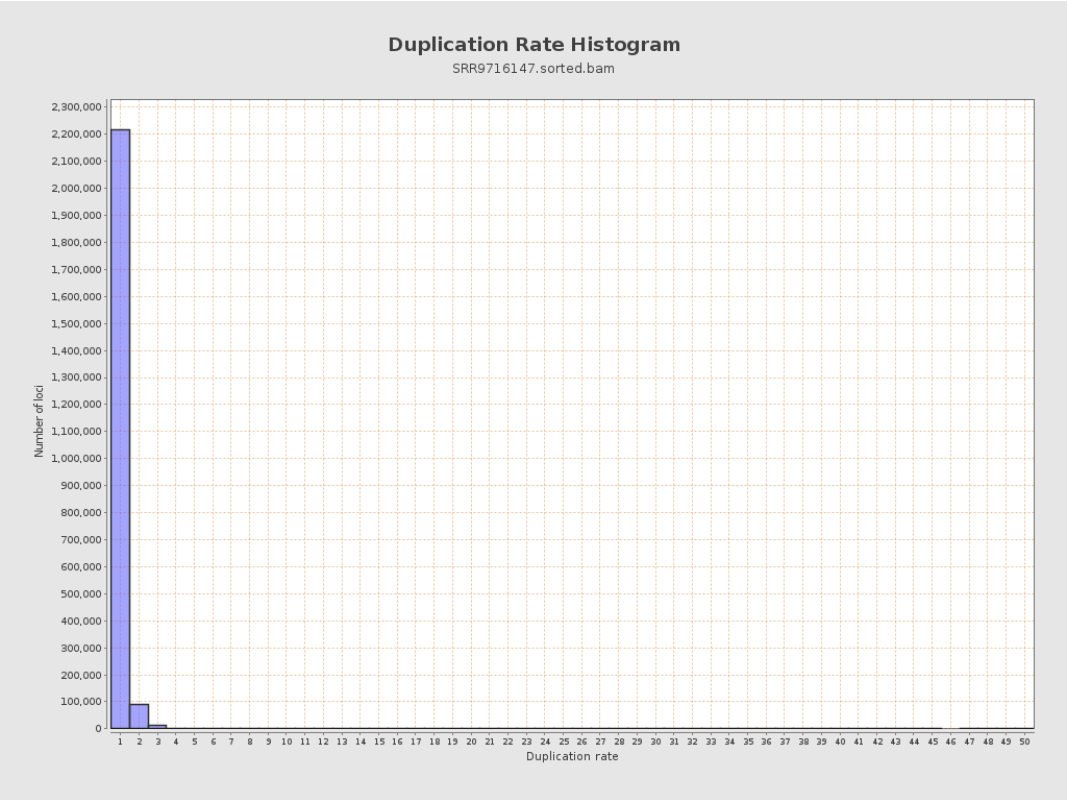
5. Results : Coverage Histogram (0-50X)



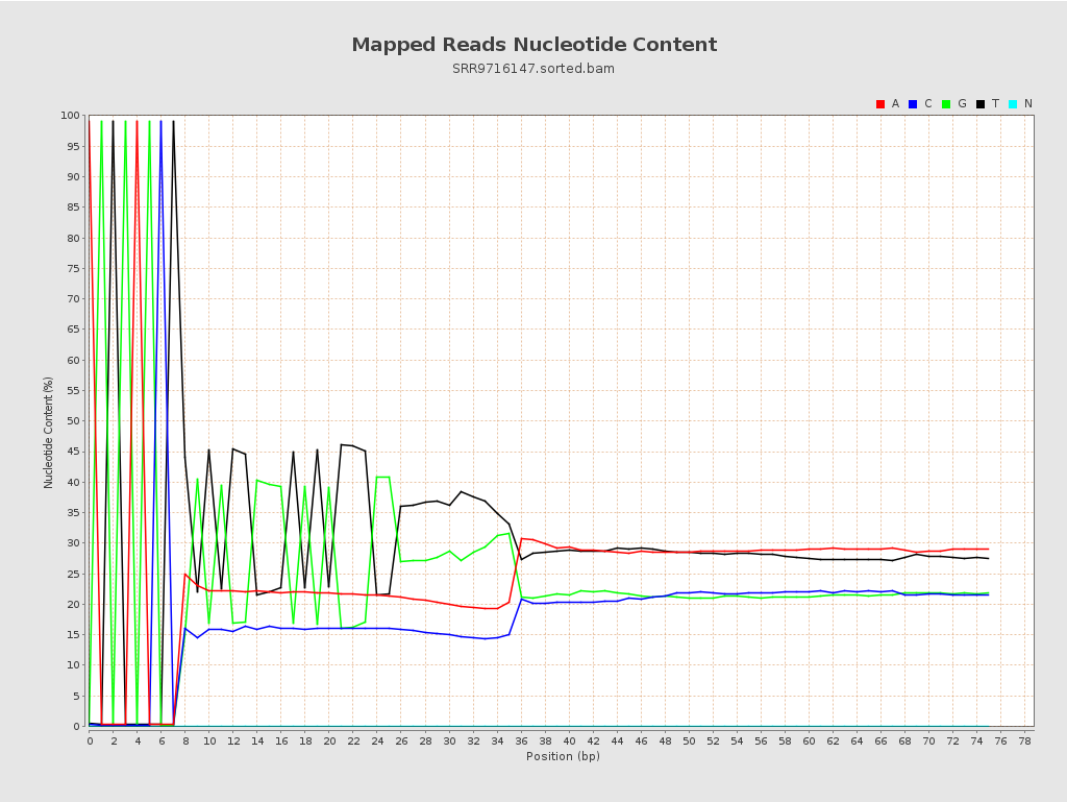
6. Results : Genome Fraction Coverage



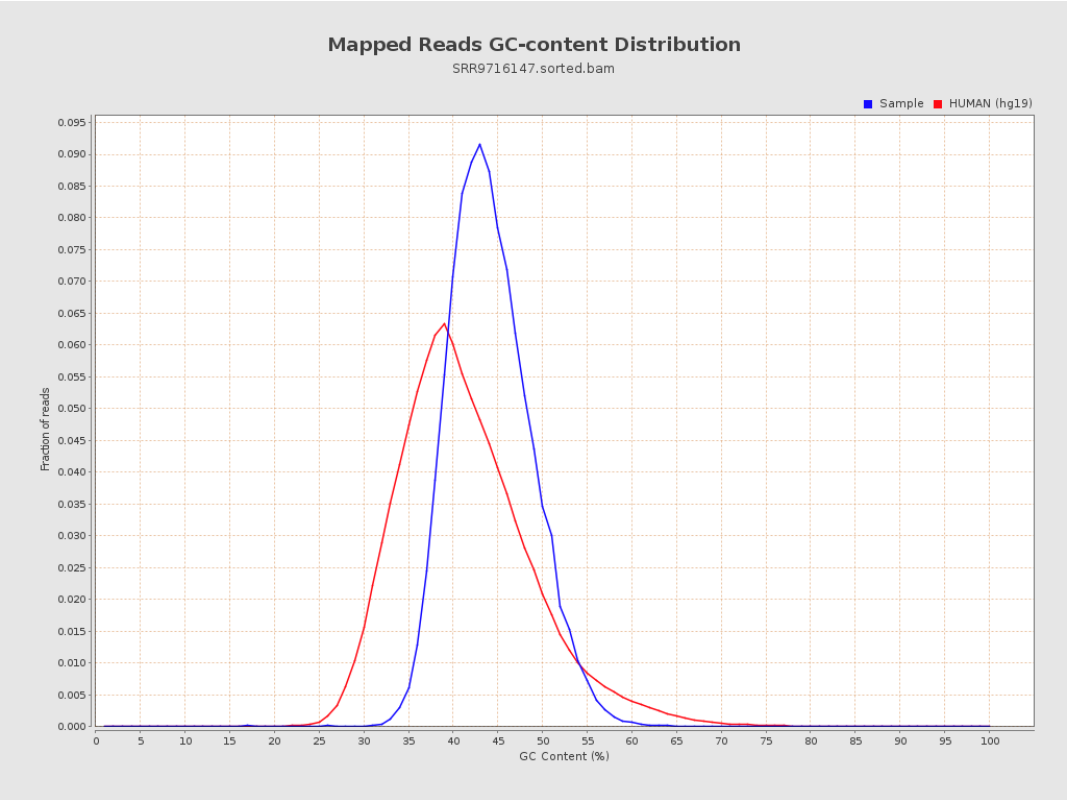
7. Results : Duplication Rate Histogram



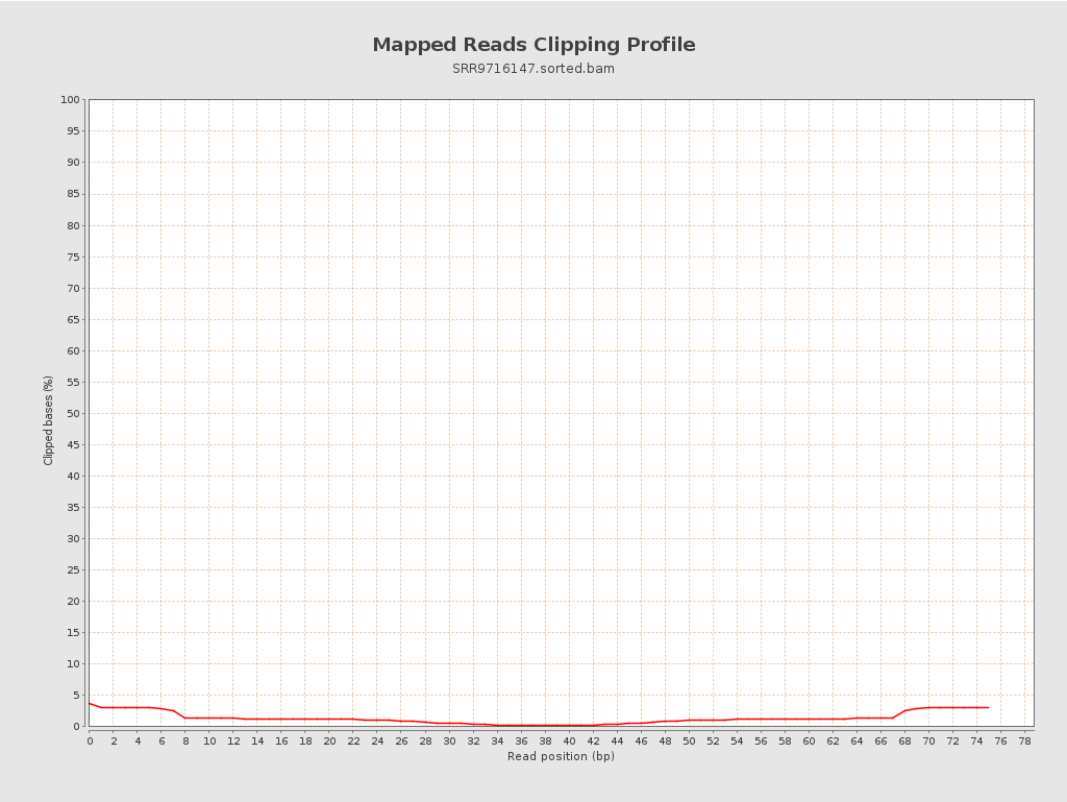
8. Results : Mapped Reads Nucleotide Content



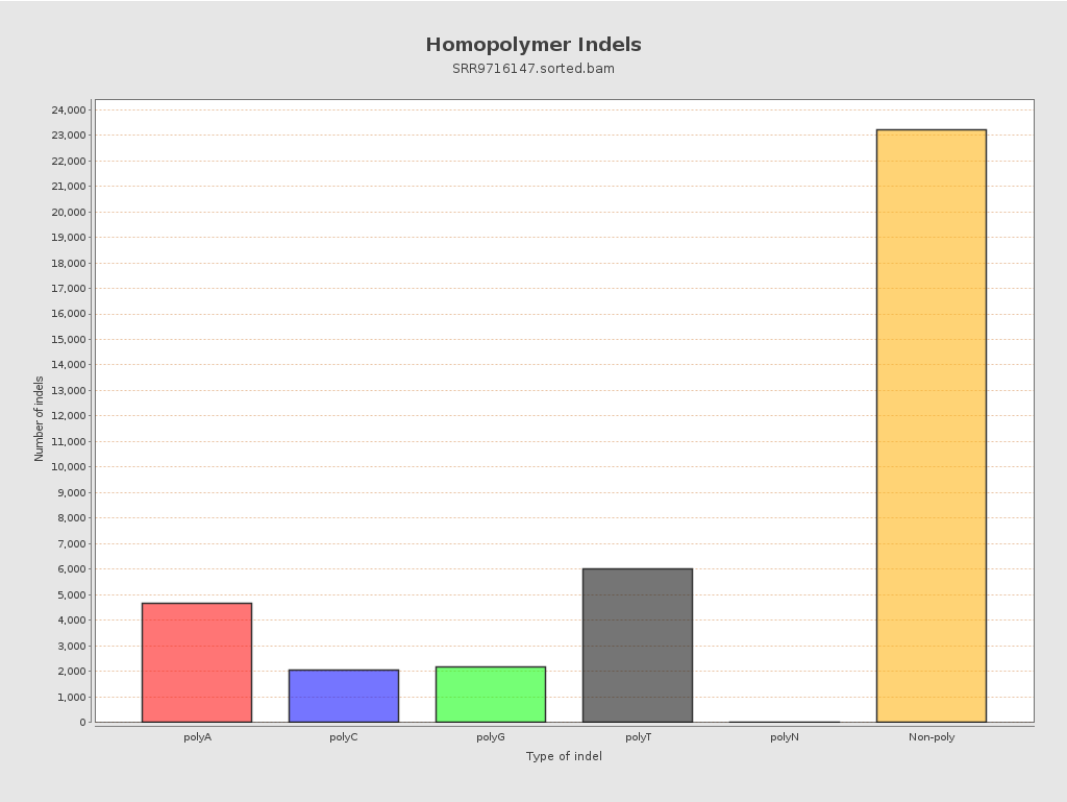
9. Results : Mapped Reads GC-content Distribution



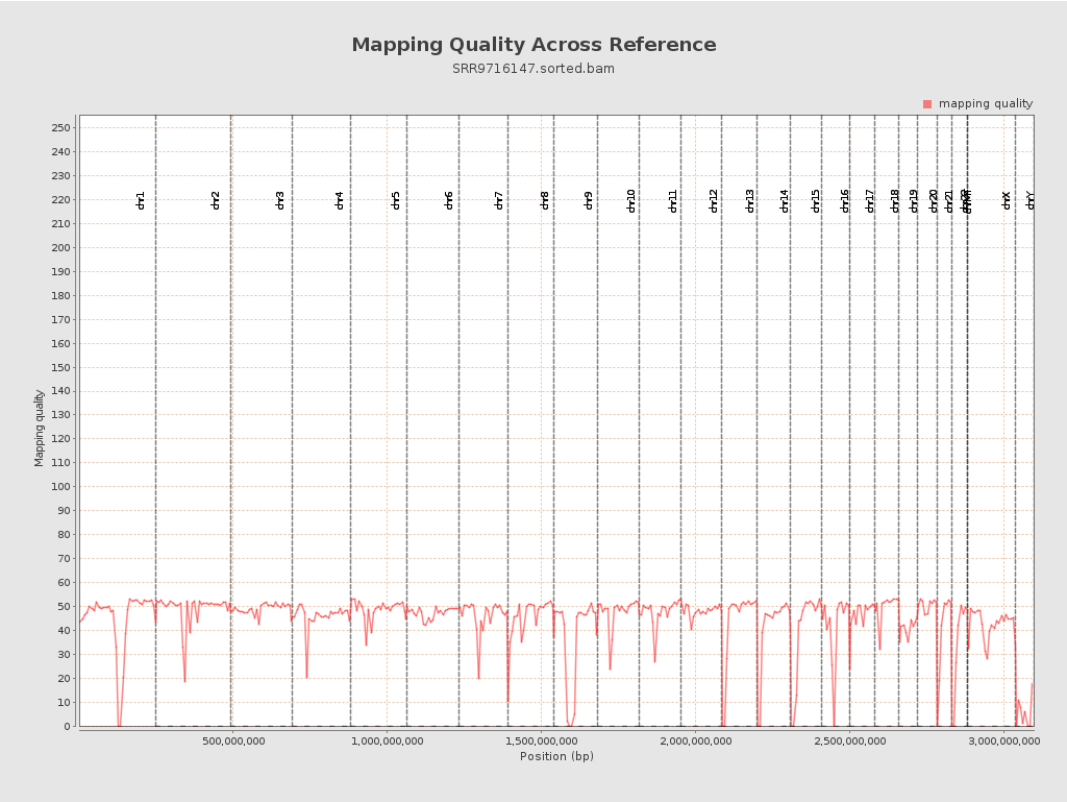
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram