Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:37:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716143.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_SRR9716143 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716143.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:37:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716143.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,858,561
Mapped reads	2,469,302 / 86.38%
Unmapped reads	389,259 / 13.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,562 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	114,290 / 4%
Duplication rate	3.45%
Clipped reads	2,475,158 / 86.59%

2.2. ACGT Content

Number/percentage of A's	37,256,890 / 26.21%
Number/percentage of C's	25,458,963 / 17.91%
Number/percentage of T's	44,425,497 / 31.25%
Number/percentage of G's	35,029,024 / 24.64%
Number/percentage of N's	1,131 / 0%
GC Percentage	42.55%

2.3. Coverage

Mean	0.0459

Standard Deviation	0.3884

2.4. Mapping Quality

Mean Mapping Quality	44.45

2.5. Mismatches and indels

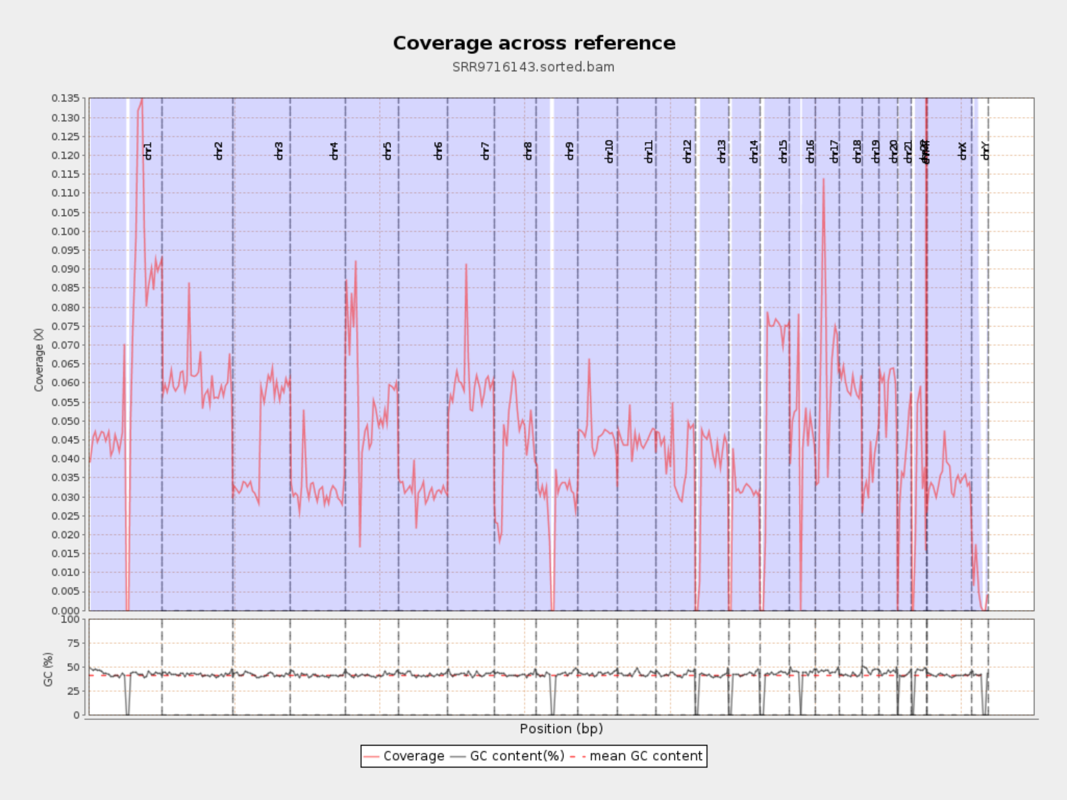
General error rate	0.53%
Mismatches	727,187
Insertions	10,355
Mapped reads with at least one insertion	0.42%
Deletions	27,573
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.79%

2.6. Chromosome stats

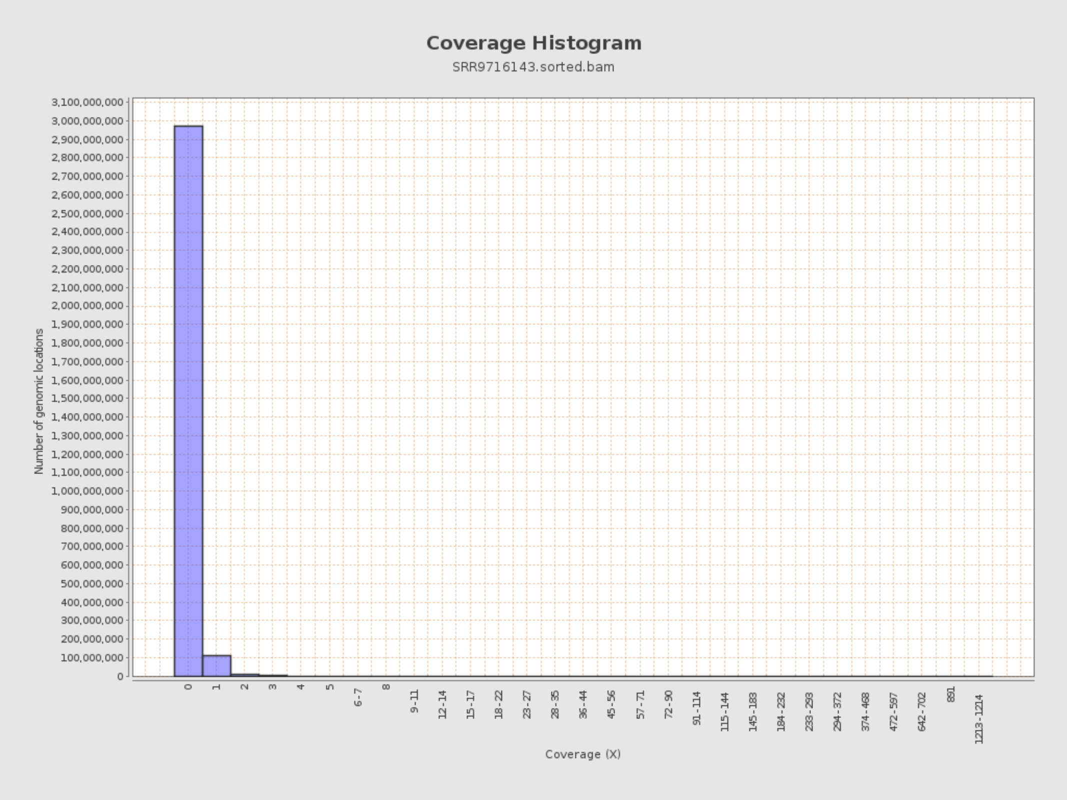
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16240132	0.0652	0.633
chr2	243199373	14705417	0.0605	0.5949
chr3	198022430	9090554	0.0459	0.2428
chr4	191154276	6075663	0.0318	0.2338
chr5	180915260	10269968	0.0568	0.2714
chr6	171115067	5414408	0.0316	0.2399
chr7	159138663	9585906	0.0602	0.6371

chr8	146364022	6437086	0.044	0.3513
chr9	141213431	3937487	0.0279	0.2866
chr10	135534747	6359682	0.0469	0.3193
chr11	135006516	6090534	0.0451	0.3673
chr12	133851895	5440404	0.0406	0.2322
chr13	115169878	4193438	0.0364	0.2179
chr14	107349540	3060567	0.0285	0.2076
chr15	102531392	6173124	0.0602	0.2878
chr16	90354753	4200472	0.0465	0.2635
chr17	81195210	5240548	0.0645	0.3199
chr18	78077248	4664394	0.0597	0.6571
chr19	59128983	2209127	0.0374	0.4848
chr20	63025520	3735461	0.0593	0.2802
chr21	48129895	1816201	0.0377	0.2344
chr22	51304566	1595963	0.0311	0.1978
chrMT	16571	11609	0.7006	0.9663
chrX	155270560	5335621	0.0344	0.2585
chrY	59373566	331091	0.0056	0.1263

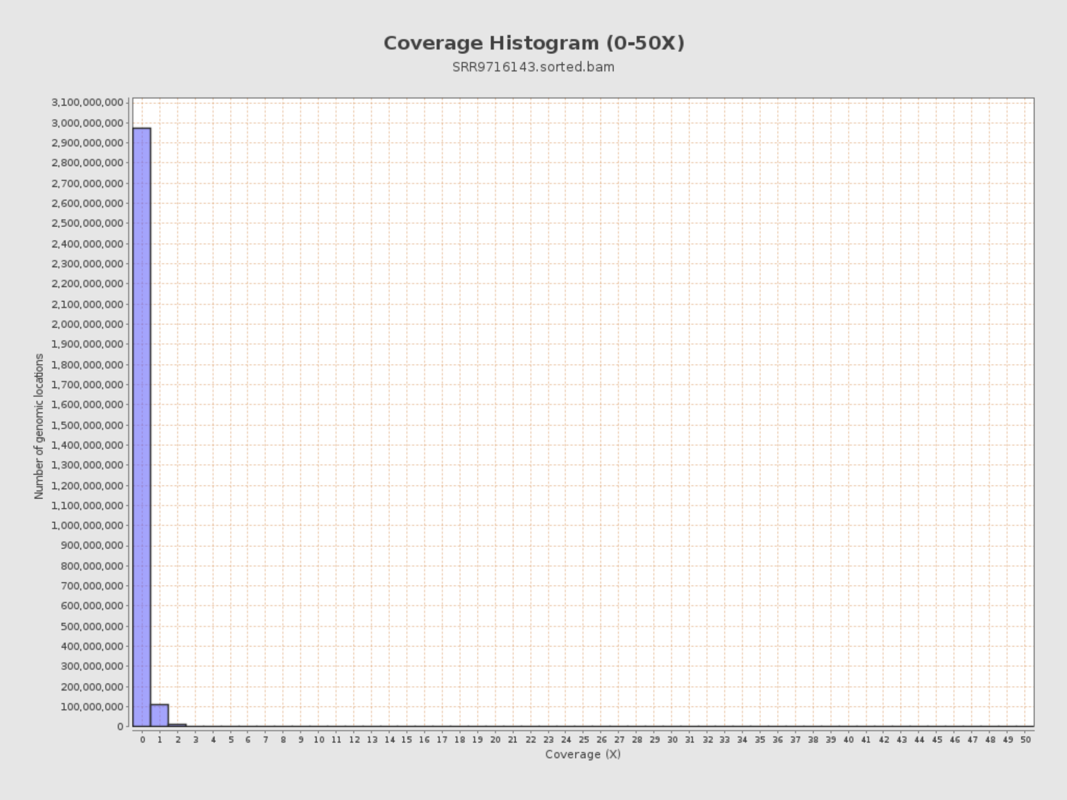
3. Results : Coverage across reference



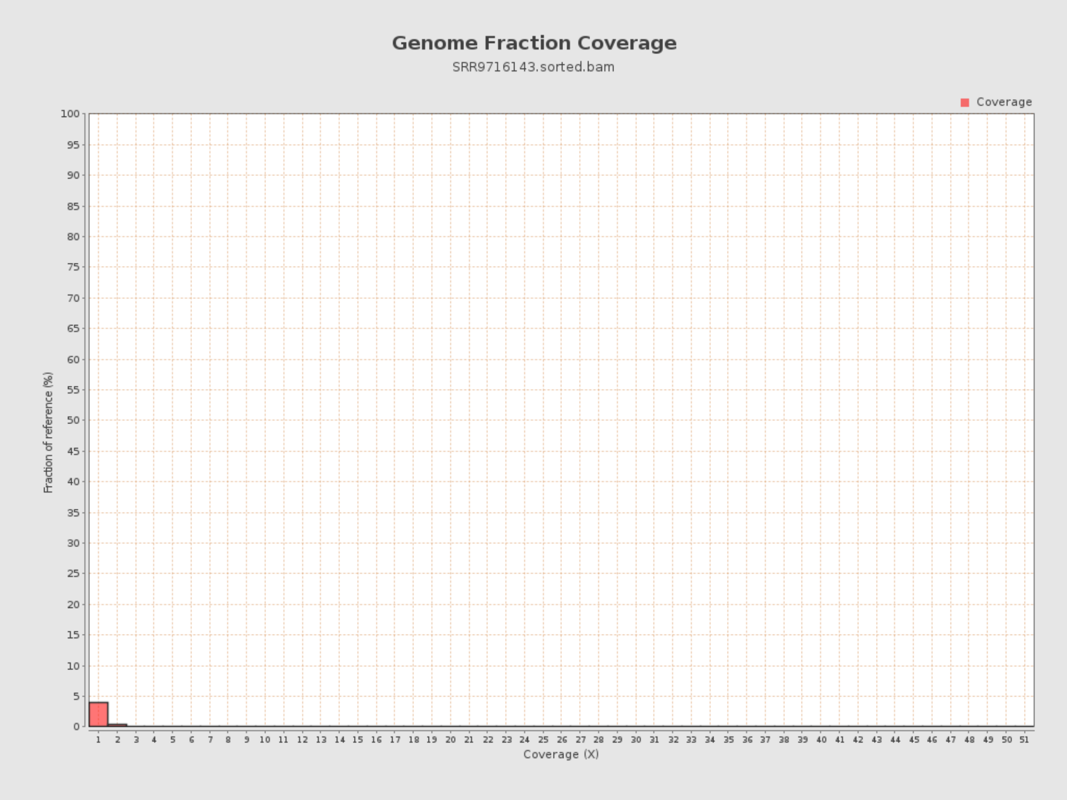
4. Results : Coverage Histogram



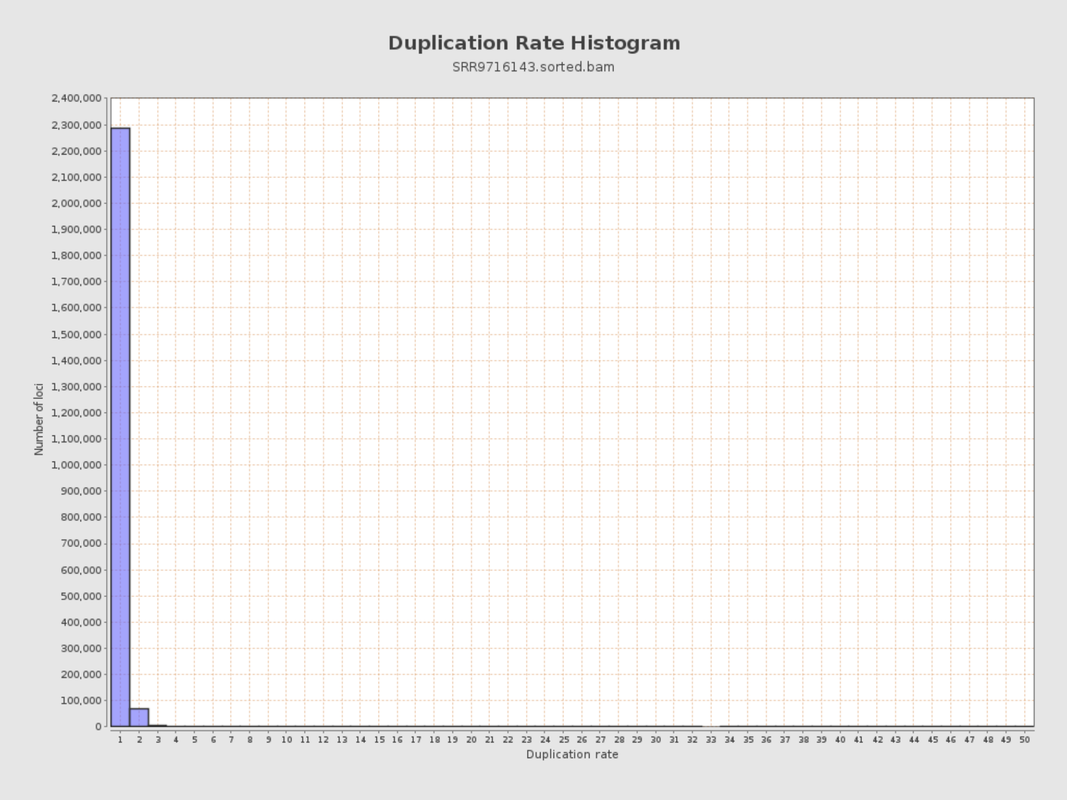
5. Results : Coverage Histogram (0-50X)



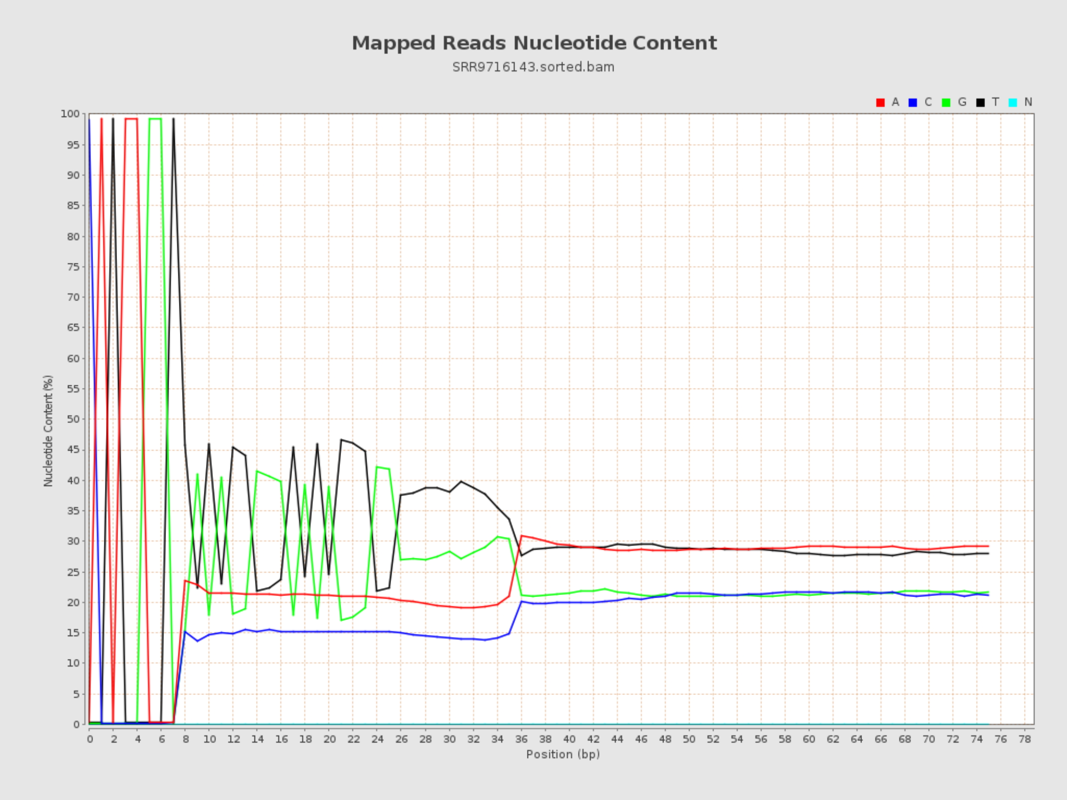
6. Results : Genome Fraction Coverage



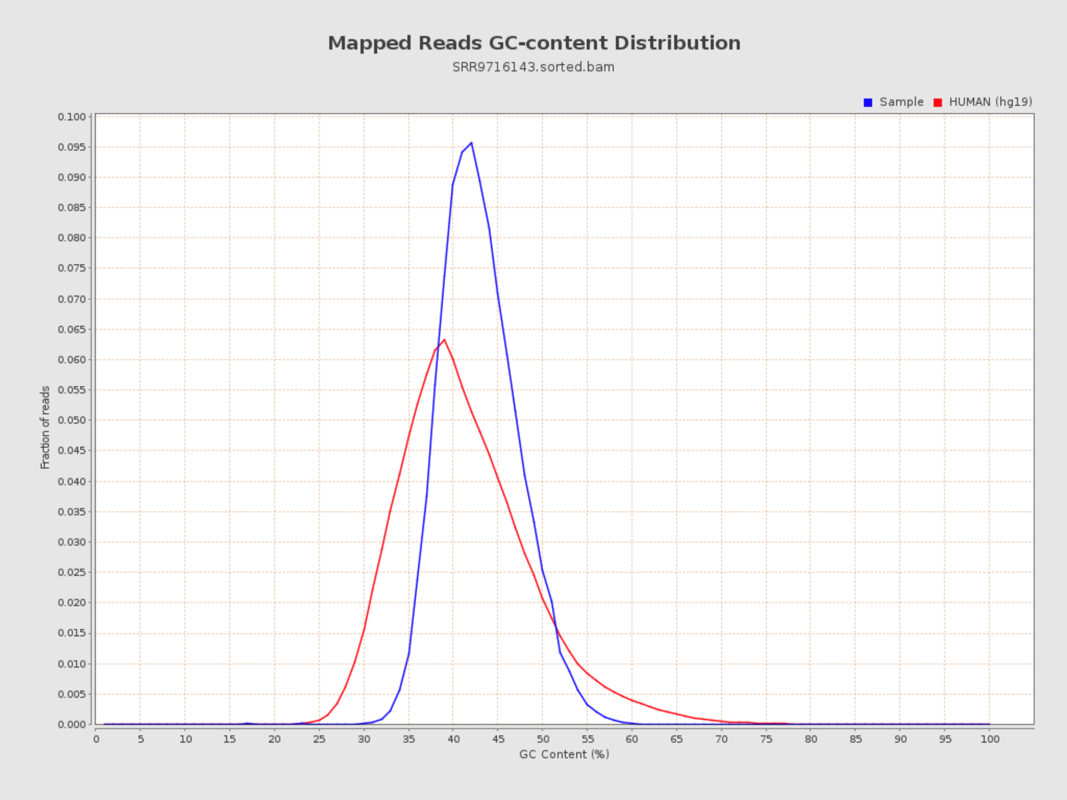
7. Results : Duplication Rate Histogram



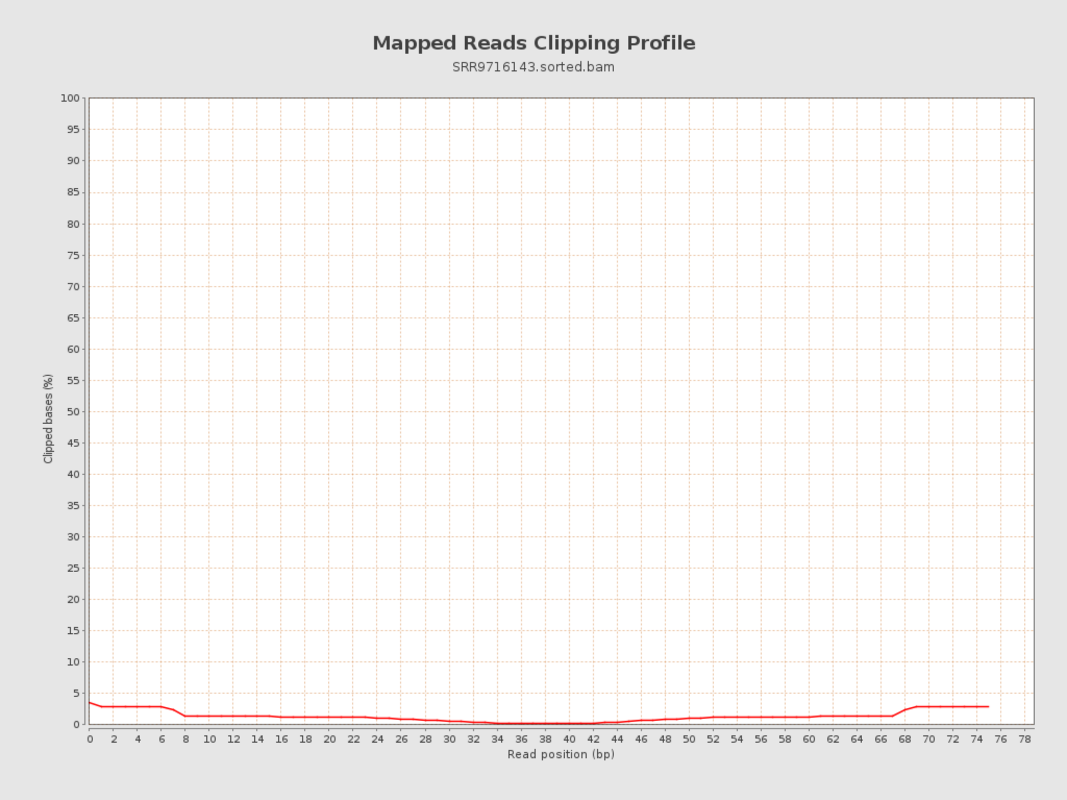
8. Results : Mapped Reads Nucleotide Content



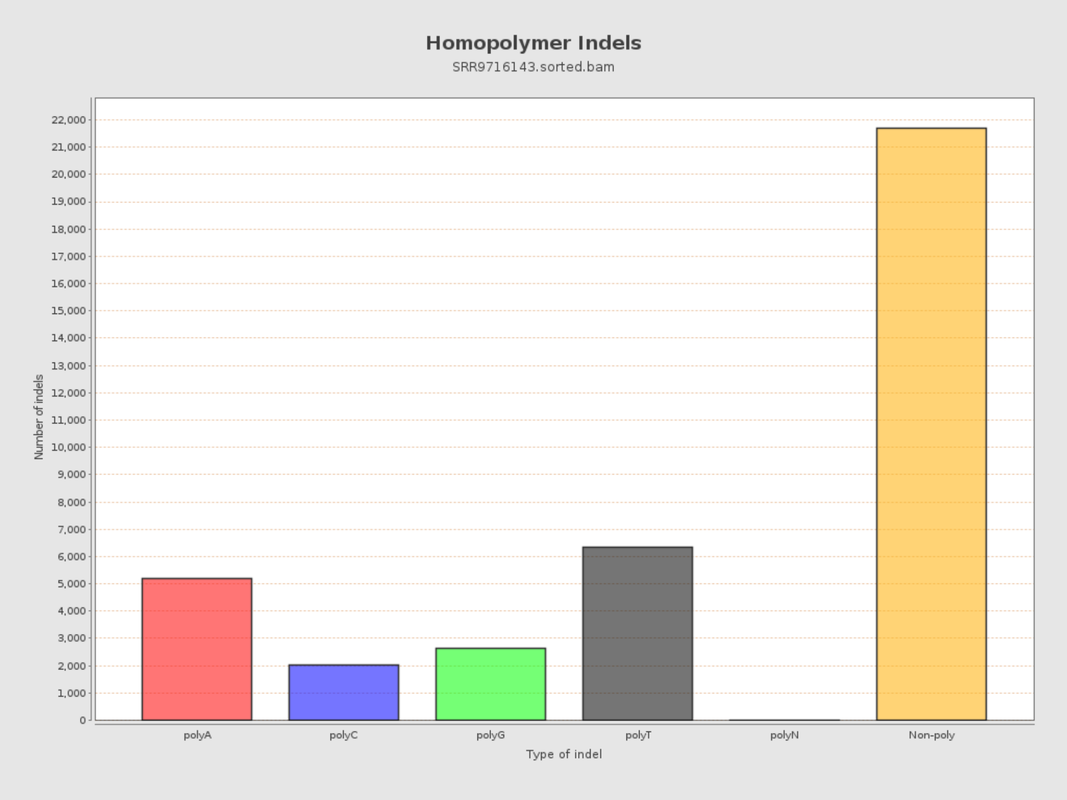
9. Results : Mapped Reads GC-content Distribution



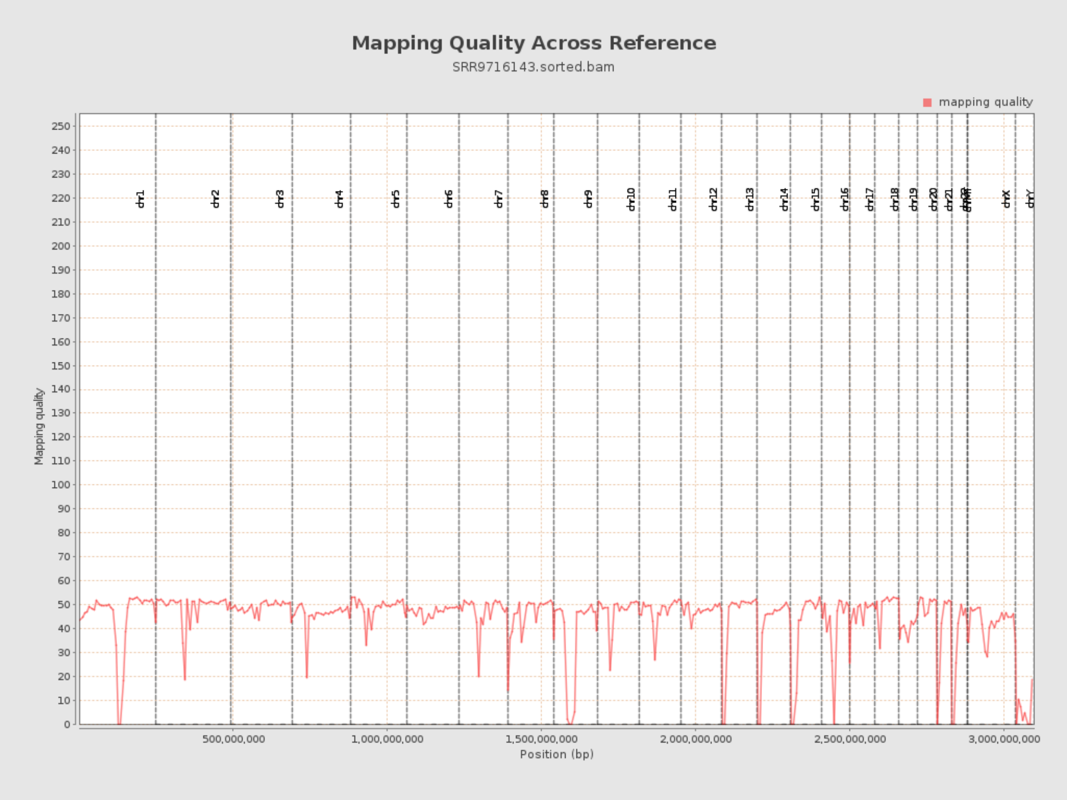
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram