Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:48:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716744.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_SRR9716744 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716744.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:48:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716744.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	924,802
Mapped reads	718,302 / 77.67%
Unmapped reads	206,500 / 22.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,012 / 0.11%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	46,100 / 4.98%
Duplication rate	5.72%
Clipped reads	717,942 / 77.63%

2.2. ACGT Content

Number/percentage of A's	7,737,070 / 20.24%
Number/percentage of C's	6,485,462 / 16.97%
Number/percentage of T's	12,975,342 / 33.95%
Number/percentage of G's	11,022,190 / 28.84%
Number/percentage of N's	739 / 0%
GC Percentage	45.81%

2.3. Coverage

Mean	0.0123

Standard Deviation	0.1365

2.4. Mapping Quality

Mean Mapping Quality	43.27

2.5. Mismatches and indels

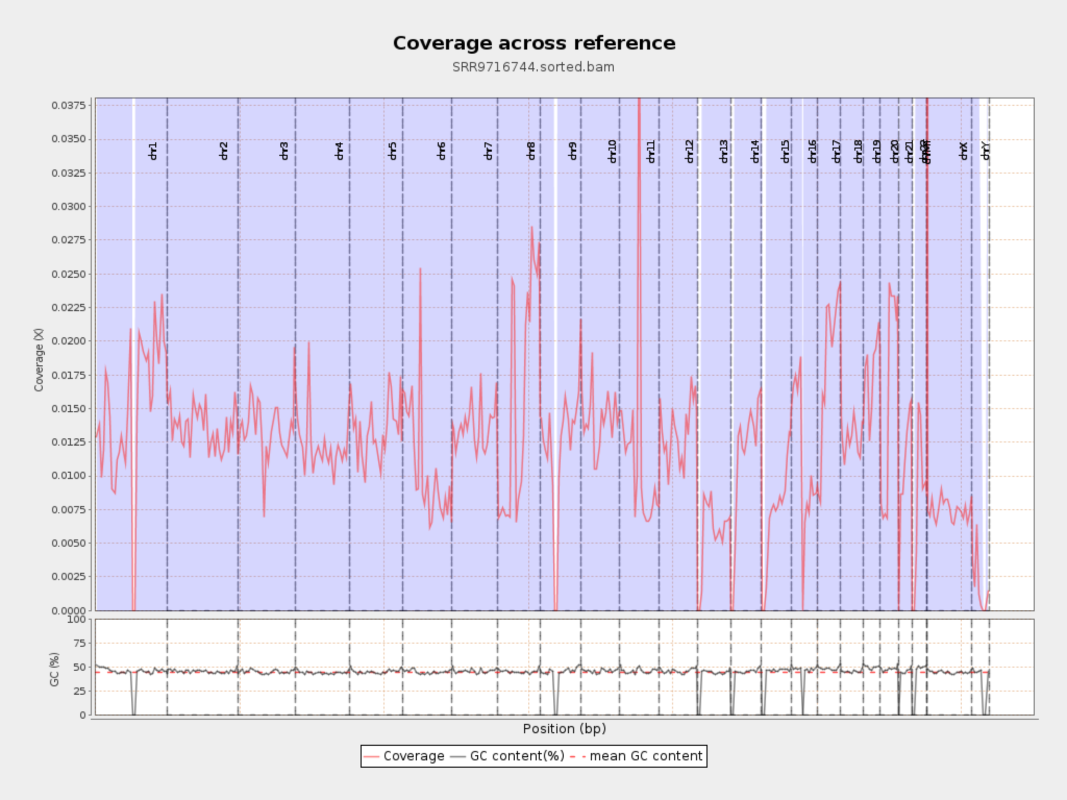
General error rate	0.67%
Mismatches	251,453
Insertions	2,337
Mapped reads with at least one insertion	0.32%
Deletions	5,584
Mapped reads with at least one deletion	0.77%
Homopolymer indels	39.84%

2.6. Chromosome stats

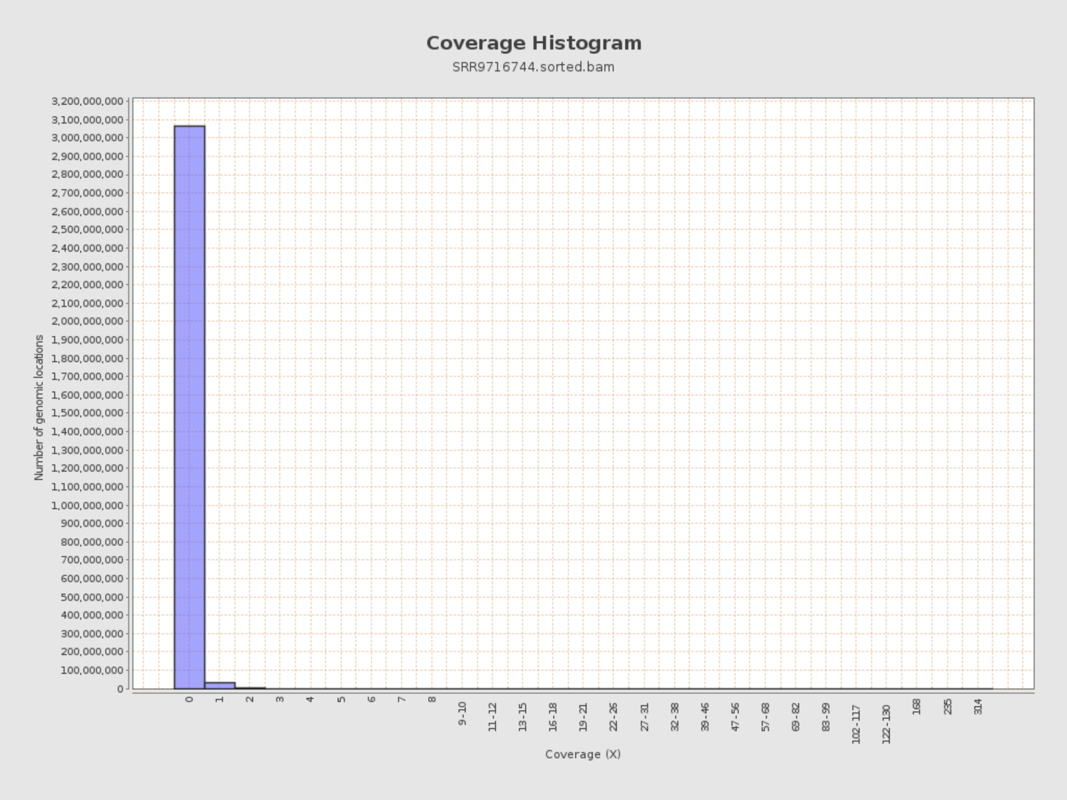
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3710664	0.0149	0.1637
chr2	243199373	3318623	0.0136	0.1802
chr3	198022430	2647251	0.0134	0.1289
chr4	191154276	2355129	0.0123	0.1273
chr5	180915260	2439194	0.0135	0.129
chr6	171115067	1847470	0.0108	0.1289
chr7	159138663	2188750	0.0138	0.1426

chr8	146364022	2314154	0.0158	0.1445
chr9	141213431	1678610	0.0119	0.1292
chr10	135534747	1930793	0.0142	0.1465
chr11	135006516	1652234	0.0122	0.1324
chr12	133851895	1774079	0.0133	0.1297
chr13	115169878	652369	0.0057	0.0842
chr14	107349540	1209780	0.0113	0.1194
chr15	102531392	727172	0.0071	0.0942
chr16	90354753	992358	0.011	0.1229
chr17	81195210	1494145	0.0184	0.158
chr18	78077248	996813	0.0128	0.1395
chr19	59128983	1043751	0.0177	0.1735
chr20	63025520	997044	0.0158	0.147
chr21	48129895	518567	0.0108	0.1195
chr22	51304566	425935	0.0083	0.1053
chrMT	16571	55643	3.3579	3.1707
chrX	155270560	1153850	0.0074	0.0988
chrY	59373566	105851	0.0018	0.0579

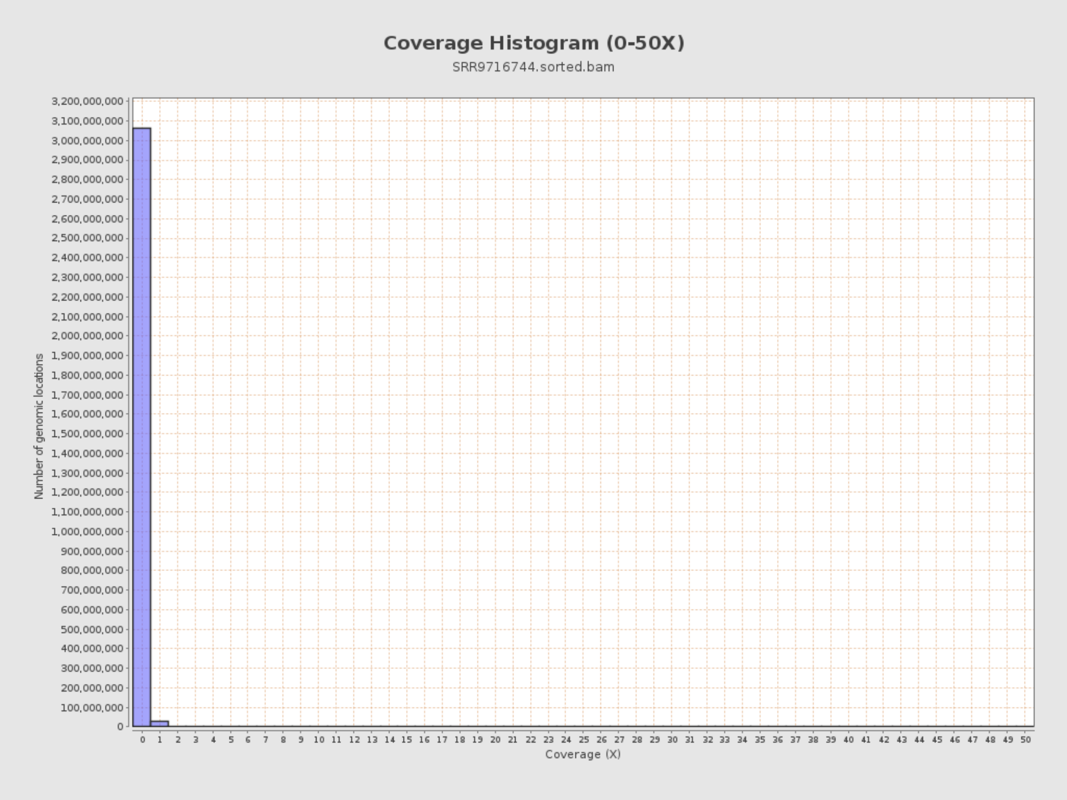
3. Results : Coverage across reference



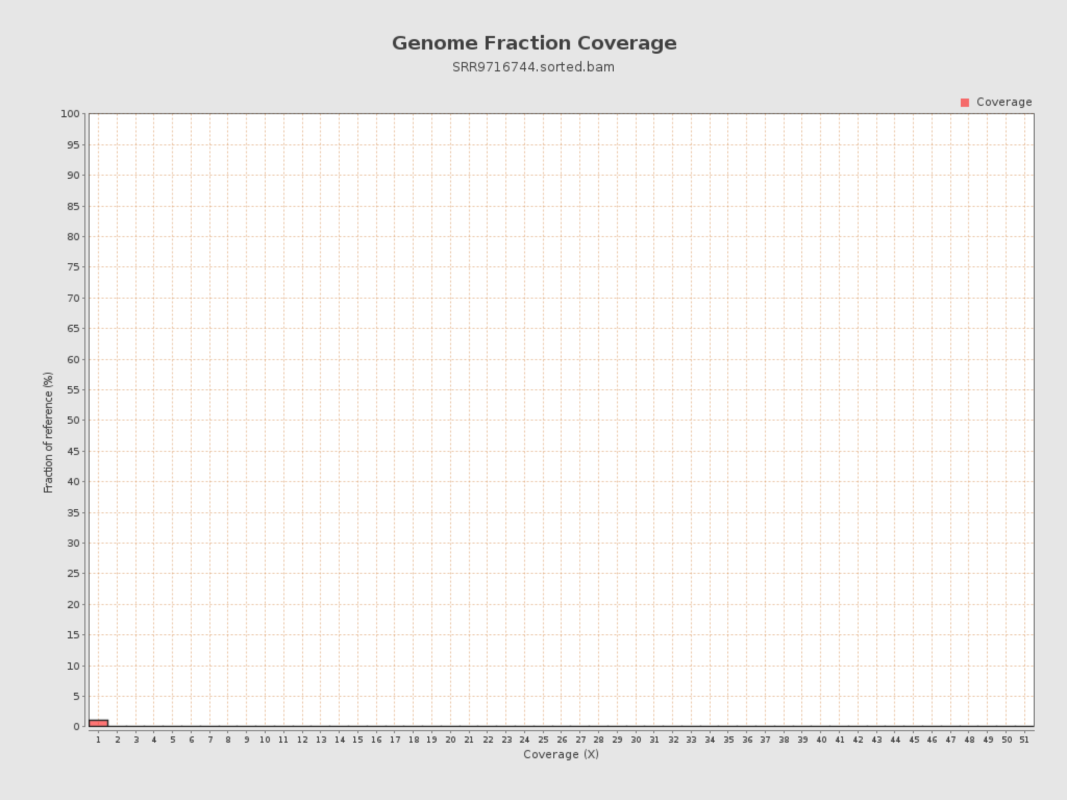
4. Results : Coverage Histogram



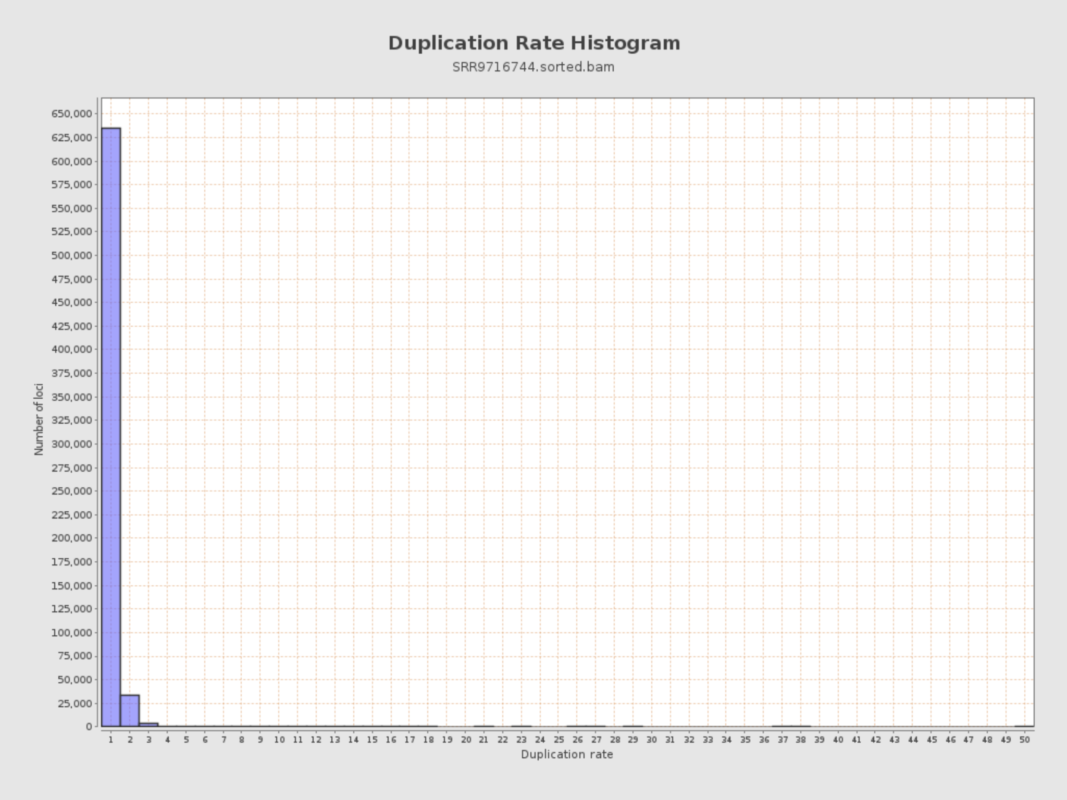
5. Results : Coverage Histogram (0-50X)



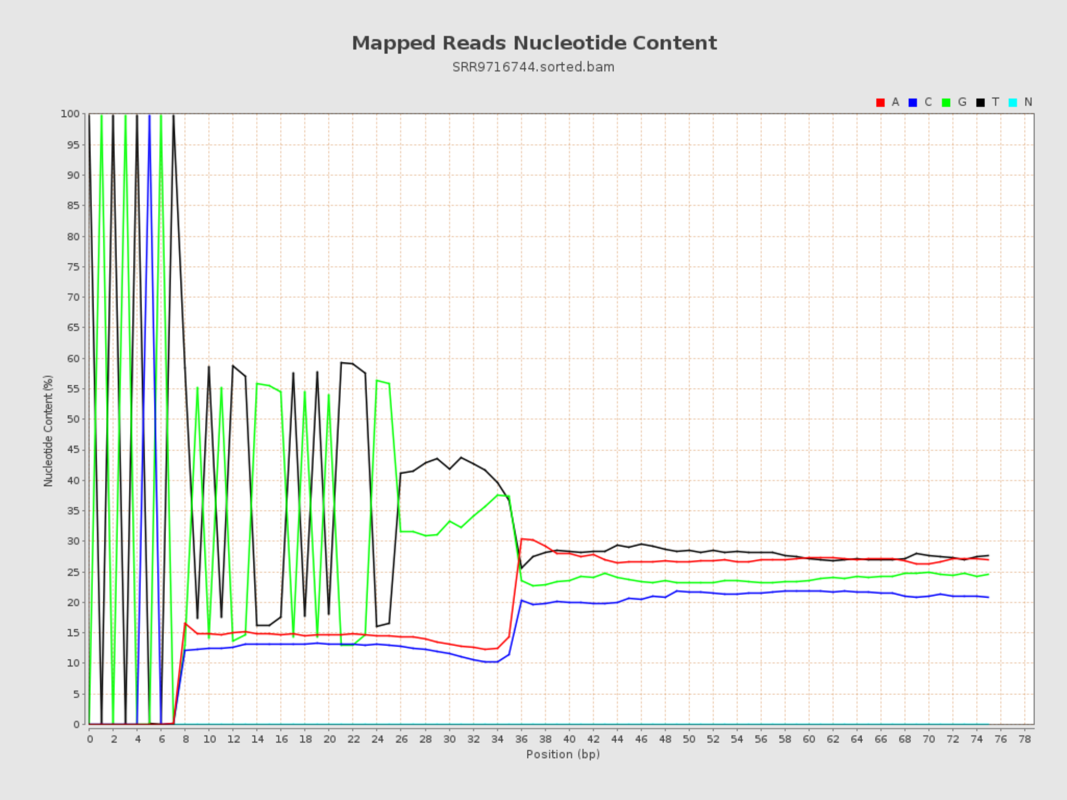
6. Results : Genome Fraction Coverage



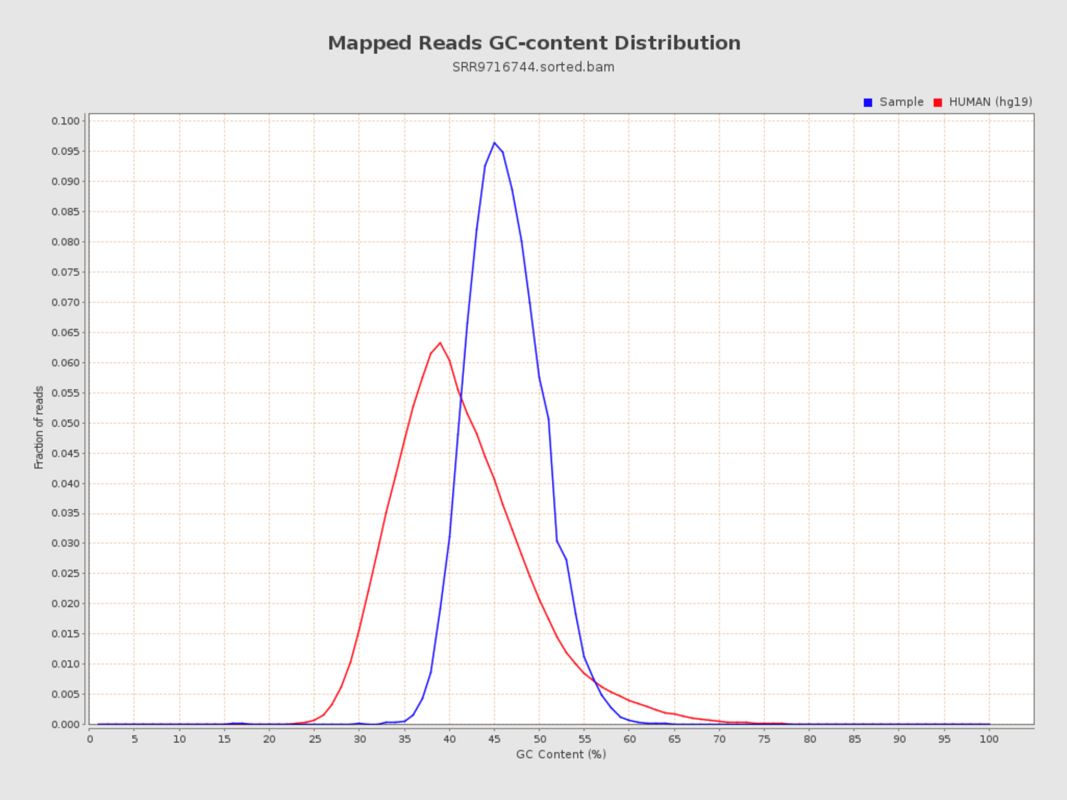
7. Results : Duplication Rate Histogram



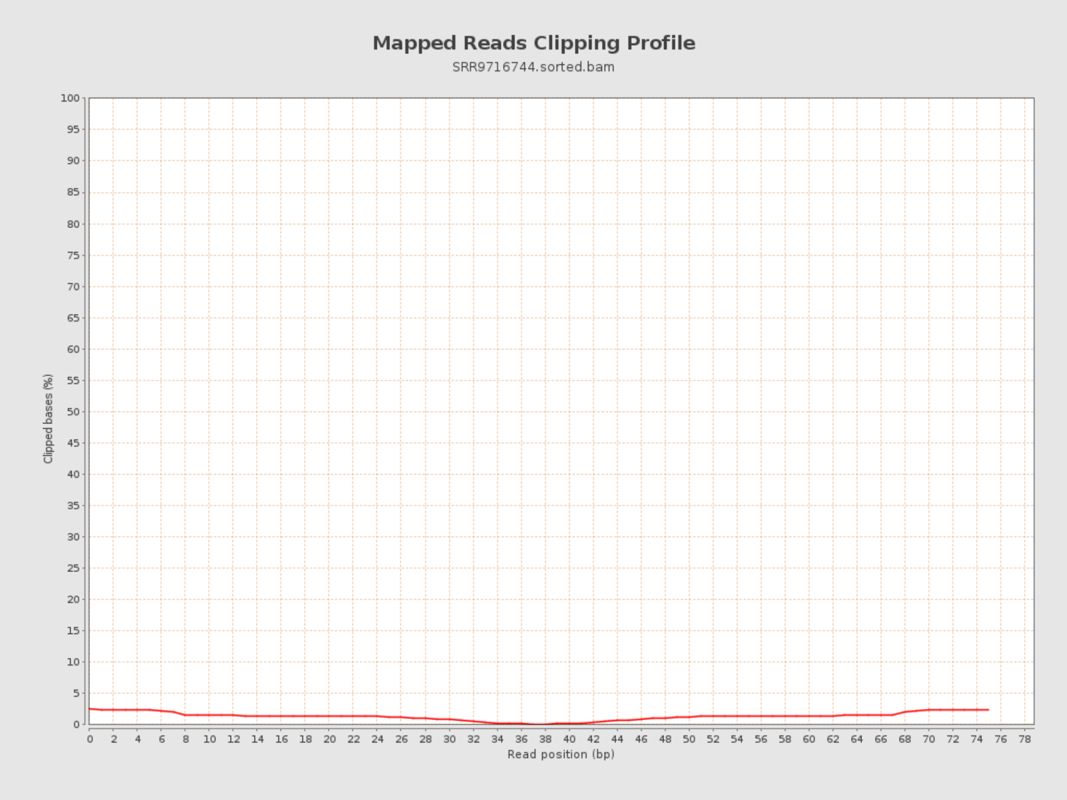
8. Results : Mapped Reads Nucleotide Content



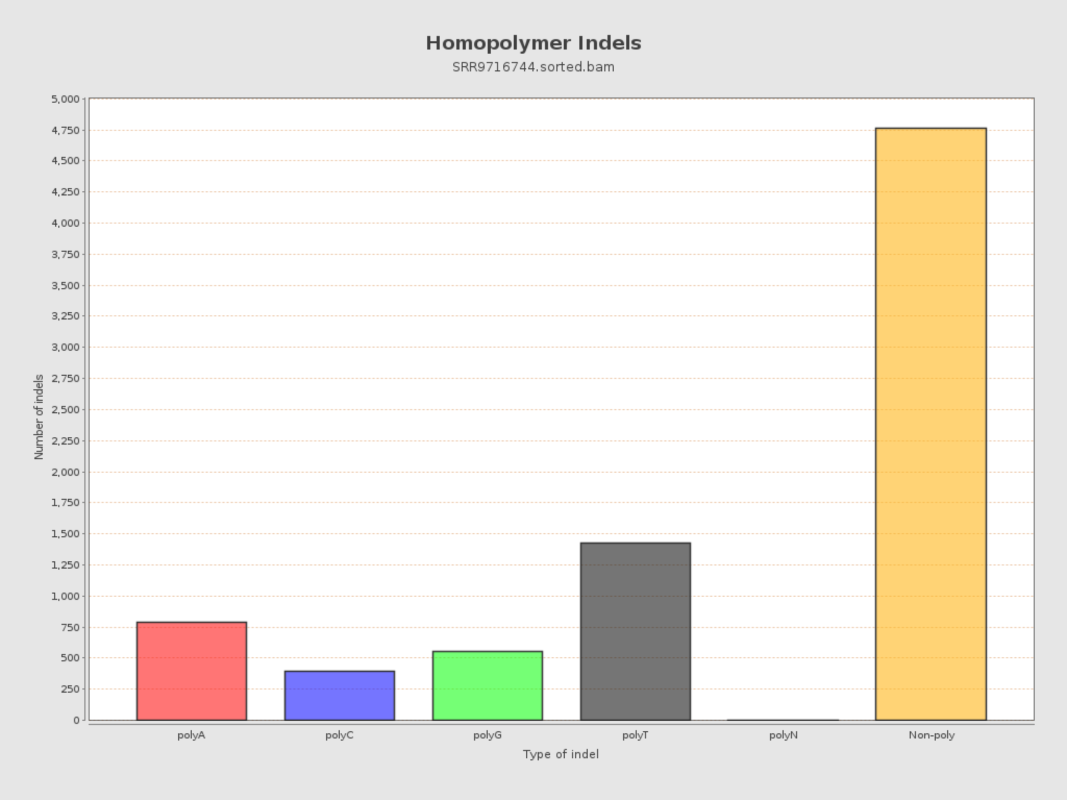
9. Results : Mapped Reads GC-content Distribution



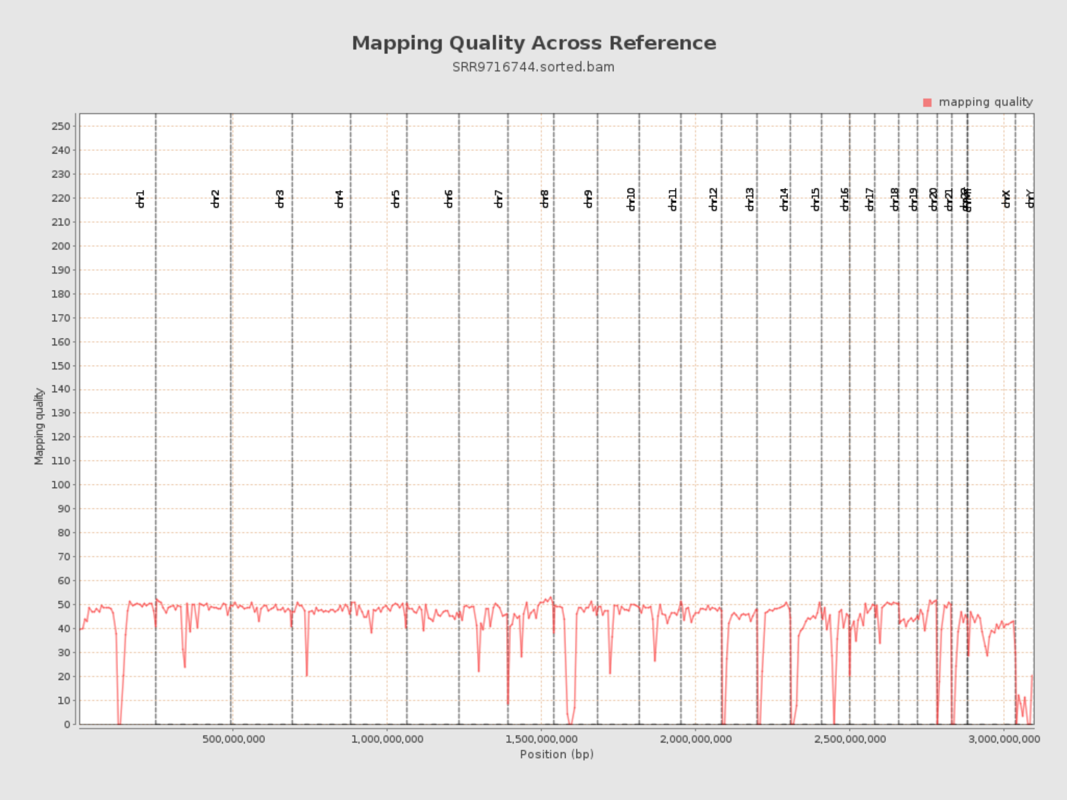
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram