Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 04:01:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617416.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_SRR617416 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617416_1.fastq.gz SRR617416_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 04:01:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617416.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,550,050 / 92.34%
Unmapped reads	2,449,950 / 7.66%
Mapped paired reads	29,550,050 / 92.34%
Mapped reads, first in pair	14,985,327 / 46.83%
Mapped reads, second in pair	14,564,723 / 45.51%
Mapped reads, both in pair	28,869,148 / 90.22%
Mapped reads, singletons	680,902 / 2.13%
Secondary alignments	0
Supplementary alignments	467,402 / 1.46%
Read min/max/mean length	30 / 100 / 100.6
Duplicated reads (estimated)	1,364,152 / 4.26%
Duplication rate	4.14%
Clipped reads	3,294,099 / 10.29%

2.2. ACGT Content

Number/percentage of A's	865,173,619 / 29.8%
Number/percentage of C's	584,107,199 / 20.12%
Number/percentage of T's	858,563,626 / 29.57%
Number/percentage of G's	594,844,626 / 20.49%
Number/percentage of N's	619,449 / 0.02%

GC Percentage	40.61%

2.3. Coverage

Mean	0.9381
Standard Deviation	2.8841

2.4. Mapping Quality

Mean Mapping Quality	53.84

2.5. Insert size

Mean	60,127.06
Standard Deviation	2,359,178.27
P25/Median/P75	172 / 213 / 277

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	30,941,021
Insertions	248,922
Mapped reads with at least one insertion	0.83%
Deletions	293,324
Mapped reads with at least one deletion	0.97%
Homopolymer indels	44.37%

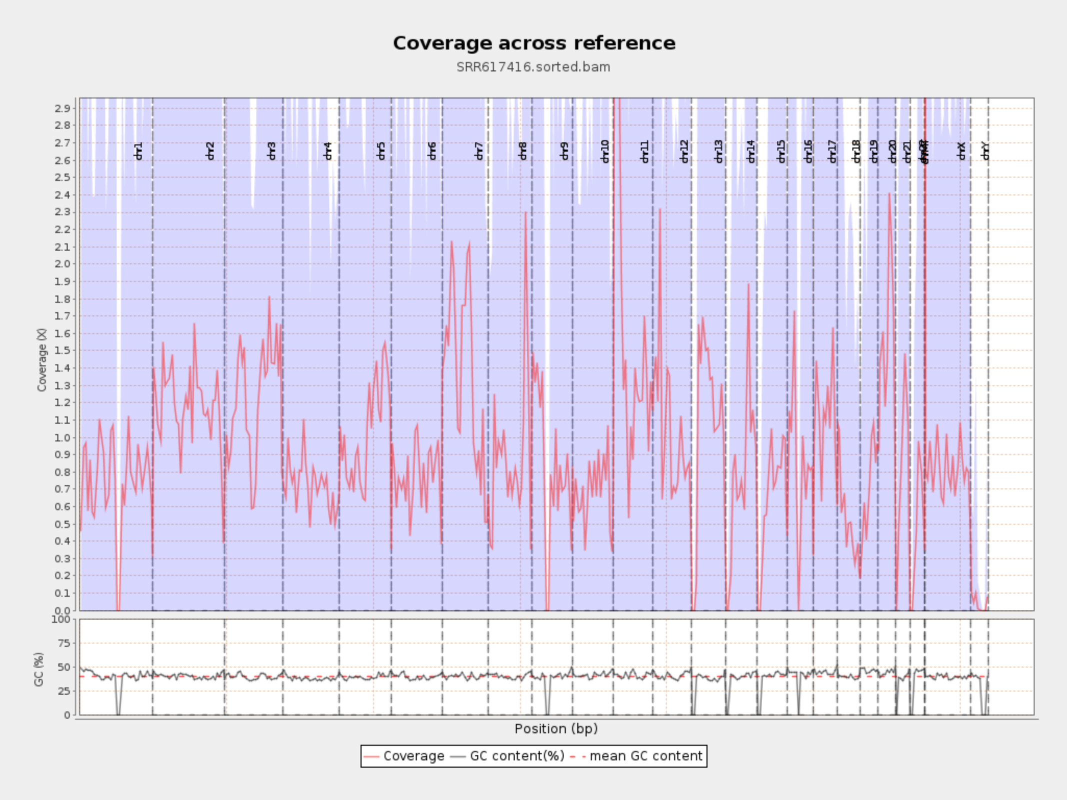
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

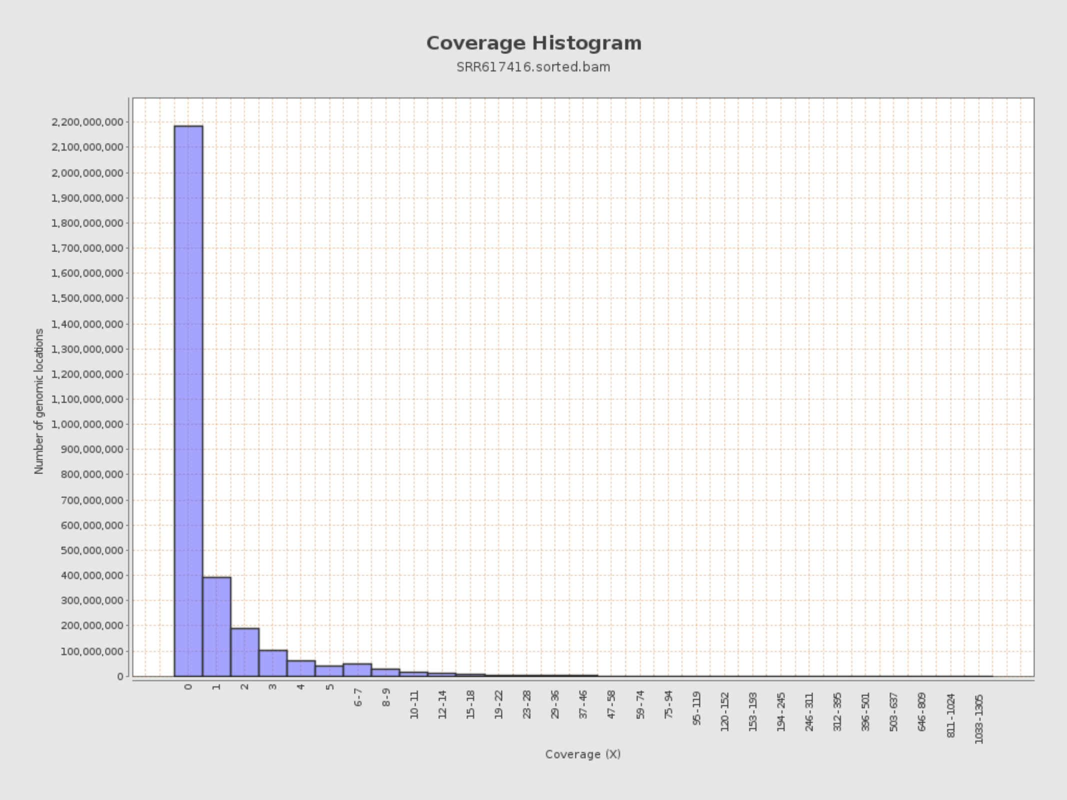
		bases	**coverage**	**deviation**
chr1	249250621	186843954	0.7496	2.691
chr2	243199373	289315147	1.1896	3.0575
chr3	198022430	245047104	1.2375	3.3729
chr4	191154276	139284886	0.7287	2.2387
chr5	180915260	185383987	1.0247	2.8164
chr6	171115067	132991641	0.7772	2.563
chr7	159138663	217218843	1.365	3.1889
chr8	146364022	128574351	0.8785	3.2141
chr9	141213431	115773474	0.8198	2.5626
chr10	135534747	93132442	0.6871	2.383
chr11	135006516	215925884	1.5994	3.7843
chr12	133851895	138293215	1.0332	2.7517
chr13	115169878	125913975	1.0933	2.7268
chr14	107349540	84253363	0.7849	2.8554
chr15	102531392	66762125	0.6511	2.3426
chr16	90354753	73330877	0.8116	3.2677
chr17	81195210	90032772	1.1088	3.6218
chr18	78077248	41414686	0.5304	1.949
chr19	59128983	41880713	0.7083	2.325
chr20	63025520	99518713	1.579	4.6843
chr21	48129895	39643147	0.8237	2.4778
chr22	51304566	23733091	0.4626	2.0741
chrMT	16571	183330	11.0633	5.2538
chrX	155270560	127180418	0.8191	2.5205

chrY	59373566	2336862	0.0394	0.6014

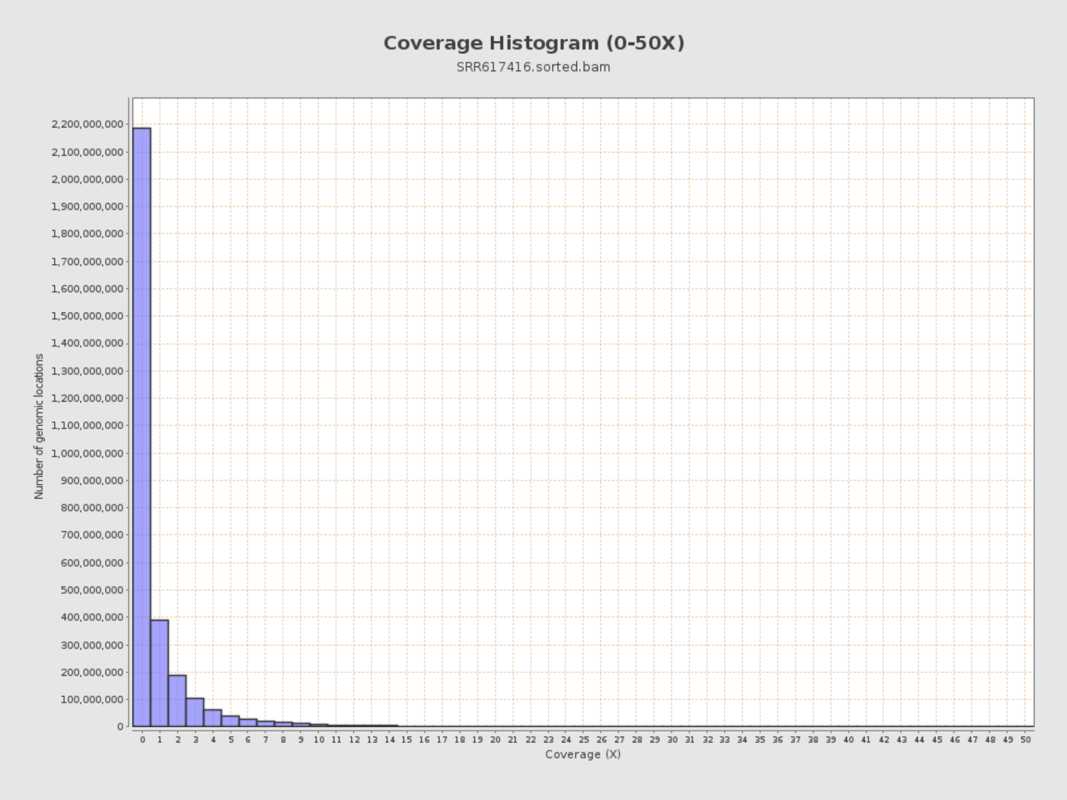
3. Results : Coverage across reference



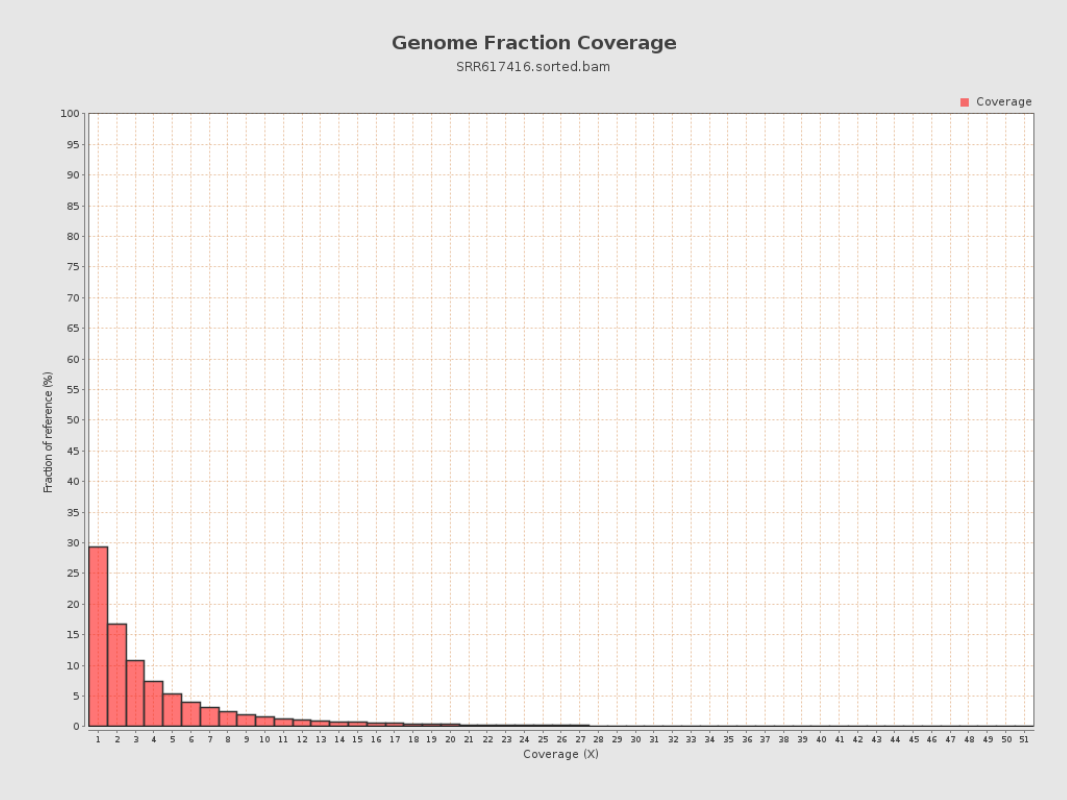
4. Results : Coverage Histogram



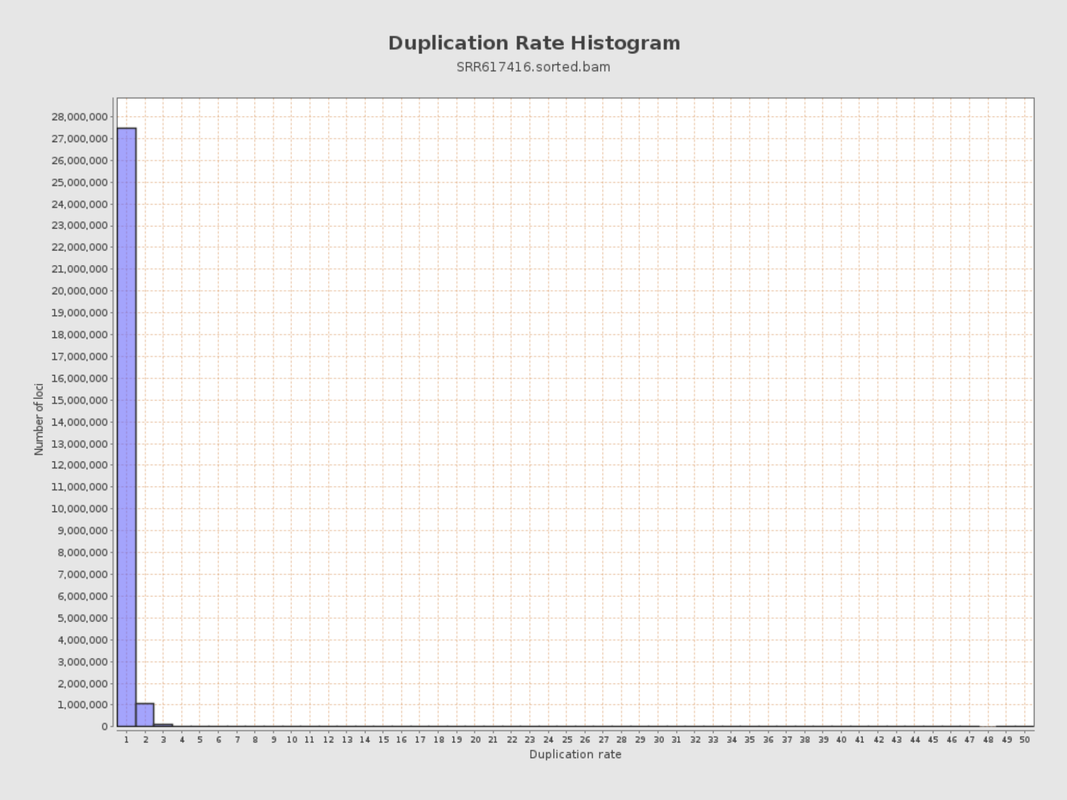
5. Results : Coverage Histogram (0-50X)



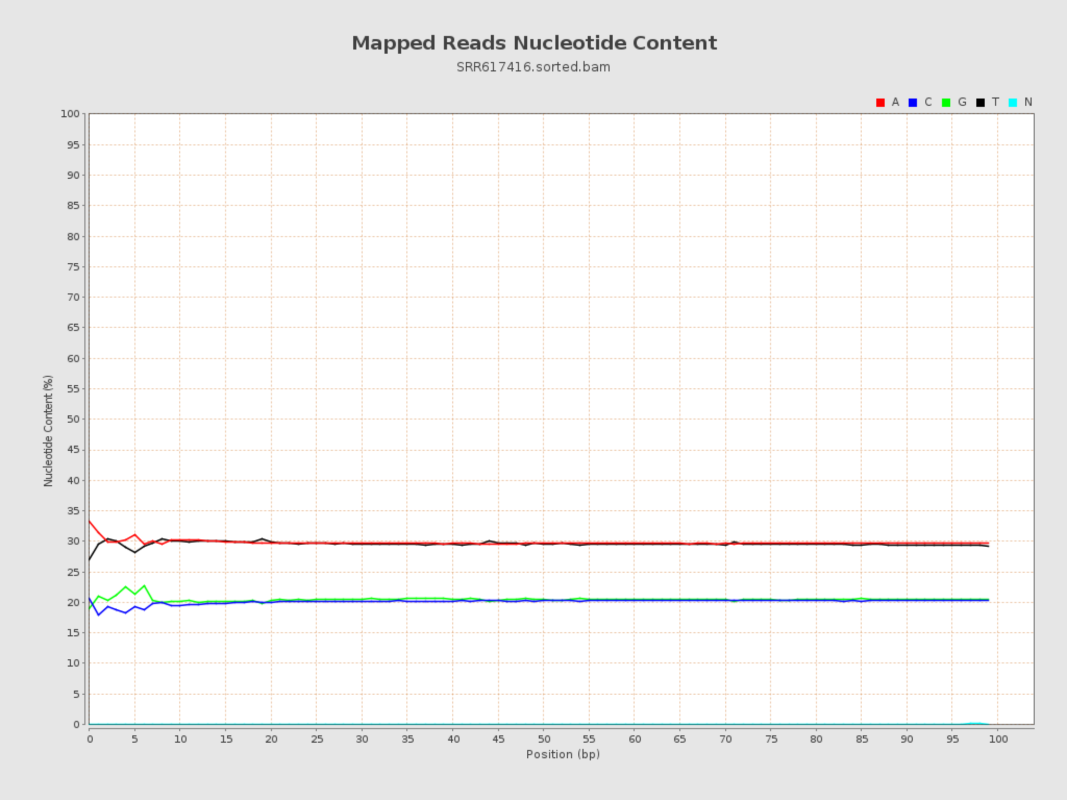
6. Results : Genome Fraction Coverage



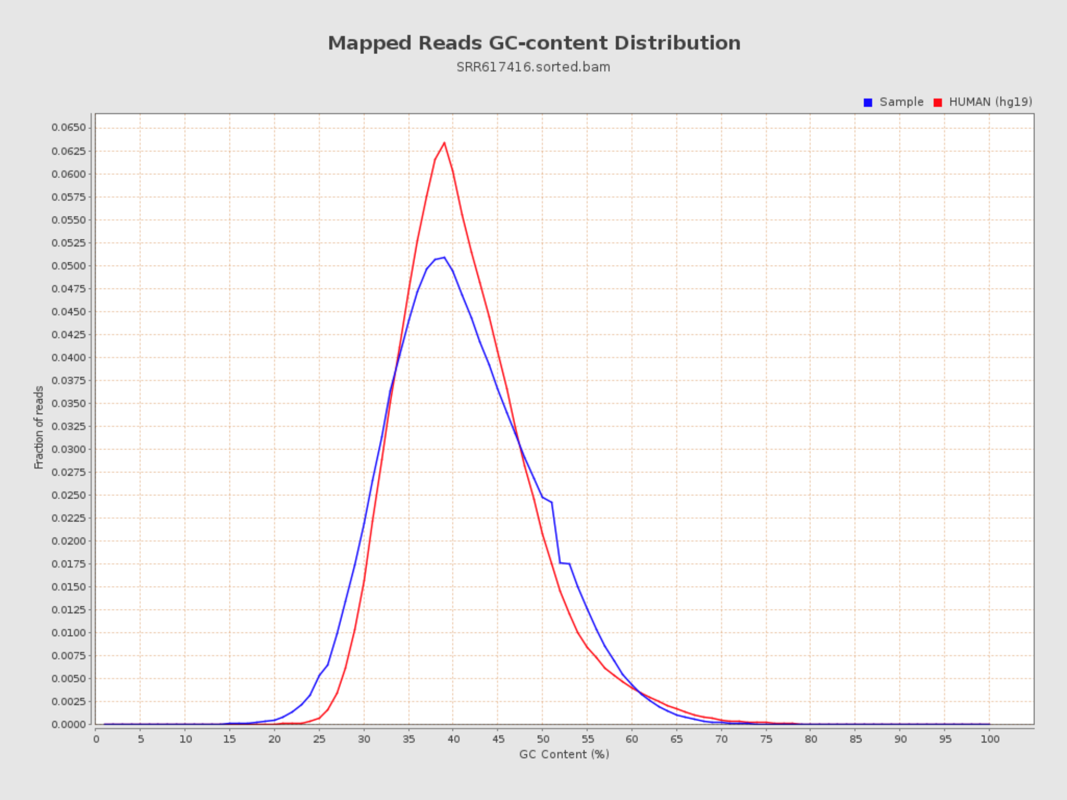
7. Results : Duplication Rate Histogram



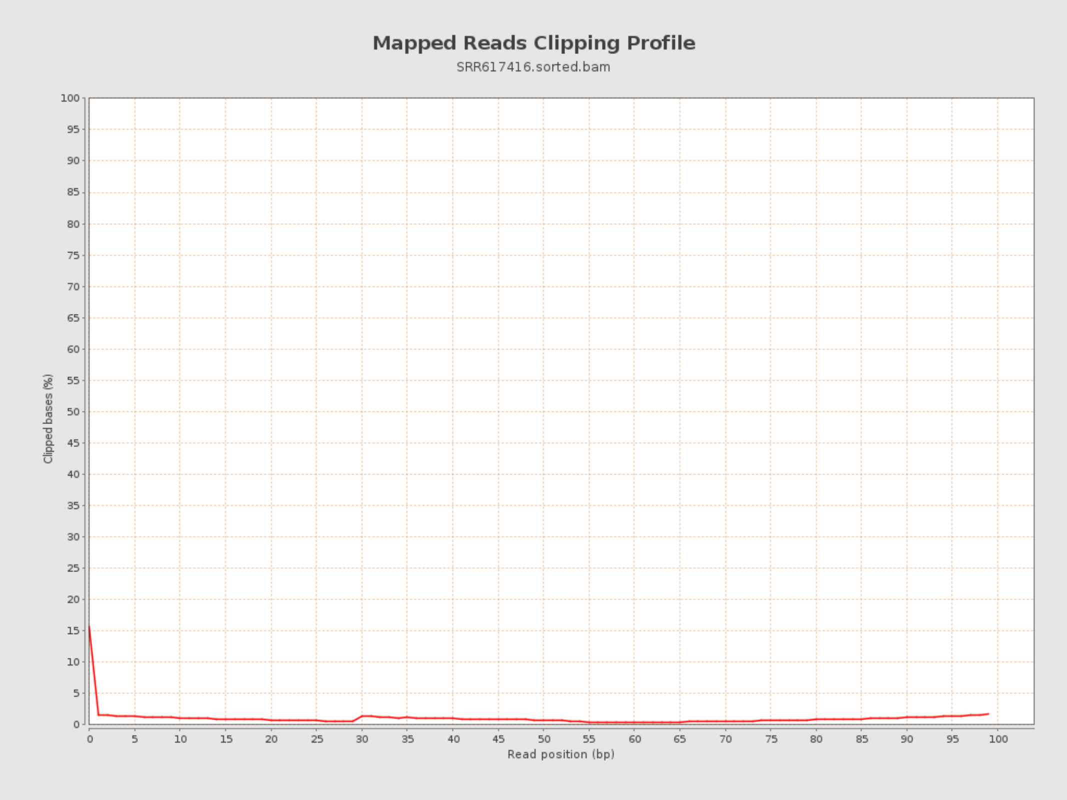
8. Results : Mapped Reads Nucleotide Content



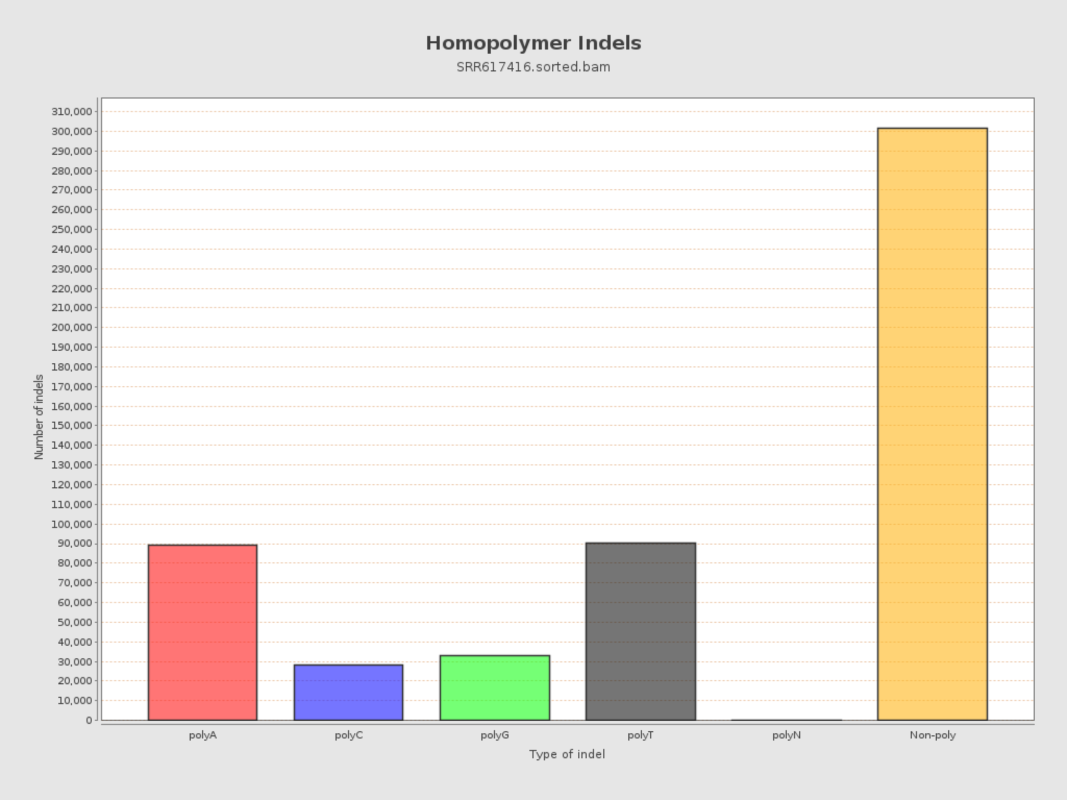
9. Results : Mapped Reads GC-content Distribution



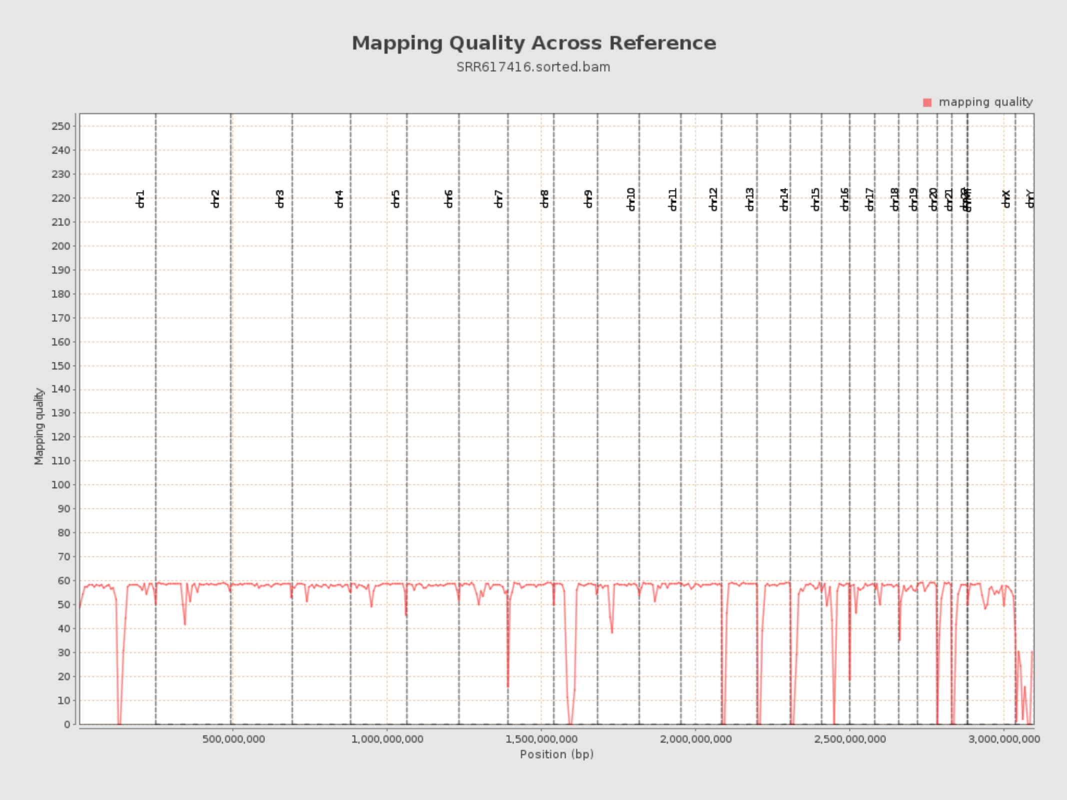
10. Results : Mapped Reads Clipping Profile



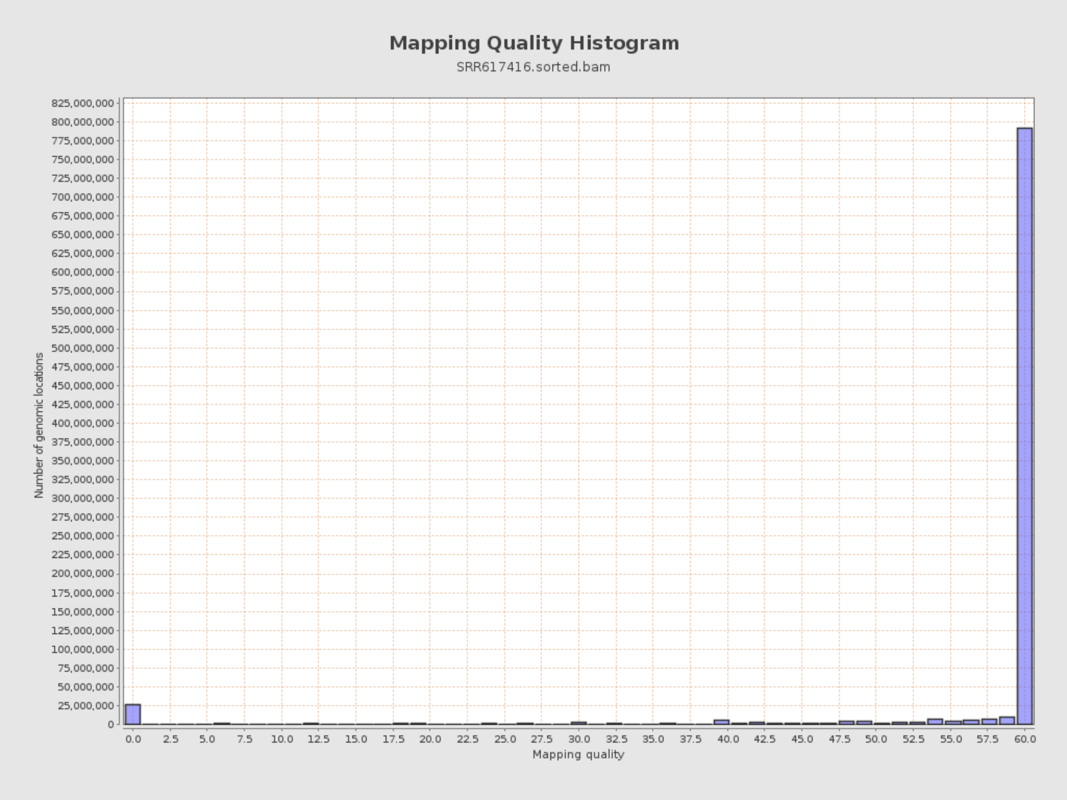
11. Results : Homopolymer Indels



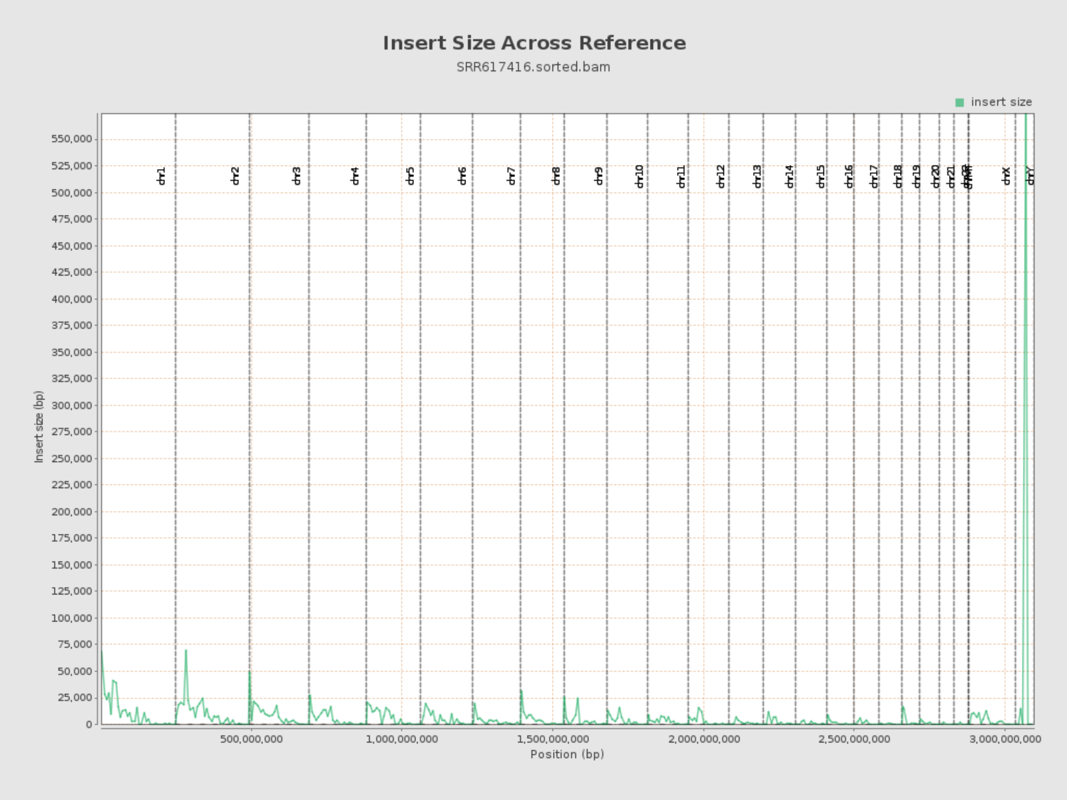
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram