Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 22:01:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617407.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_SRR617407 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617407_1.fastq.gz SRR617407_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 22:01:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617407.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,751,592
Mapped reads	17,556,503 / 77.17%
Unmapped reads	5,195,089 / 22.83%
Mapped paired reads	17,556,503 / 77.17%
Mapped reads, first in pair	9,682,134 / 42.56%
Mapped reads, second in pair	7,874,369 / 34.61%
Mapped reads, both in pair	15,540,502 / 68.31%
Mapped reads, singletons	2,016,001 / 8.86%
Secondary alignments	0
Supplementary alignments	241,739 / 1.06%
Read min/max/mean length	30 / 100 / 100.43
Duplicated reads (estimated)	505,292 / 2.22%
Duplication rate	2.62%
Clipped reads	2,816,758 / 12.38%

2.2. ACGT Content

Number/percentage of A's	508,011,106 / 29.9%
Number/percentage of C's	340,345,077 / 20.03%
Number/percentage of T's	502,621,923 / 29.59%
Number/percentage of G's	347,452,710 / 20.45%
Number/percentage of N's	440,155 / 0.03%

GC Percentage	40.49%

2.3. Coverage

Mean	0.5489
Standard Deviation	1.7429

2.4. Mapping Quality

Mean Mapping Quality	53.11

2.5. Insert size

Mean	58,838.72
Standard Deviation	2,319,329.56
P25/Median/P75	166 / 202 / 257

2.6. Mismatches and indels

General error rate	1.99%
Mismatches	33,506,025
Insertions	149,370
Mapped reads with at least one insertion	0.84%
Deletions	169,873
Mapped reads with at least one deletion	0.95%
Homopolymer indels	42.8%

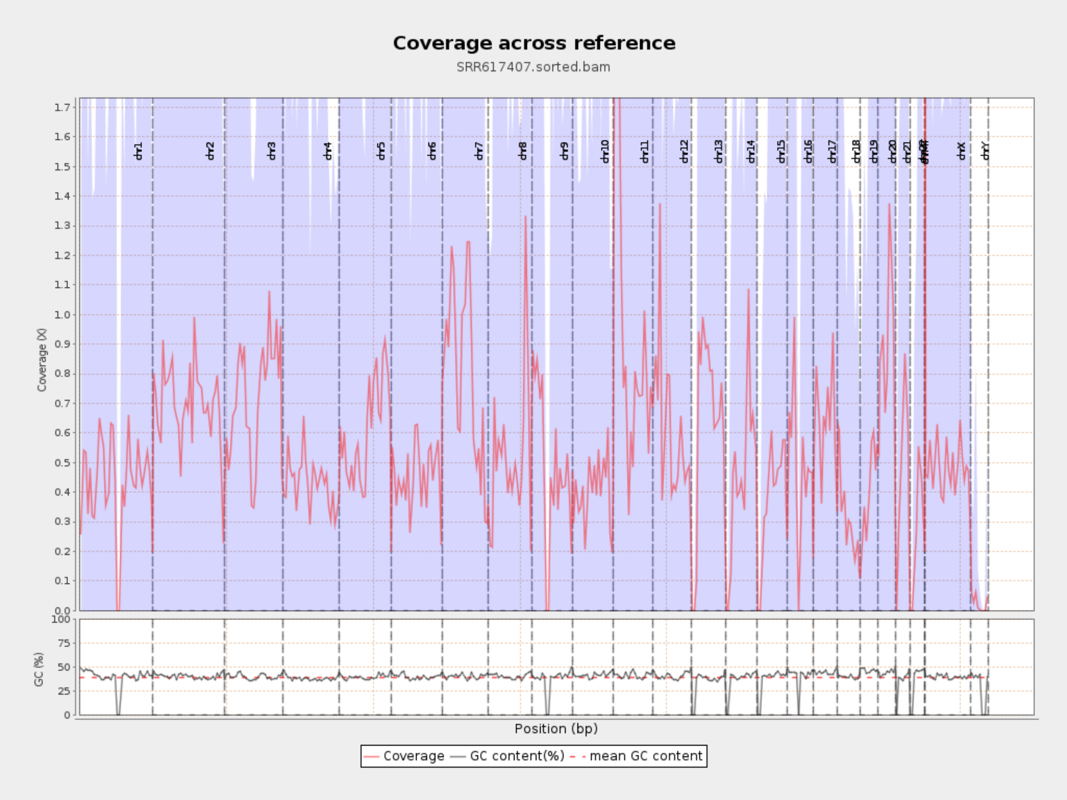
2.7. Chromosome stats

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

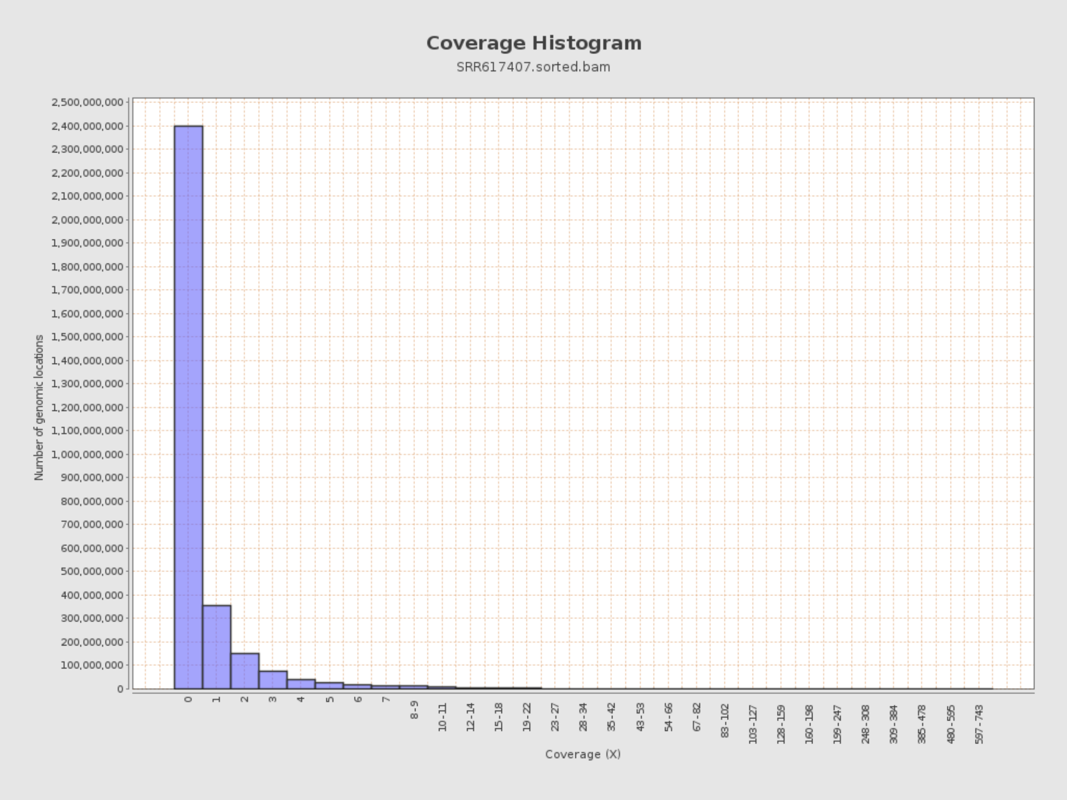
		bases	coverage	deviation
chr1	249250621	109055487	0.4375	1.618
chr2	243199373	169902577	0.6986	1.8858
chr3	198022430	143592531	0.7251	2.0254
chr4	191154276	82892390	0.4336	1.3982
chr5	180915260	109636767	0.606	1.7375
chr6	171115067	78353339	0.4579	1.5658
chr7	159138663	127219287	0.7994	1.9605
chr8	146364022	75278417	0.5143	1.887
chr9	141213431	67986430	0.4814	1.5506
chr10	135534747	54549461	0.4025	1.4399
chr11	135006516	125755519	0.9315	2.2825
chr12	133851895	80867970	0.6042	1.6844
chr13	115169878	74407208	0.6461	1.6877
chr14	107349540	49173305	0.4581	1.7044
chr15	102531392	38713473	0.3776	1.4302
chr16	90354753	42188575	0.4669	1.9296
chr17	81195210	51406103	0.6331	2.1179
chr18	78077248	24536194	0.3143	1.2019
chr19	59128983	23664265	0.4002	1.3615
chr20	63025520	56639979	0.8987	2.7053
chr21	48129895	23301166	0.4841	1.5209
chr22	51304566	13404762	0.2613	1.2161
chrMT	16571	100658	6.0743	3.3899
chrX	155270560	75190412	0.4843	1.5515

chrY	59373566	1431501	0.0241	0.3705

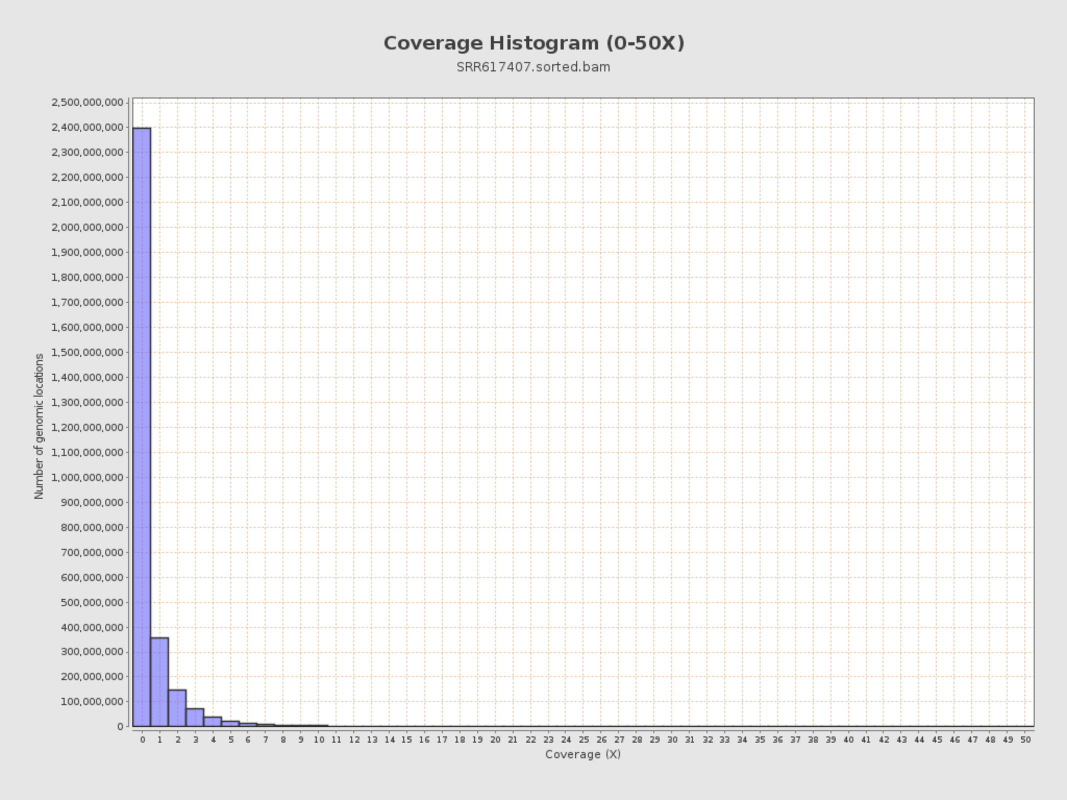
3. Results : Coverage across reference



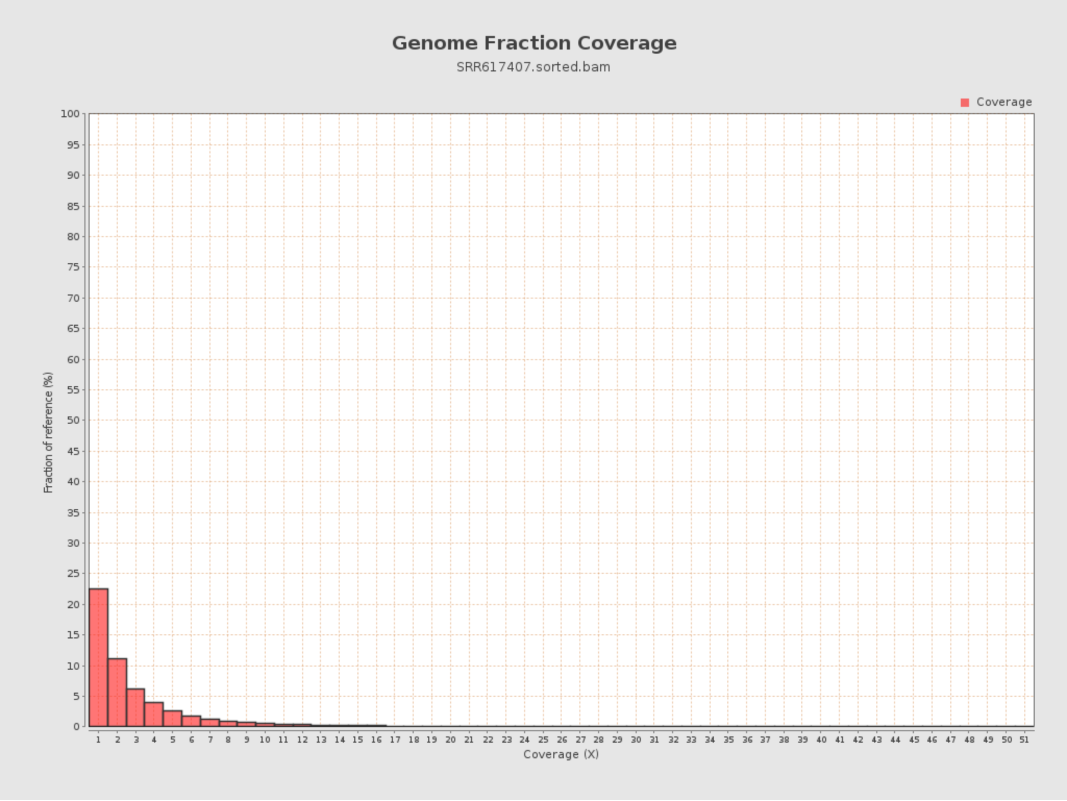
4. Results : Coverage Histogram



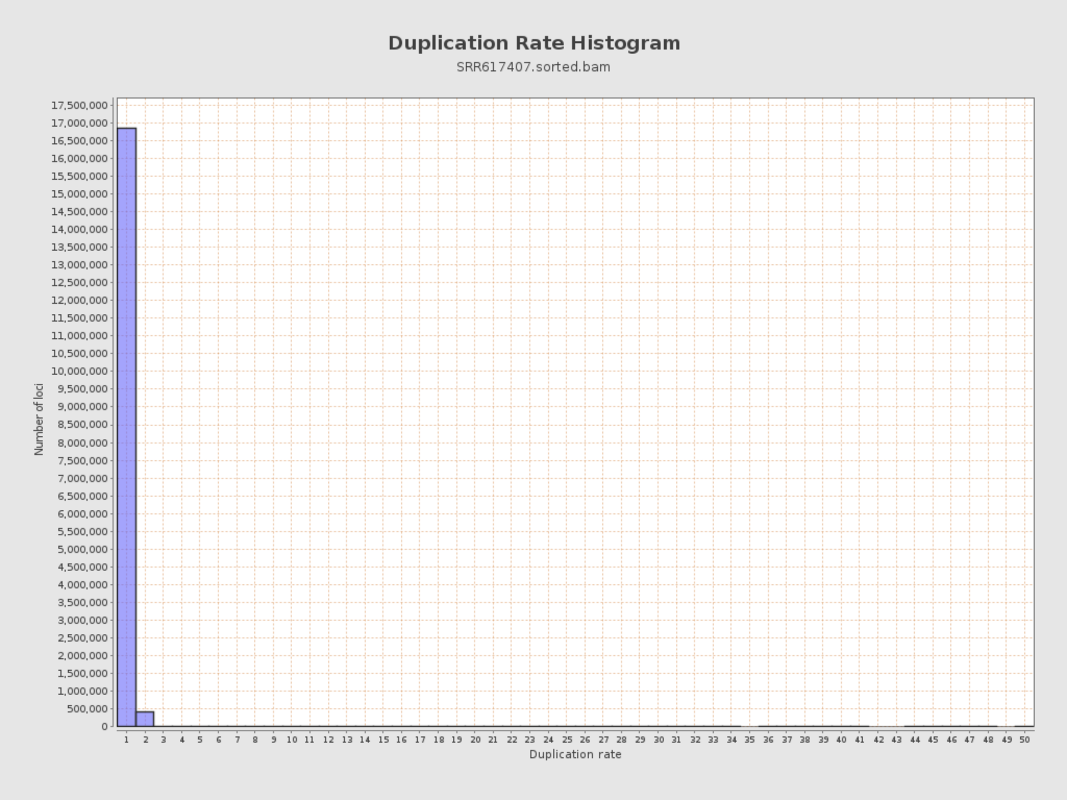
5. Results : Coverage Histogram (0-50X)



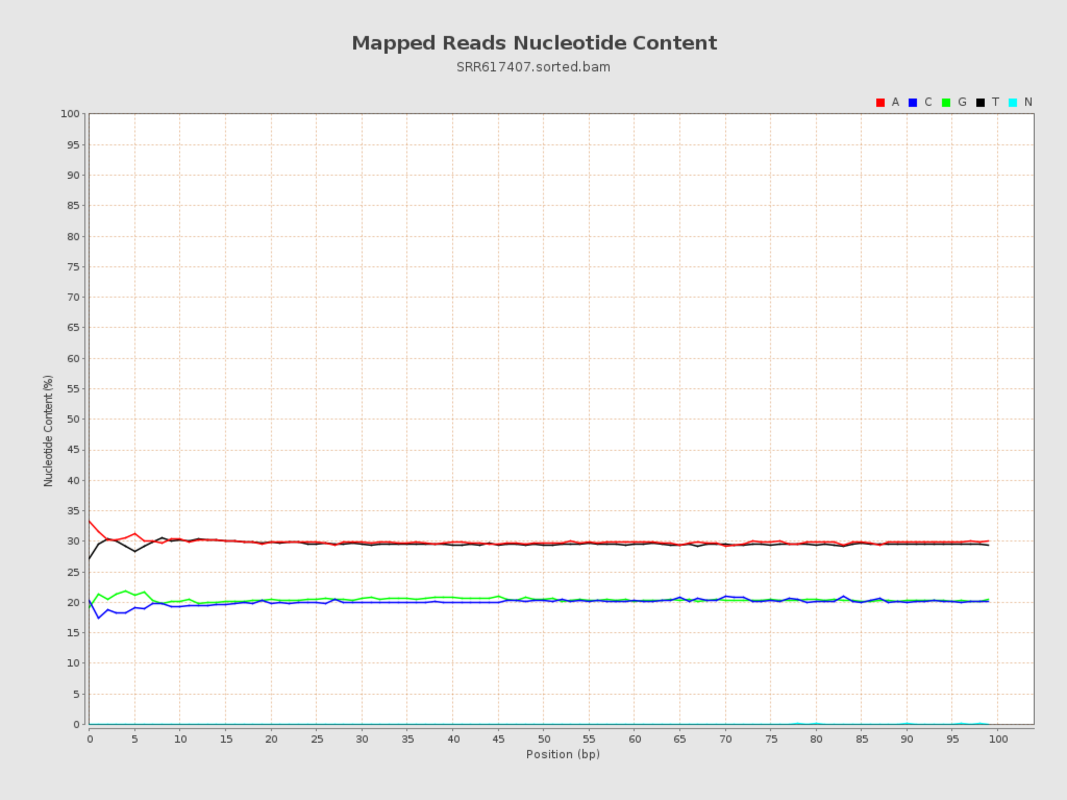
6. Results : Genome Fraction Coverage



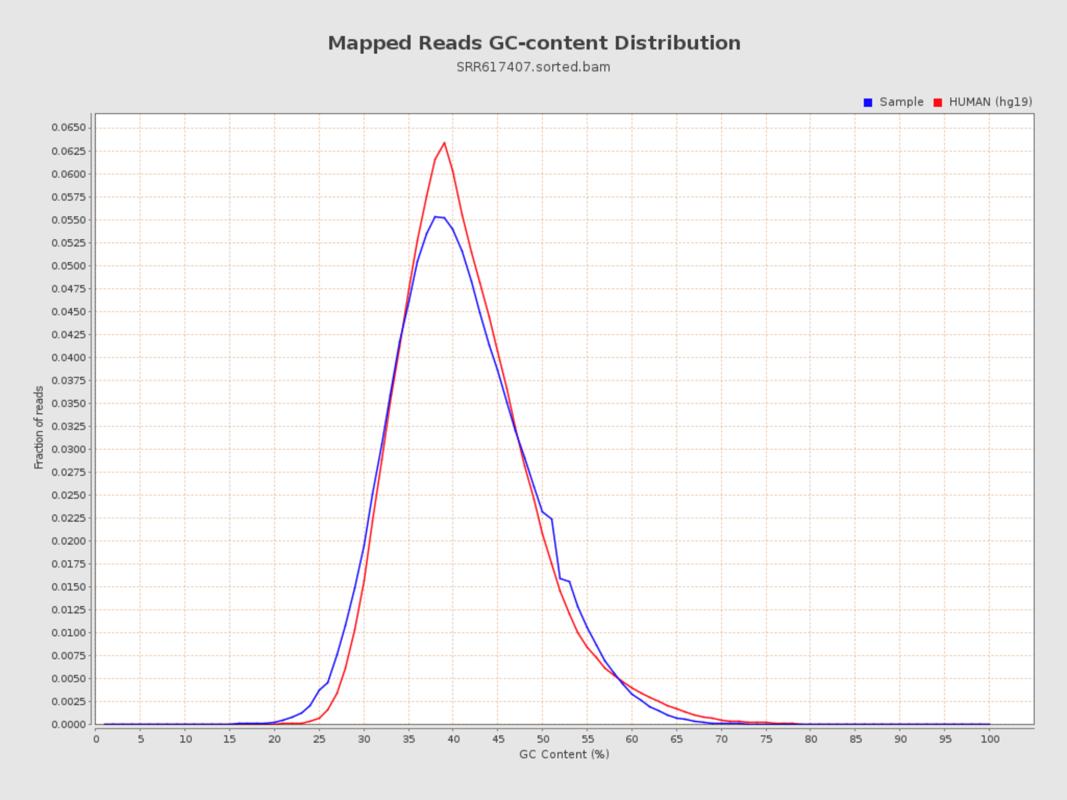
7. Results : Duplication Rate Histogram



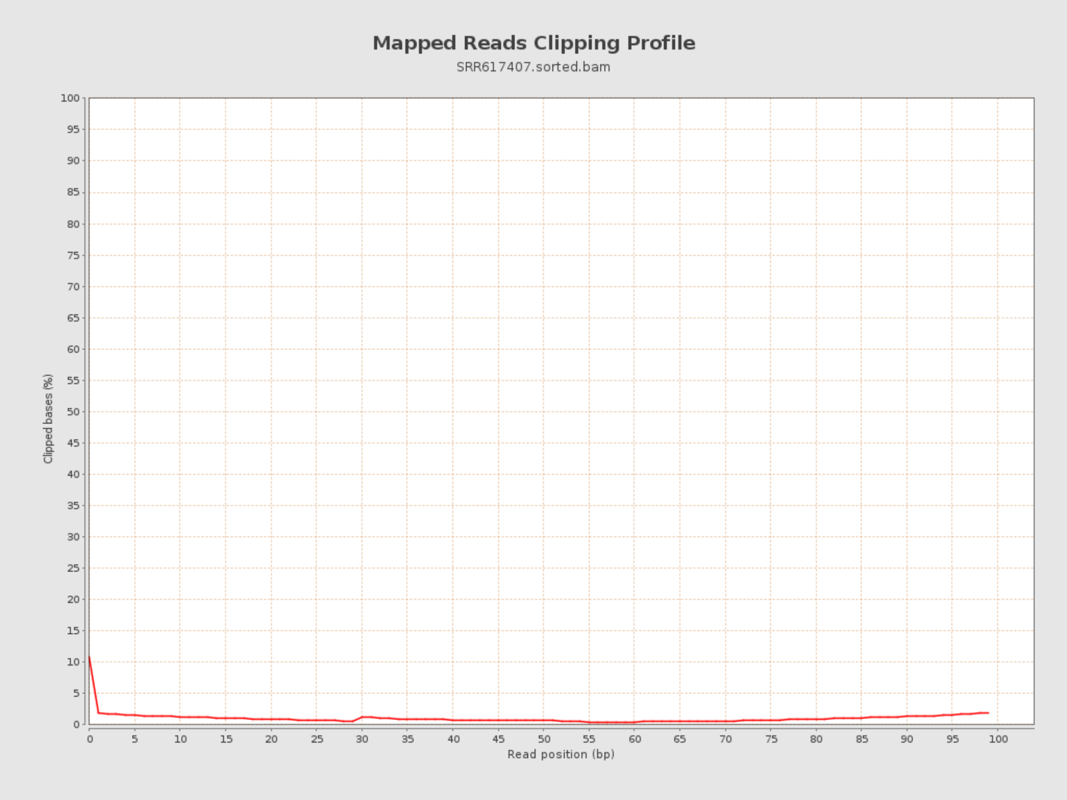
8. Results : Mapped Reads Nucleotide Content



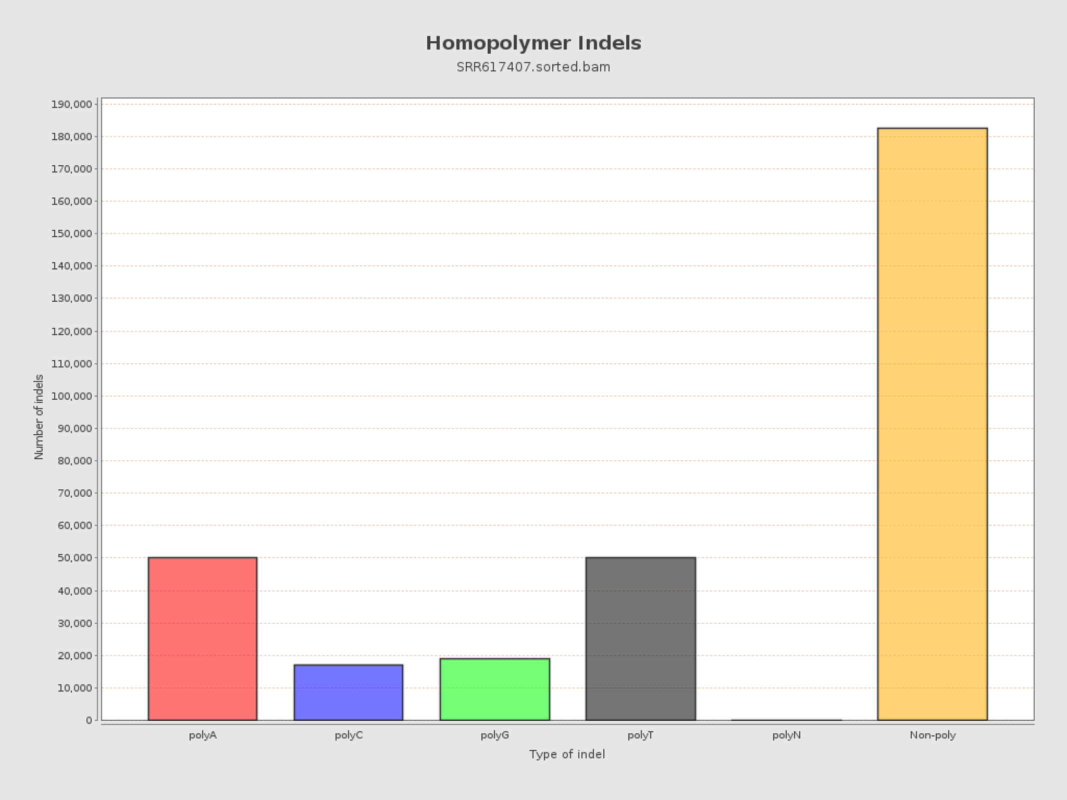
9. Results : Mapped Reads GC-content Distribution



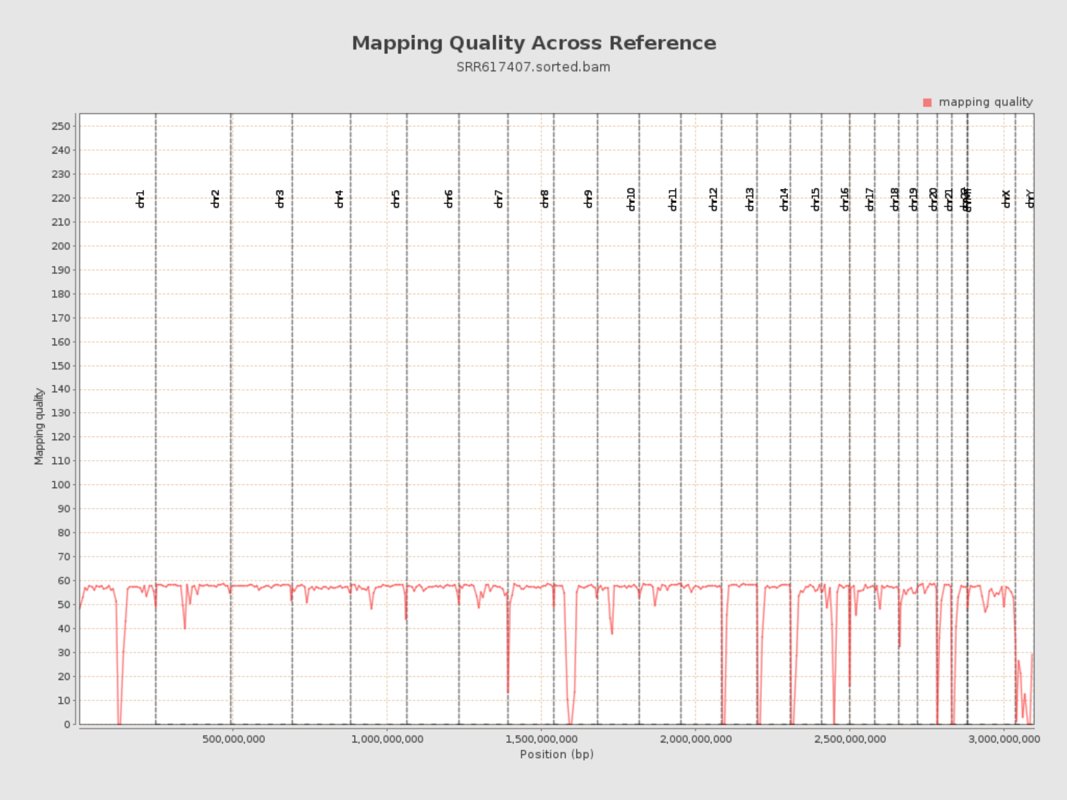
10. Results : Mapped Reads Clipping Profile



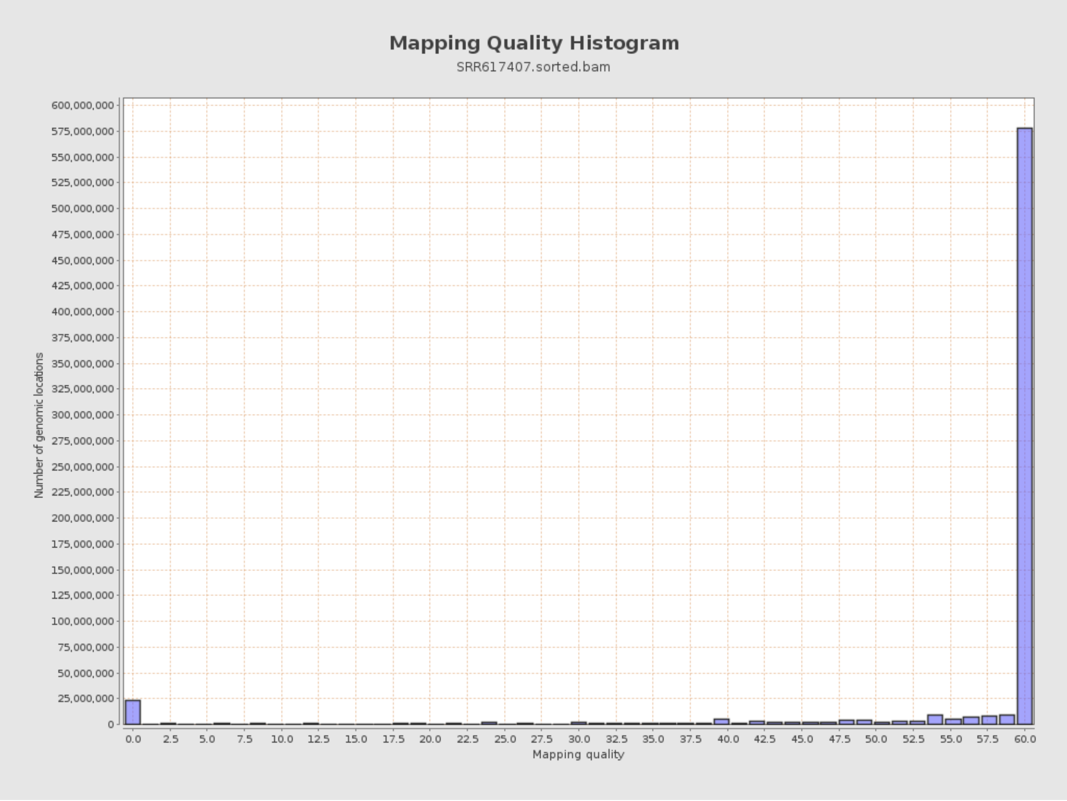
11. Results : Homopolymer Indels



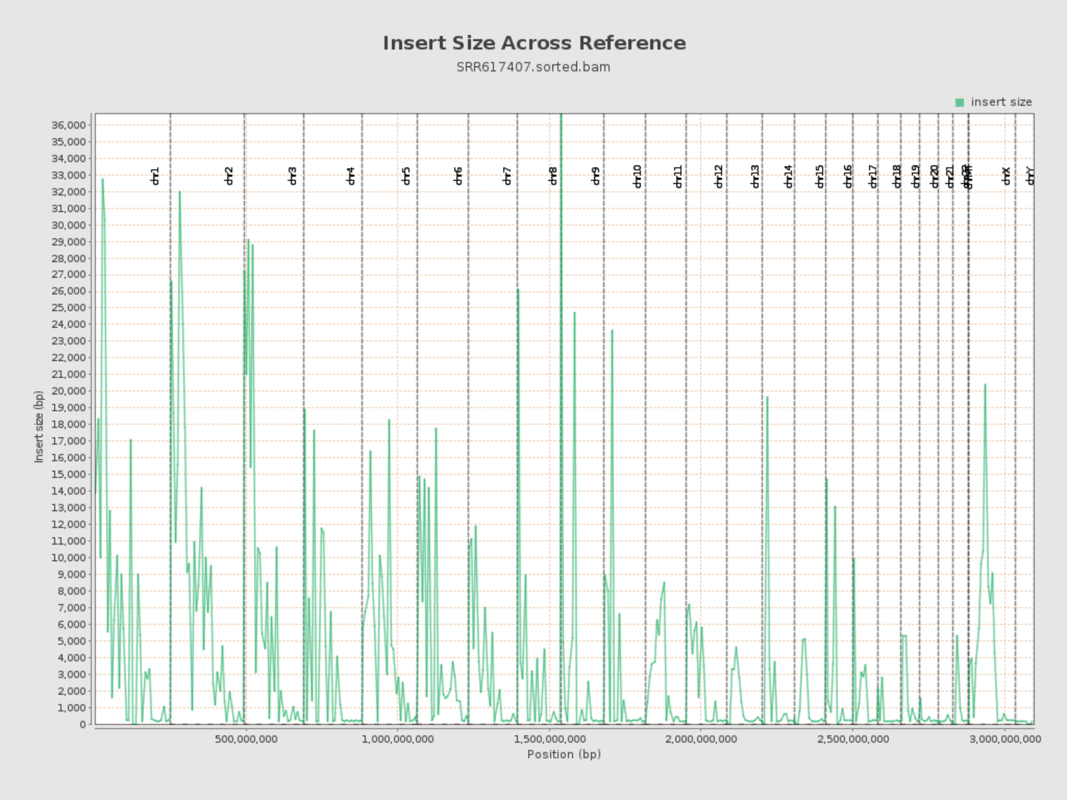
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram