Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 08:39:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617423.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_SRR617423 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617423_1.fastq.gz SRR617423_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 08:39:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617423.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,082,792 / 94.01%
Unmapped reads	1,917,208 / 5.99%
Mapped paired reads	30,082,792 / 94.01%
Mapped reads, first in pair	15,186,146 / 47.46%
Mapped reads, second in pair	14,896,646 / 46.55%
Mapped reads, both in pair	29,485,068 / 92.14%
Mapped reads, singletons	597,724 / 1.87%
Secondary alignments	0
Supplementary alignments	490,991 / 1.53%
Read min/max/mean length	30 / 100 / 100.63
Duplicated reads (estimated)	1,418,828 / 4.43%
Duplication rate	4.22%
Clipped reads	3,218,759 / 10.06%

2.2. ACGT Content

Number/percentage of A's	883,848,250 / 29.86%
Number/percentage of C's	594,623,168 / 20.09%
Number/percentage of T's	875,751,640 / 29.59%
Number/percentage of G's	605,410,249 / 20.45%
Number/percentage of N's	441,046 / 0.01%

GC Percentage	40.54%

2.3. Coverage

Mean	0.9564
Standard Deviation	2.9404

2.4. Mapping Quality

Mean Mapping Quality	53.88

2.5. Insert size

Mean	60,053.7
Standard Deviation	2,335,780.49
P25/Median/P75	170 / 209 / 270

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	26,865,353
Insertions	243,343
Mapped reads with at least one insertion	0.8%
Deletions	289,602
Mapped reads with at least one deletion	0.94%
Homopolymer indels	45.04%

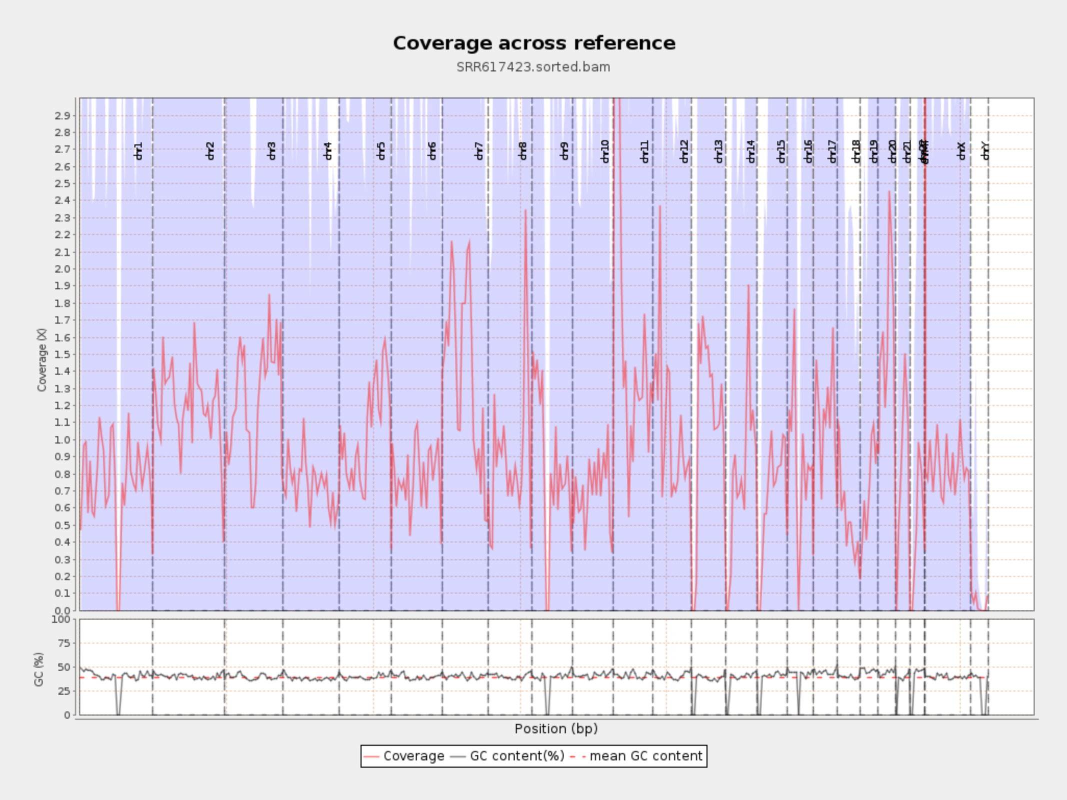
2.7. Chromosome stats

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

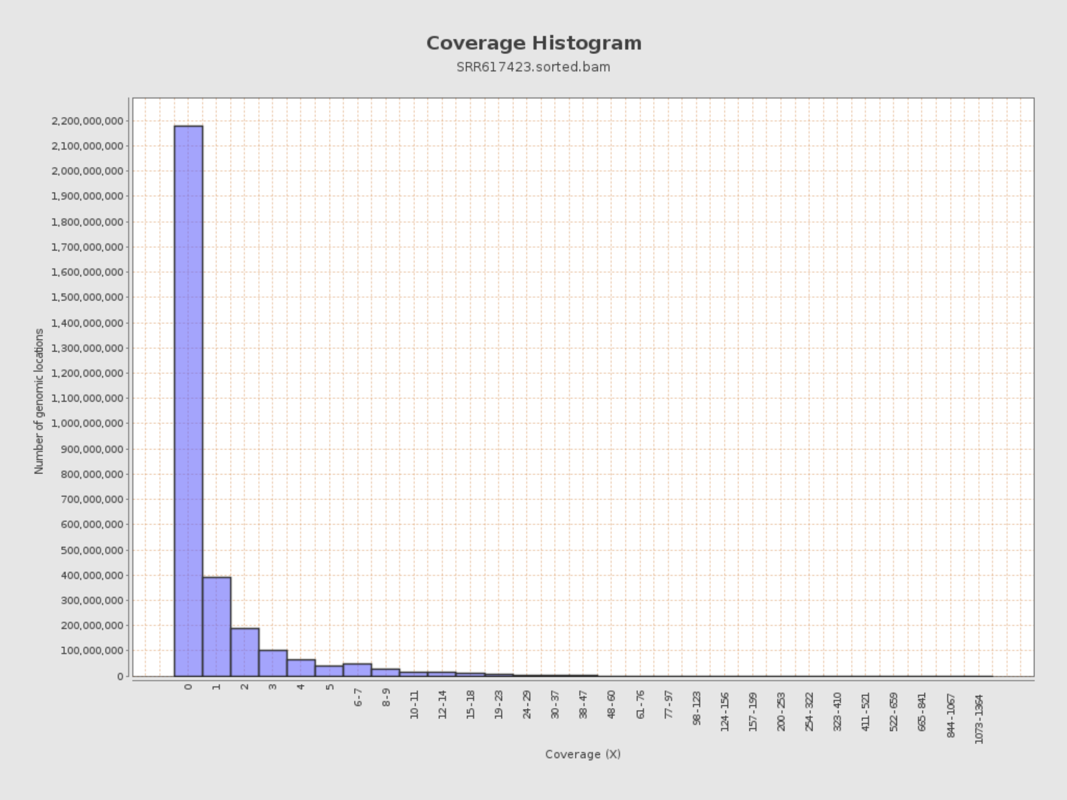
		bases	coverage	deviation
chr1	249250621	190545909	0.7645	2.7554
chr2	243199373	294924145	1.2127	3.1254
chr3	198022430	249911806	1.262	3.4292
chr4	191154276	141995972	0.7428	2.2894
chr5	180915260	189235640	1.046	2.8698
chr6	171115067	135577943	0.7923	2.6003
chr7	159138663	221531402	1.3921	3.2469
chr8	146364022	131117734	0.8958	3.2605
chr9	141213431	118371962	0.8382	2.6213
chr10	135534747	94977598	0.7008	2.4253
chr11	135006516	220074198	1.6301	3.8502
chr12	133851895	141478109	1.057	2.8097
chr13	115169878	128349417	1.1144	2.7814
chr14	107349540	85824037	0.7995	2.8934
chr15	102531392	68008270	0.6633	2.3887
chr16	90354753	74805833	0.8279	3.3377
chr17	81195210	91175267	1.1229	3.7228
chr18	78077248	42489038	0.5442	2.0225
chr19	59128983	42517224	0.7191	2.3551
chr20	63025520	100969900	1.602	4.7581
chr21	48129895	40358999	0.8385	2.5262
chr22	51304566	23937807	0.4666	2.087
chrMT	16571	188941	11.4019	5.6544
chrX	155270560	129963032	0.837	2.5825

chrY	59373566	2396462	0.0404	0.631

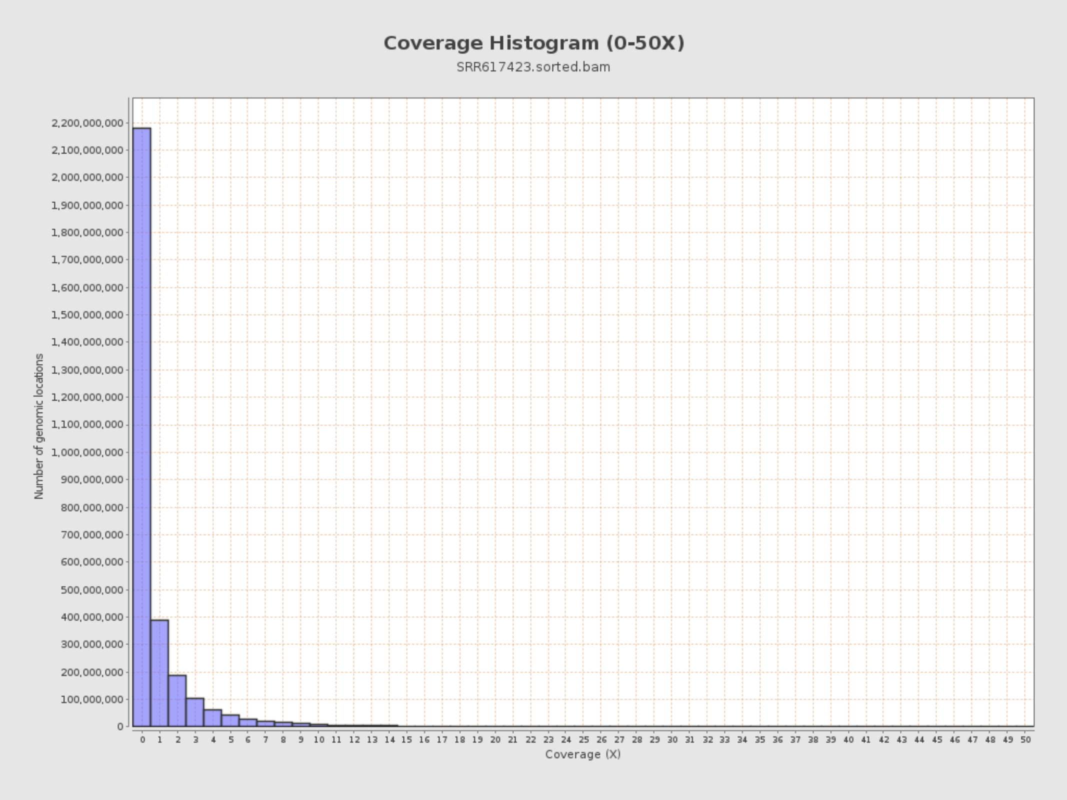
3. Results : Coverage across reference



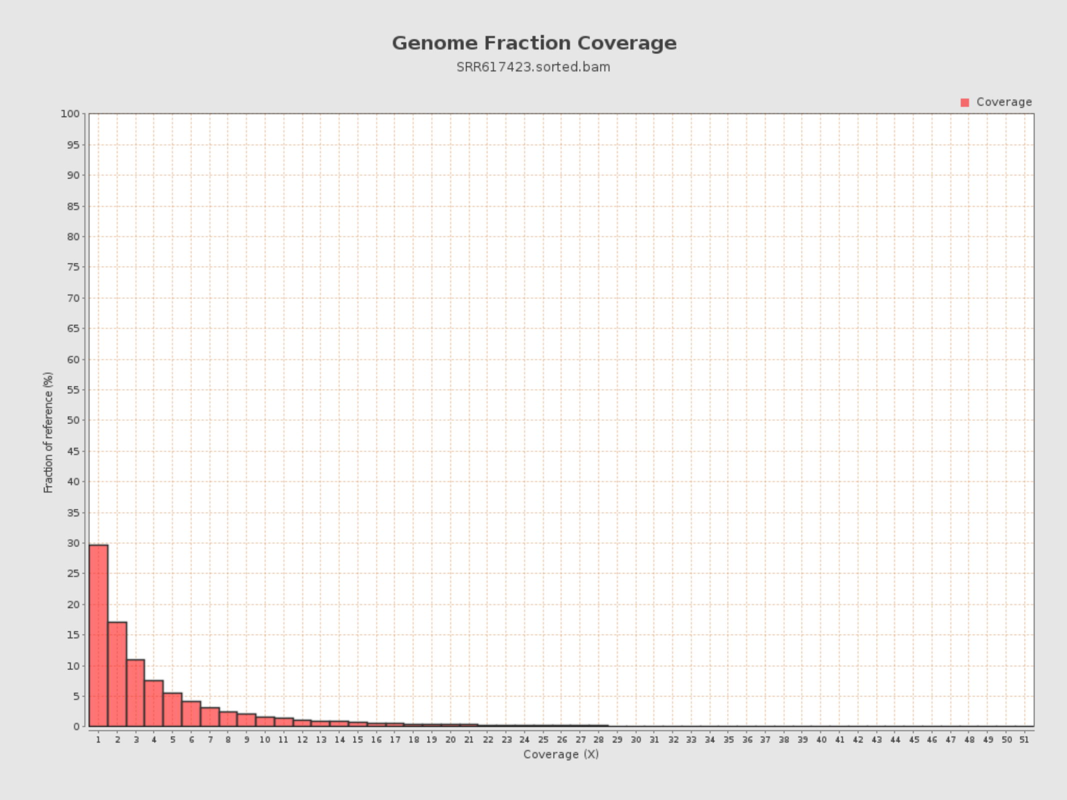
4. Results : Coverage Histogram



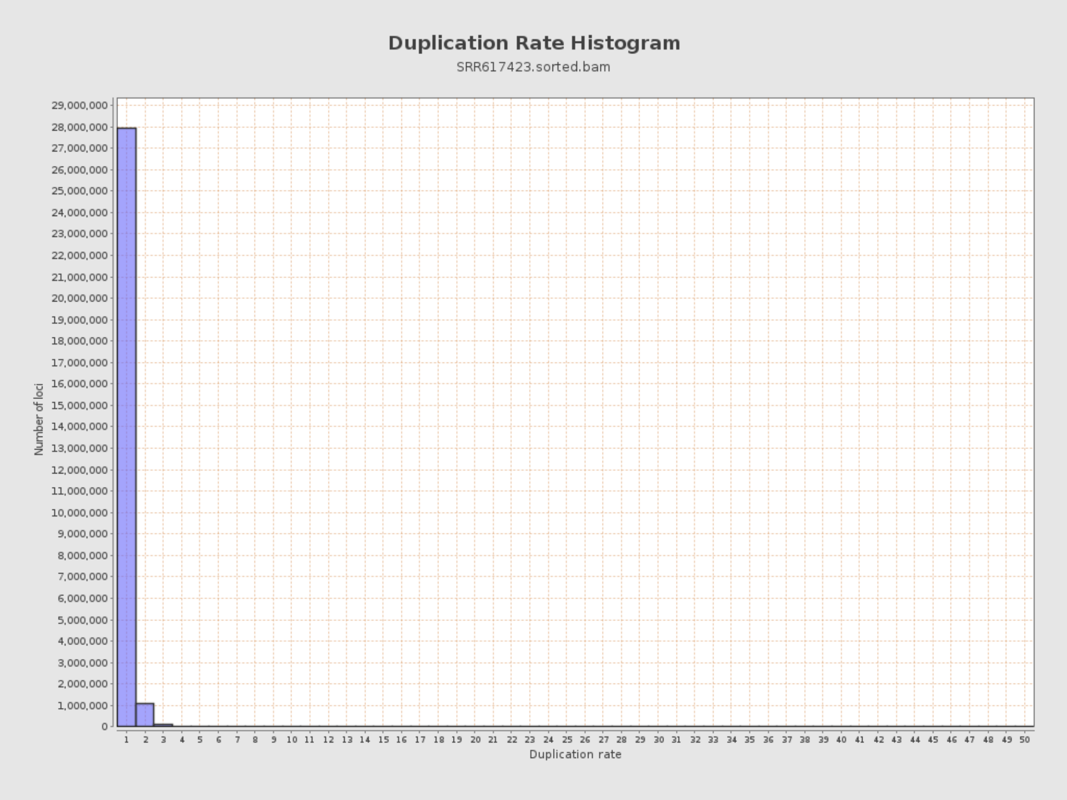
5. Results : Coverage Histogram (0-50X)



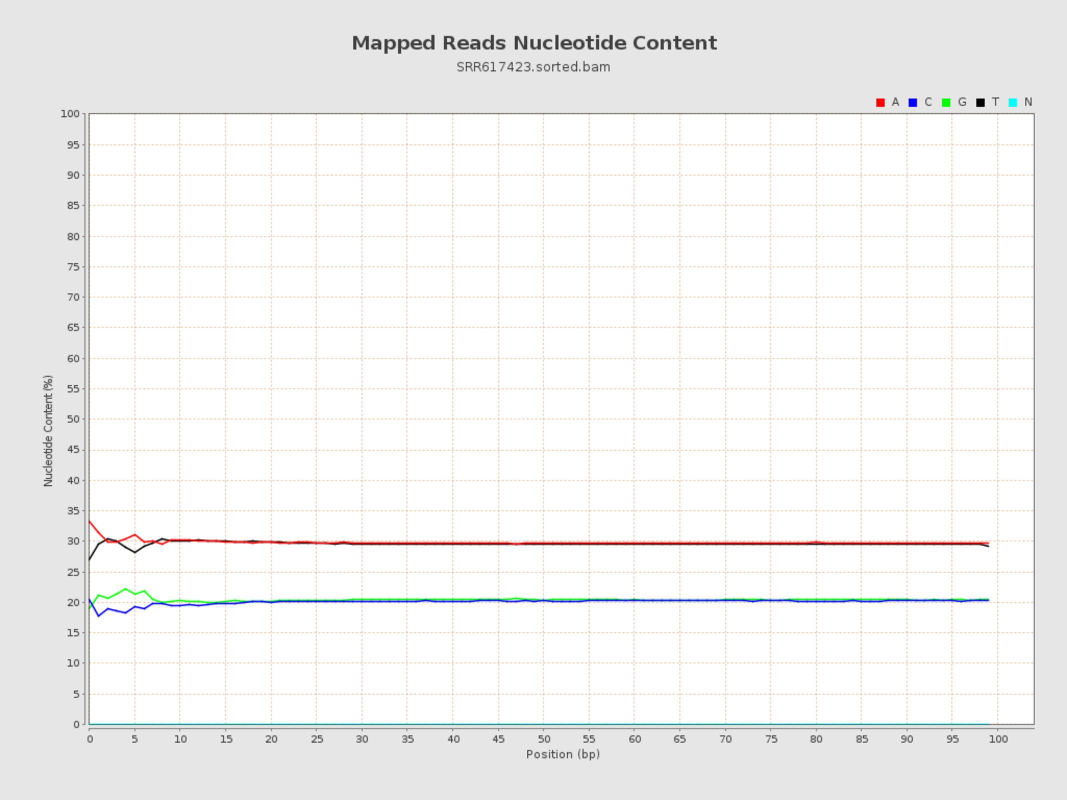
6. Results : Genome Fraction Coverage



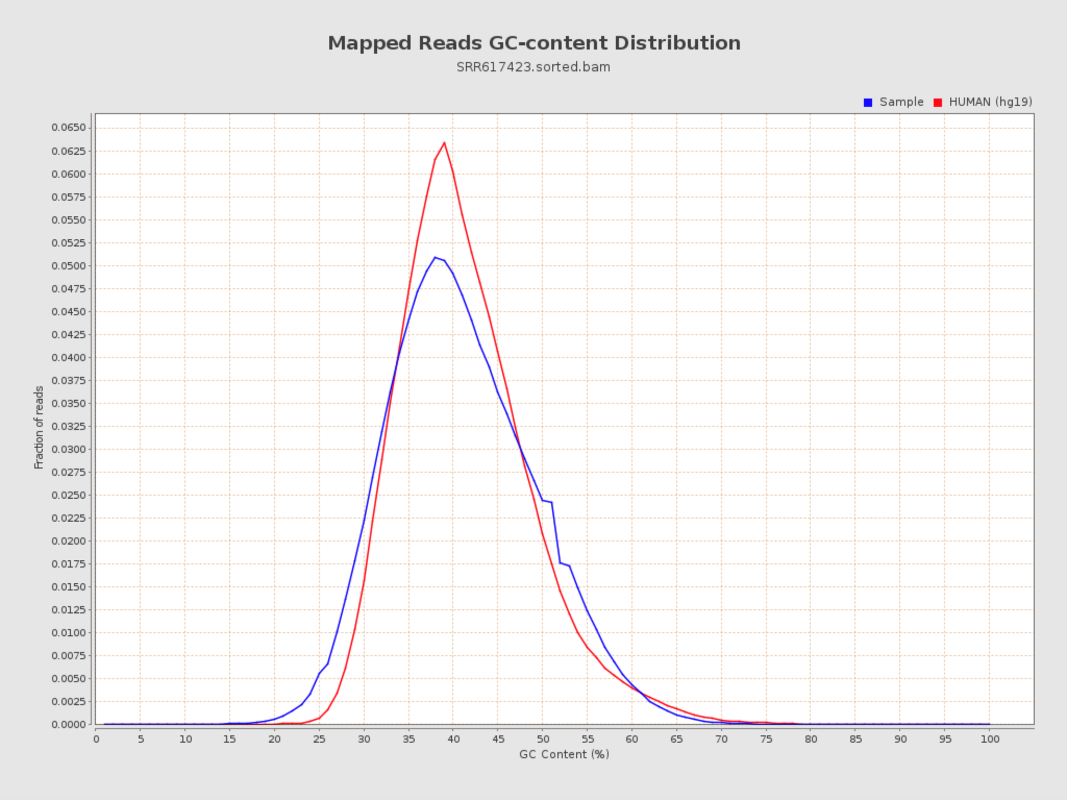
7. Results : Duplication Rate Histogram



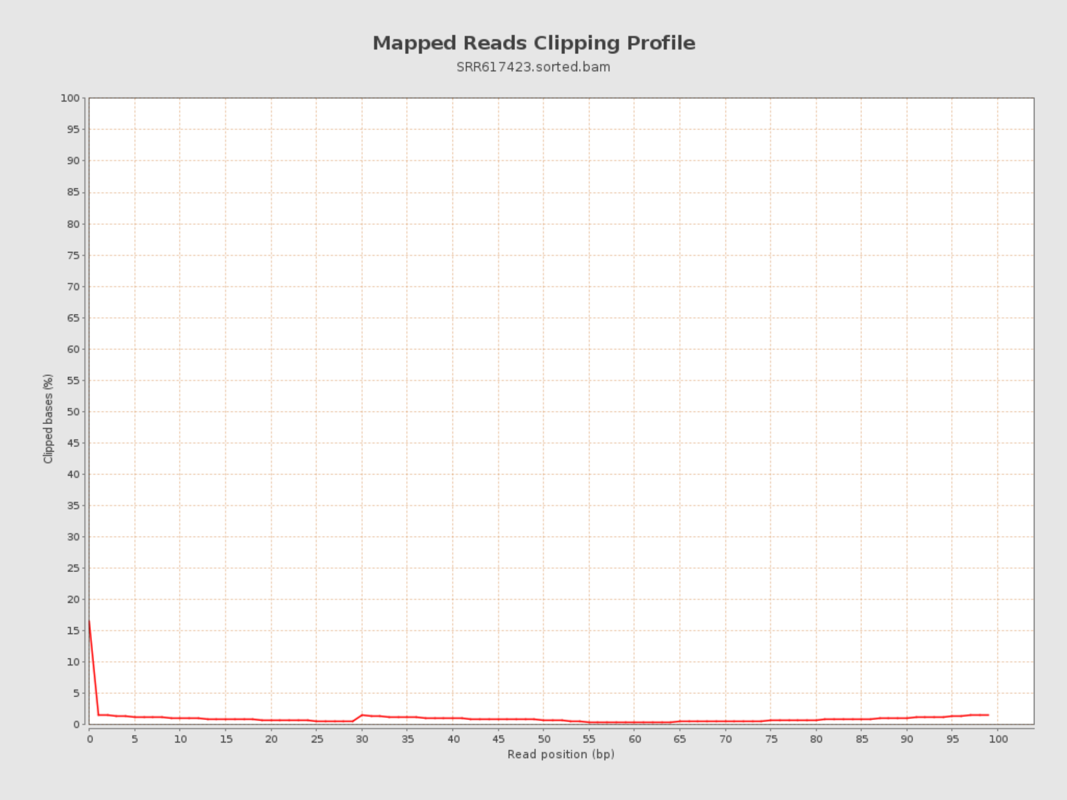
8. Results : Mapped Reads Nucleotide Content



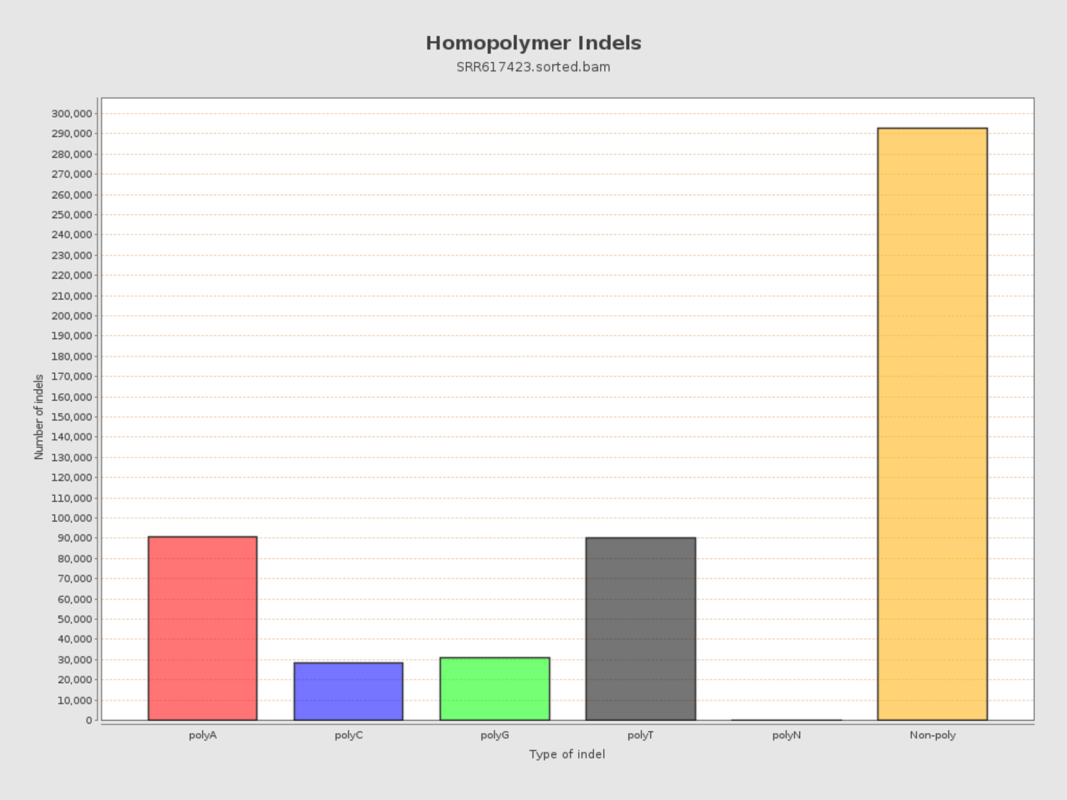
9. Results : Mapped Reads GC-content Distribution



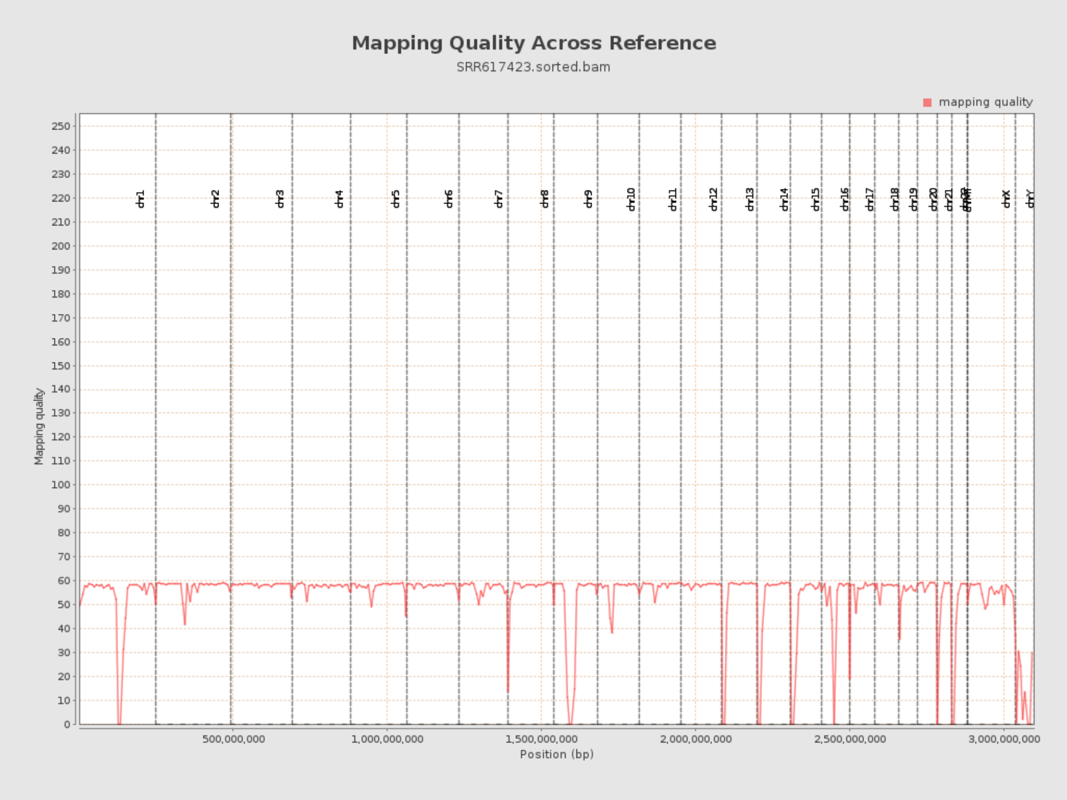
10. Results : Mapped Reads Clipping Profile



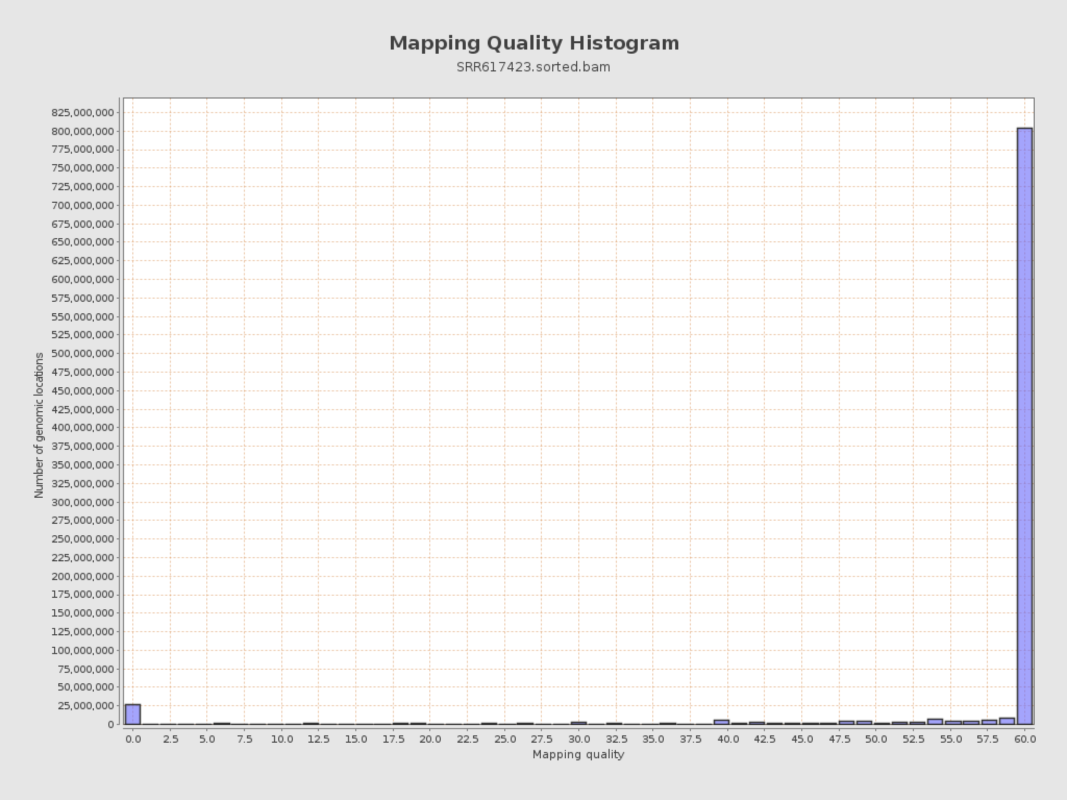
11. Results : Homopolymer Indels



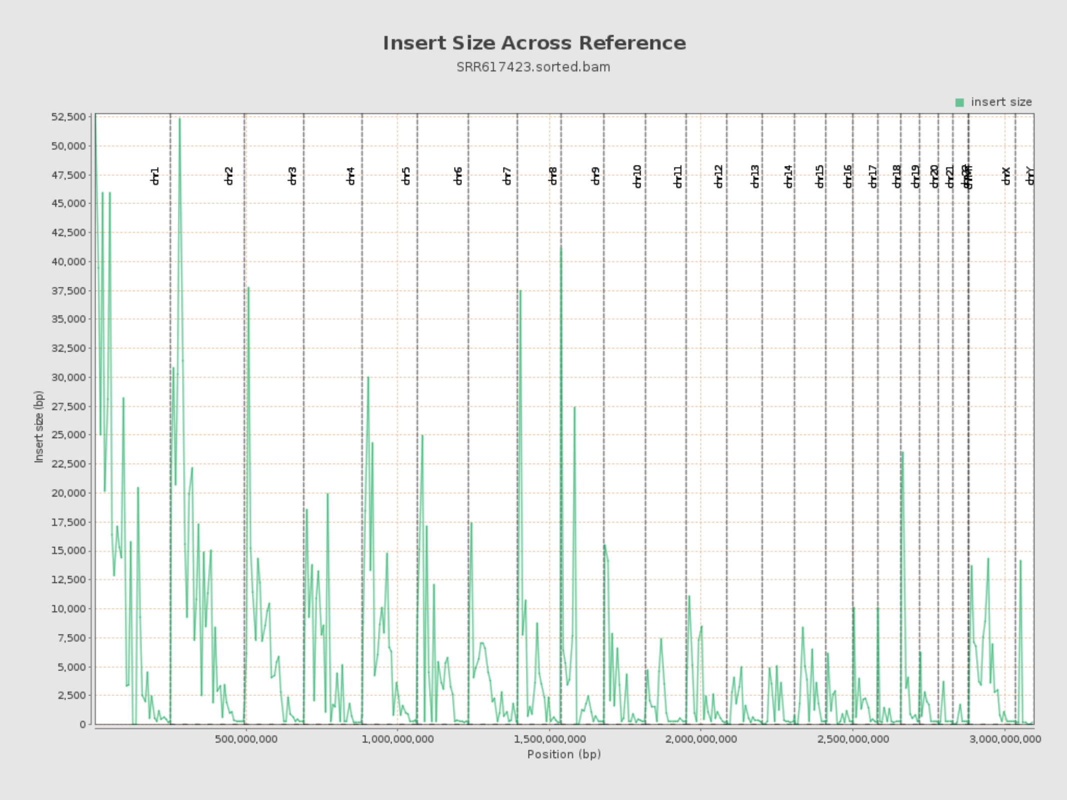
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram