Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 23:44:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006210.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_SRR1006210 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006210_1.fastq.gz SRR1006210_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 23:44:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006210.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,685,594
Mapped reads	2,200,787 / 81.95%
Unmapped reads	484,807 / 18.05%
Mapped paired reads	2,200,787 / 81.95%
Mapped reads, first in pair	1,103,647 / 41.1%
Mapped reads, second in pair	1,097,140 / 40.85%
Mapped reads, both in pair	2,030,980 / 75.62%
Mapped reads, singletons	169,807 / 6.32%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	55,894 / 2.08%
Duplication rate	2.19%
Clipped reads	125,300 / 4.67%

2.2. ACGT Content

Number/percentage of A's	23,605,187 / 27.71%
Number/percentage of C's	18,365,585 / 21.56%
Number/percentage of T's	24,118,108 / 28.31%
Number/percentage of G's	19,090,836 / 22.41%
Number/percentage of N's	4,085 / 0%
GC Percentage	43.97%

2.3. Coverage

Mean	0.0275
Standard Deviation	0.2102

2.4. Mapping Quality

Mean Mapping Quality	48.05

2.5. Insert size

Mean	53,661.58
Standard Deviation	2,195,751.06
P25/Median/P75	76 / 119 / 162

2.6. Mismatches and indels

General error rate	0.3%
Mismatches	248,372
Insertions	2,640
Mapped reads with at least one insertion	0.12%
Deletions	8,446
Mapped reads with at least one deletion	0.38%
Homopolymer indels	45.38%

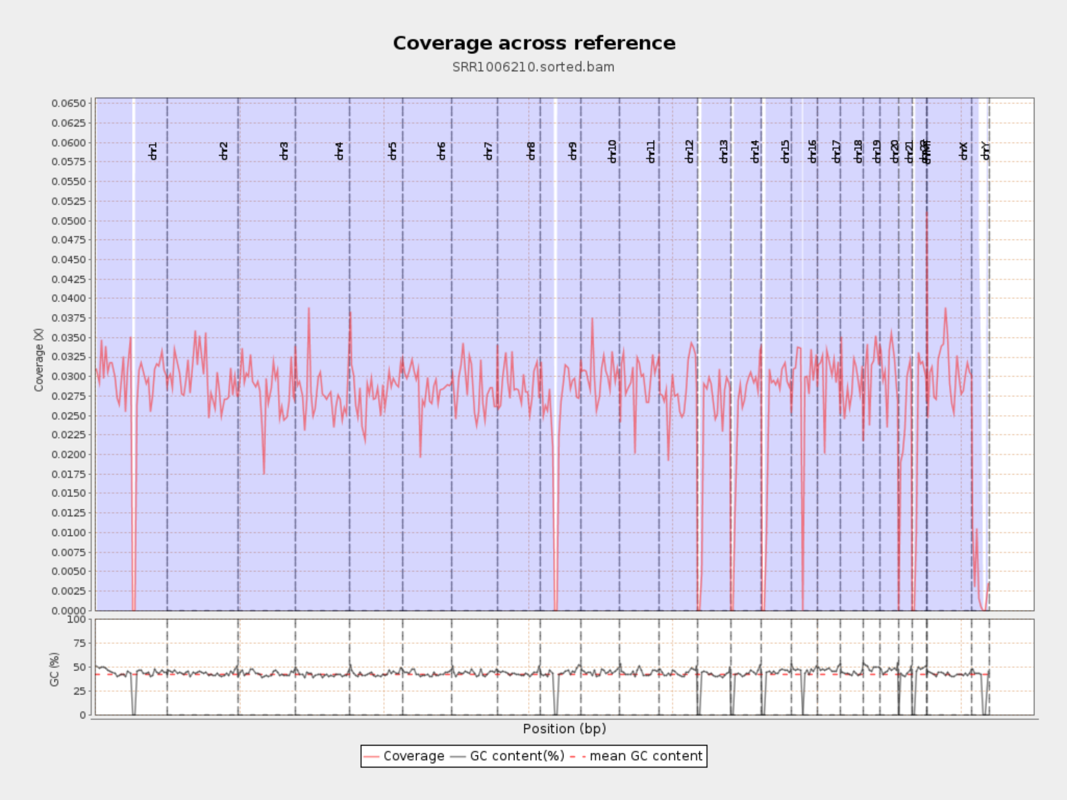
2.7. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**

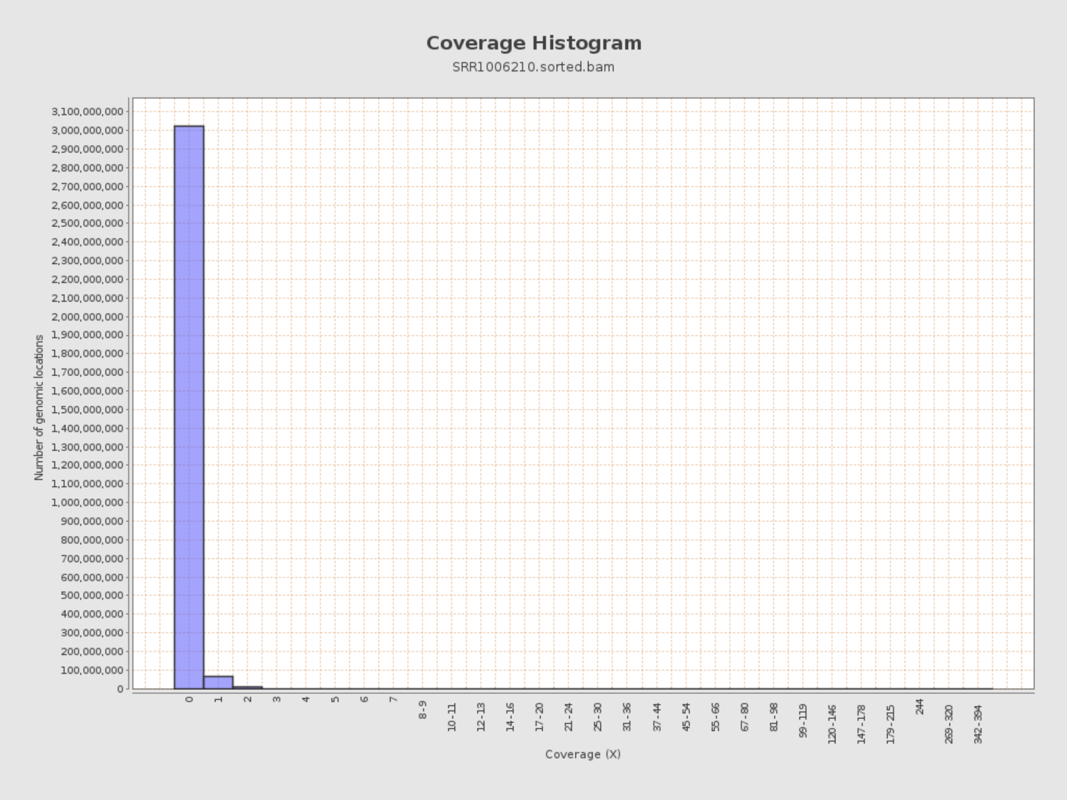
chr1	249250621	7083930	0.0284	0.2575
chr2	243199373	7223739	0.0297	0.2168
chr3	198022430	5595508	0.0283	0.1865
chr4	191154276	5326161	0.0279	0.1927
chr5	180915260	5066810	0.028	0.1856
chr6	171115067	4899402	0.0286	0.1985
chr7	159138663	4516221	0.0284	0.2339
chr8	146364022	4199317	0.0287	0.2721
chr9	141213431	3474467	0.0246	0.1898
chr10	135534747	4117071	0.0304	0.2268
chr11	135006516	3987270	0.0295	0.2105
chr12	133851895	3770486	0.0282	0.1869
chr13	115169878	2680258	0.0233	0.1688
chr14	107349540	2602604	0.0242	0.2293
chr15	102531392	2460538	0.024	0.1724
chr16	90354753	2556769	0.0283	0.1997
chr17	81195210	2454710	0.0302	0.199
chr18	78077248	2263424	0.029	0.2614
chr19	59128983	1831837	0.031	0.2257
chr20	63025520	1925198	0.0305	0.1954
chr21	48129895	1112087	0.0231	0.1802
chr22	51304566	1113347	0.0217	0.1706
chrMT	16571	848	0.0512	0.268
chrX	155270560	4729687	0.0305	0.202

chrY	59373566	203139	0.0034	0.0962

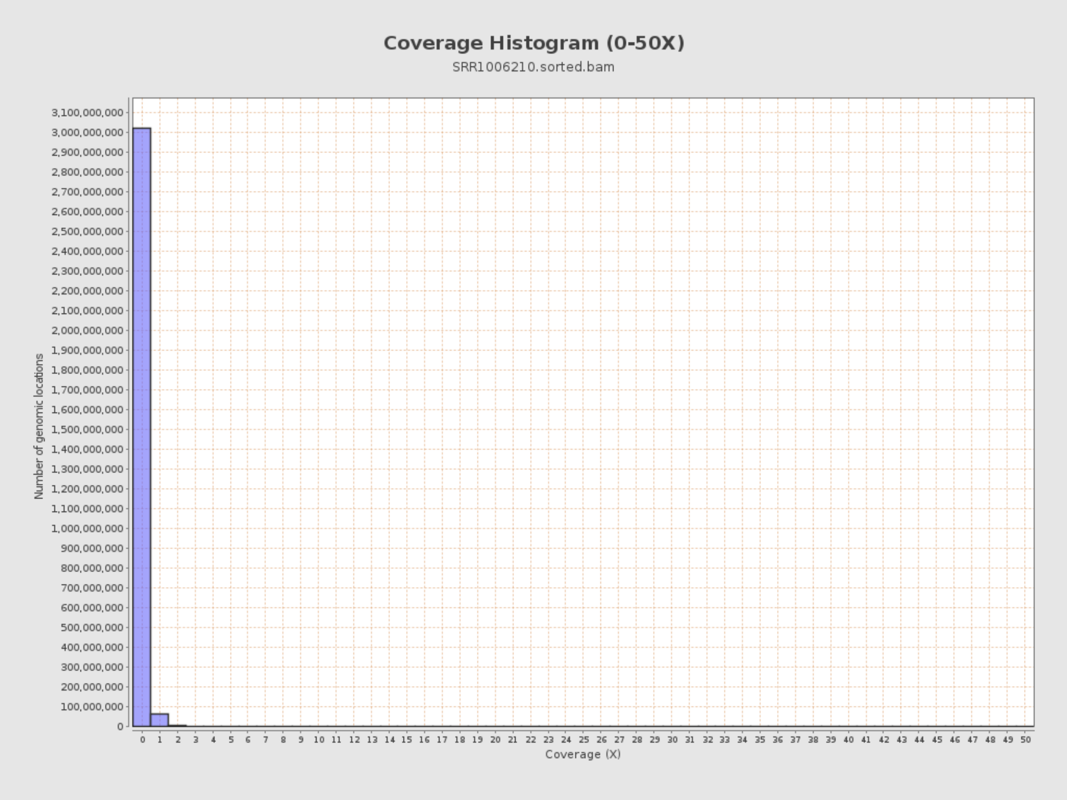
3. Results : Coverage across reference



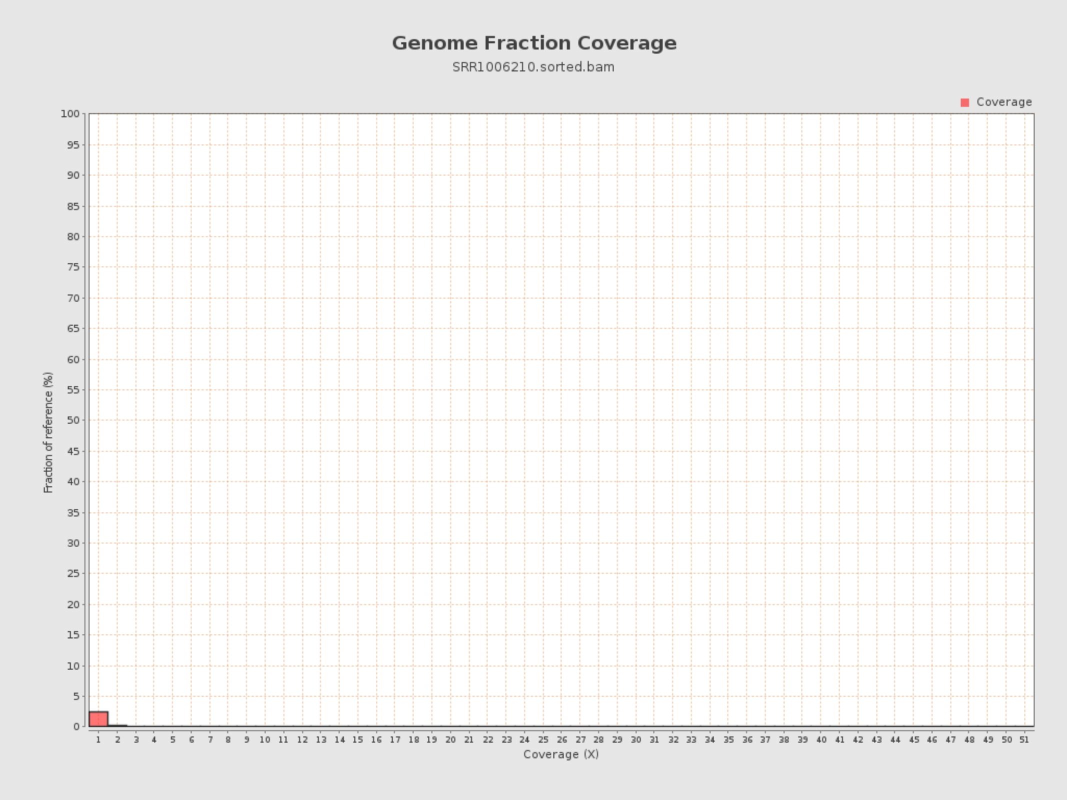
4. Results : Coverage Histogram



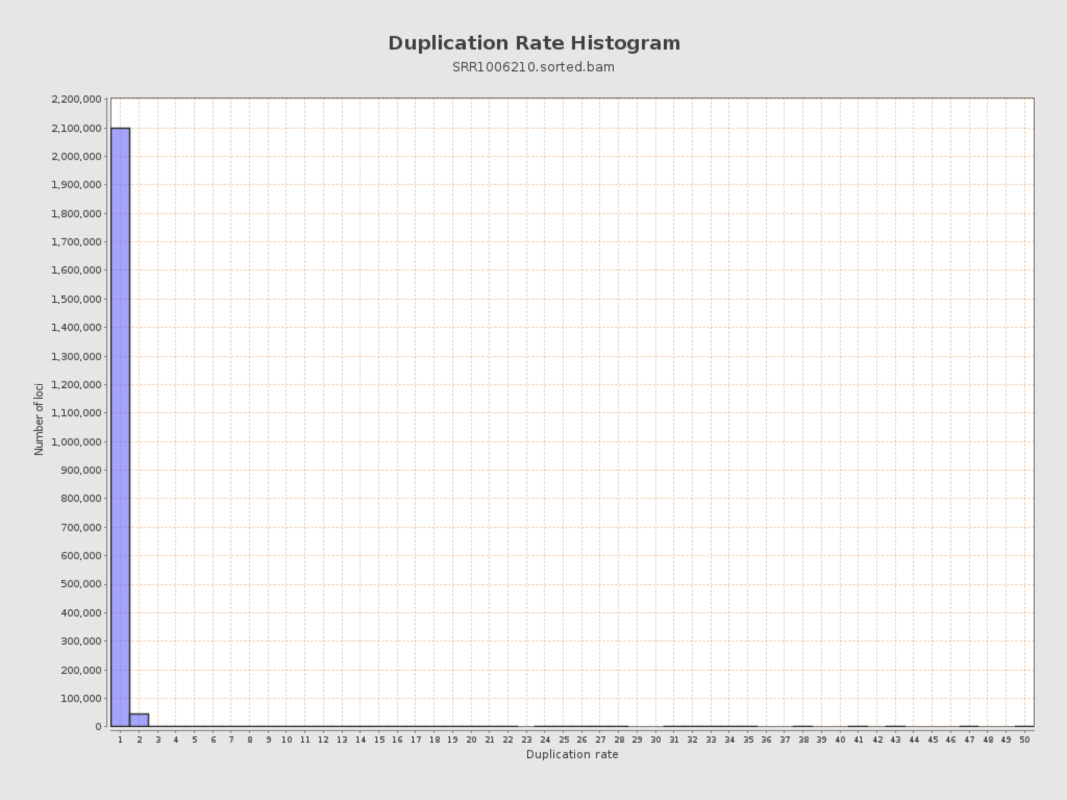
5. Results : Coverage Histogram (0-50X)



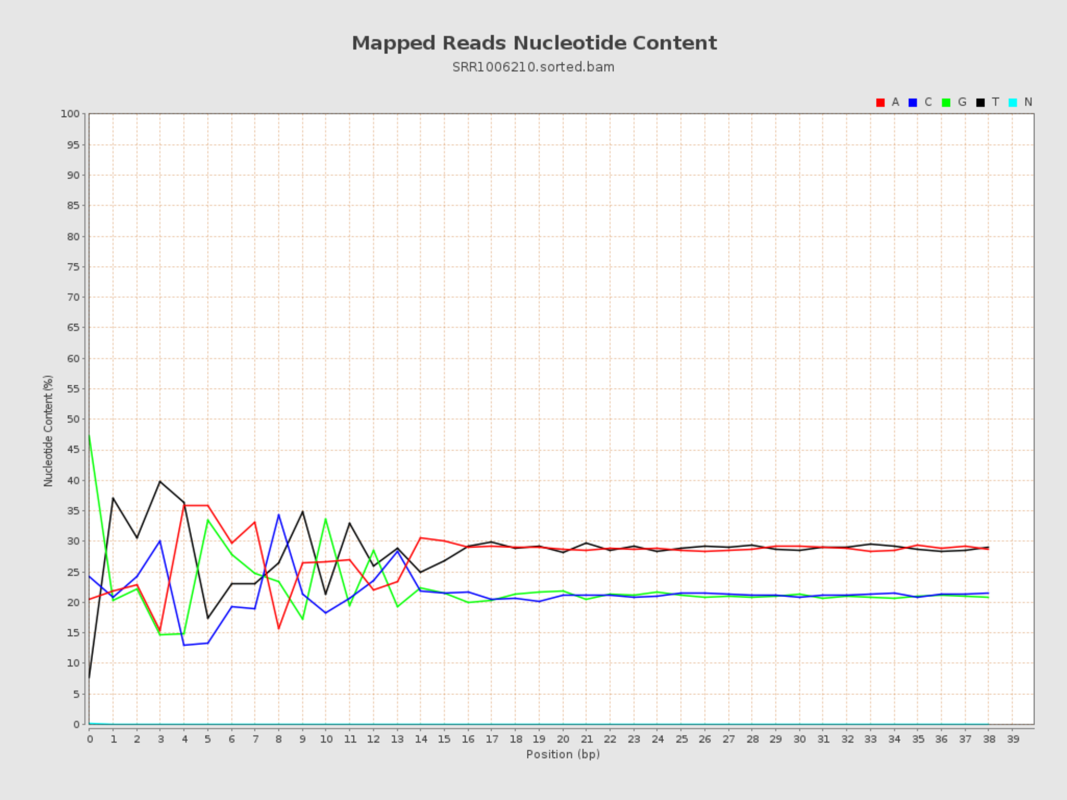
6. Results : Genome Fraction Coverage



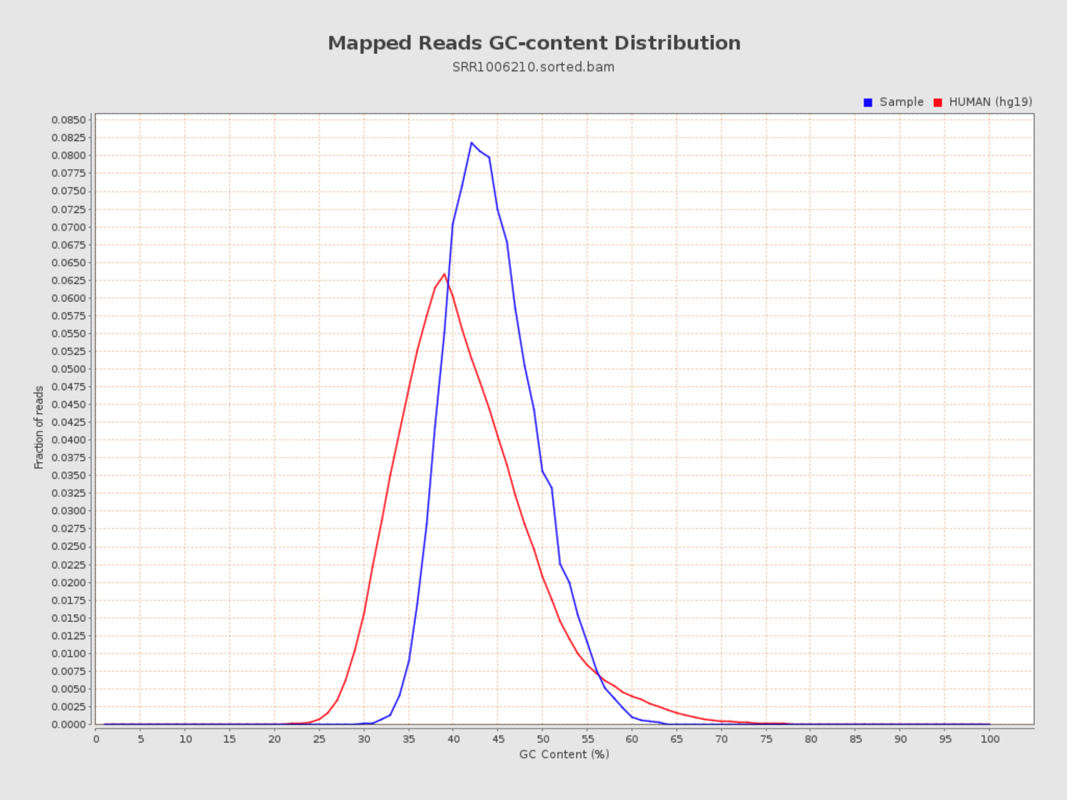
7. Results : Duplication Rate Histogram



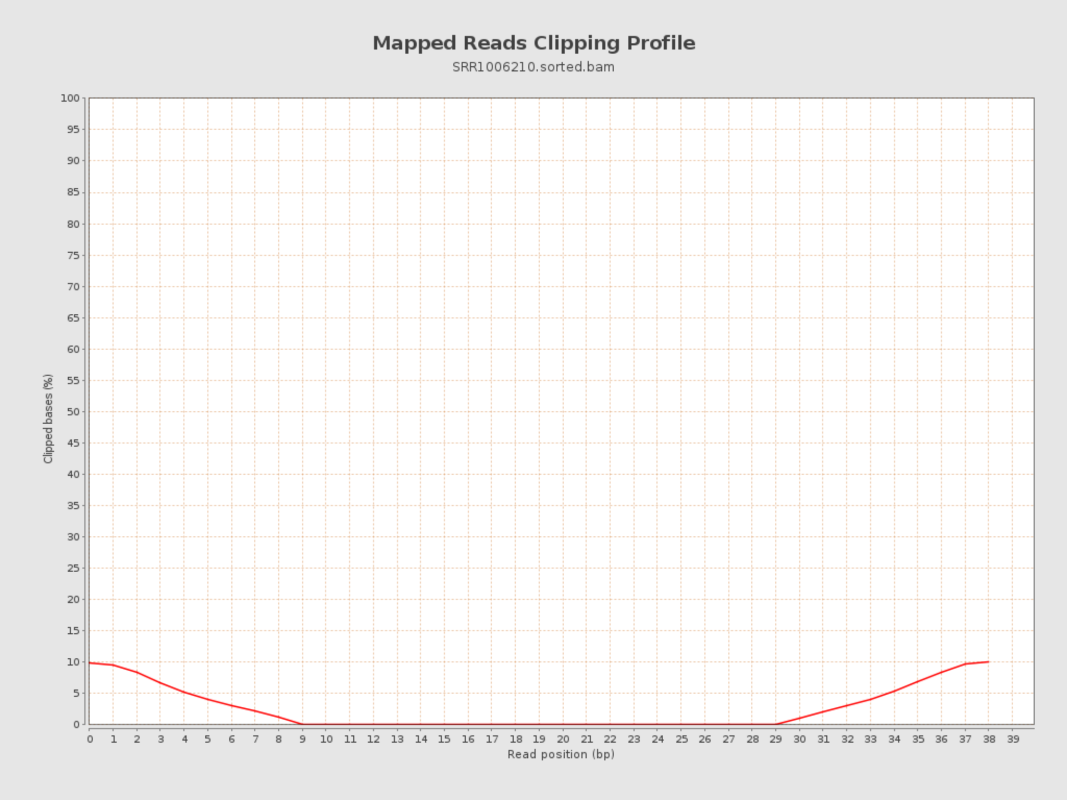
8. Results : Mapped Reads Nucleotide Content



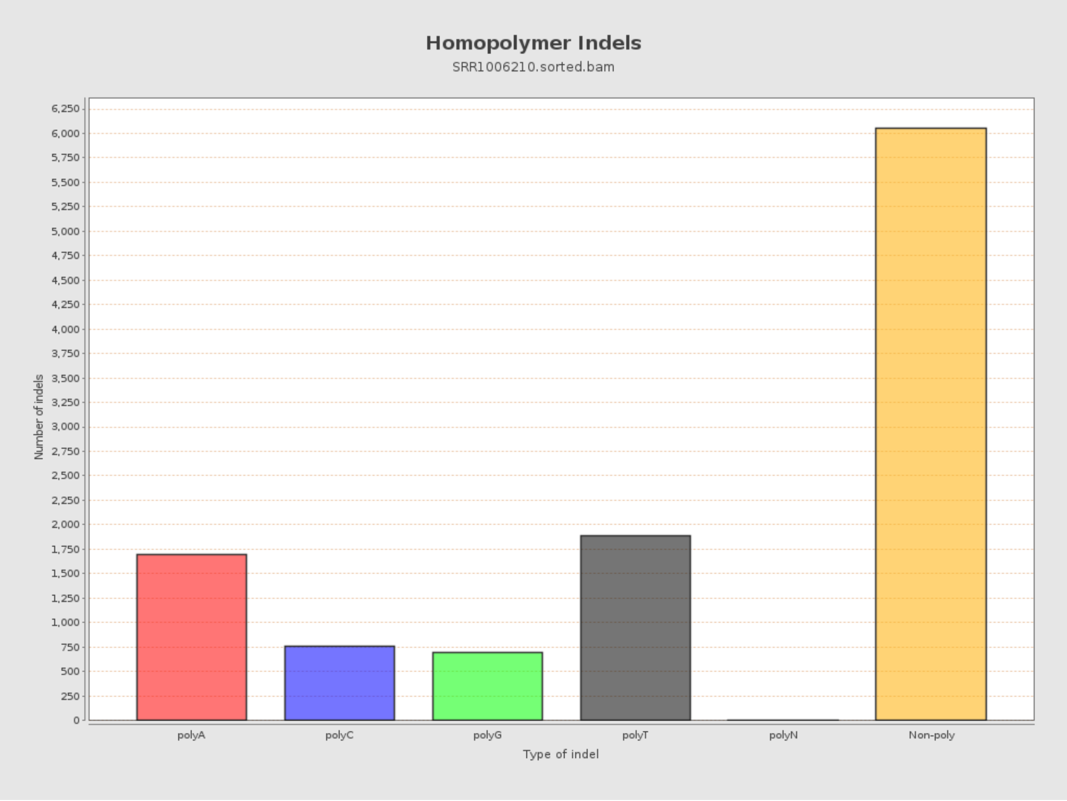
9. Results : Mapped Reads GC-content Distribution



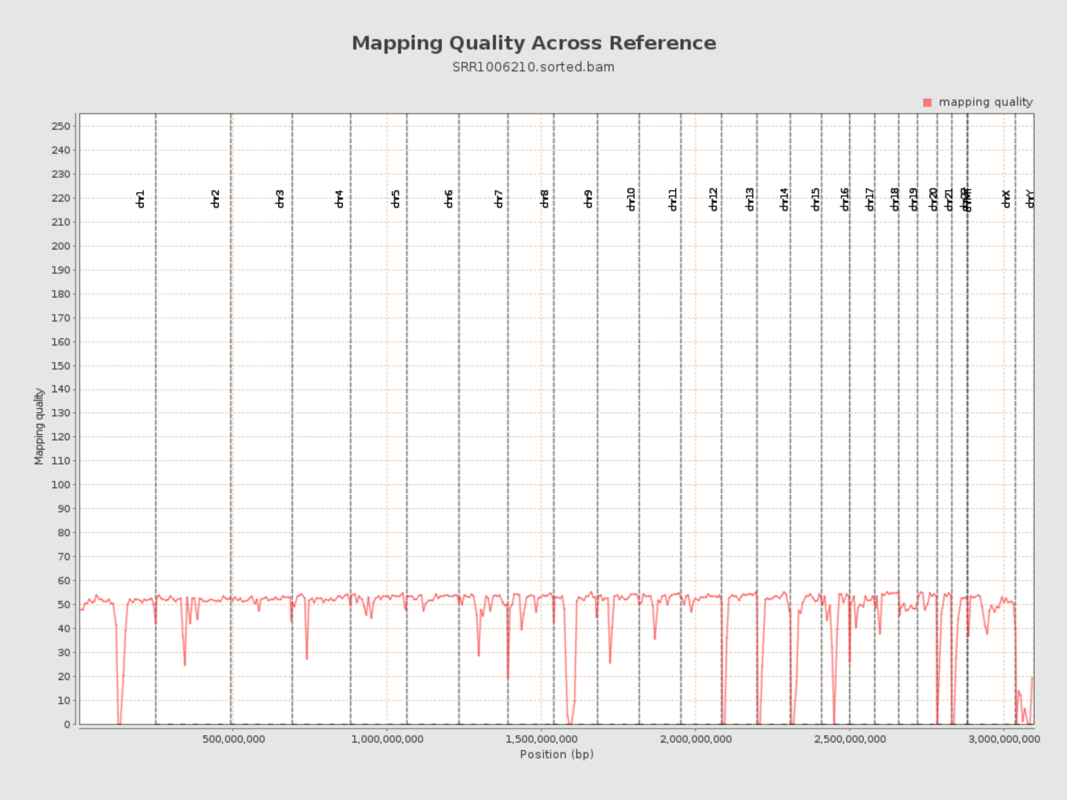
10. Results : Mapped Reads Clipping Profile



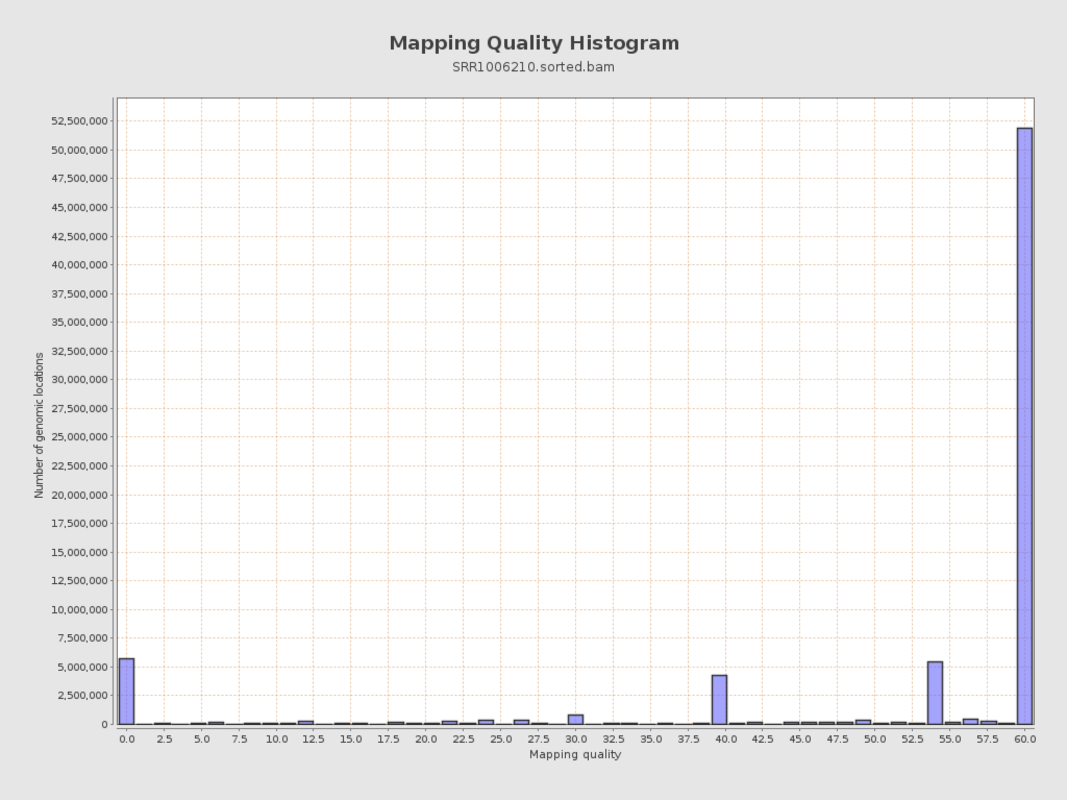
11. Results : Homopolymer Indels



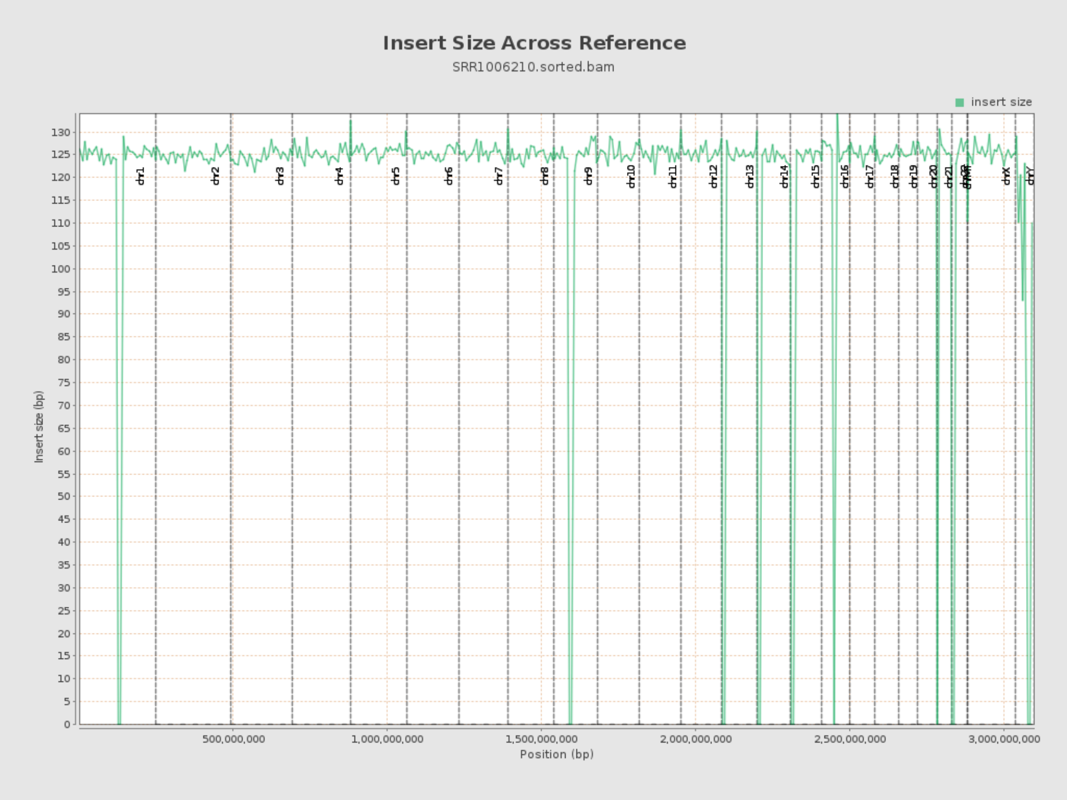
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram