Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 21:39:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006156.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_SRR1006156 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006156_1.fastq.gz SRR1006156_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 21:39:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006156.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,951,026
Mapped reads	9,568,704 / 87.38%
Unmapped reads	1,382,322 / 12.62%
Mapped paired reads	9,568,704 / 87.38%
Mapped reads, first in pair	4,857,535 / 44.36%
Mapped reads, second in pair	4,711,169 / 43.02%
Mapped reads, both in pair	8,786,260 / 80.23%
Mapped reads, singletons	782,444 / 7.14%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	915,128 / 8.36%
Duplication rate	8.59%
Clipped reads	829,874 / 7.58%

2.2. ACGT Content

Number/percentage of A's	99,563,598 / 26.97%
Number/percentage of C's	81,294,207 / 22.03%
Number/percentage of T's	102,677,148 / 27.82%
Number/percentage of G's	85,546,985 / 23.18%
Number/percentage of N's	14,368 / 0%
GC Percentage	45.2%

2.3. Coverage

Mean	0.1192
Standard Deviation	0.7623

2.4. Mapping Quality

Mean Mapping Quality	46.46

2.5. Insert size

Mean	66,346.04
Standard Deviation	2,528,666.13
P25/Median/P75	64 / 92 / 126

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	1,846,971
Insertions	12,452
Mapped reads with at least one insertion	0.13%
Deletions	30,820
Mapped reads with at least one deletion	0.32%
Homopolymer indels	44.68%

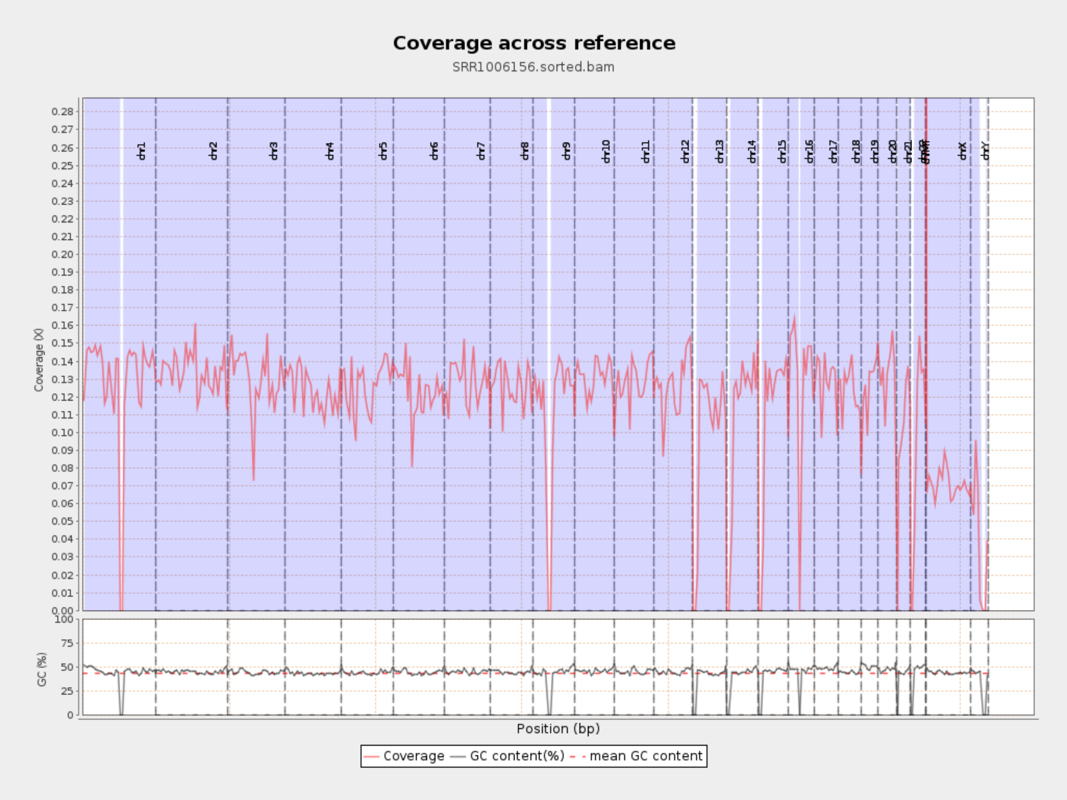
2.7. Chromosome stats

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

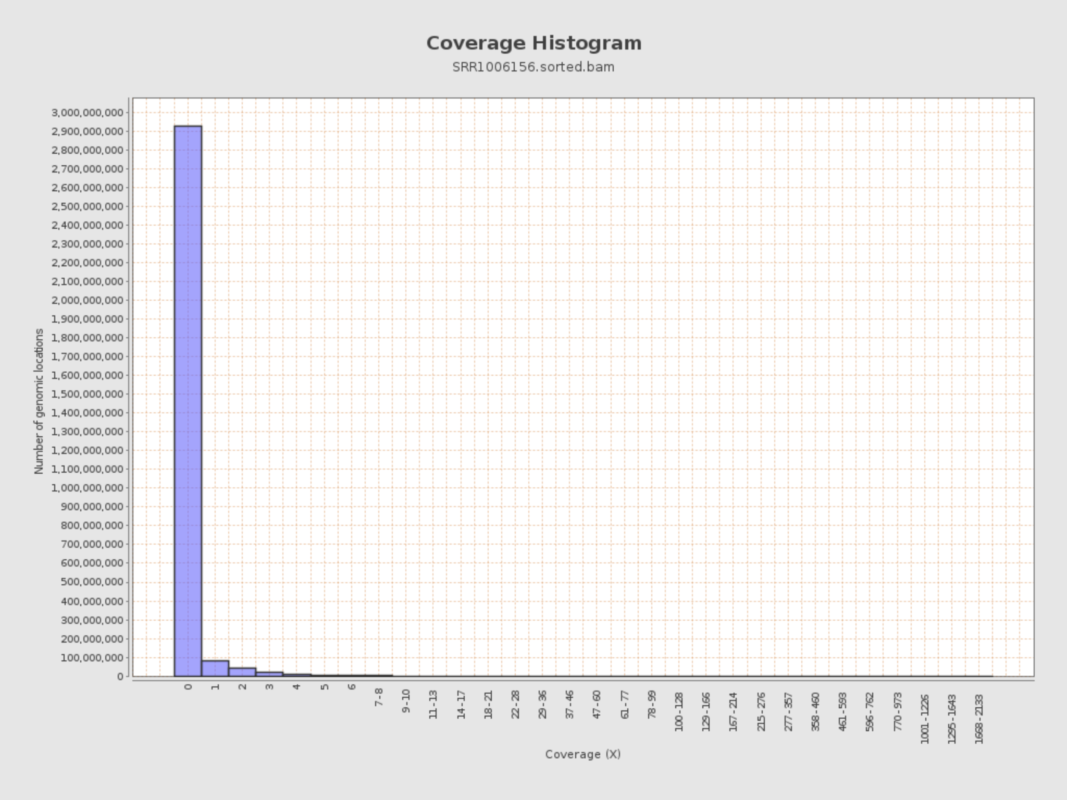
chr1	249250621	31902134	0.128	0.8714
chr2	243199373	32570191	0.1339	0.7684
chr3	198022430	25725415	0.1299	0.6577
chr4	191154276	23733435	0.1242	0.6831
chr5	180915260	22902232	0.1266	0.6501
chr6	171115067	21095133	0.1233	0.7257
chr7	159138663	20582640	0.1293	0.9146
chr8	146364022	18453642	0.1261	1.0059
chr9	141213431	15609153	0.1105	0.6523
chr10	135534747	17850914	0.1317	0.6979
chr11	135006516	17394395	0.1288	1.3021
chr12	133851895	17110224	0.1278	0.658
chr13	115169878	11437516	0.0993	0.5802
chr14	107349540	11479531	0.1069	0.6128
chr15	102531392	10891504	0.1062	0.6087
chr16	90354753	11316585	0.1252	0.677
chr17	81195210	10535110	0.1298	0.7526
chr18	78077248	9677536	0.1239	0.9029
chr19	59128983	7413752	0.1254	0.8473
chr20	63025520	8395862	0.1332	0.6831
chr21	48129895	4816751	0.1001	0.6265
chr22	51304566	4793874	0.0934	0.6358
chrMT	16571	28732	1.7339	2.5898
chrX	155270560	11051141	0.0712	0.5137

chrY	59373566	2367584	0.0399	0.3778

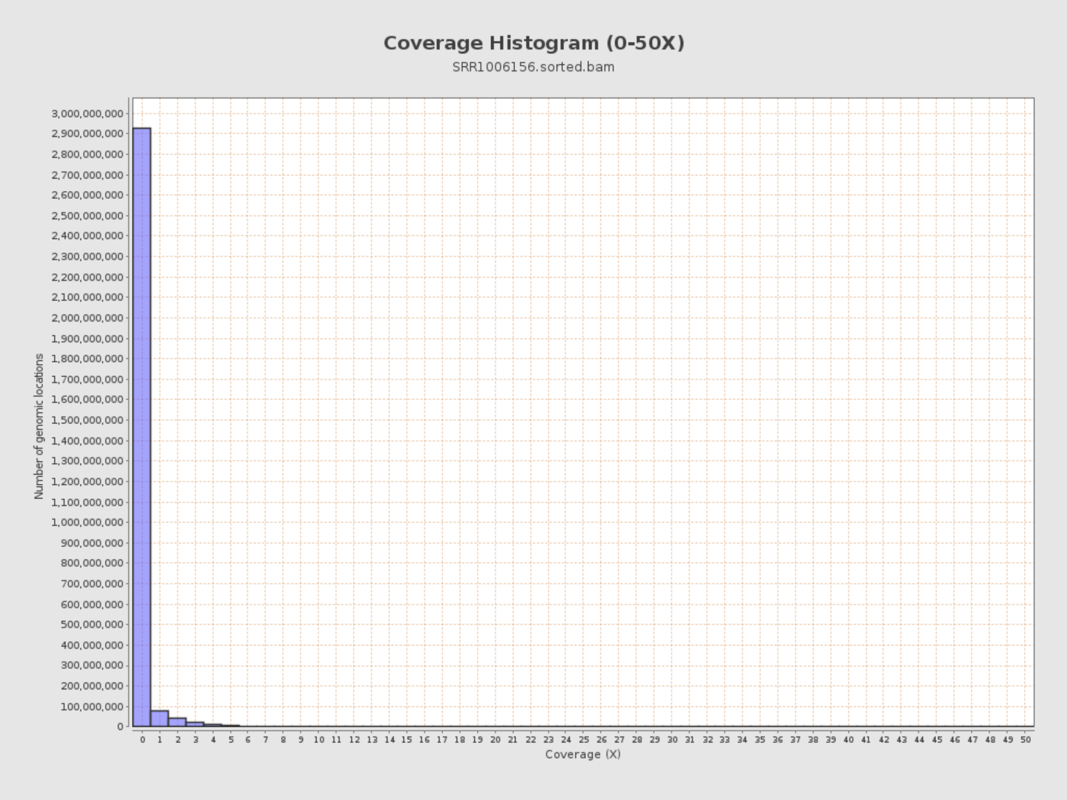
3. Results : Coverage across reference



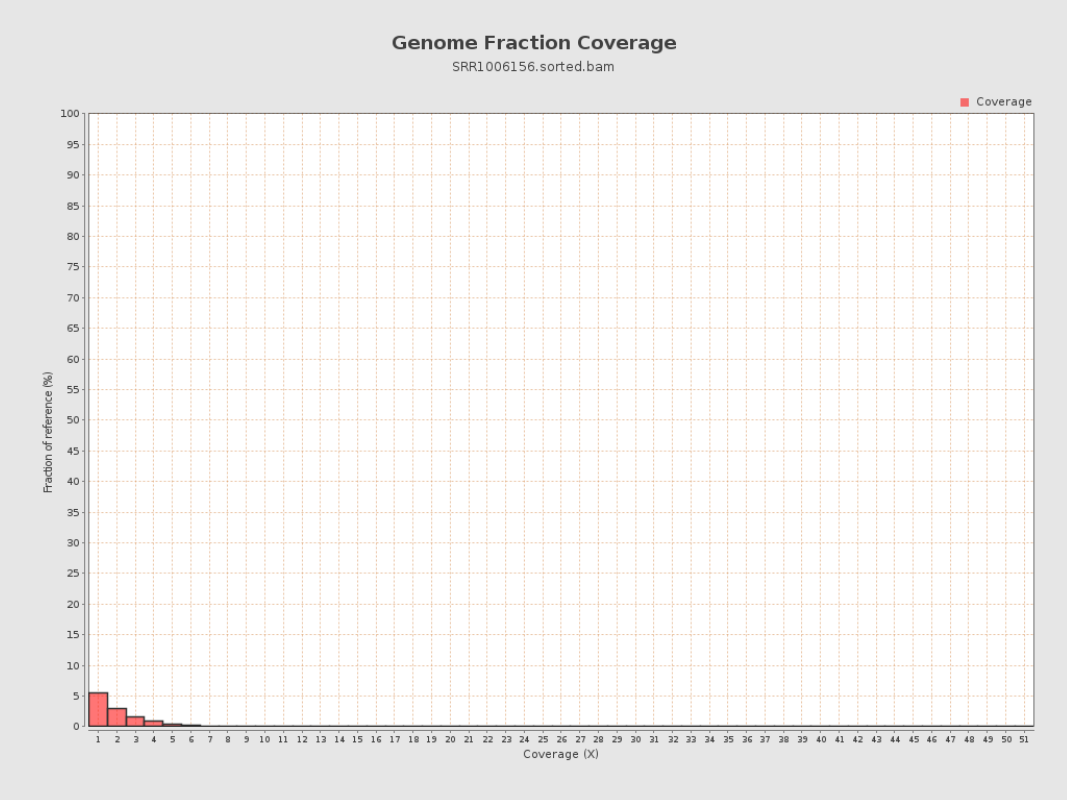
4. Results : Coverage Histogram



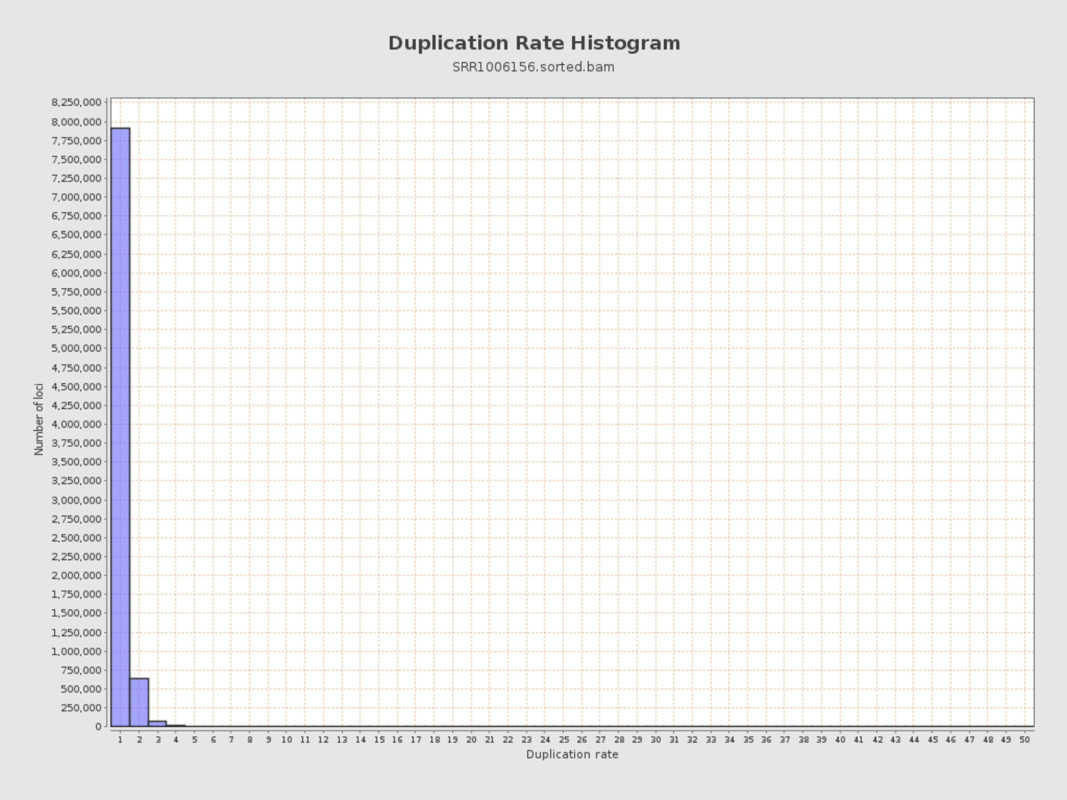
5. Results : Coverage Histogram (0-50X)



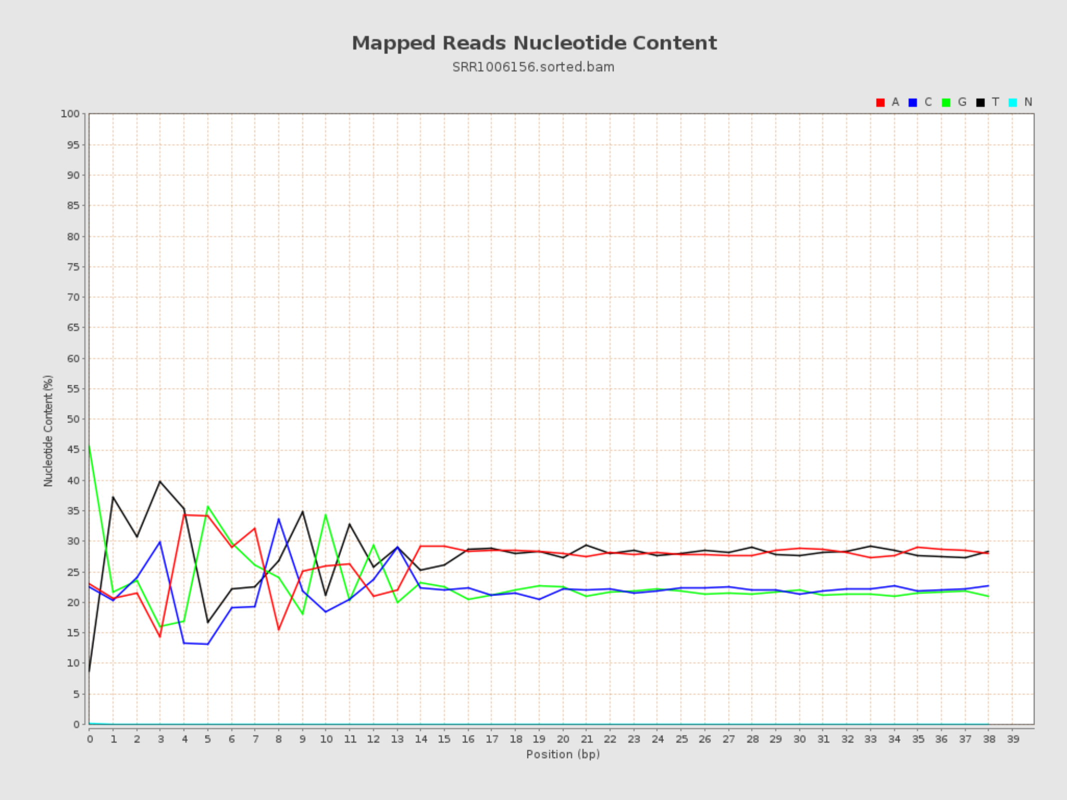
6. Results : Genome Fraction Coverage



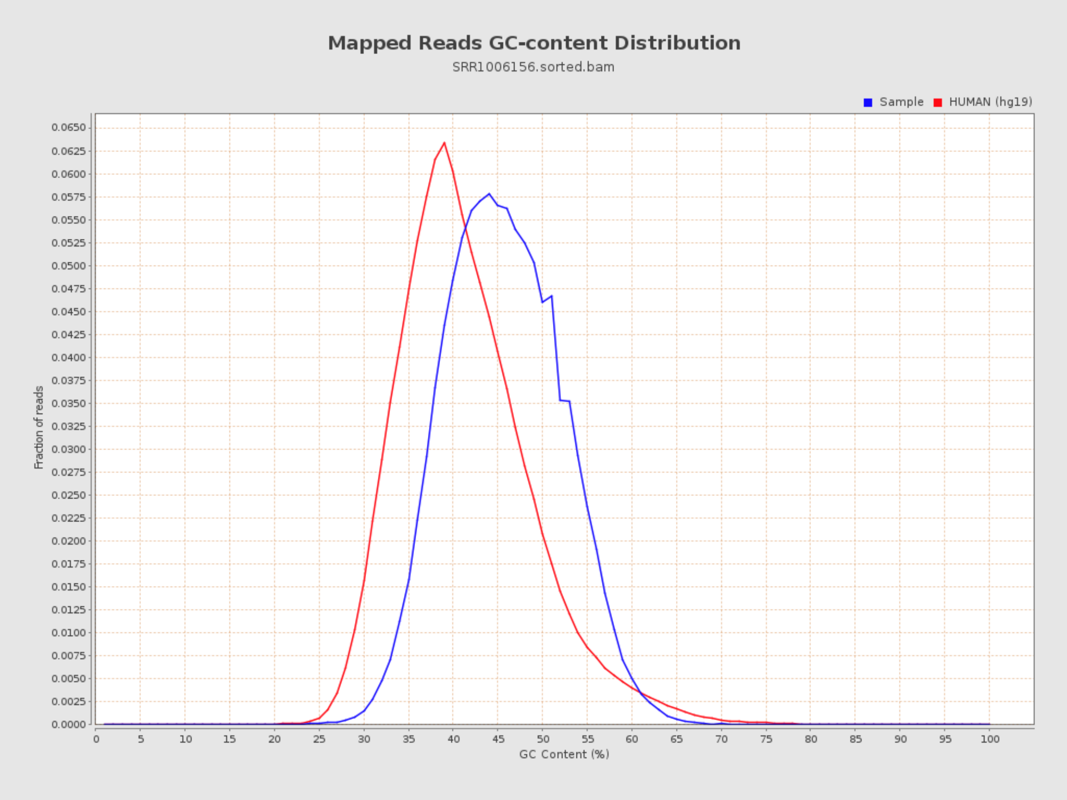
7. Results : Duplication Rate Histogram



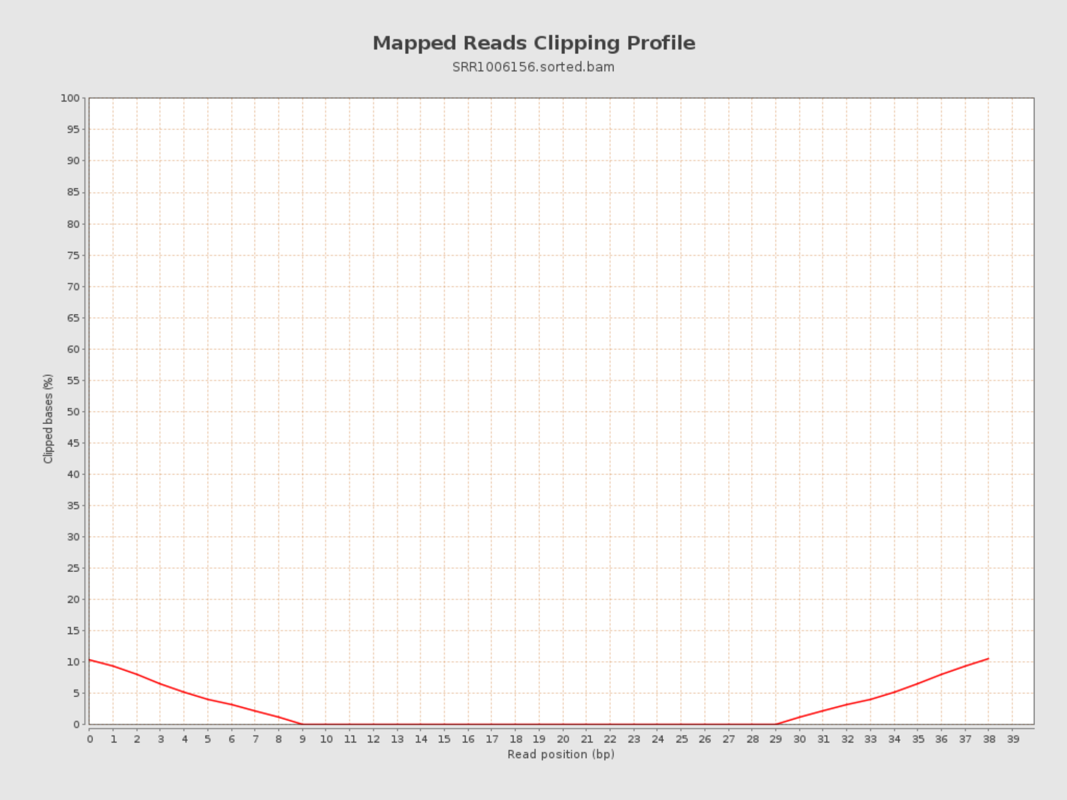
8. Results : Mapped Reads Nucleotide Content



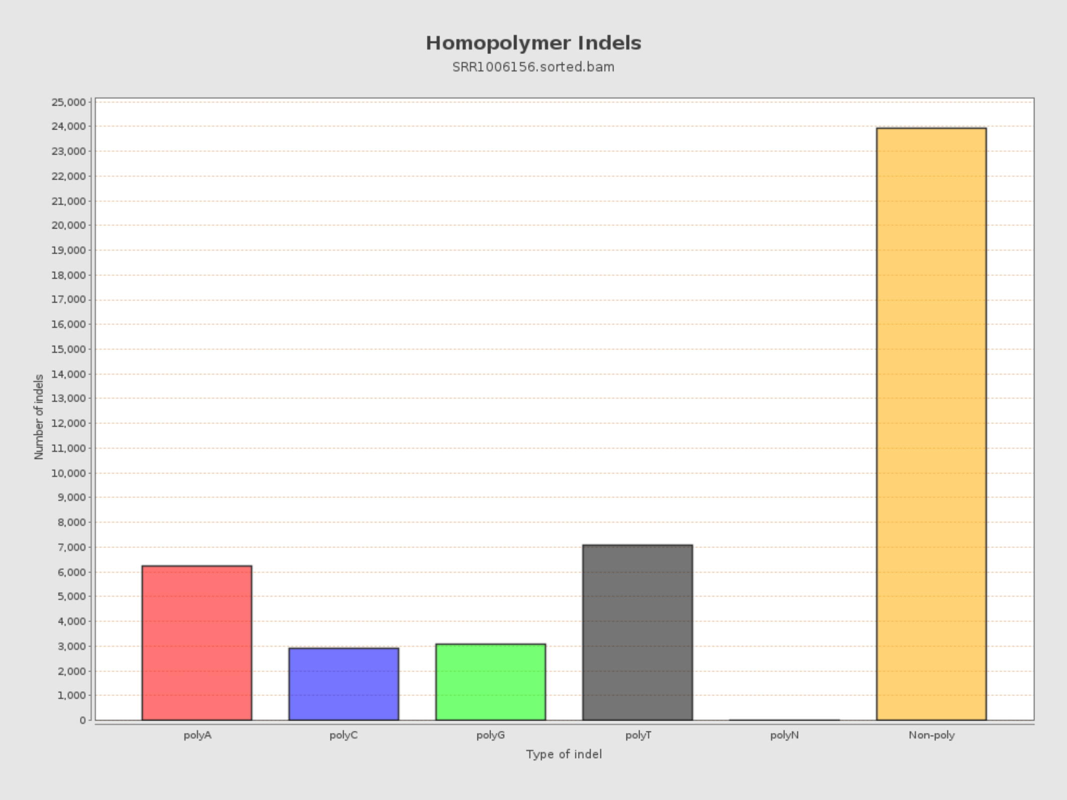
9. Results : Mapped Reads GC-content Distribution



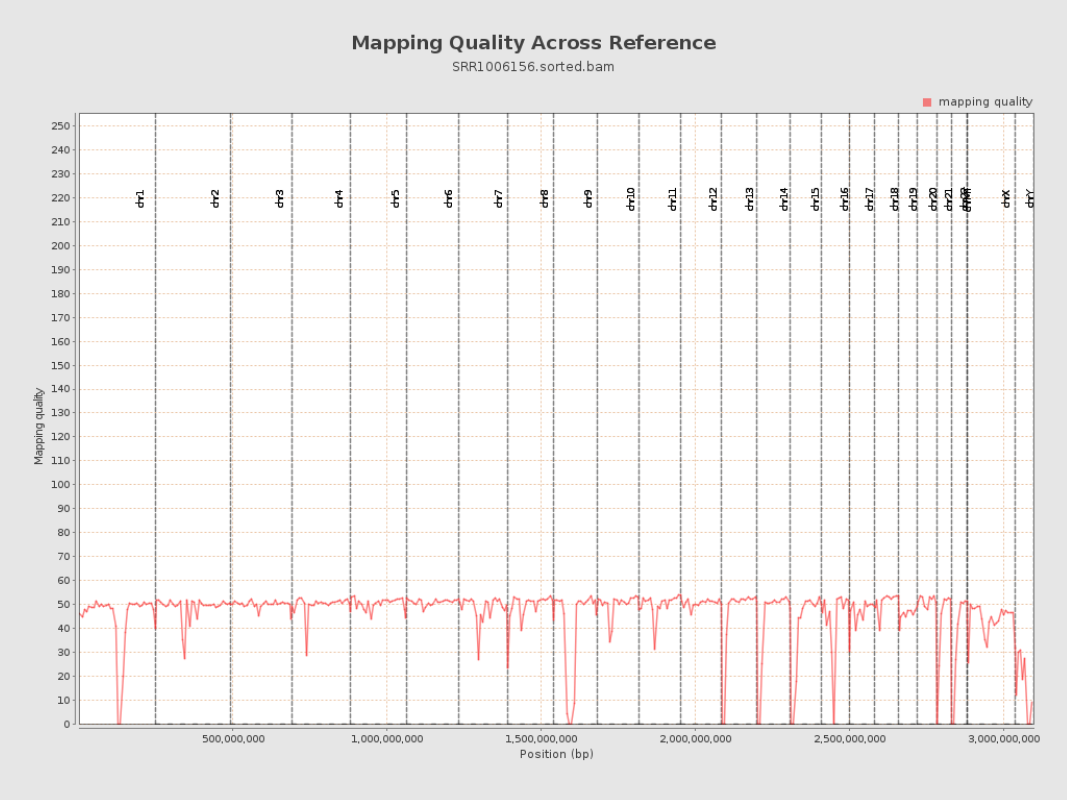
10. Results : Mapped Reads Clipping Profile



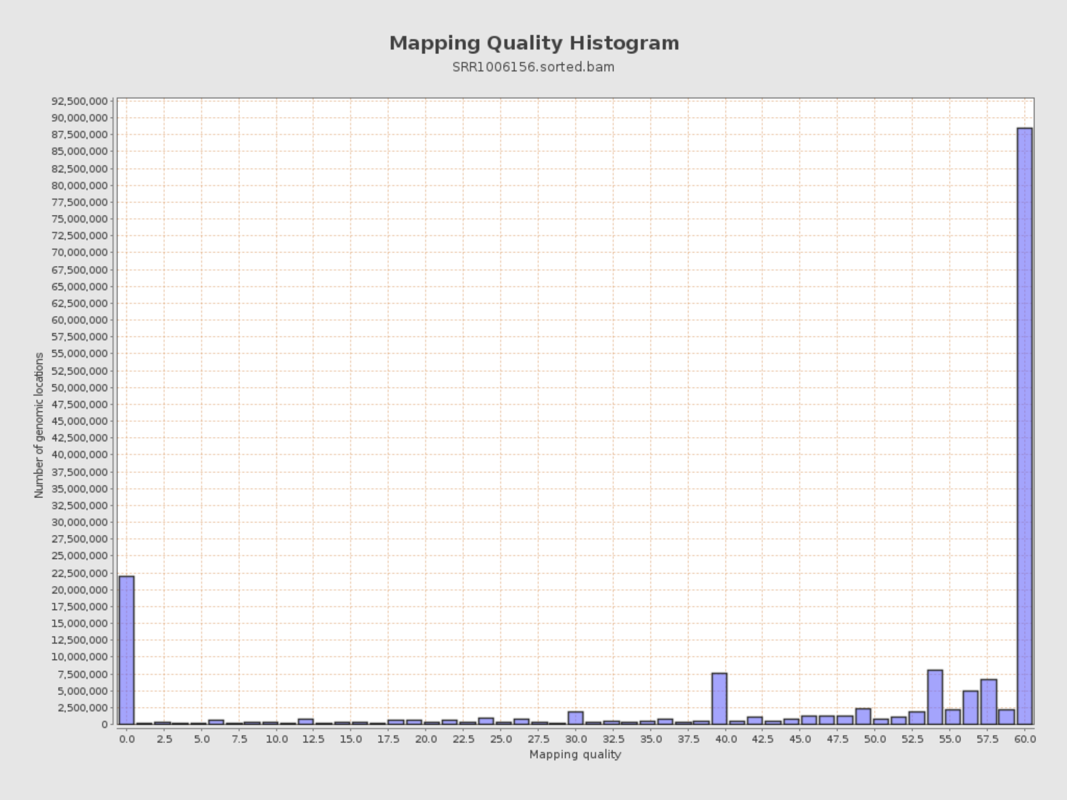
11. Results : Homopolymer Indels



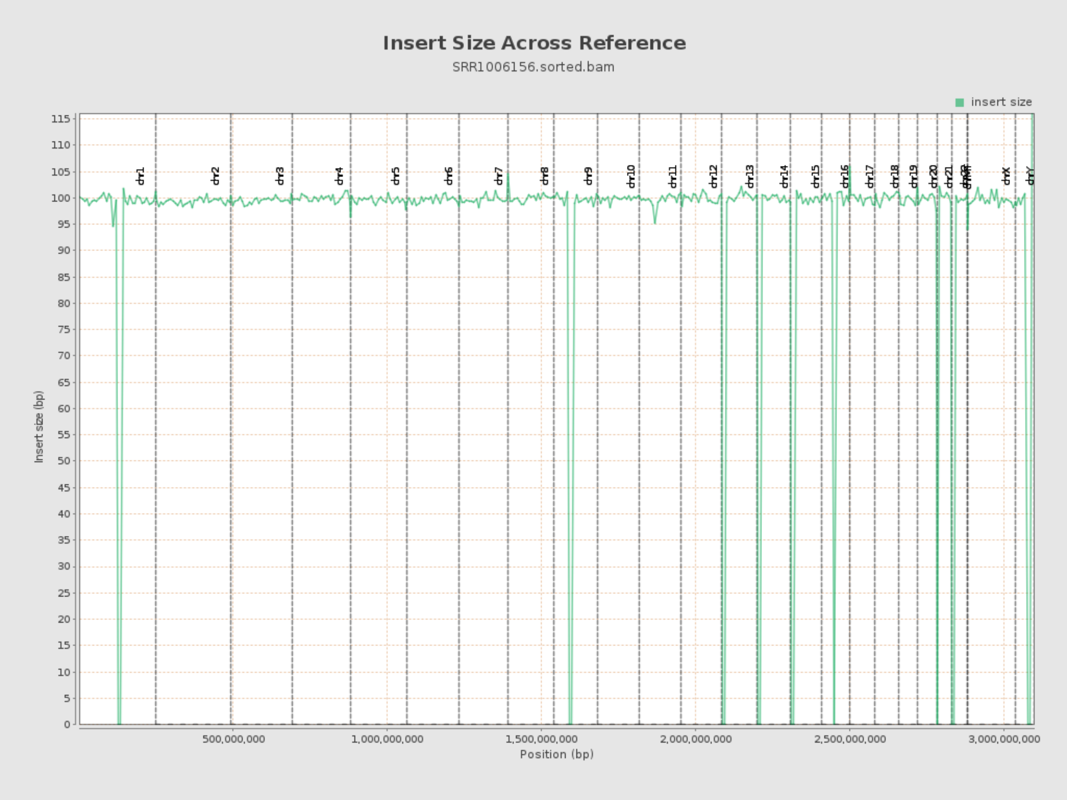
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram