Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 15:52:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006042.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_SRR1006042 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006042_1.fastq.gz SRR1006042_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 15:52:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006042.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,783,358
Mapped reads	12,211,637 / 88.6%
Unmapped reads	1,571,721 / 11.4%
Mapped paired reads	12,211,637 / 88.6%
Mapped reads, first in pair	6,200,619 / 44.99%
Mapped reads, second in pair	6,011,018 / 43.61%
Mapped reads, both in pair	11,297,074 / 81.96%
Mapped reads, singletons	914,563 / 6.64%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	883,560 / 6.41%
Duplication rate	6.44%
Clipped reads	856,991 / 6.22%

2.2. ACGT Content

Number/percentage of A's	130,106,409 / 27.55%
Number/percentage of C's	103,126,764 / 21.84%
Number/percentage of T's	133,075,528 / 28.18%
Number/percentage of G's	105,749,593 / 22.39%
Number/percentage of N's	190,995 / 0.04%
GC Percentage	44.23%

2.3. Coverage

Mean	0.1526
Standard Deviation	0.8069

2.4. Mapping Quality

Mean Mapping Quality	47.12

2.5. Insert size

Mean	52,706.14
Standard Deviation	2,238,331.69
P25/Median/P75	65 / 92 / 133

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	2,681,014
Insertions	13,720
Mapped reads with at least one insertion	0.11%
Deletions	38,113
Mapped reads with at least one deletion	0.31%
Homopolymer indels	46.61%

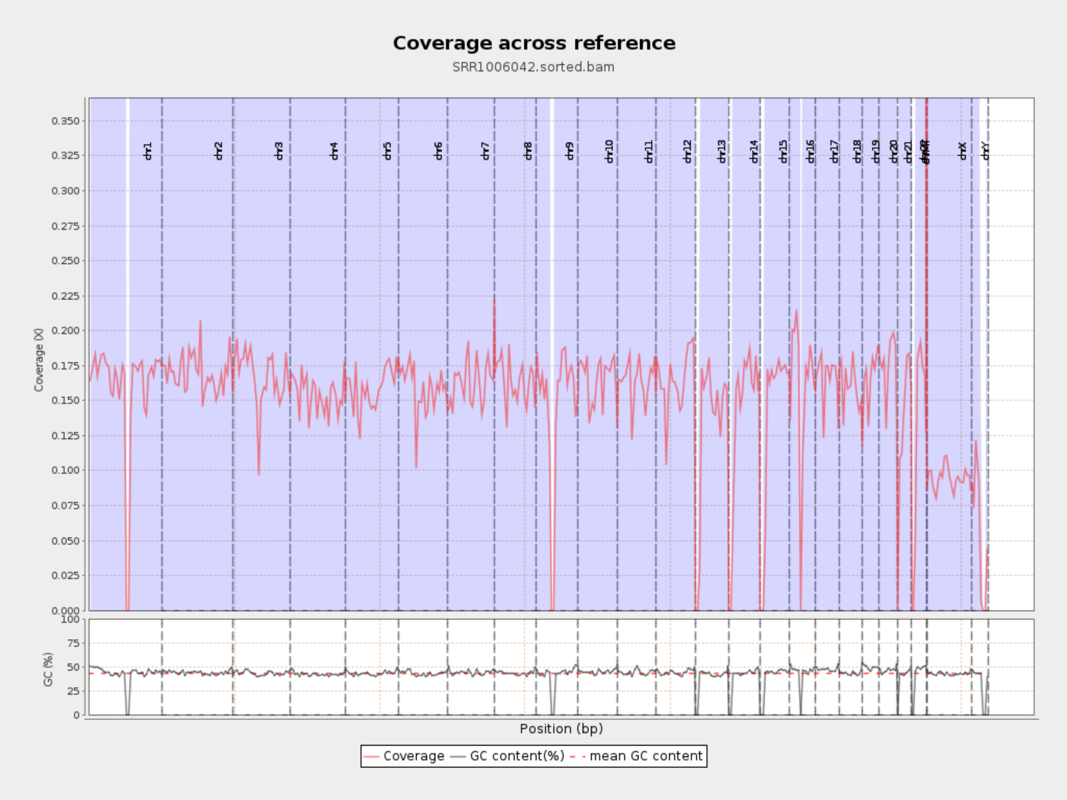
2.7. Chromosome stats

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

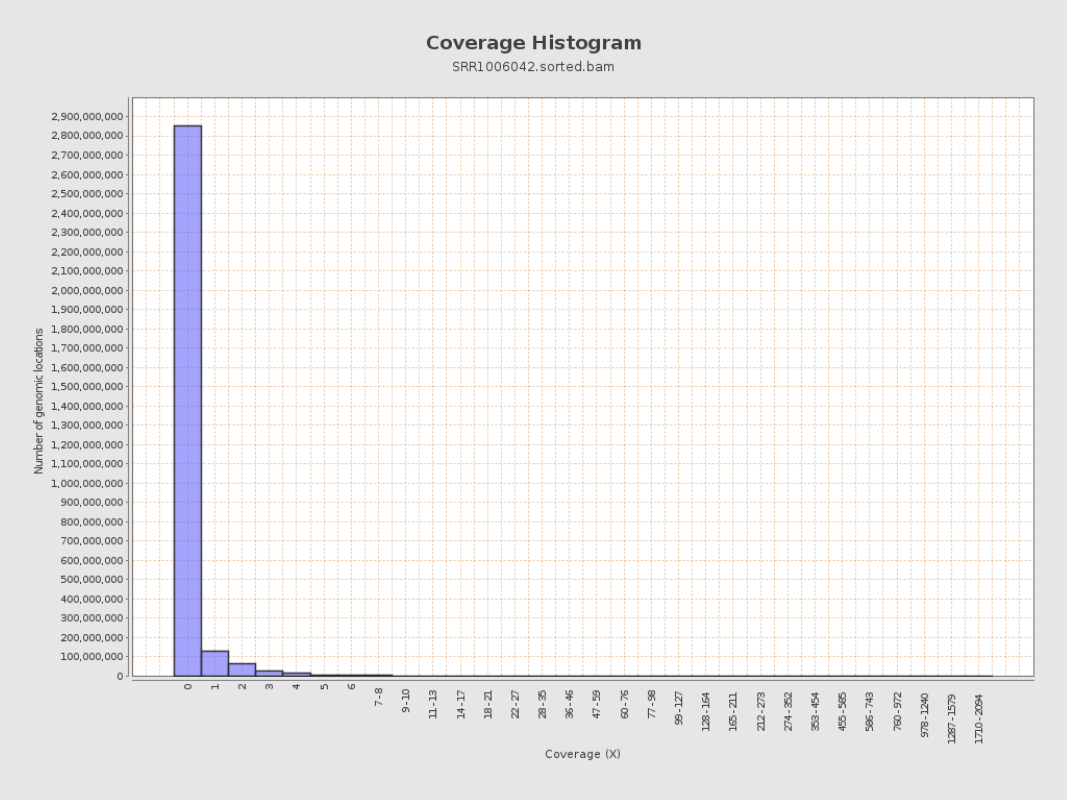
chr1	249250621	39566143	0.1587	0.8646
chr2	243199373	41398736	0.1702	0.8647
chr3	198022430	33053347	0.1669	0.6836
chr4	191154276	29441712	0.154	0.688
chr5	180915260	28711234	0.1587	0.6668
chr6	171115067	27260405	0.1593	0.7733
chr7	159138663	25938823	0.163	1.1108
chr8	146364022	24032413	0.1642	0.9526
chr9	141213431	20300661	0.1438	0.7528
chr10	135534747	22624033	0.1669	0.7233
chr11	135006516	22179323	0.1643	1.2937
chr12	133851895	21980875	0.1642	0.6847
chr13	115169878	14970858	0.13	0.6067
chr14	107349540	14785998	0.1377	0.6514
chr15	102531392	14134506	0.1379	0.6326
chr16	90354753	14539288	0.1609	0.7353
chr17	81195210	13461762	0.1658	0.82
chr18	78077248	12564225	0.1609	1.0874
chr19	59128983	9851514	0.1666	0.9064
chr20	63025520	11033550	0.1751	0.7222
chr21	48129895	6428697	0.1336	0.7015
chr22	51304566	6183400	0.1205	0.6502
chrMT	16571	60486	3.6501	4.5924
chrX	155270560	14708252	0.0947	0.5596

chrY	59373566	3087173	0.052	0.4237

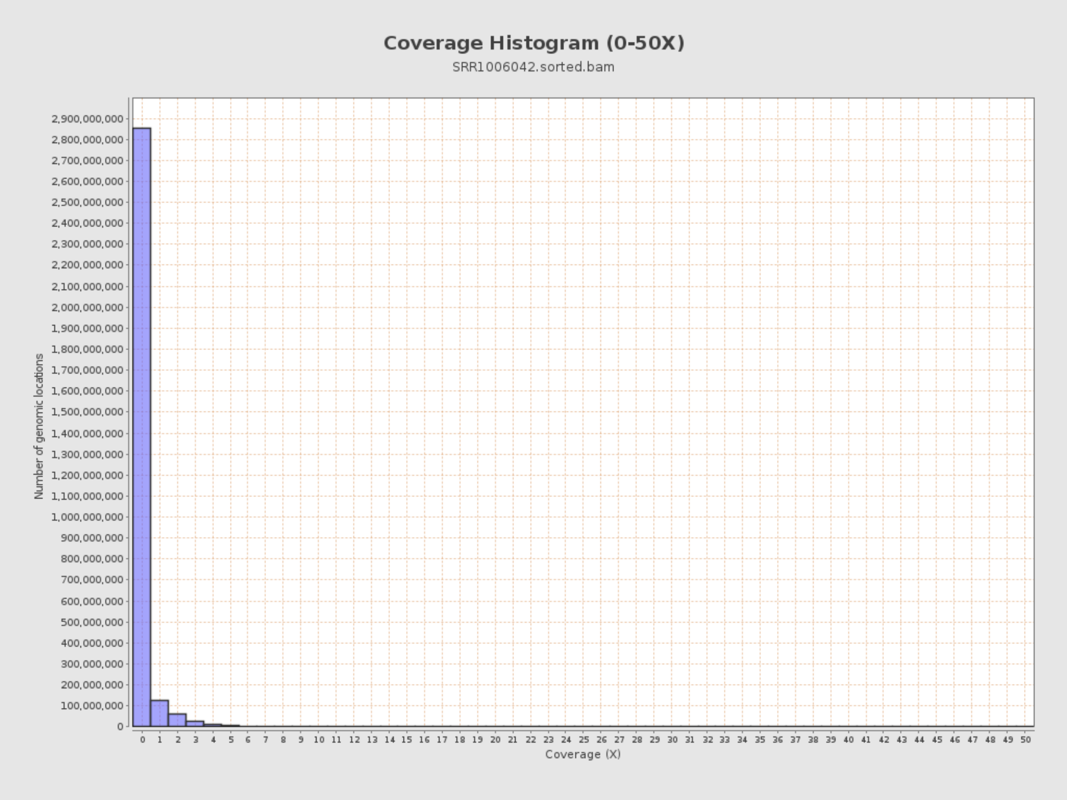
3. Results : Coverage across reference



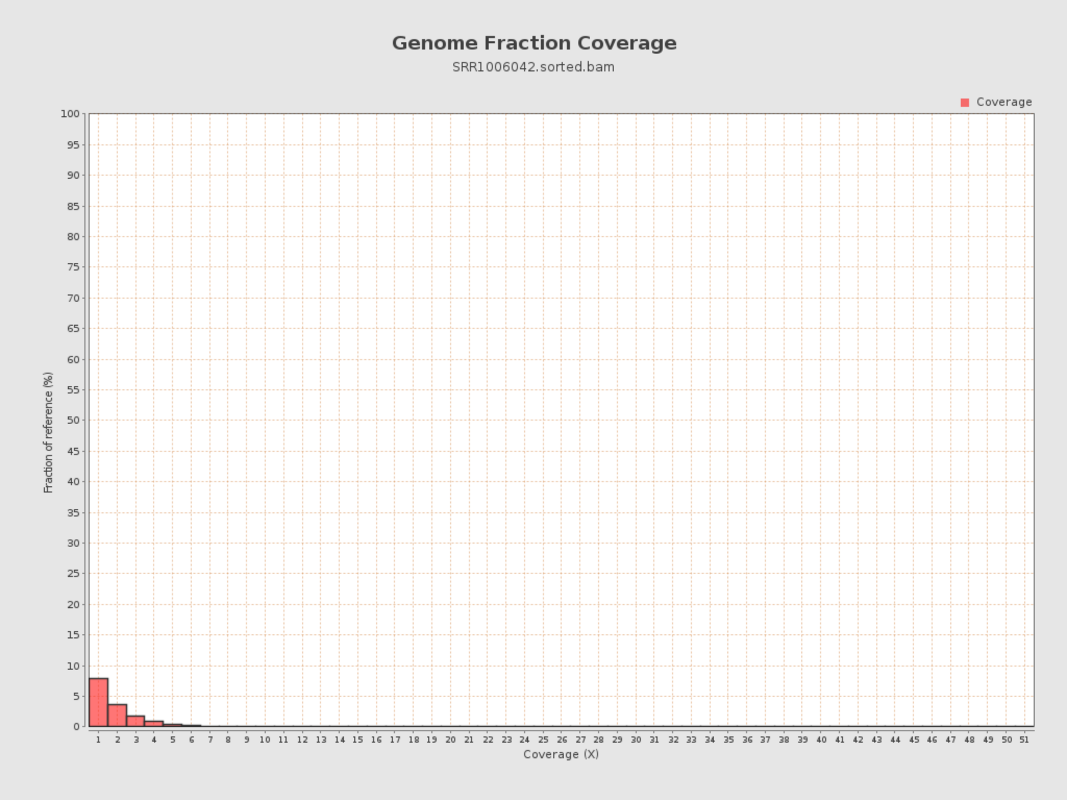
4. Results : Coverage Histogram



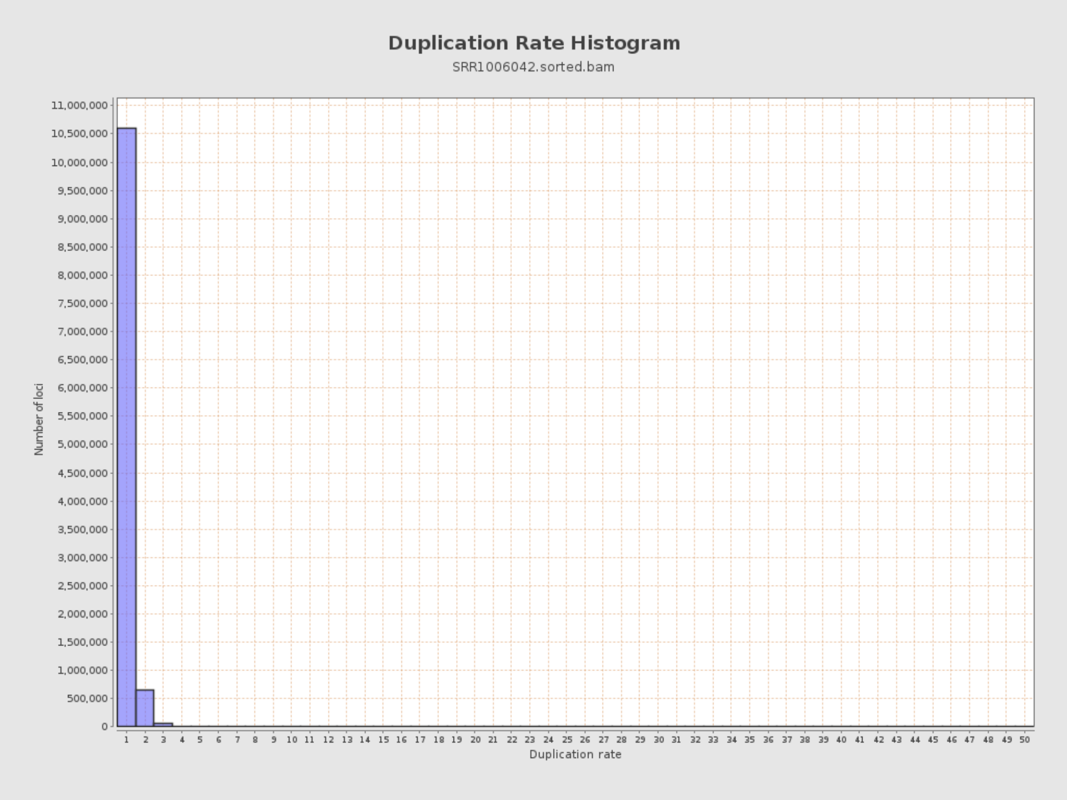
5. Results : Coverage Histogram (0-50X)



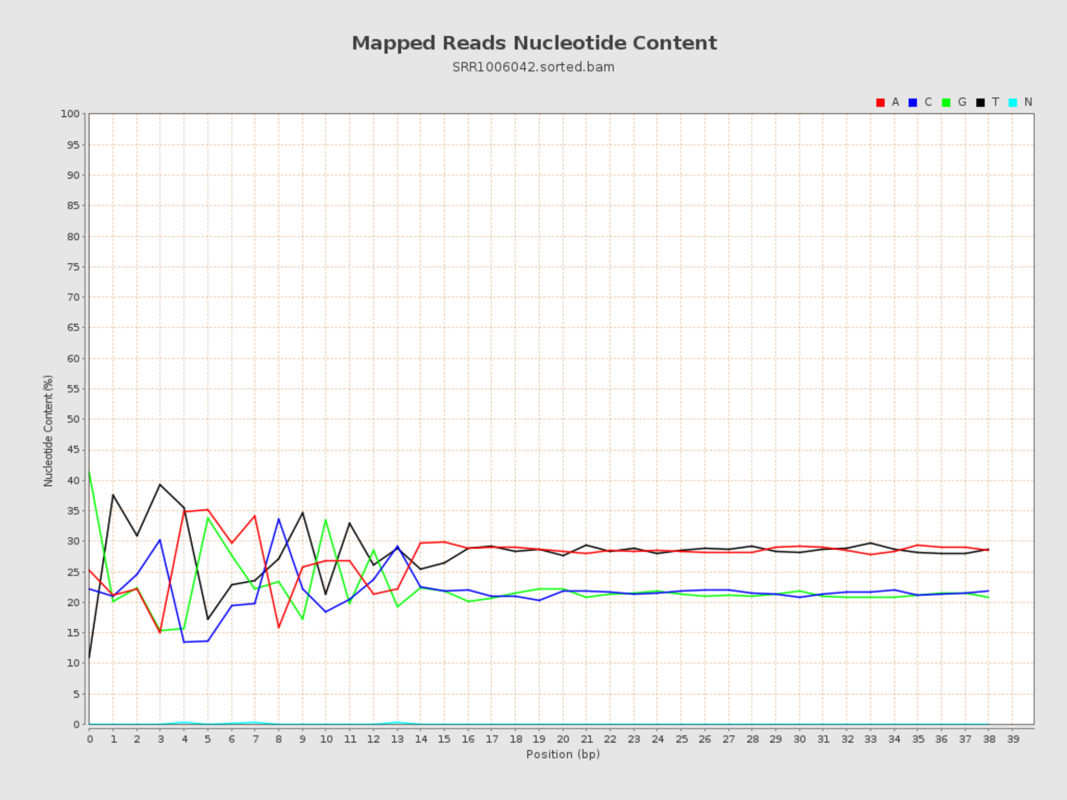
6. Results : Genome Fraction Coverage



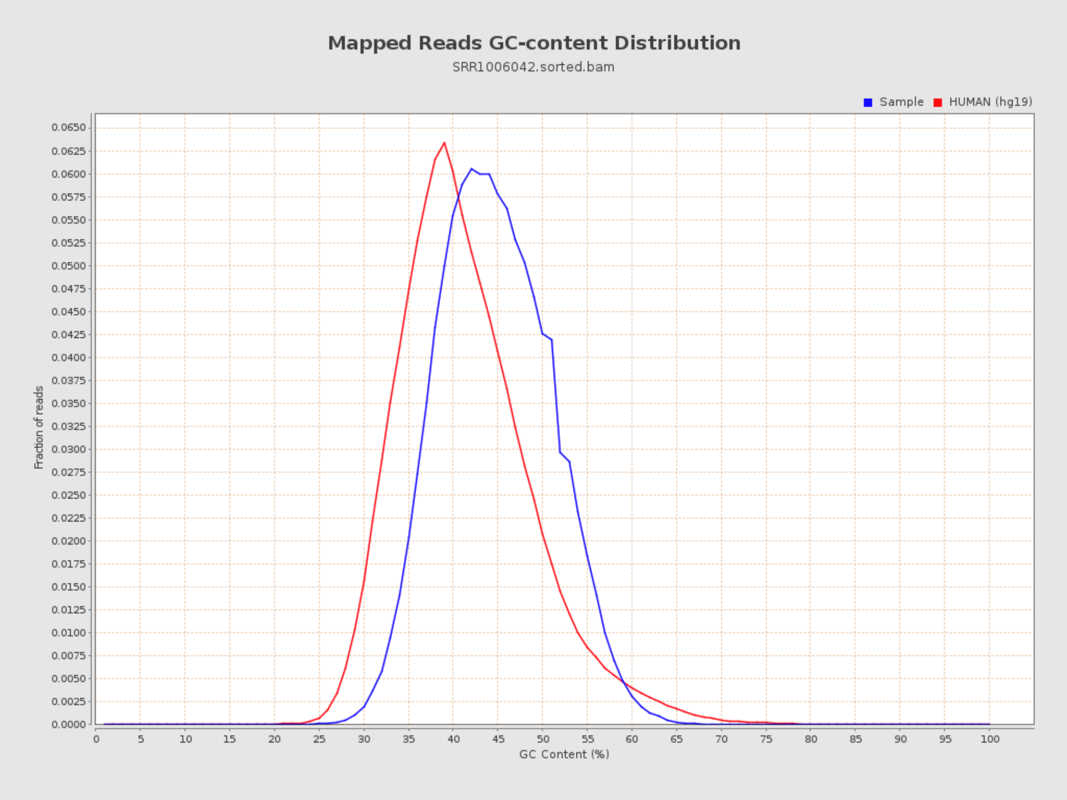
7. Results : Duplication Rate Histogram



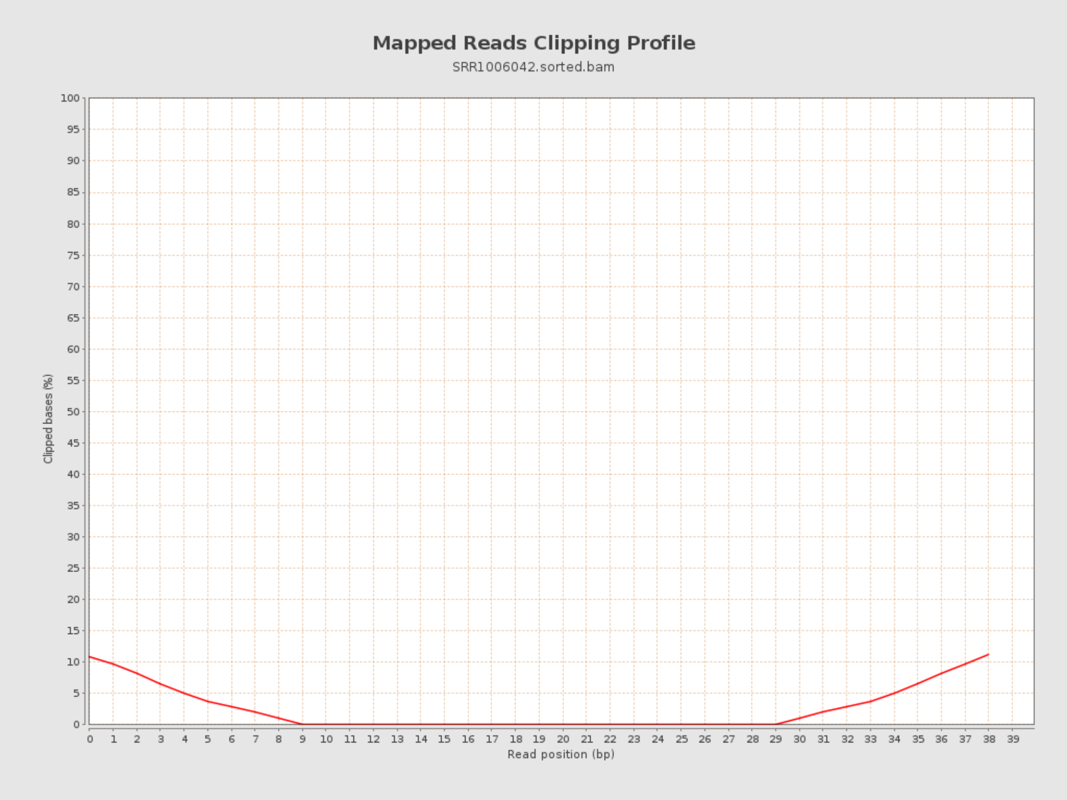
8. Results : Mapped Reads Nucleotide Content



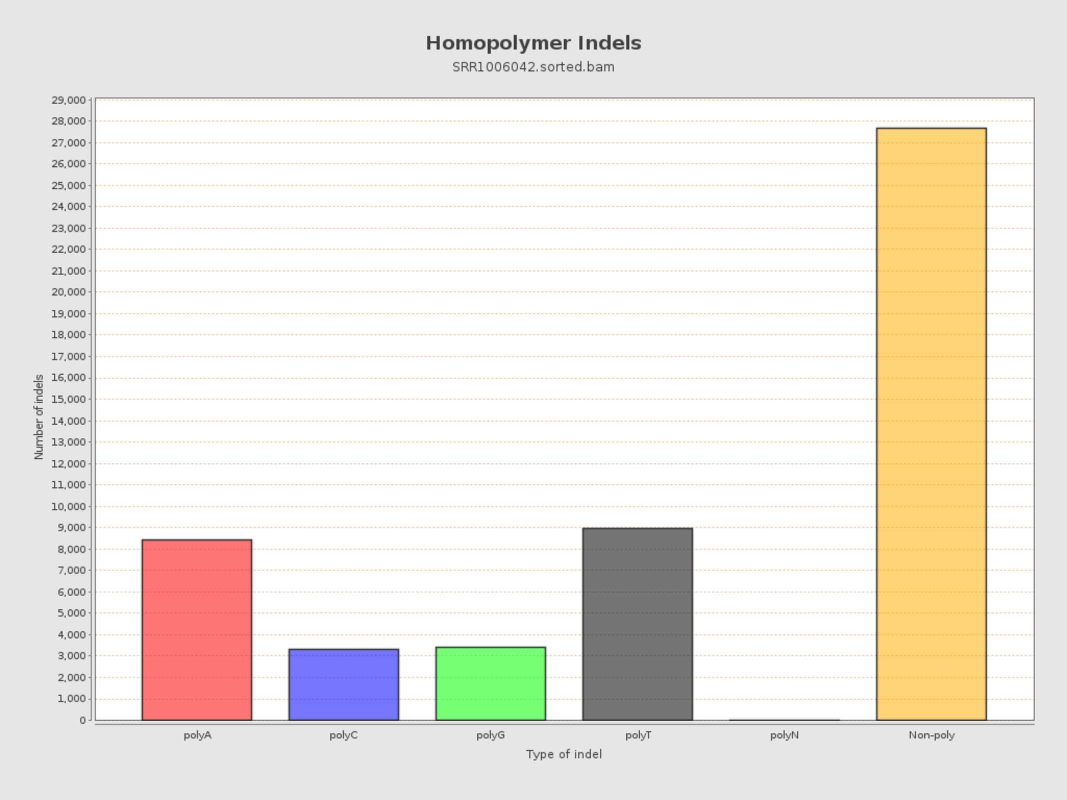
9. Results : Mapped Reads GC-content Distribution



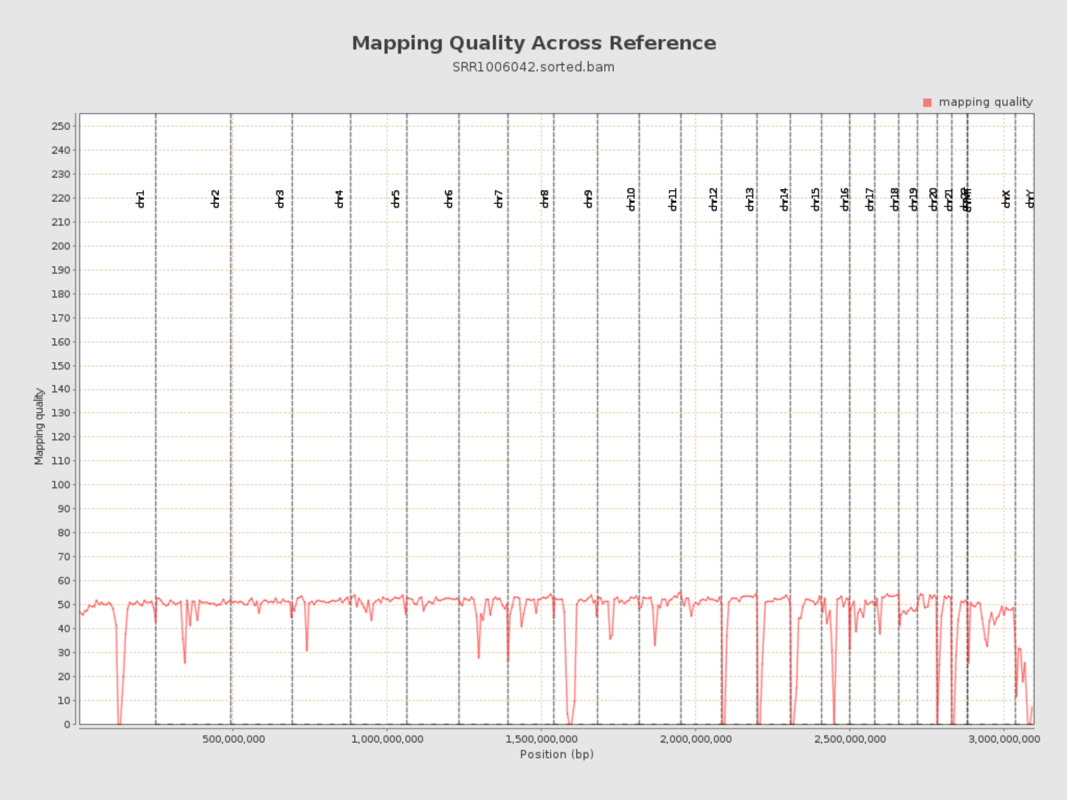
10. Results : Mapped Reads Clipping Profile



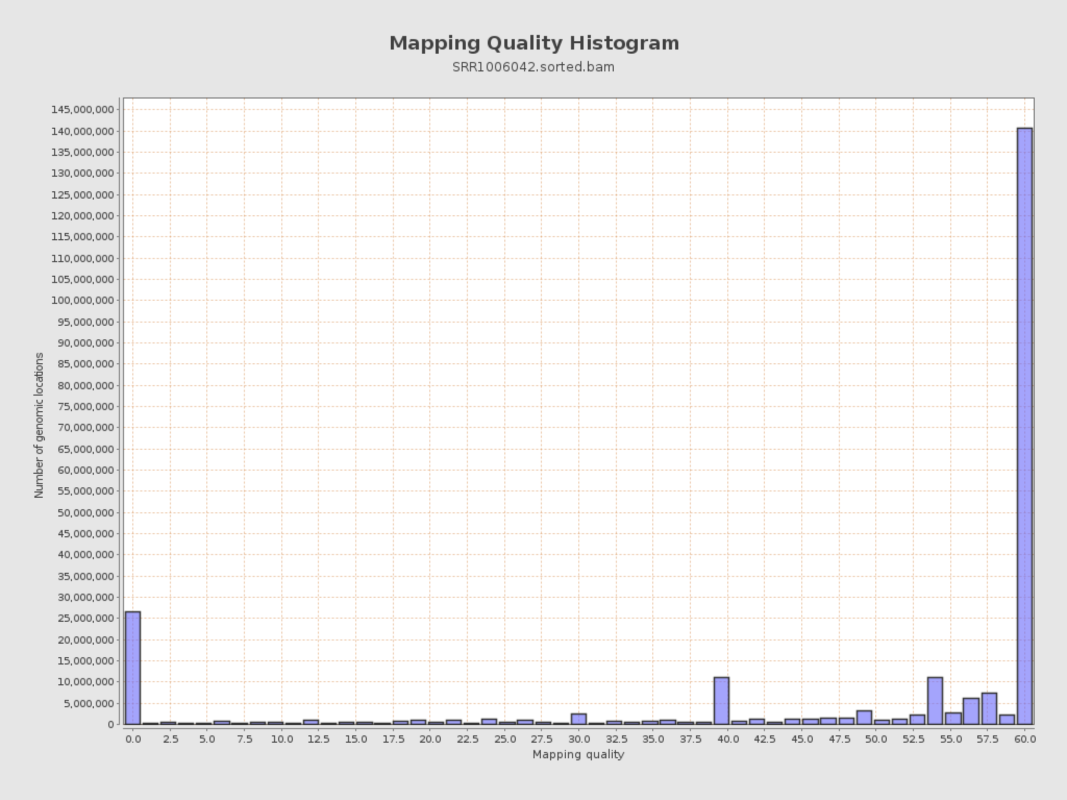
11. Results : Homopolymer Indels



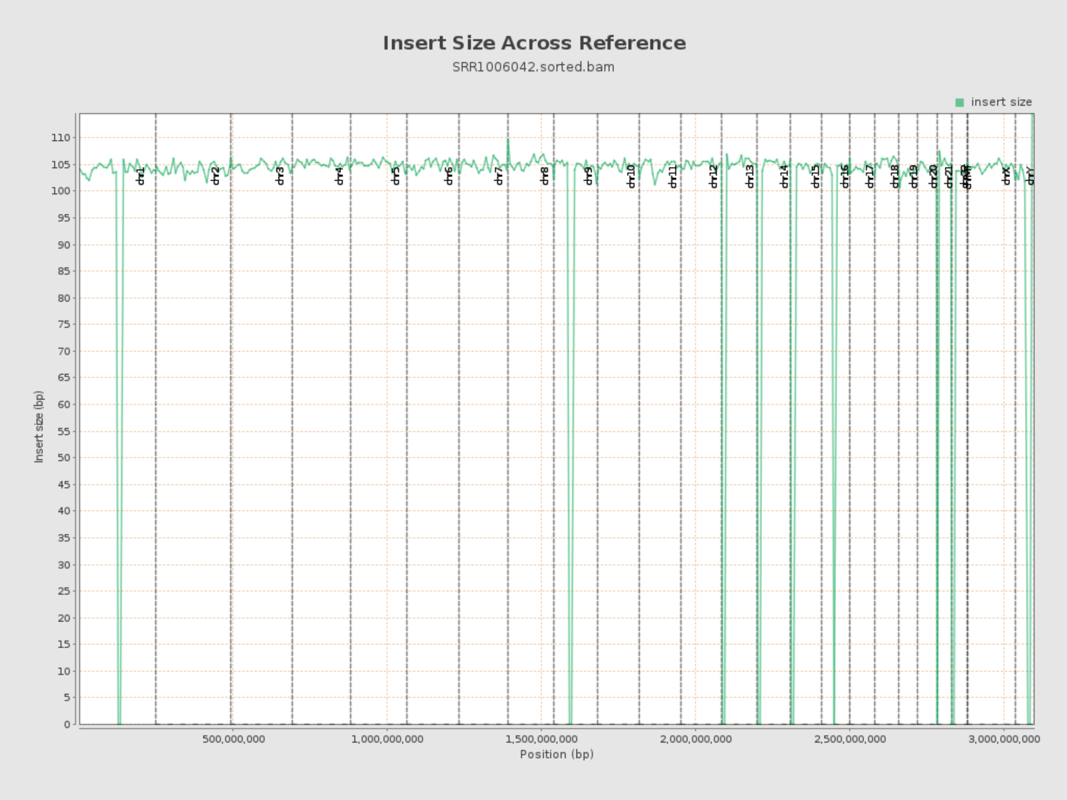
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram