

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 22:31:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006165.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_SRR1006165 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006165_1.fastq.gz SRR1006165_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 22:31:15 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006165.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,995,916
Mapped reads	3,383,122 / 84.66%
Unmapped reads	612,794 / 15.34%
Mapped paired reads	3,383,122 / 84.66%
Mapped reads, first in pair	1,700,774 / 42.56%
Mapped reads, second in pair	1,682,348 / 42.1%
Mapped reads, both in pair	3,122,498 / 78.14%
Mapped reads, singletons	260,624 / 6.52%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	96,825 / 2.42%
Duplication rate	2.42%
Clipped reads	180,160 / 4.51%

2.2. ACGT Content

Number/percentage of A's	36,736,206 / 28.05%
Number/percentage of C's	28,208,103 / 21.54%
Number/percentage of T's	37,486,853 / 28.62%
Number/percentage of G's	28,543,669 / 21.79%
Number/percentage of N's	4,906 / 0%
GC Percentage	43.33%

2.3. Coverage

Mean	0.0423
Standard Deviation	0.2882

2.4. Mapping Quality

Mean Mapping Quality	48.24
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2.5. Insert size

Mean	80,401.25
Standard Deviation	2,677,874.62
P25/Median/P75	108 / 175 / 235

2.6. Mismatches and indels

General error rate	0.3%
Mismatches	387,055
Insertions	3,750
Mapped reads with at least one insertion	0.11%
Deletions	12,996
Mapped reads with at least one deletion	0.38%
Homopolymer indels	44.64%

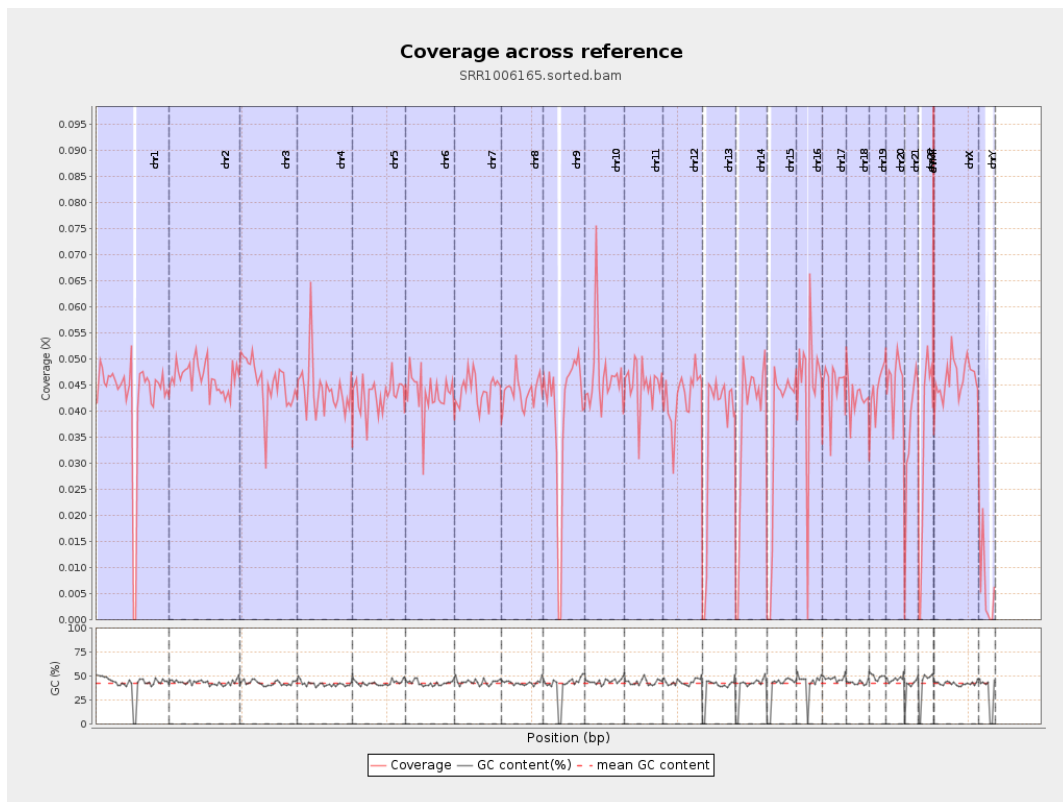
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

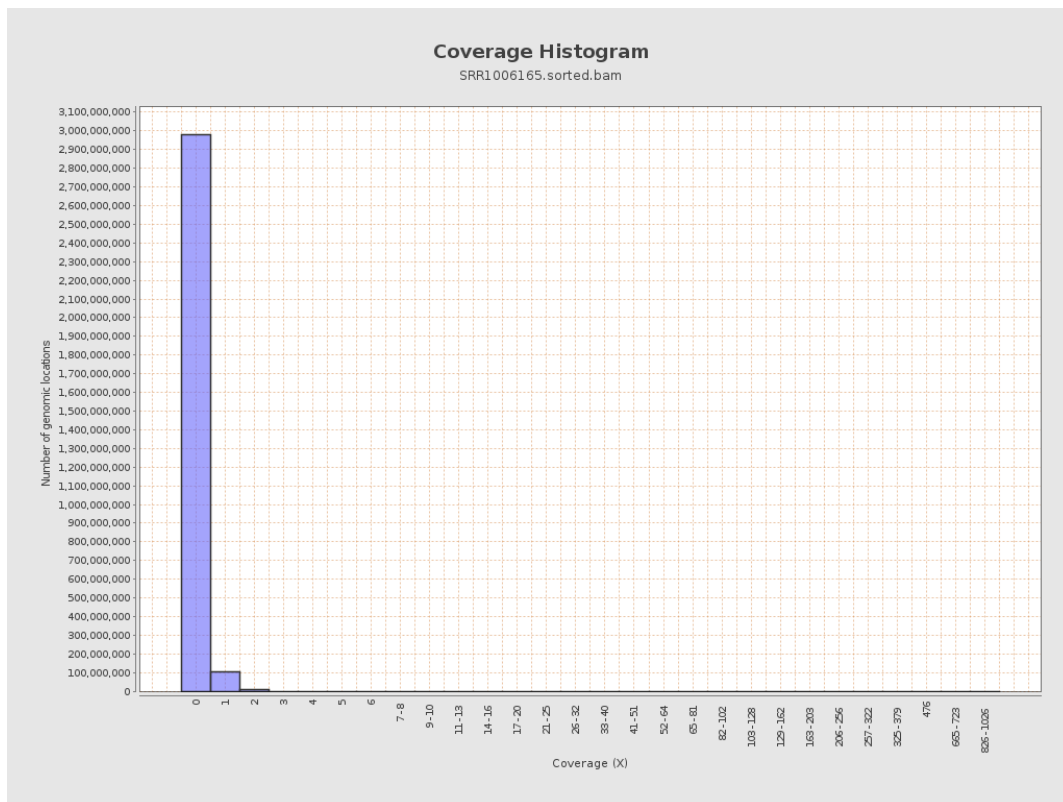
chr1	249250621	10605200	0.0425	0.3904
chr2	243199373	11309575	0.0465	0.2657
chr3	198022430	8991427	0.0454	0.2312
chr4	191154276	8405812	0.044	0.2469
chr5	180915260	7789009	0.0431	0.2256
chr6	171115067	7419173	0.0434	0.2438
chr7	159138663	7006604	0.044	0.2934
chr8	146364022	6412501	0.0438	0.548
chr9	141213431	5593789	0.0396	0.2345
chr10	135534747	6313735	0.0466	0.3306
chr11	135006516	6090567	0.0451	0.254
chr12	133851895	5697268	0.0426	0.2249
chr13	115169878	4126295	0.0358	0.2043
chr14	107349540	4088216	0.0381	0.2974
chr15	102531392	3703173	0.0361	0.2061
chr16	90354753	4047445	0.0448	0.2951
chr17	81195210	3628052	0.0447	0.2355
chr18	78077248	3331989	0.0427	0.3344
chr19	59128983	2608408	0.0441	0.3106
chr20	63025520	2859600	0.0454	0.2362
chr21	48129895	1731995	0.036	0.2206
chr22	51304566	1709942	0.0333	0.2008
chrMT	16571	2562	0.1546	0.4212
chrX	155270560	7163312	0.0461	0.2431

chrY	59373566	361492	0.0061	0.1781
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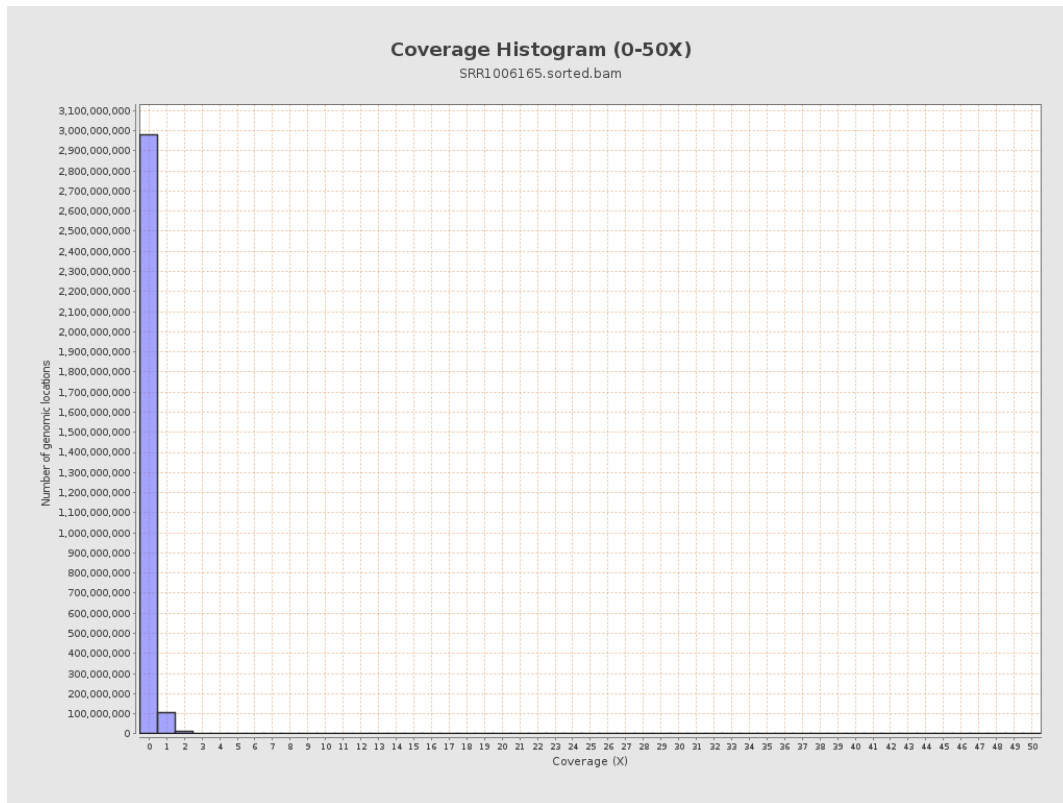
3. Results : Coverage across reference



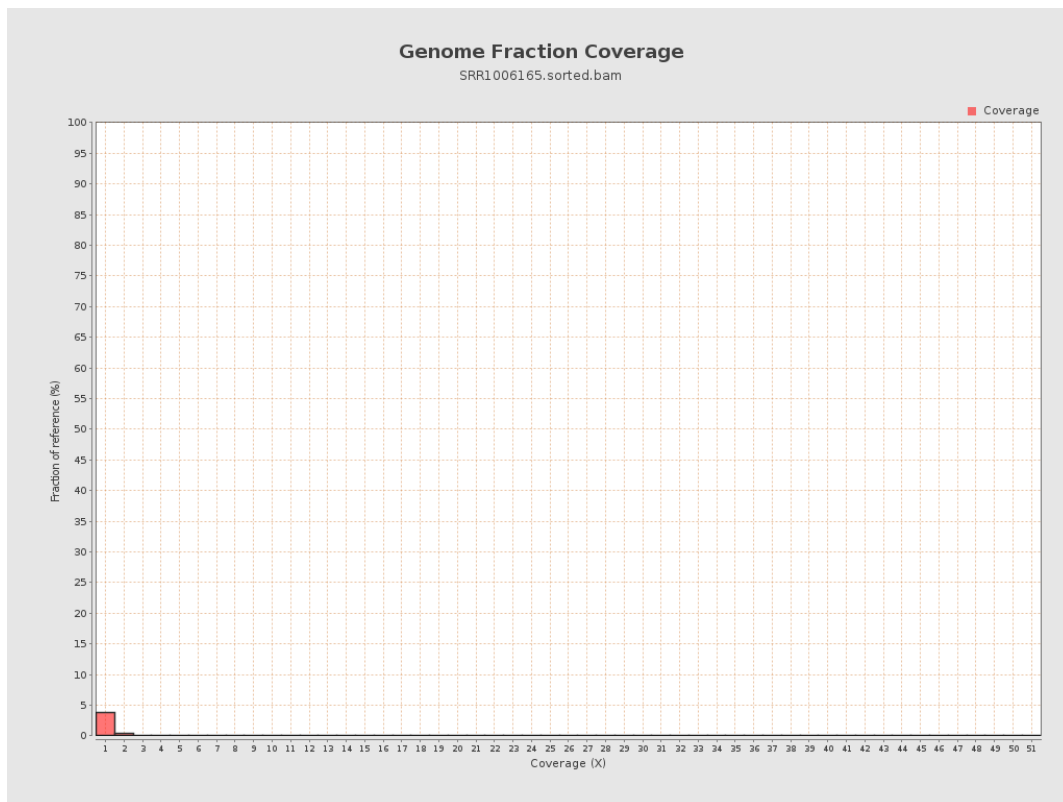
4. Results : Coverage Histogram



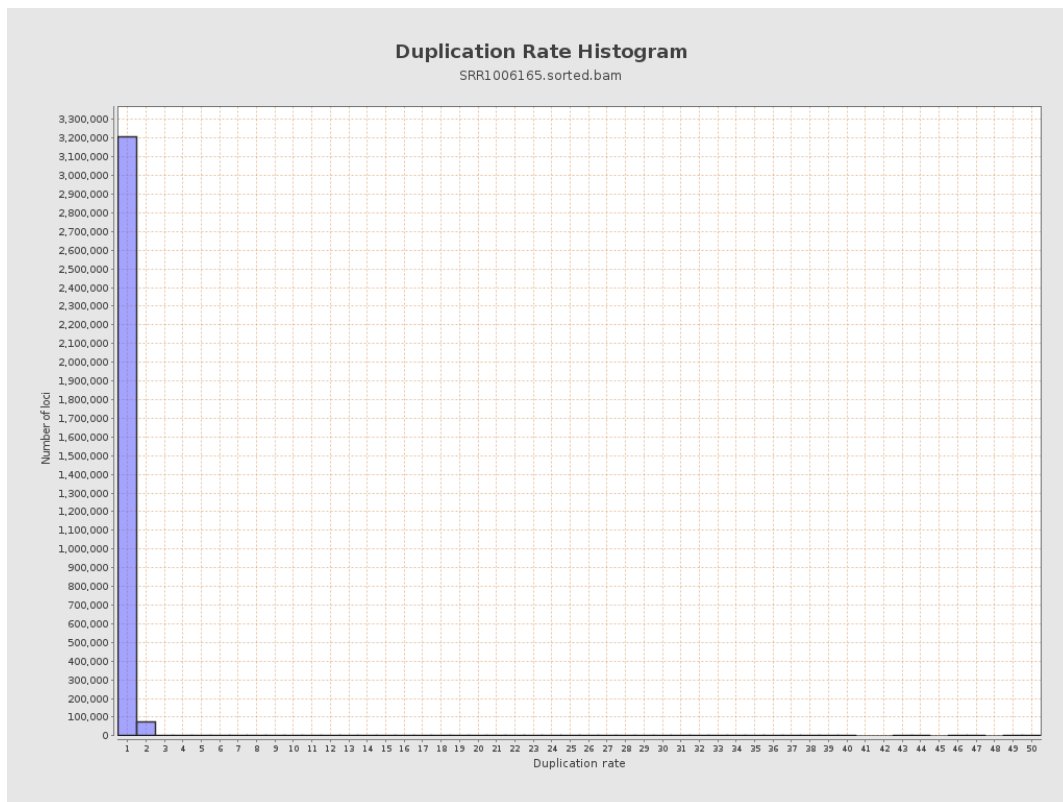
5. Results : Coverage Histogram (0-50X)



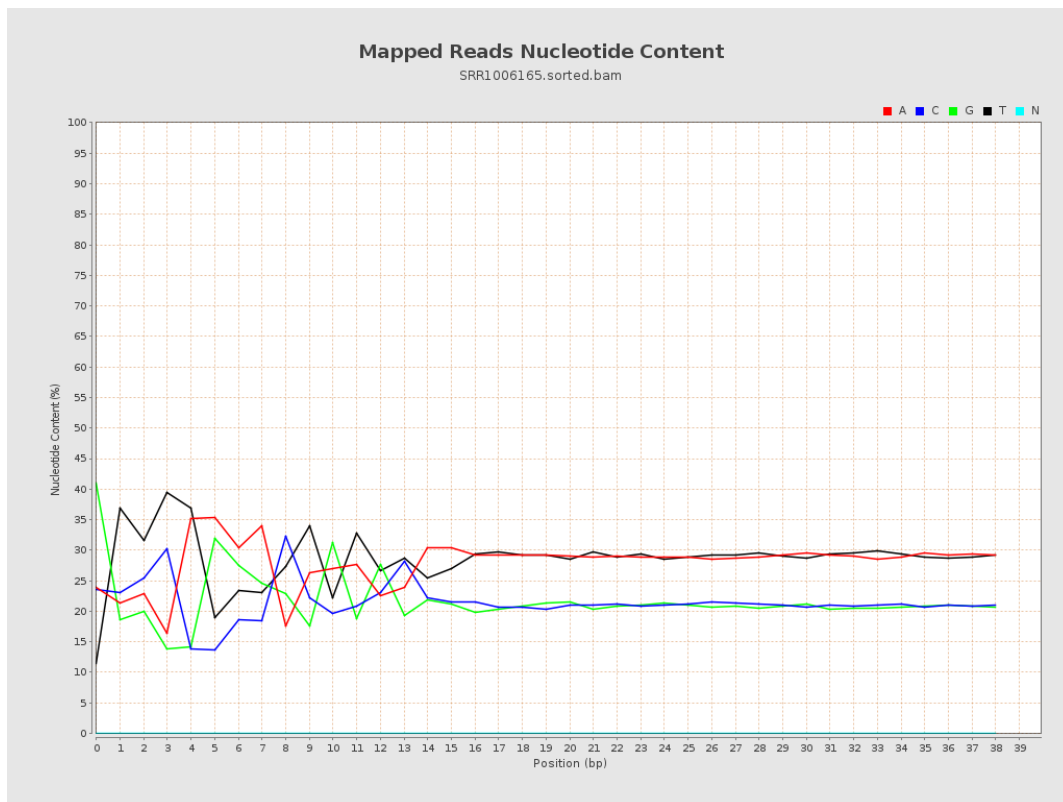
6. Results : Genome Fraction Coverage



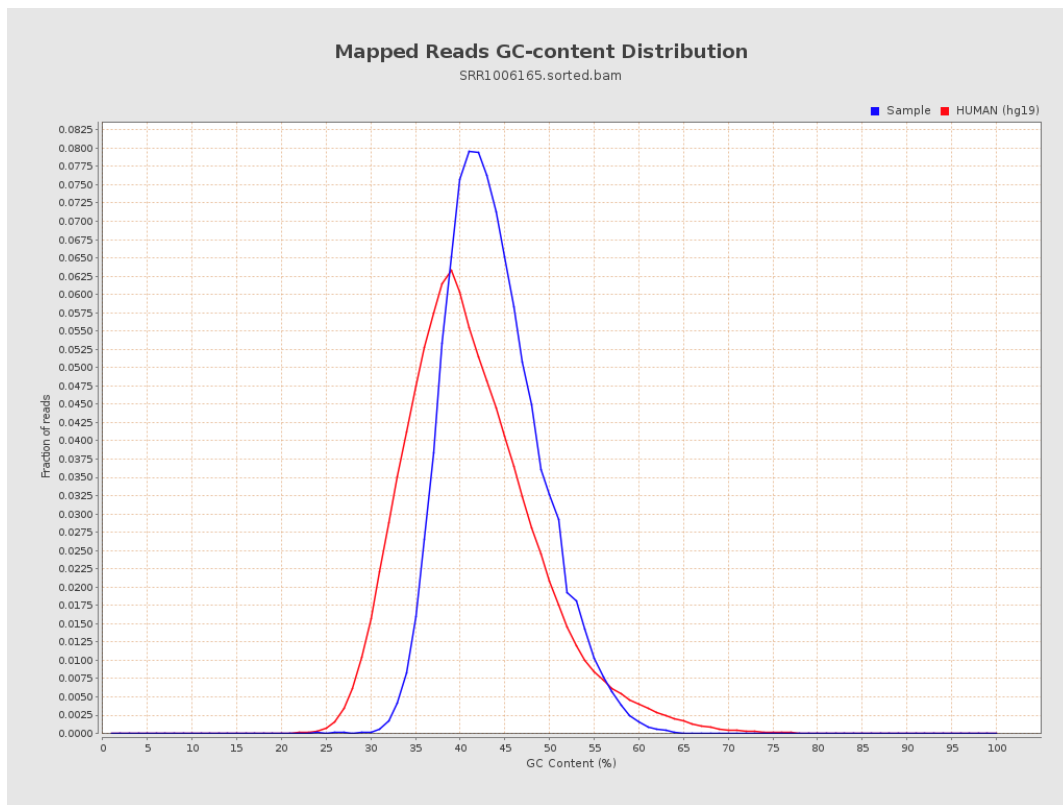
7. Results : Duplication Rate Histogram



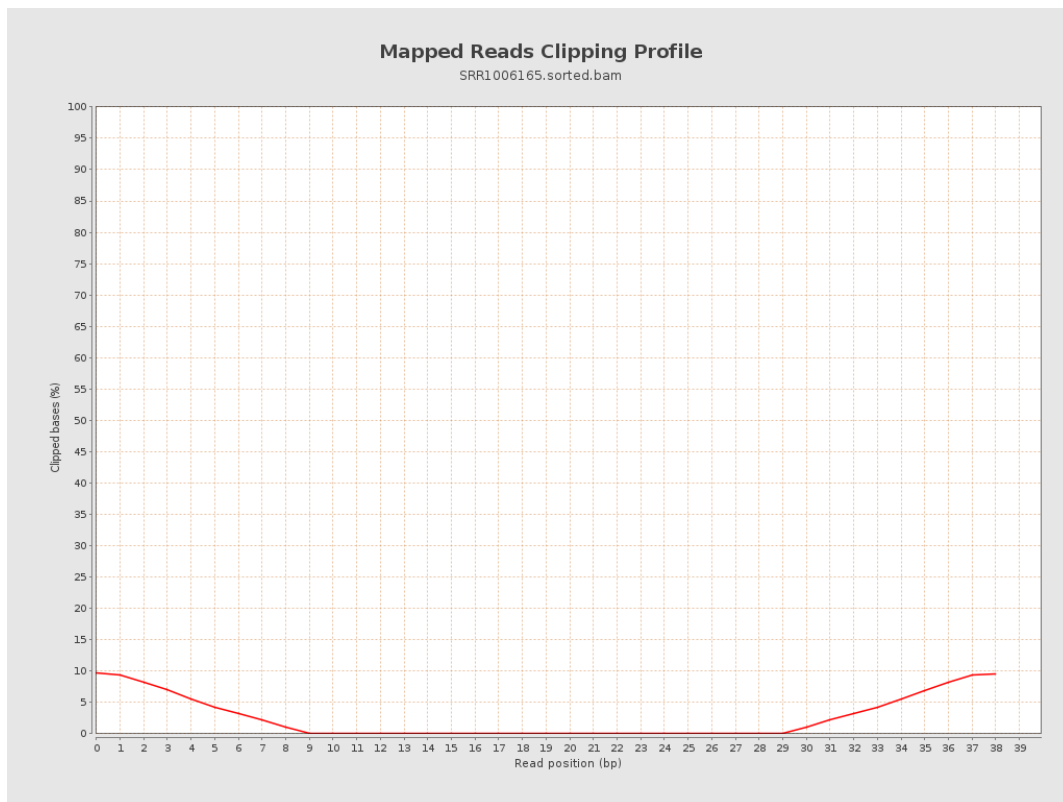
8. Results : Mapped Reads Nucleotide Content



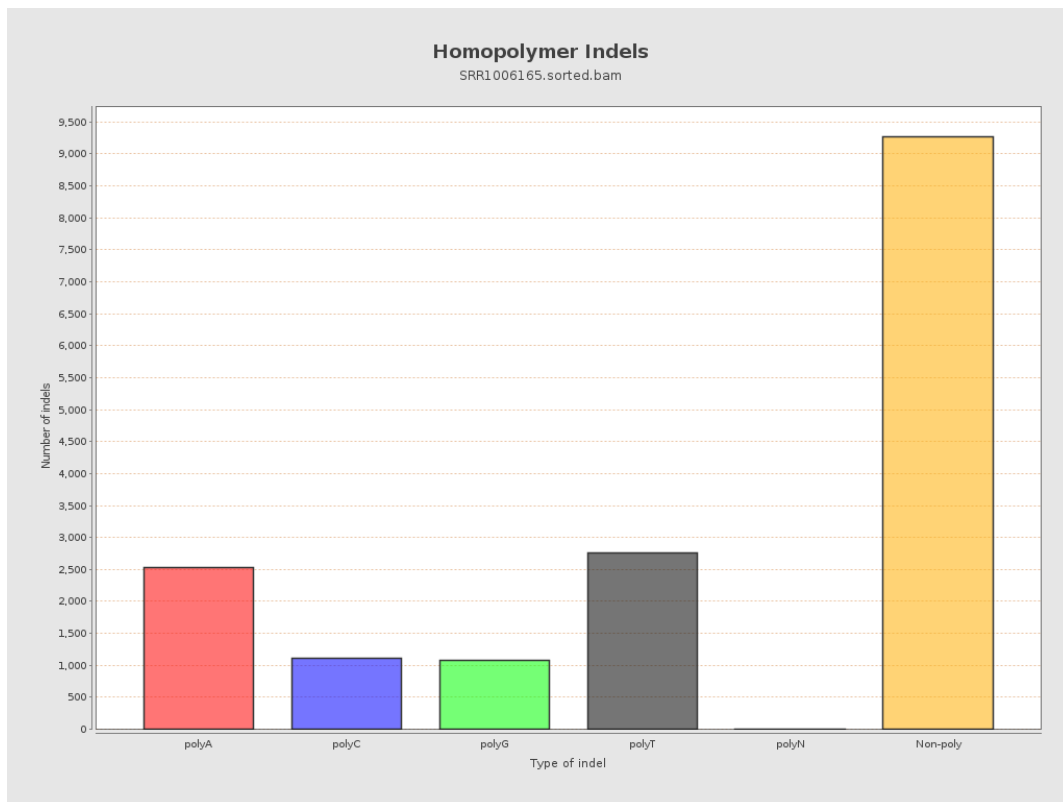
9. Results : Mapped Reads GC-content Distribution



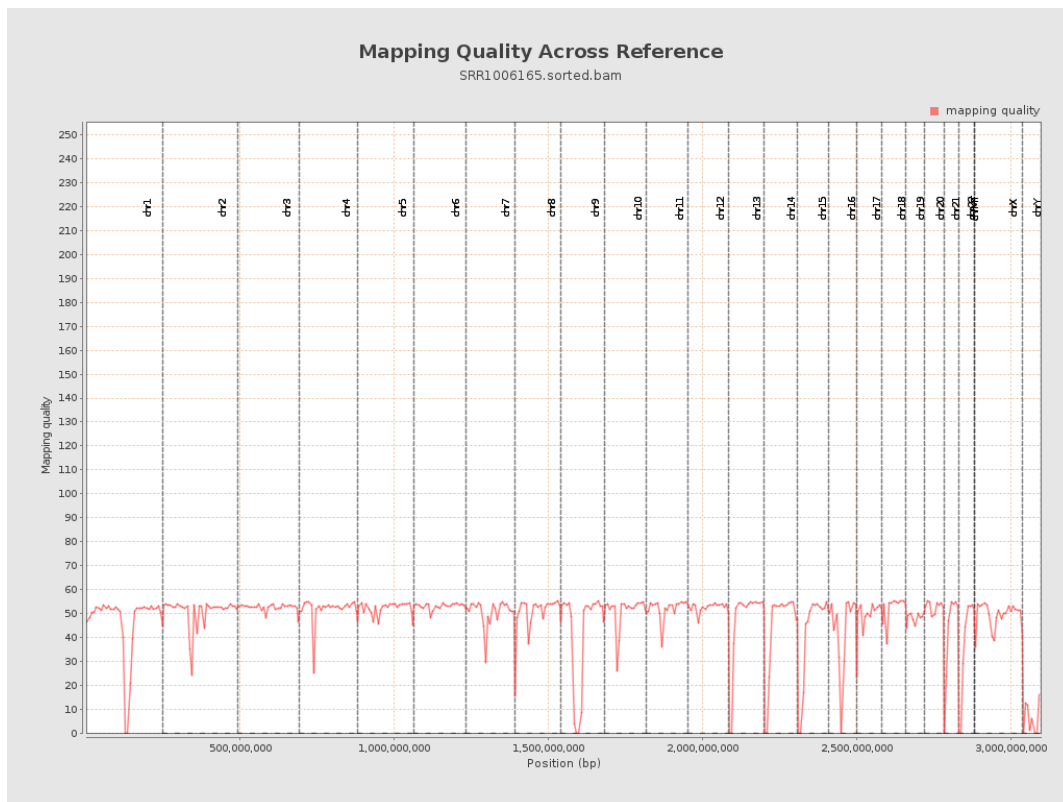
10. Results : Mapped Reads Clipping Profile



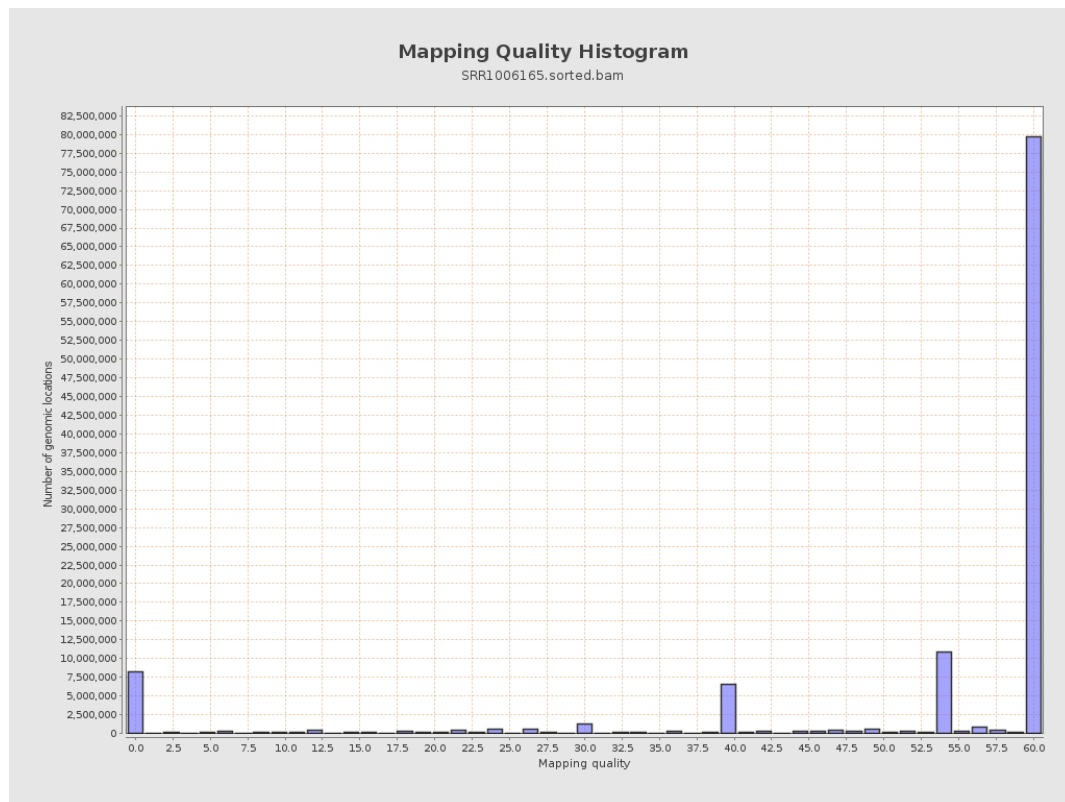
11. Results : Homopolymer Indels



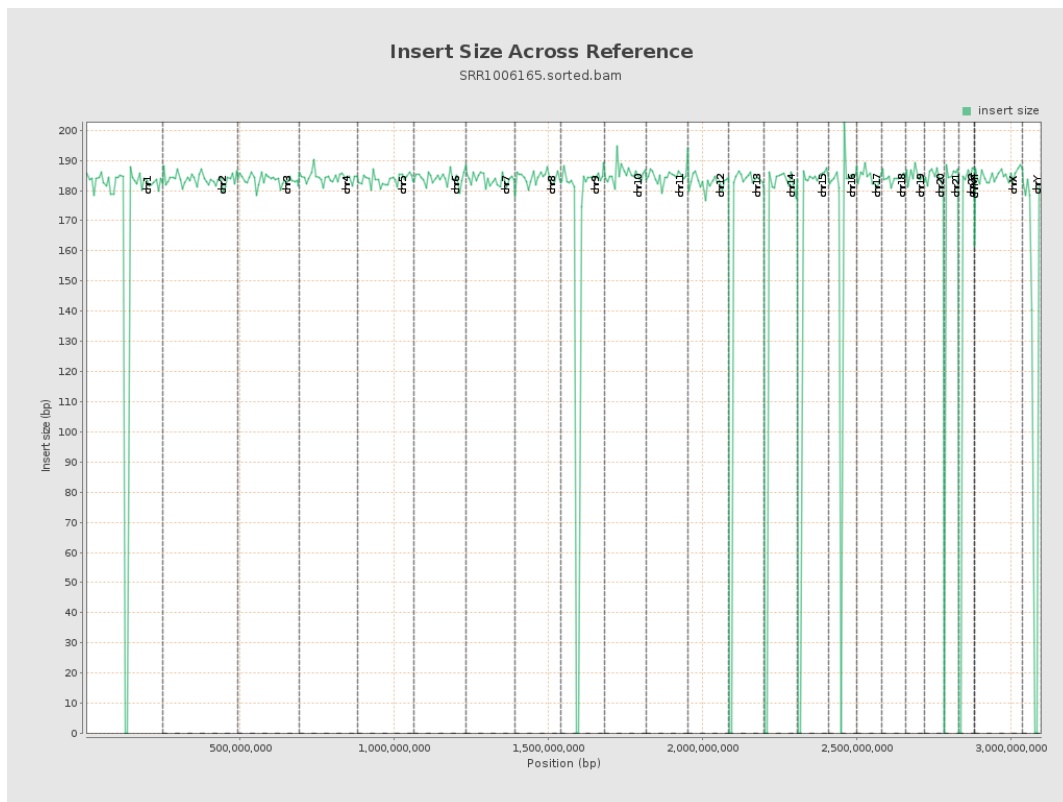
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

