

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 23:57:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006221.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_SRR1006221 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006221_1.fastq.gz SRR1006221_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 23:57:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006221.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,089,438
Mapped reads	10,748,598 / 88.91%
Unmapped reads	1,340,840 / 11.09%
Mapped paired reads	10,748,598 / 88.91%
Mapped reads, first in pair	5,423,412 / 44.86%
Mapped reads, second in pair	5,325,186 / 44.05%
Mapped reads, both in pair	9,911,728 / 81.99%
Mapped reads, singletons	836,870 / 6.92%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	621,514 / 5.14%
Duplication rate	5.03%
Clipped reads	666,787 / 5.52%

2.2. ACGT Content

Number/percentage of A's	116,730,290 / 28.08%
Number/percentage of C's	88,956,411 / 21.4%
Number/percentage of T's	118,965,898 / 28.61%
Number/percentage of G's	91,103,177 / 21.91%
Number/percentage of N's	17,458 / 0%
GC Percentage	43.31%

2.3. Coverage

Mean	0.1343
Standard Deviation	0.6945

2.4. Mapping Quality

Mean Mapping Quality	48.25
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2.5. Insert size

Mean	73,359.32
Standard Deviation	2,595,029.22
P25/Median/P75	103 / 136 / 187

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	1,649,744
Insertions	11,640
Mapped reads with at least one insertion	0.11%
Deletions	39,241
Mapped reads with at least one deletion	0.37%
Homopolymer indels	44.79%

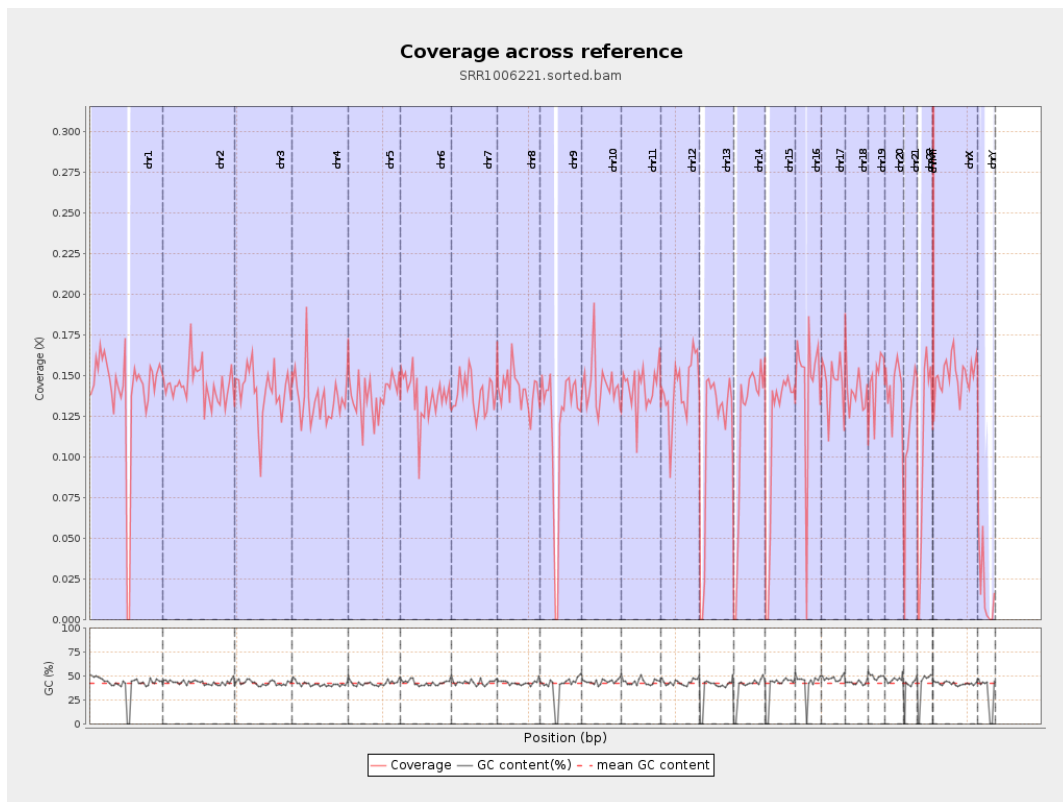
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

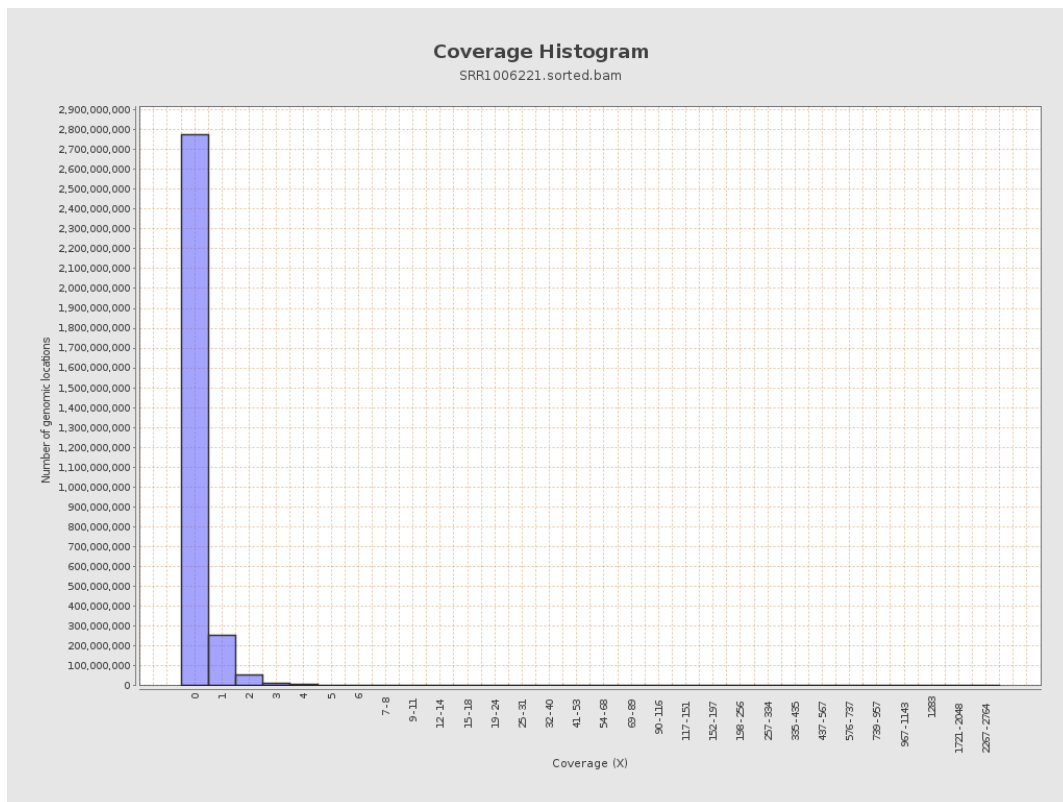
chr1	249250621	34710744	0.1393	1.0792
chr2	243199373	35100194	0.1443	0.6431
chr3	198022430	27665555	0.1397	0.4583
chr4	191154276	26021596	0.1361	0.5329
chr5	180915260	24861419	0.1374	0.4538
chr6	171115067	23415833	0.1368	0.5239
chr7	159138663	22041605	0.1385	0.8089
chr8	146364022	20661211	0.1412	1.4308
chr9	141213431	17124482	0.1213	0.5464
chr10	135534747	19460681	0.1436	0.7419
chr11	135006516	19201735	0.1422	0.6087
chr12	133851895	19072557	0.1425	0.4695
chr13	115169878	13099581	0.1137	0.4112
chr14	107349540	12875776	0.1199	0.5026
chr15	102531392	11656386	0.1137	0.4116
chr16	90354753	12933054	0.1431	0.6499
chr17	81195210	11889049	0.1464	0.5035
chr18	78077248	10935625	0.1401	0.962
chr19	59128983	8650952	0.1463	0.7634
chr20	63025520	8936959	0.1418	0.4854
chr21	48129895	5610403	0.1166	0.519
chr22	51304566	5451028	0.1062	0.4143
chrMT	16571	52124	3.1455	2.678
chrX	155270560	23330779	0.1503	0.5364

chrY	59373566	1065842	0.018	0.4085
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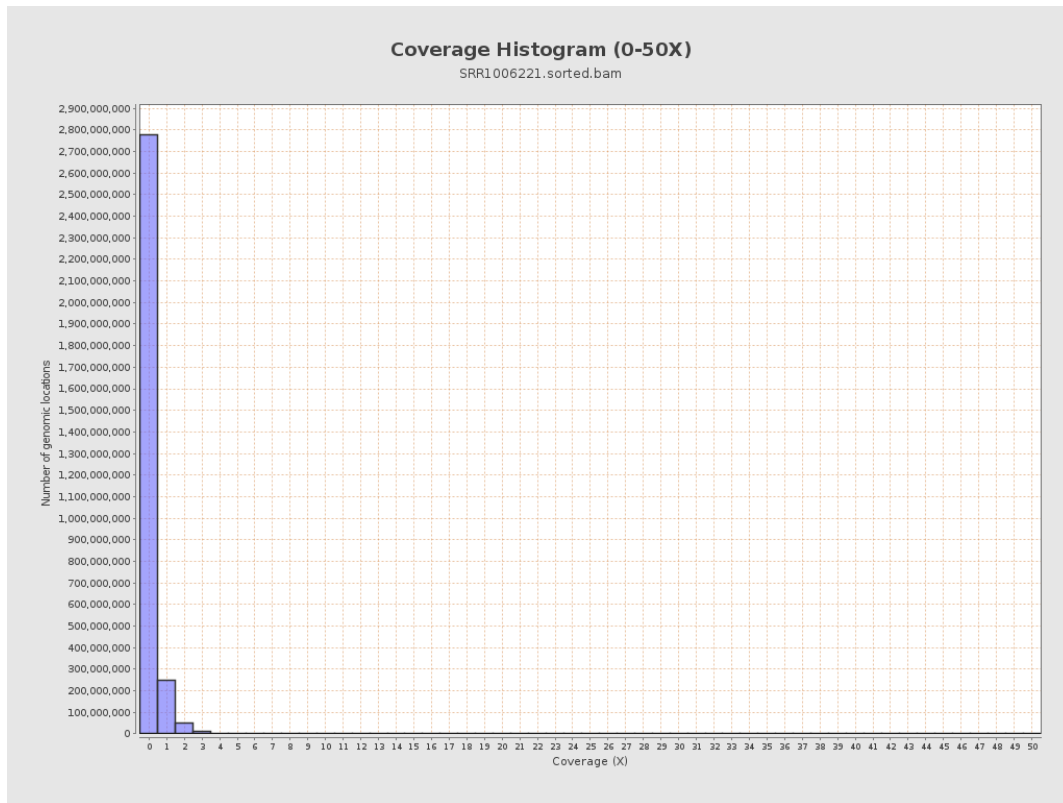
3. Results : Coverage across reference



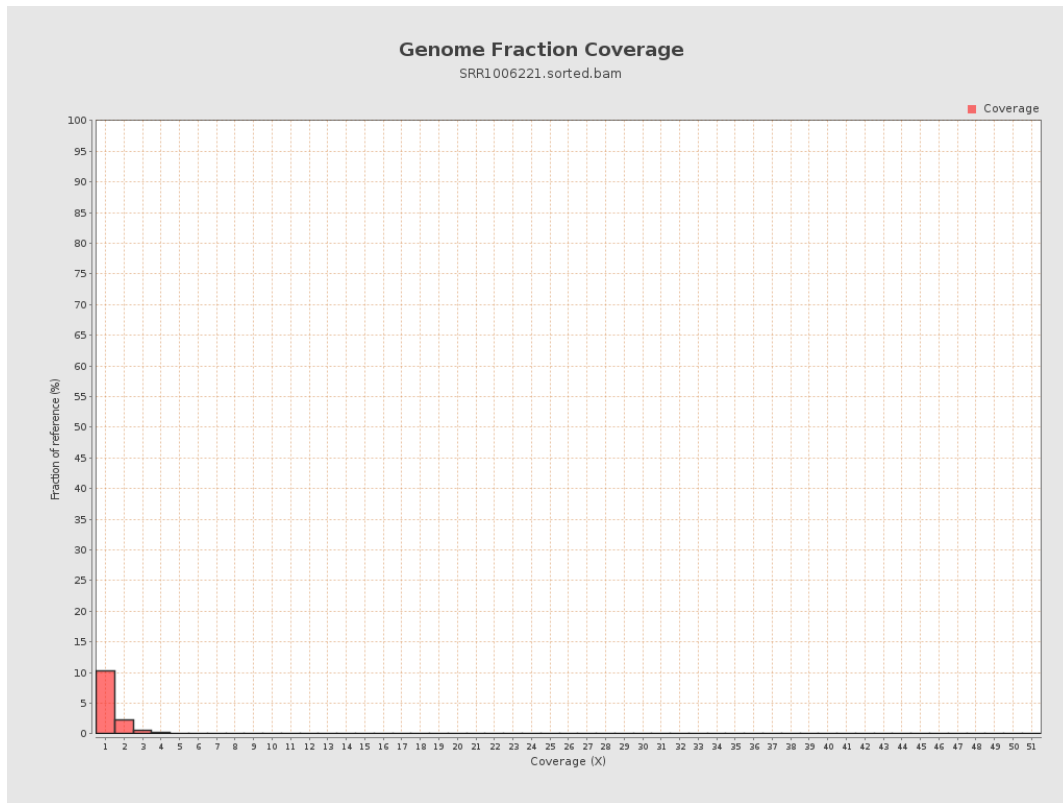
4. Results : Coverage Histogram



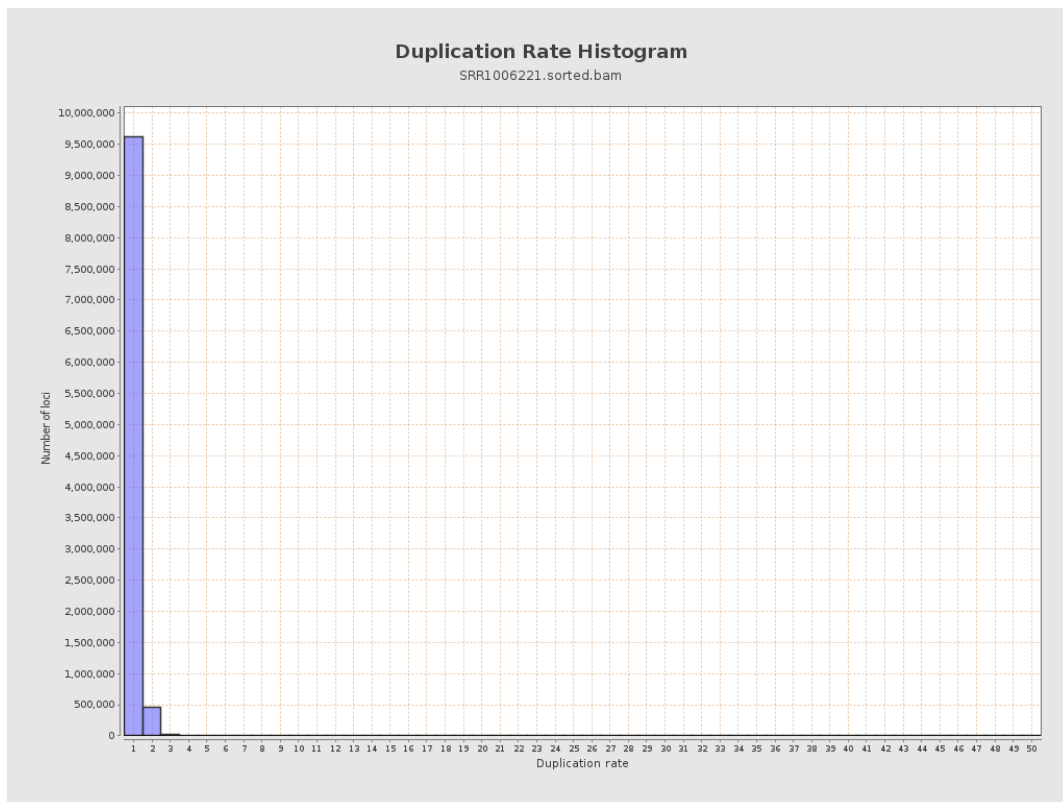
5. Results : Coverage Histogram (0-50X)



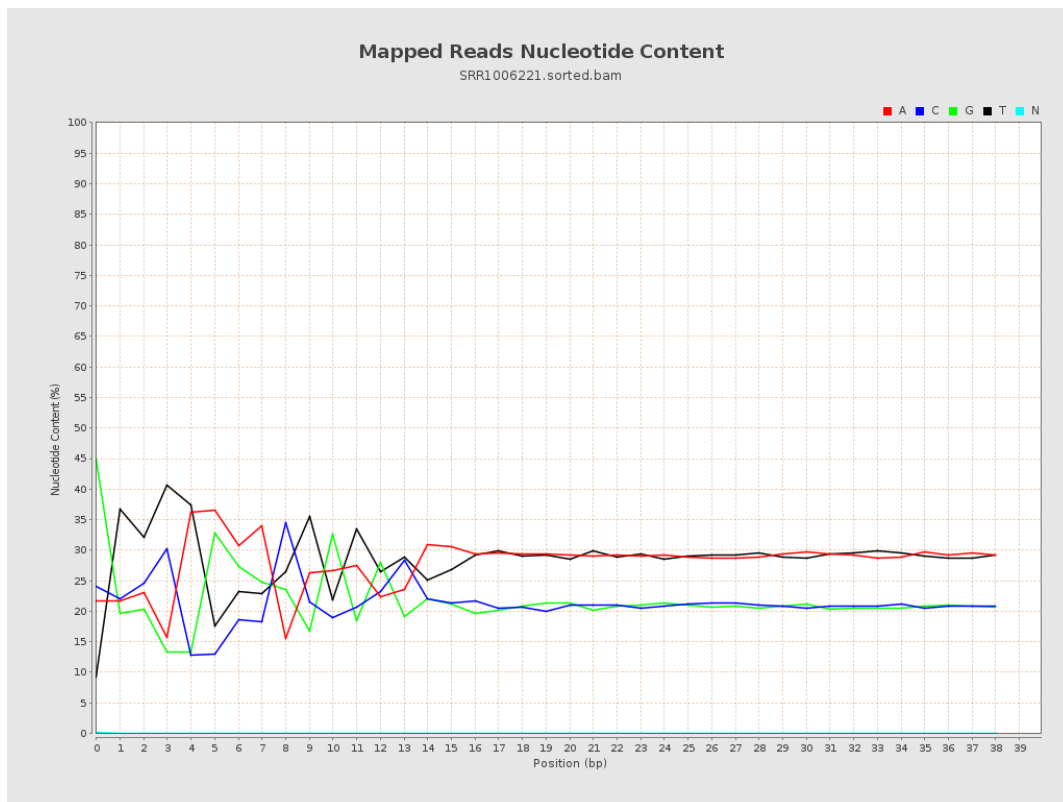
6. Results : Genome Fraction Coverage



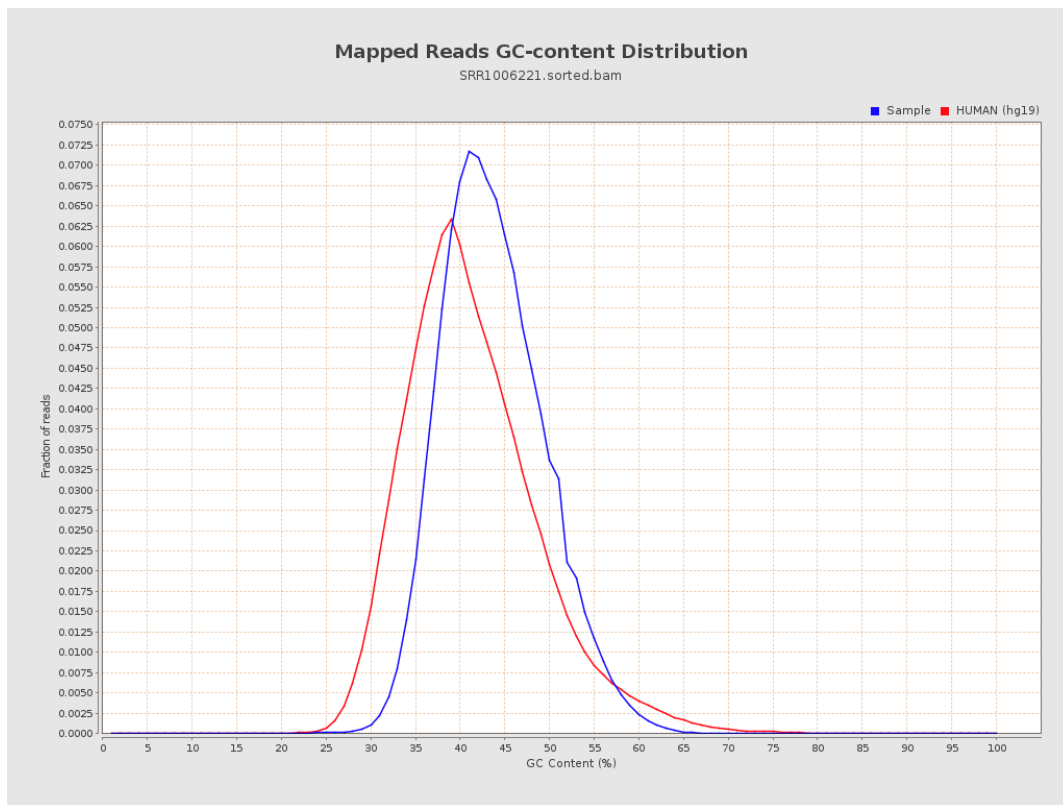
7. Results : Duplication Rate Histogram



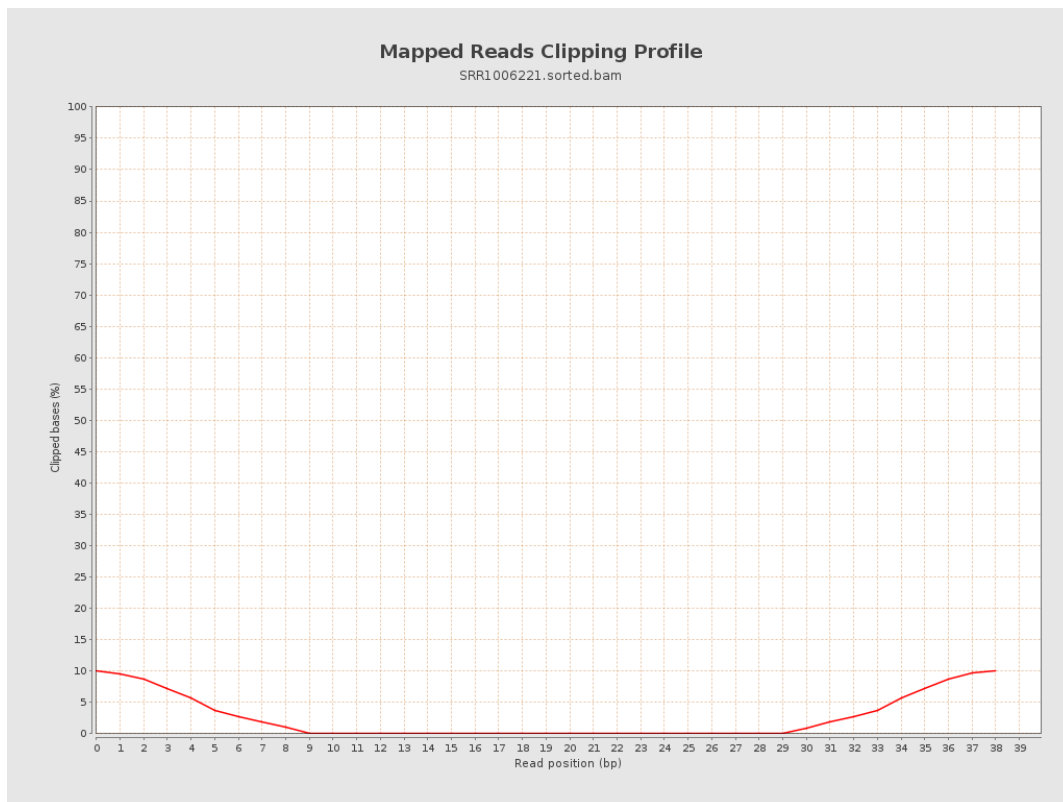
8. Results : Mapped Reads Nucleotide Content



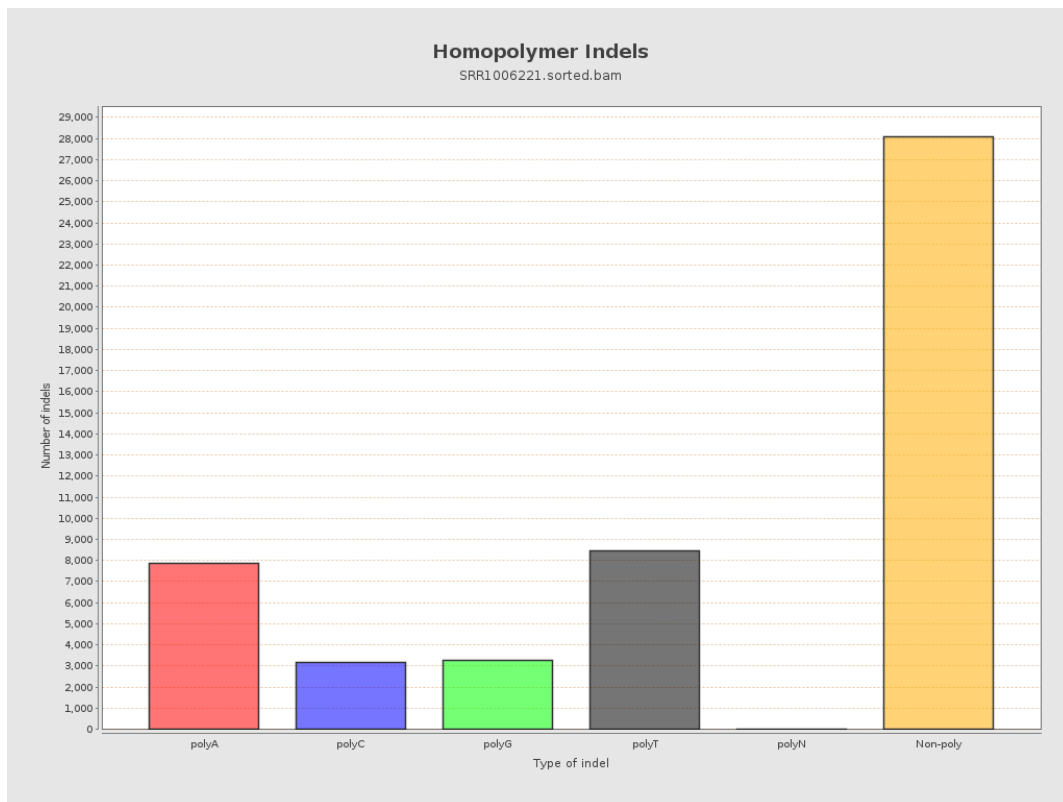
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



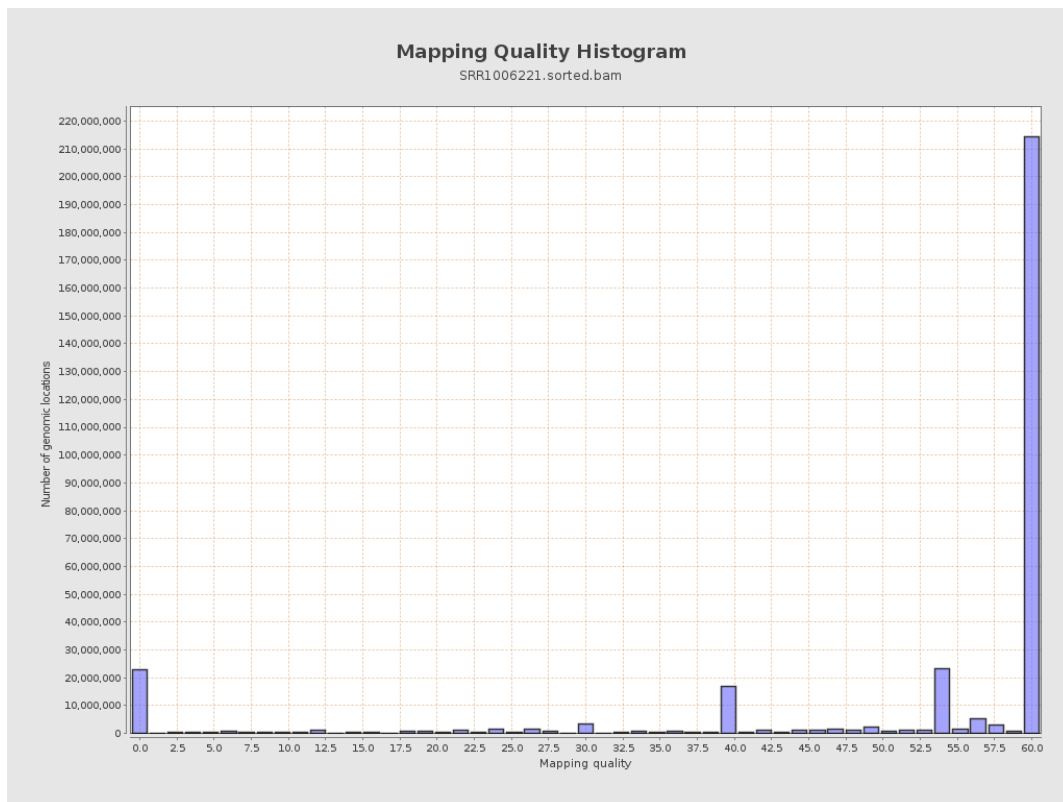
11. Results : Homopolymer Indels



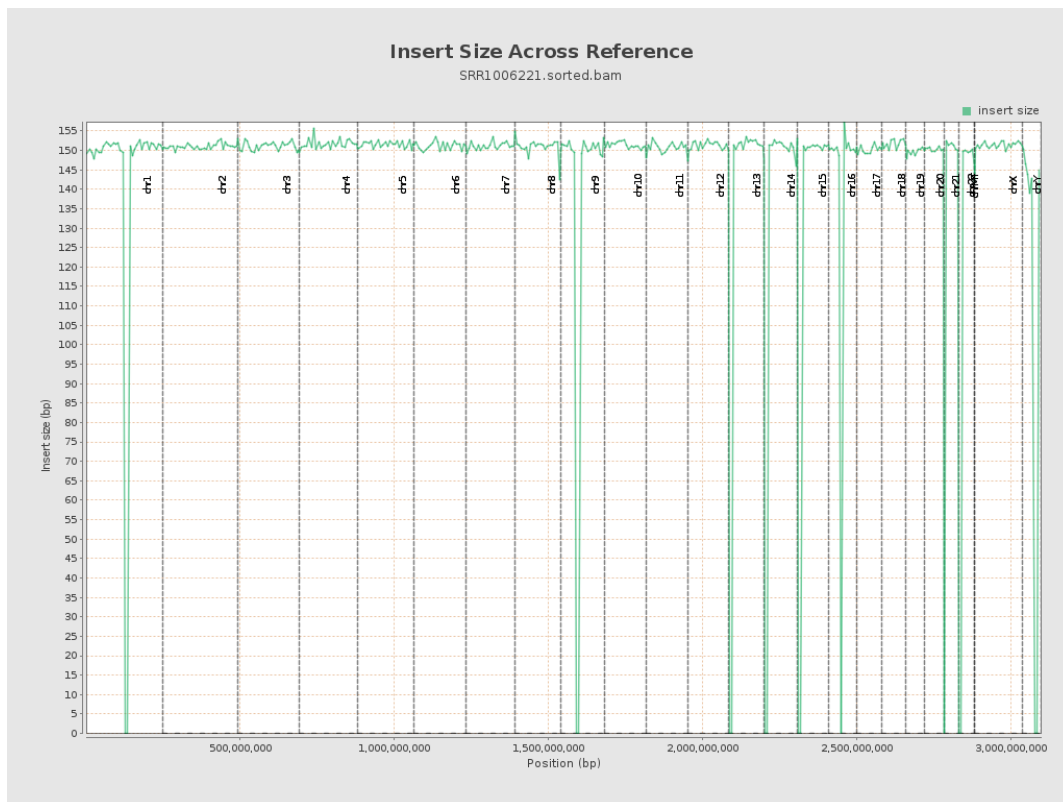
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

