

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 17:47:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006074.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_SRR1006074 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006074_1.fastq.gz SRR1006074_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 17:47:15 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006074.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,076,894
Mapped reads	4,407,122 / 86.81%
Unmapped reads	669,772 / 13.19%
Mapped paired reads	4,407,122 / 86.81%
Mapped reads, first in pair	2,234,015 / 44%
Mapped reads, second in pair	2,173,107 / 42.8%
Mapped reads, both in pair	4,018,184 / 79.15%
Mapped reads, singletons	388,938 / 7.66%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	193,384 / 3.81%
Duplication rate	4.01%
Clipped reads	393,092 / 7.74%

2.2. ACGT Content

Number/percentage of A's	44,760,524 / 26.34%
Number/percentage of C's	38,325,194 / 22.55%
Number/percentage of T's	46,232,275 / 27.21%
Number/percentage of G's	40,612,253 / 23.9%
Number/percentage of N's	6,825 / 0%
GC Percentage	46.45%

2.3. Coverage

Mean	0.0549
Standard Deviation	0.3553

2.4. Mapping Quality

Mean Mapping Quality	46.29
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2.5. Insert size

Mean	63,226.01
Standard Deviation	2,485,005.12
P25/Median/P75	62 / 88 / 119

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	784,863
Insertions	5,827
Mapped reads with at least one insertion	0.13%
Deletions	15,047
Mapped reads with at least one deletion	0.34%
Homopolymer indels	44.18%

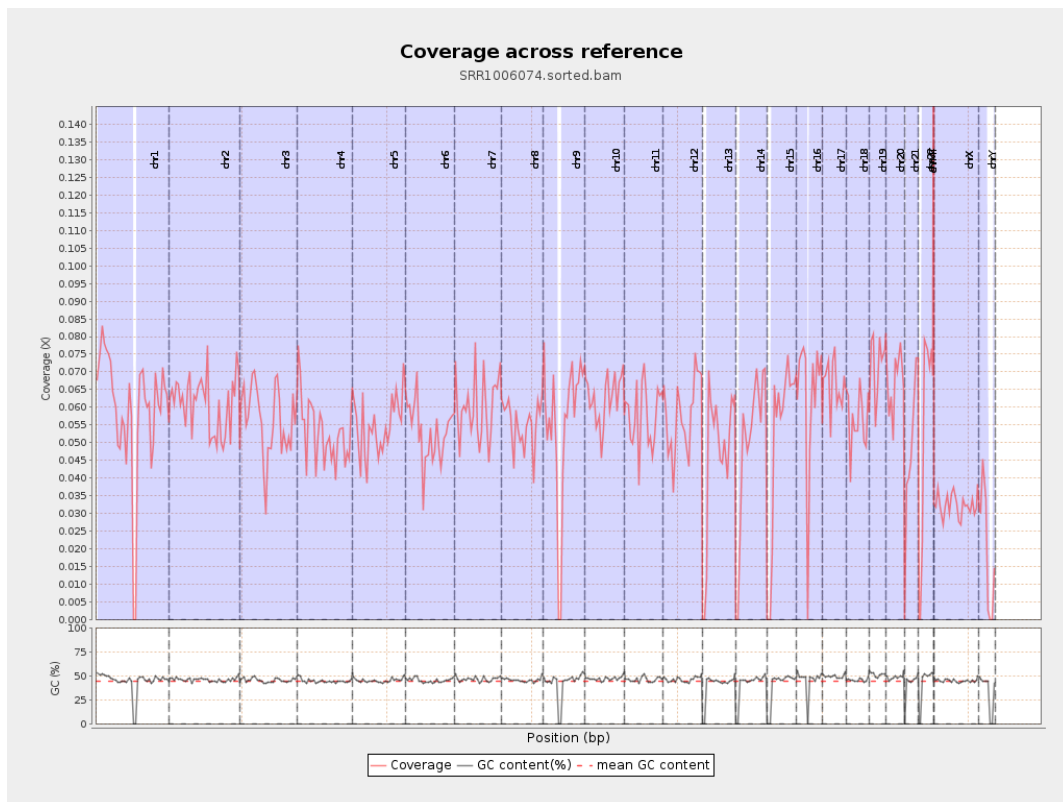
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

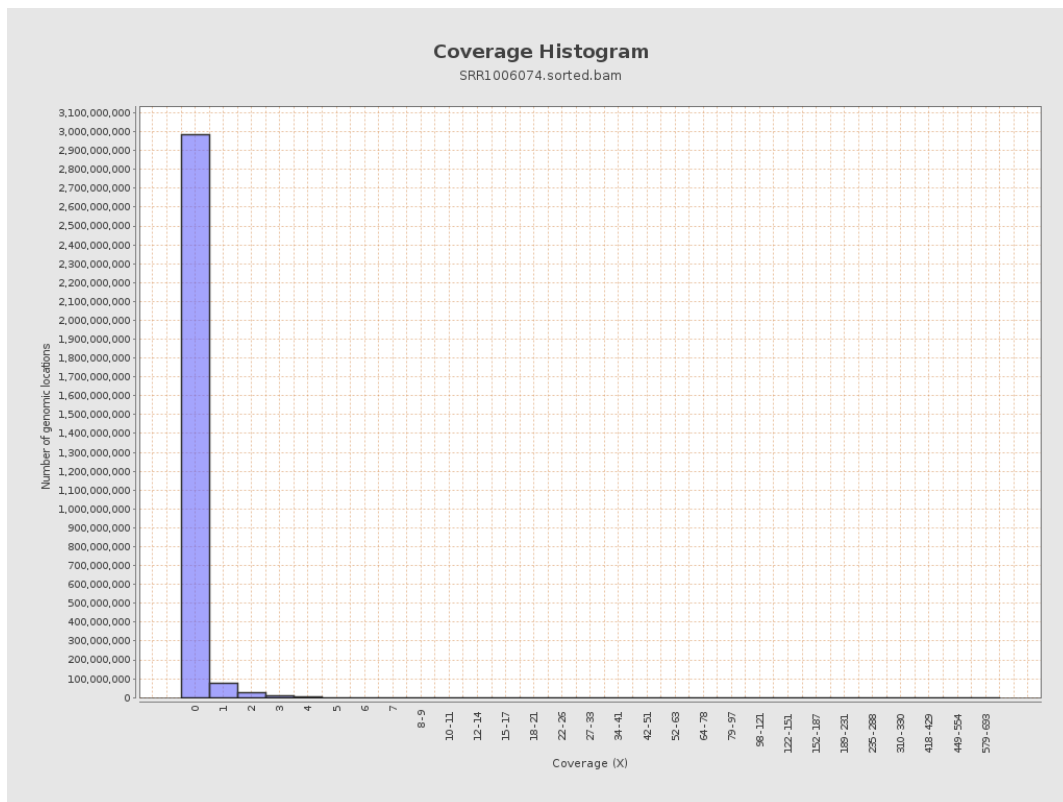
chr1	249250621	14721103	0.0591	0.3784
chr2	243199373	14836345	0.061	0.3896
chr3	198022430	11147154	0.0563	0.3284
chr4	191154276	10063846	0.0526	0.3296
chr5	180915260	9875967	0.0546	0.3246
chr6	171115067	9095777	0.0532	0.348
chr7	159138663	9493795	0.0597	0.4119
chr8	146364022	8076307	0.0552	0.3509
chr9	141213431	7590441	0.0538	0.3329
chr10	135534747	8452315	0.0624	0.3615
chr11	135006516	7775101	0.0576	0.4884
chr12	133851895	7681145	0.0574	0.336
chr13	115169878	5308989	0.0461	0.3005
chr14	107349540	5315436	0.0495	0.3146
chr15	102531392	5355547	0.0522	0.3215
chr16	90354753	5737227	0.0635	0.3799
chr17	81195210	5405809	0.0666	0.3798
chr18	78077248	4384341	0.0562	0.3729
chr19	59128983	4271204	0.0722	0.4282
chr20	63025520	4198236	0.0666	0.3676
chr21	48129895	2366333	0.0492	0.3357
chr22	51304566	2658495	0.0518	0.3435
chrMT	16571	3993	0.241	0.5974
chrX	155270560	5001342	0.0322	0.2505

chrY	59373566	1140077	0.0192	0.2058
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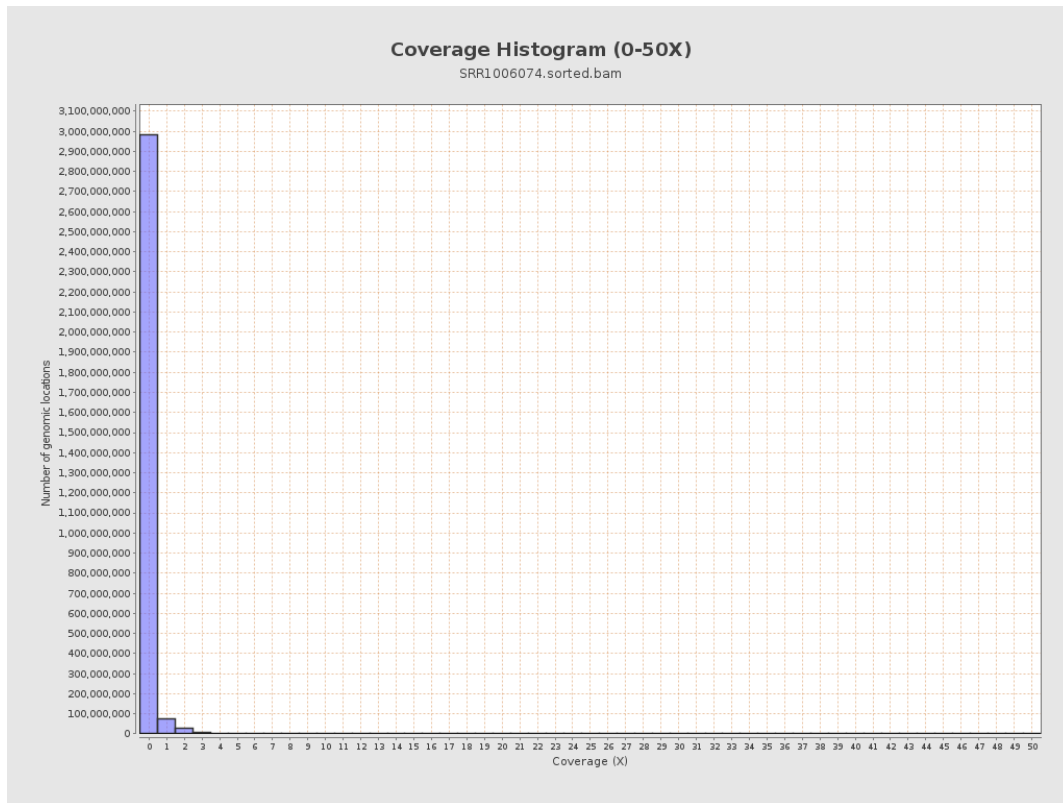
3. Results : Coverage across reference



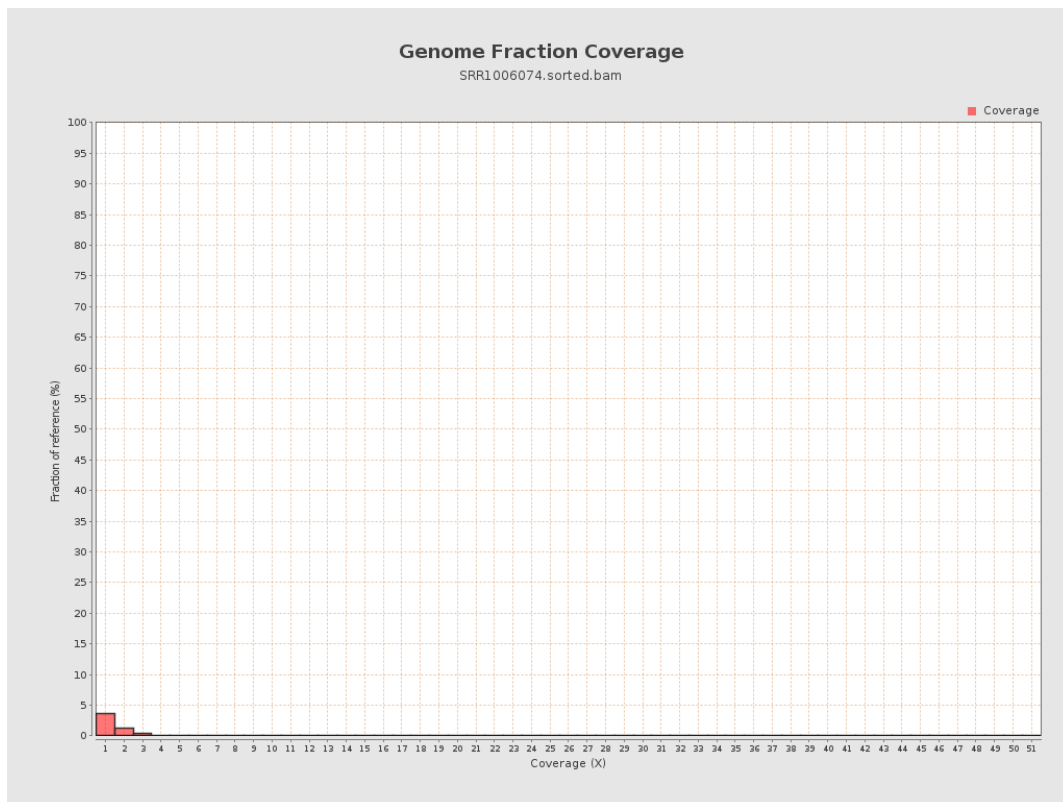
4. Results : Coverage Histogram



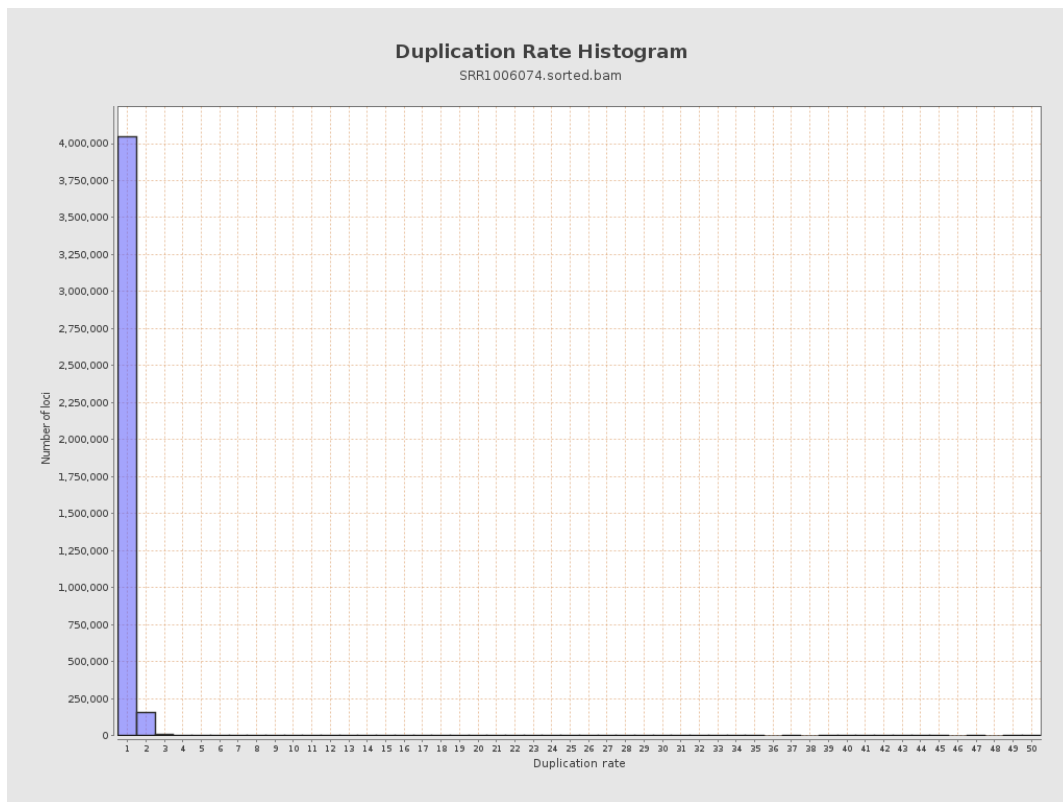
5. Results : Coverage Histogram (0-50X)



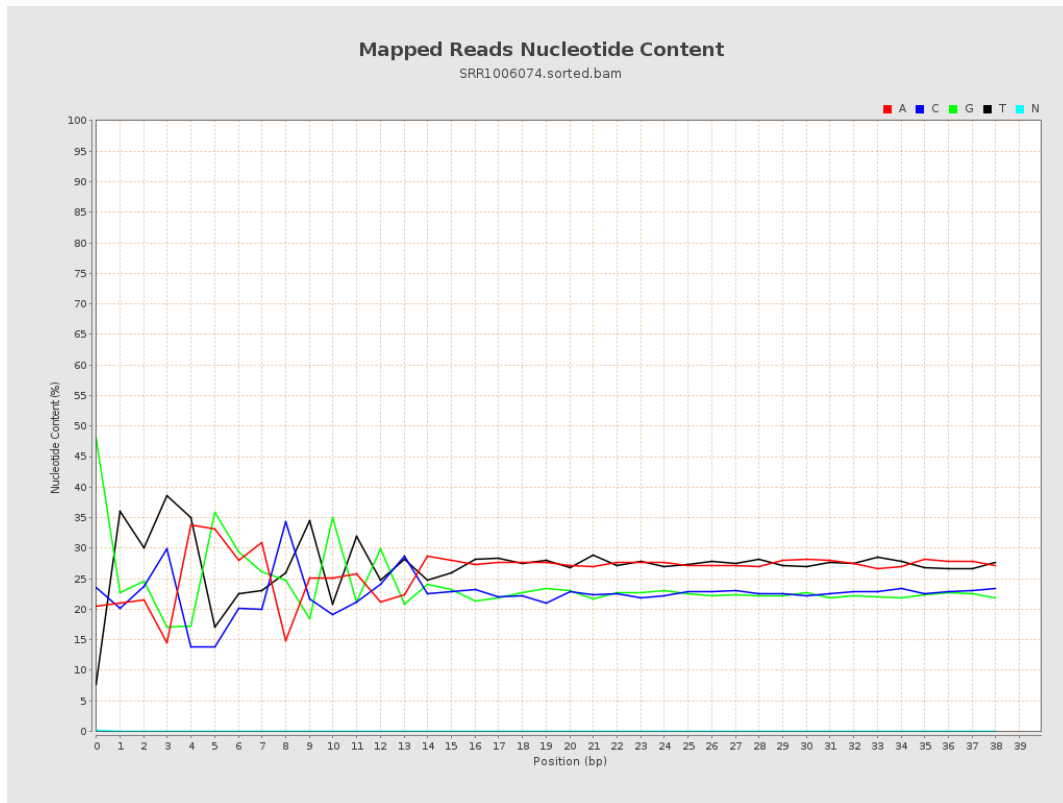
6. Results : Genome Fraction Coverage



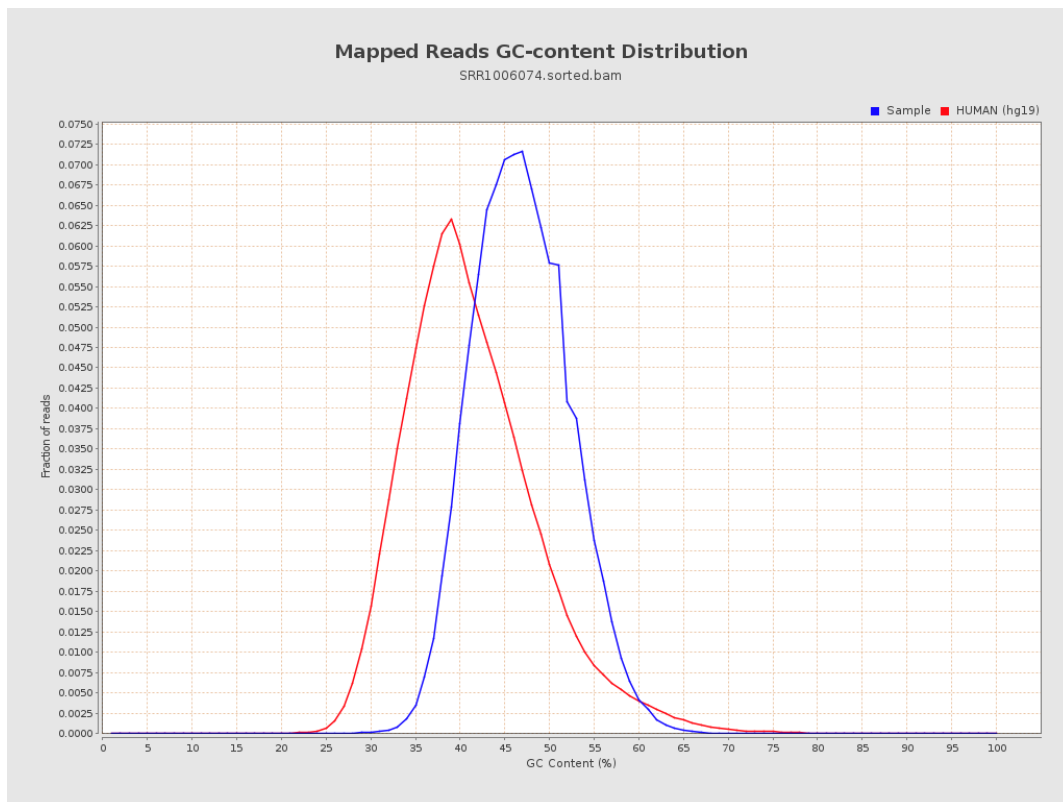
7. Results : Duplication Rate Histogram



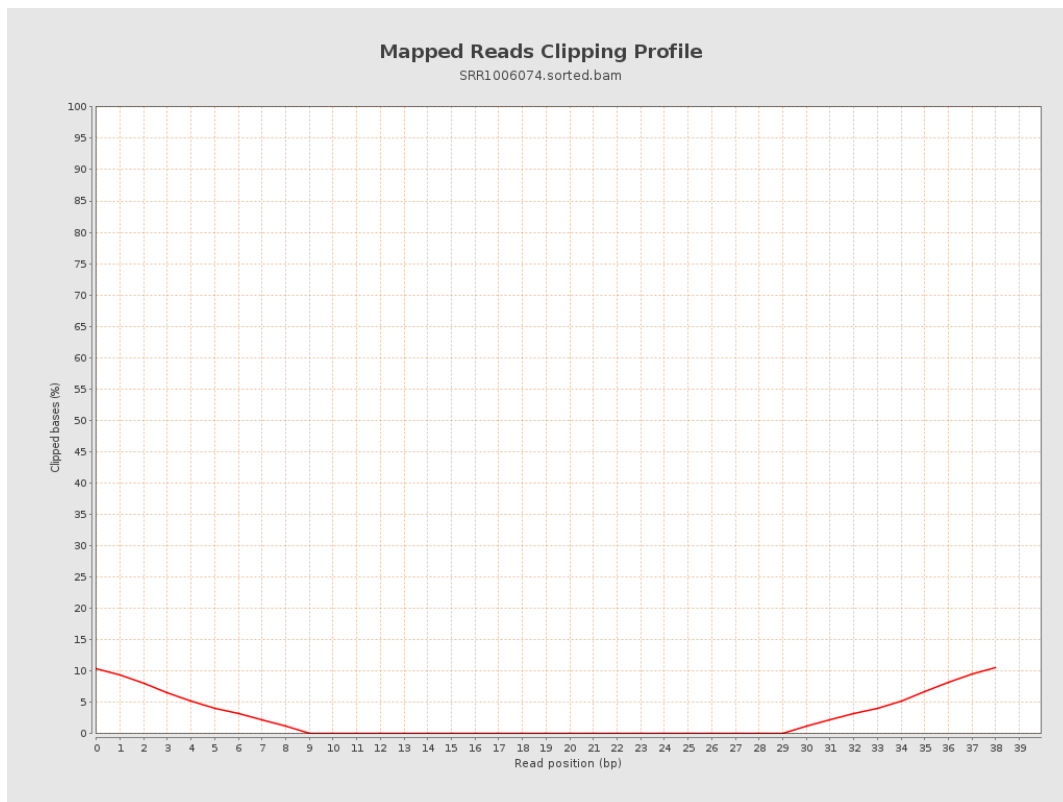
8. Results : Mapped Reads Nucleotide Content



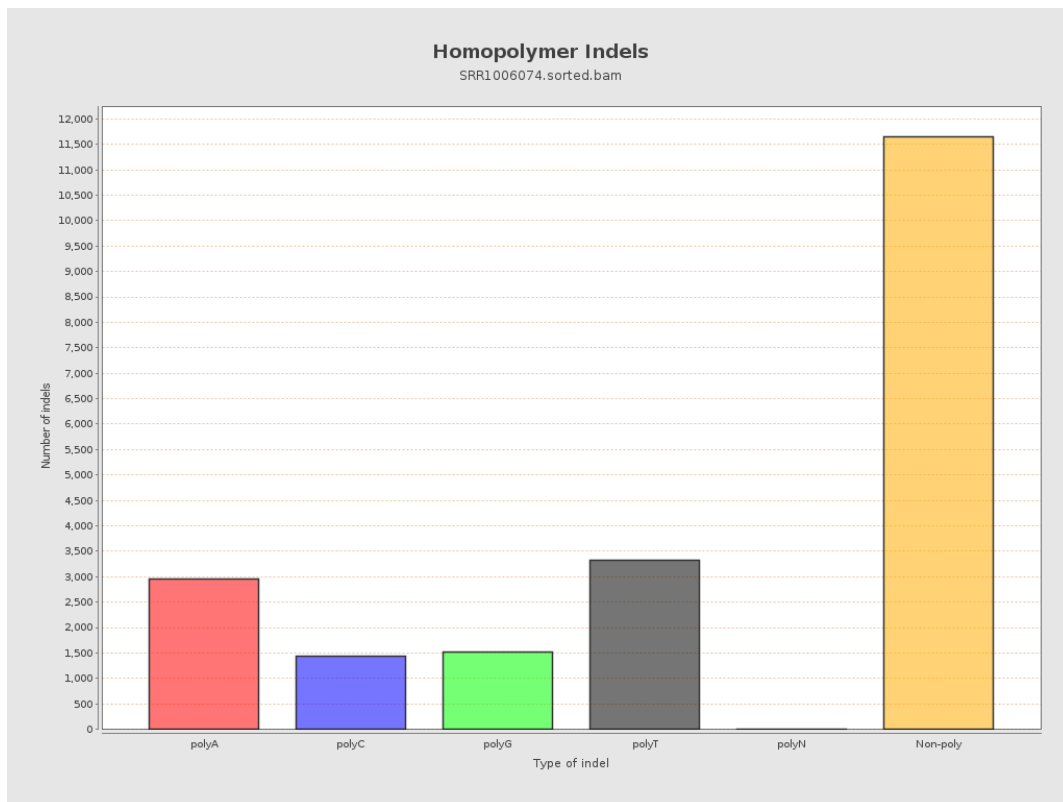
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



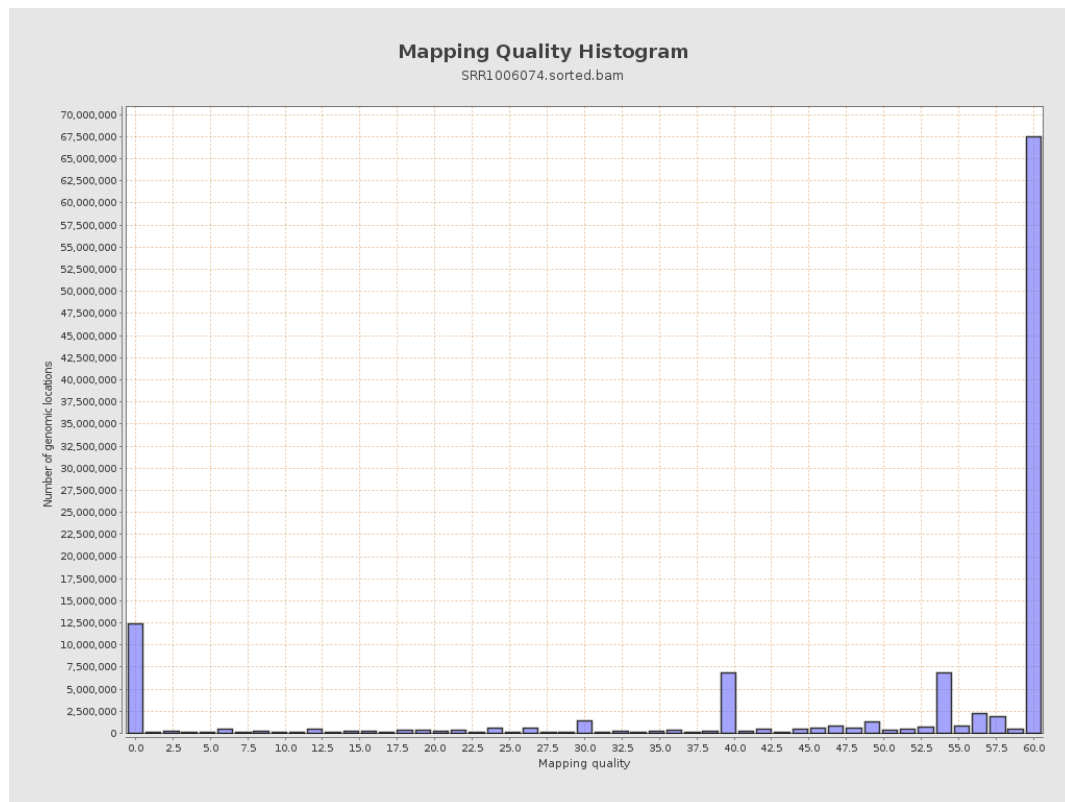
11. Results : Homopolymer Indels



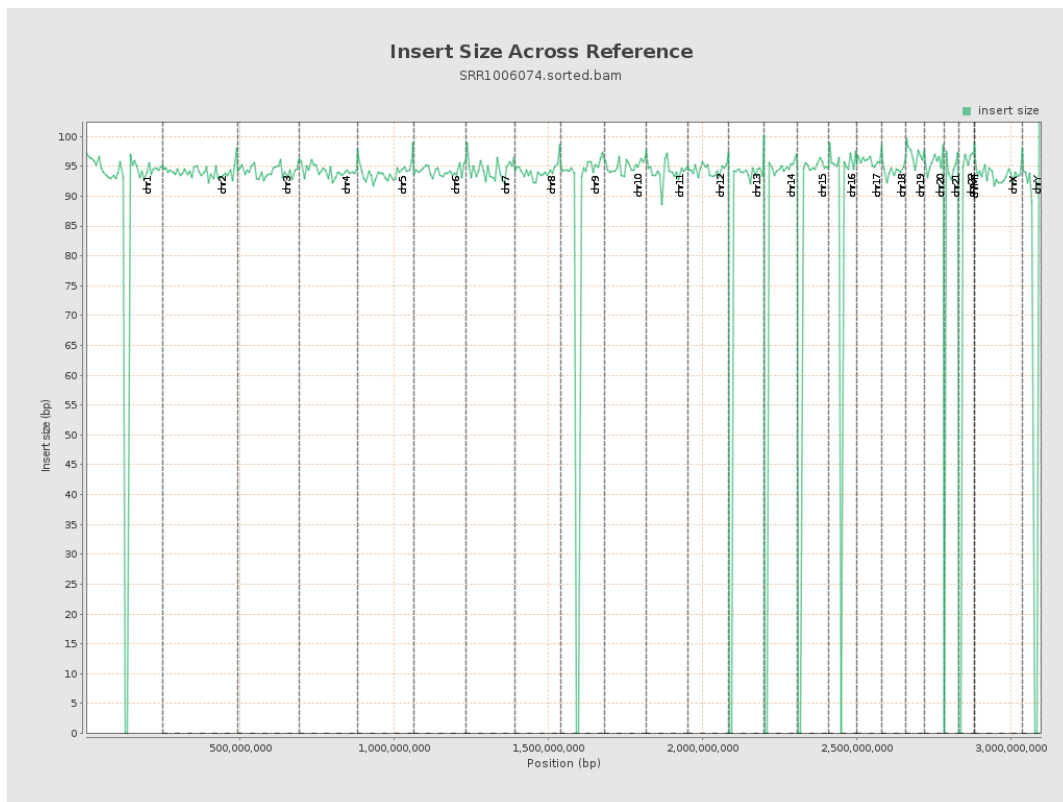
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

