

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 15:34:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173974.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_SRR10173974 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173974_1.fastq.gz SRR10173974_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 15:34:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173974.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,424,230
Mapped reads	13,044,658 / 97.17%
Unmapped reads	379,572 / 2.83%
Mapped paired reads	13,044,658 / 97.17%
Mapped reads, first in pair	6,540,772 / 48.72%
Mapped reads, second in pair	6,503,886 / 48.45%
Mapped reads, both in pair	12,796,834 / 95.33%
Mapped reads, singletons	247,824 / 1.85%
Secondary alignments	0
Supplementary alignments	1,289,610 / 9.61%
Read min/max/mean length	30 / 133 / 128.23
Duplicated reads (estimated)	10,279,525 / 76.57%
Duplication rate	65.11%
Clipped reads	5,253,373 / 39.13%

2.2. ACGT Content

Number/percentage of A's	458,763,328 / 29.76%
Number/percentage of C's	307,155,362 / 19.93%
Number/percentage of T's	457,597,497 / 29.69%
Number/percentage of G's	317,833,197 / 20.62%
Number/percentage of N's	18,512 / 0%

GC Percentage	40.55%
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2.3. Coverage

Mean	0.4982
Standard Deviation	6.7127

2.4. Mapping Quality

Mean Mapping Quality	52.75
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2.5. Insert size

Mean	907,435.6
Standard Deviation	8,712,155.99
P25/Median/P75	148 / 207 / 298

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	16,193,550
Insertions	160,775
Mapped reads with at least one insertion	1.19%
Deletions	346,265
Mapped reads with at least one deletion	2.59%
Homopolymer indels	43.24%

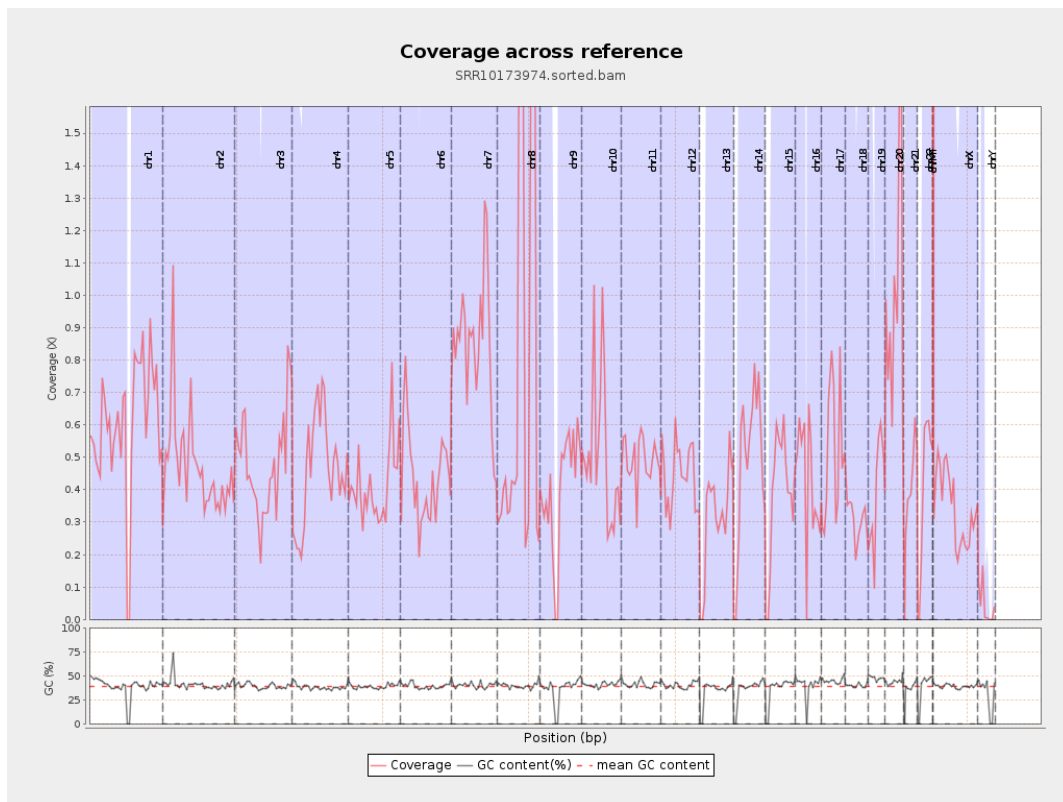
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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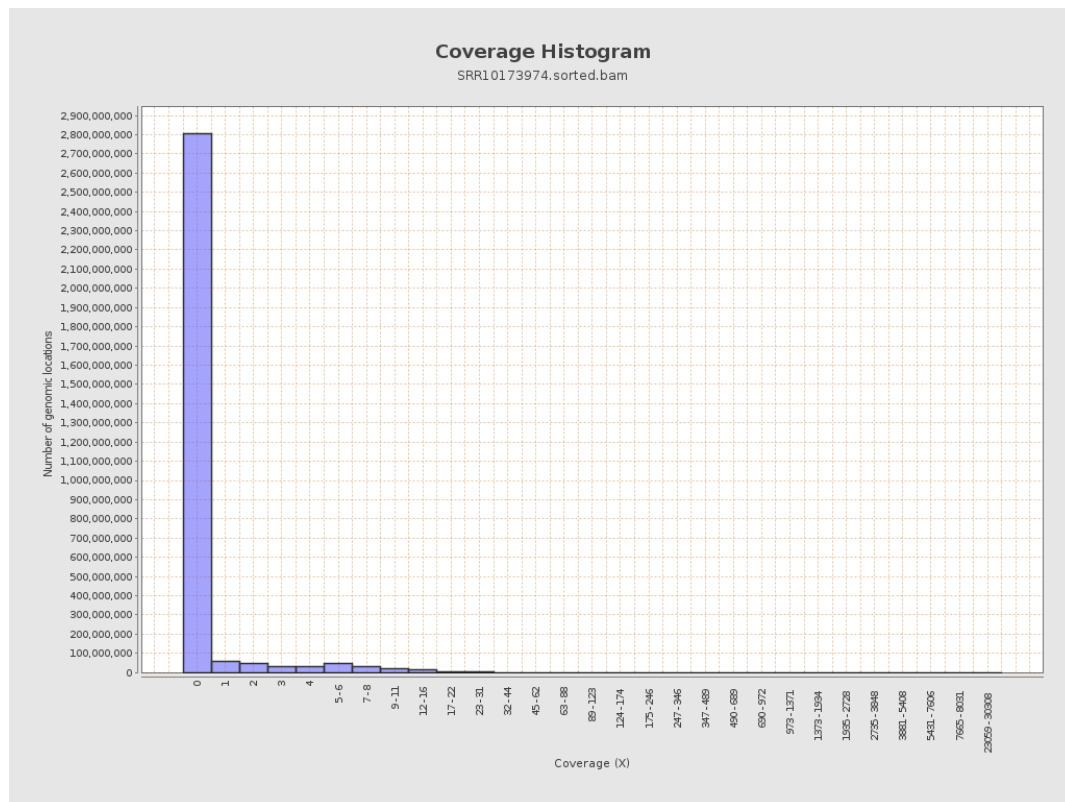
		bases	coverage	deviation
chr1	249250621	149922035	0.6015	3.3421
chr2	243199373	114360863	0.4702	21.0835
chr3	198022430	94431803	0.4769	2.0662
chr4	191154276	89004841	0.4656	2.867
chr5	180915260	75321202	0.4163	1.9
chr6	171115067	75506190	0.4413	2.1486
chr7	159138663	134071913	0.8425	6.218
chr8	146364022	135567647	0.9262	4.2453
chr9	141213431	56229938	0.3982	2.8549
chr10	135534747	68635207	0.5064	6.8226
chr11	135006516	66290577	0.491	2.1666
chr12	133851895	60180140	0.4496	2.0201
chr13	115169878	36423421	0.3163	1.6619
chr14	107349540	53798432	0.5012	2.13
chr15	102531392	39062500	0.381	1.8464
chr16	90354753	38738019	0.4287	2.9338
chr17	81195210	41644185	0.5129	2.5845
chr18	78077248	24662998	0.3159	3.6139
chr19	59128983	22851517	0.3865	2.6266
chr20	63025520	65645152	1.0416	3.1861
chr21	48129895	18977997	0.3943	2.1818
chr22	51304566	20772119	0.4049	1.8217
chrMT	16571	4375781	264.0626	170.3223
chrX	155270560	53195021	0.3426	1.7631

chrY	59373566	2557049	0.0431	1.6399
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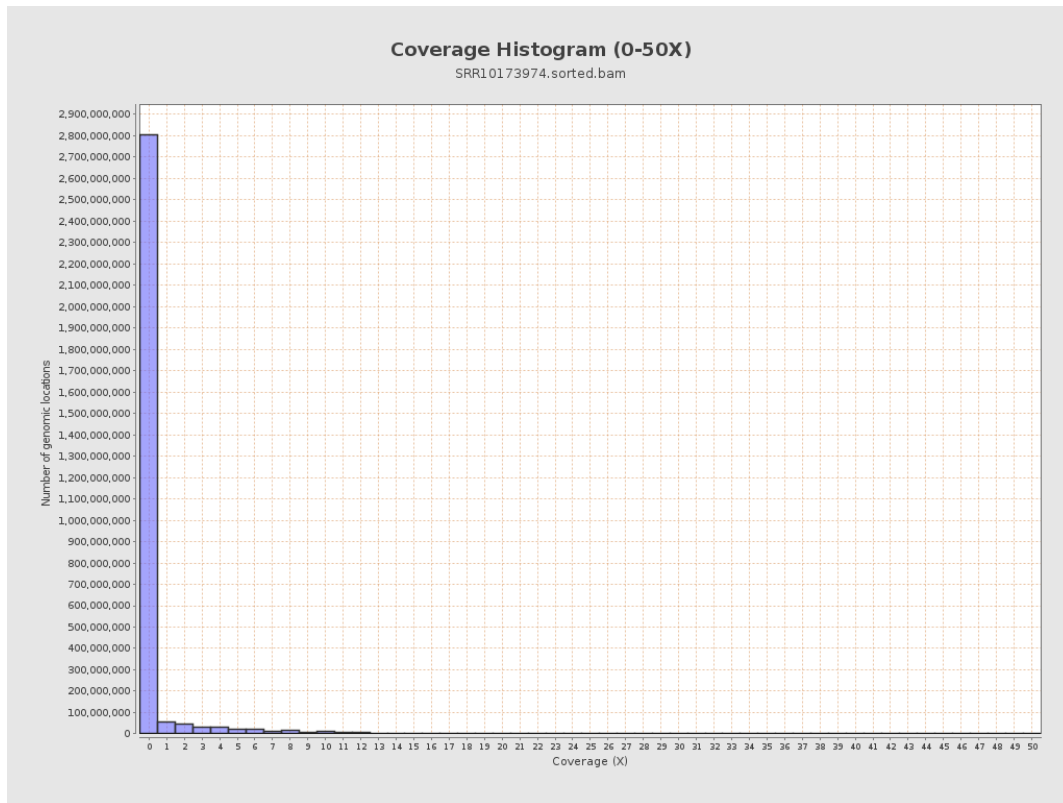
3. Results : Coverage across reference



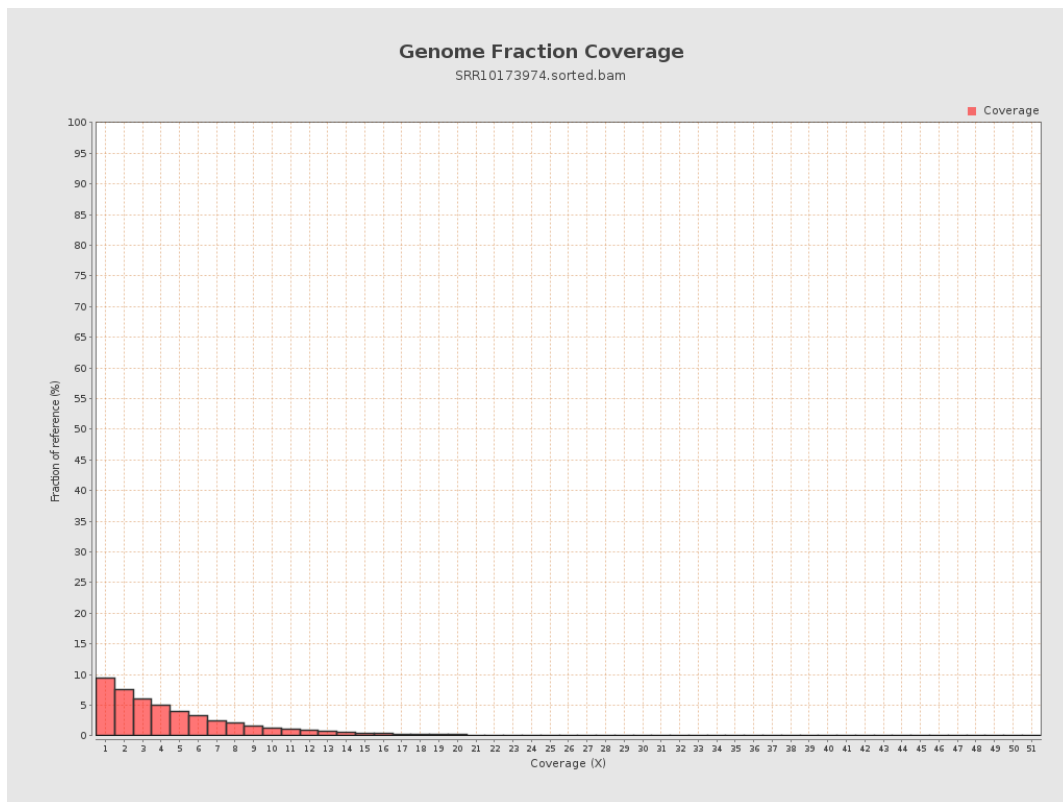
4. Results : Coverage Histogram



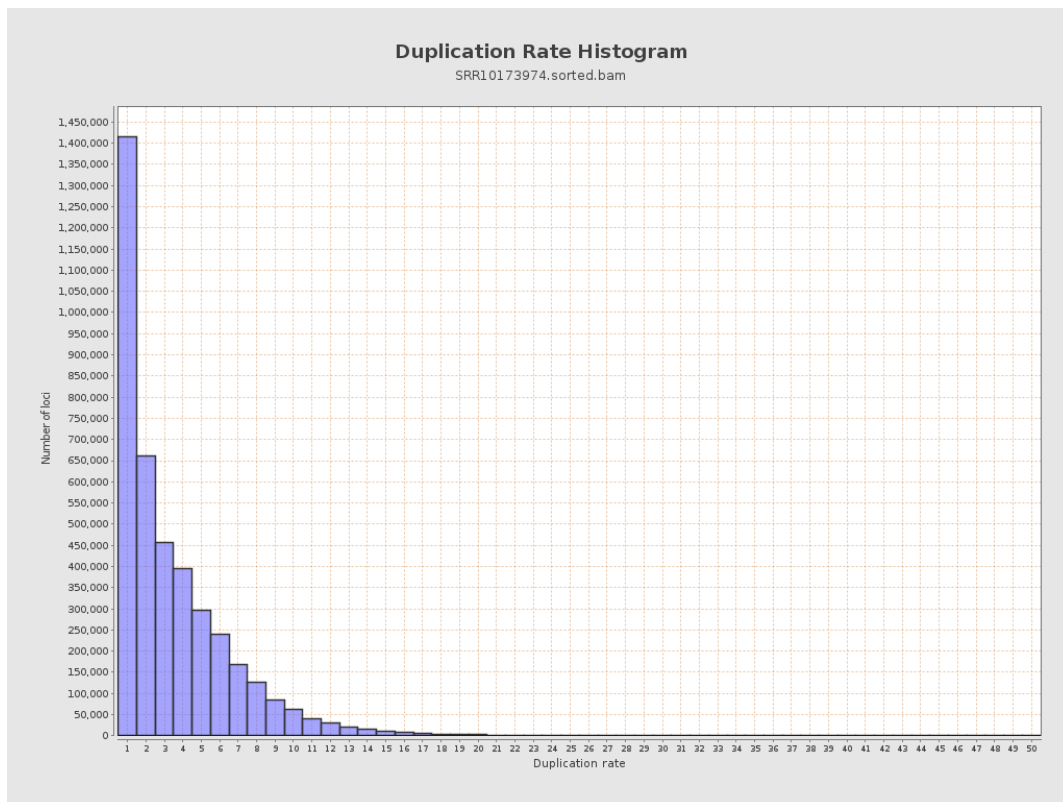
5. Results : Coverage Histogram (0-50X)



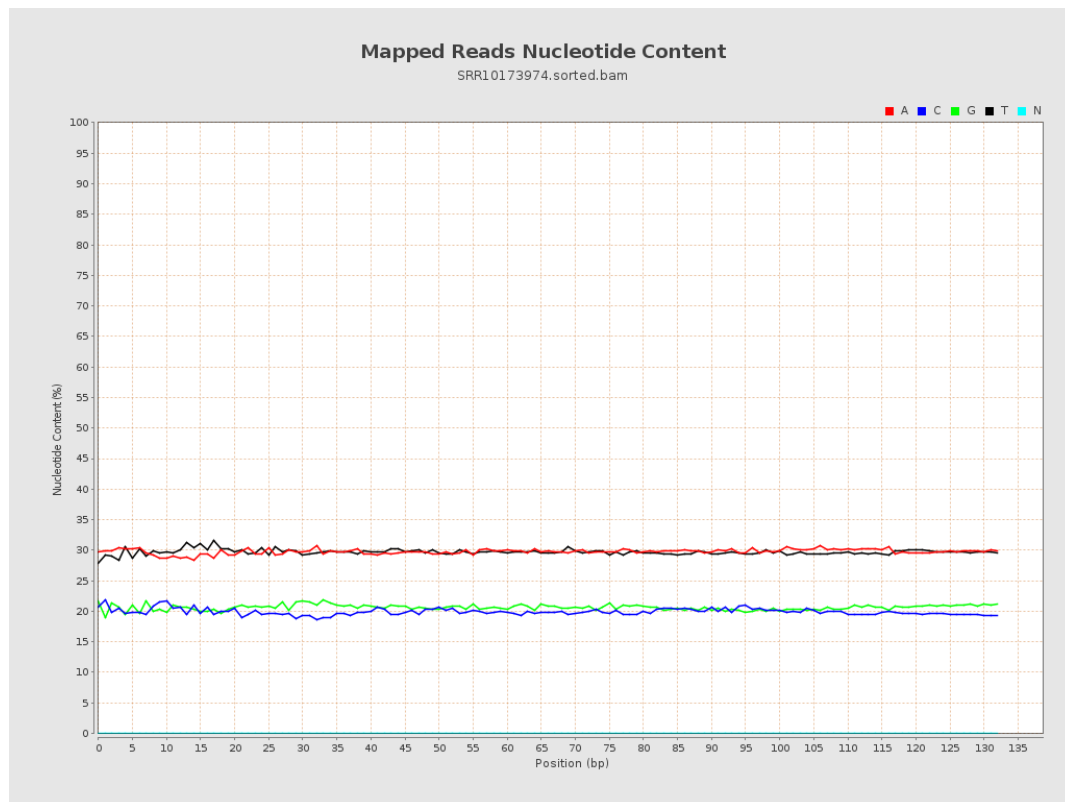
6. Results : Genome Fraction Coverage



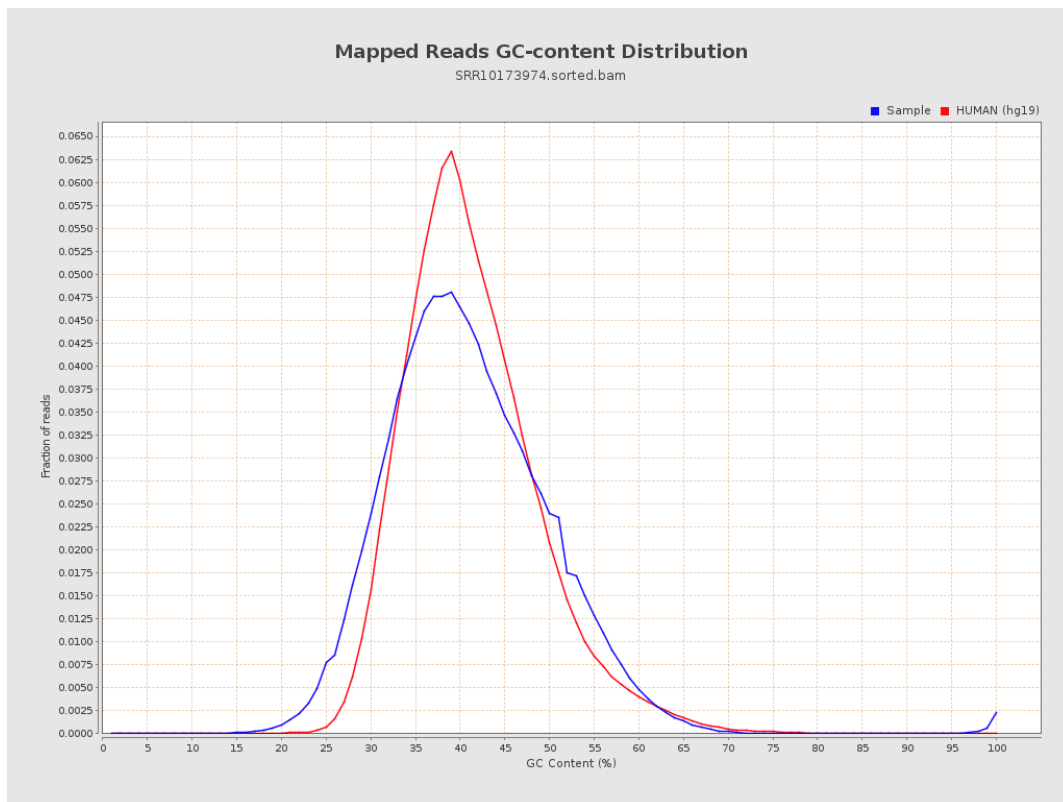
7. Results : Duplication Rate Histogram



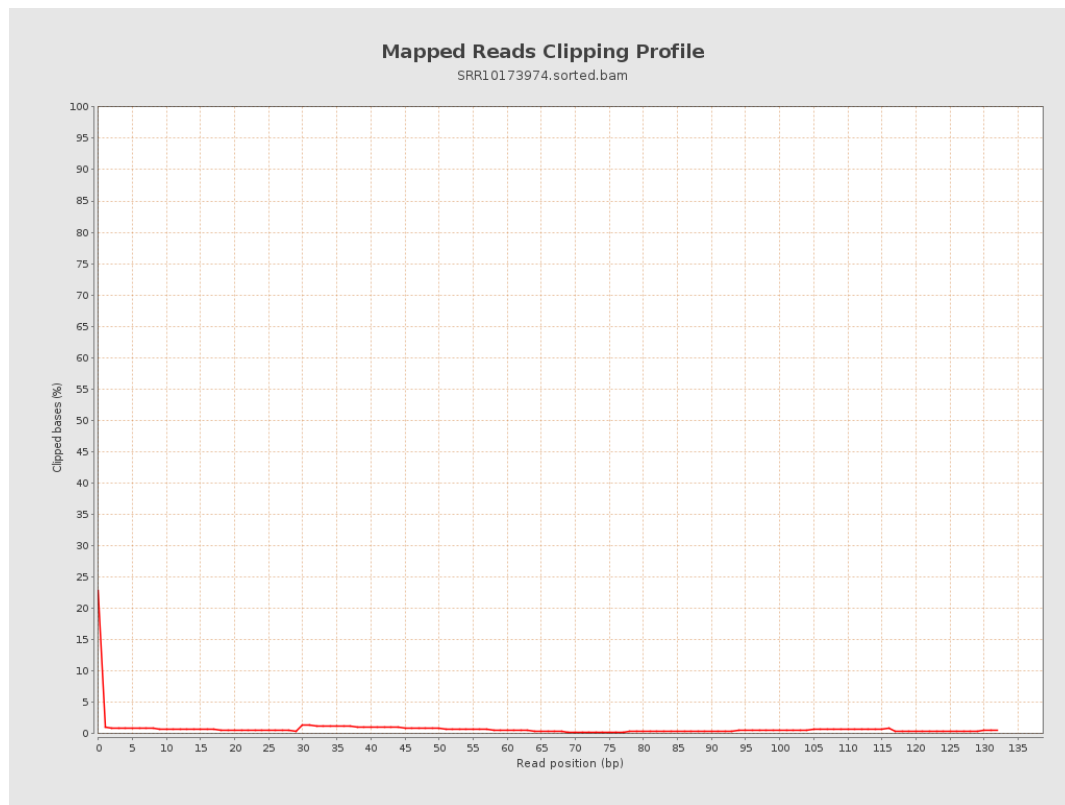
8. Results : Mapped Reads Nucleotide Content



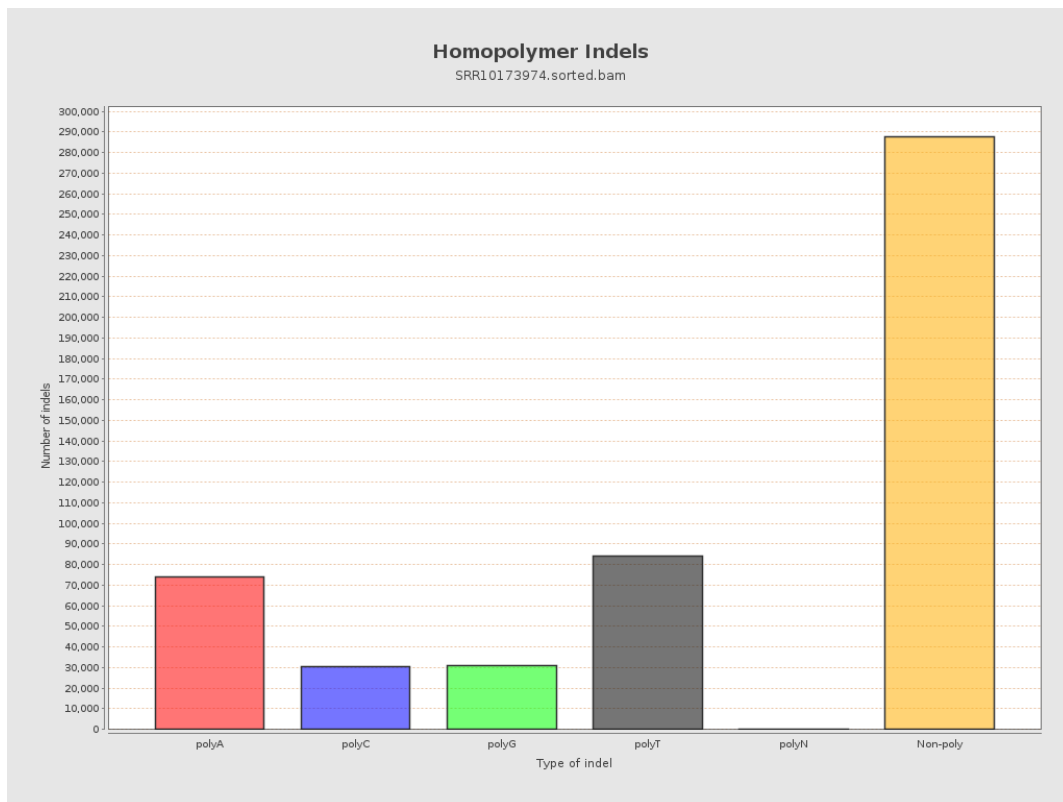
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



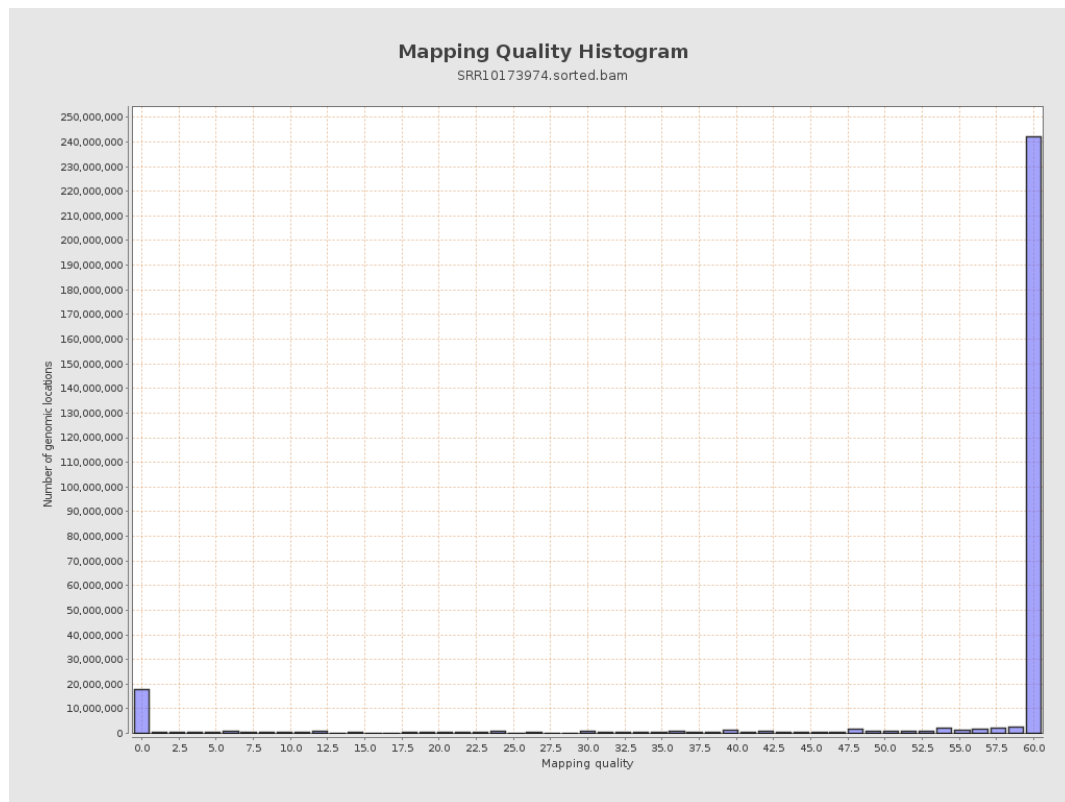
11. Results : Homopolymer Indels



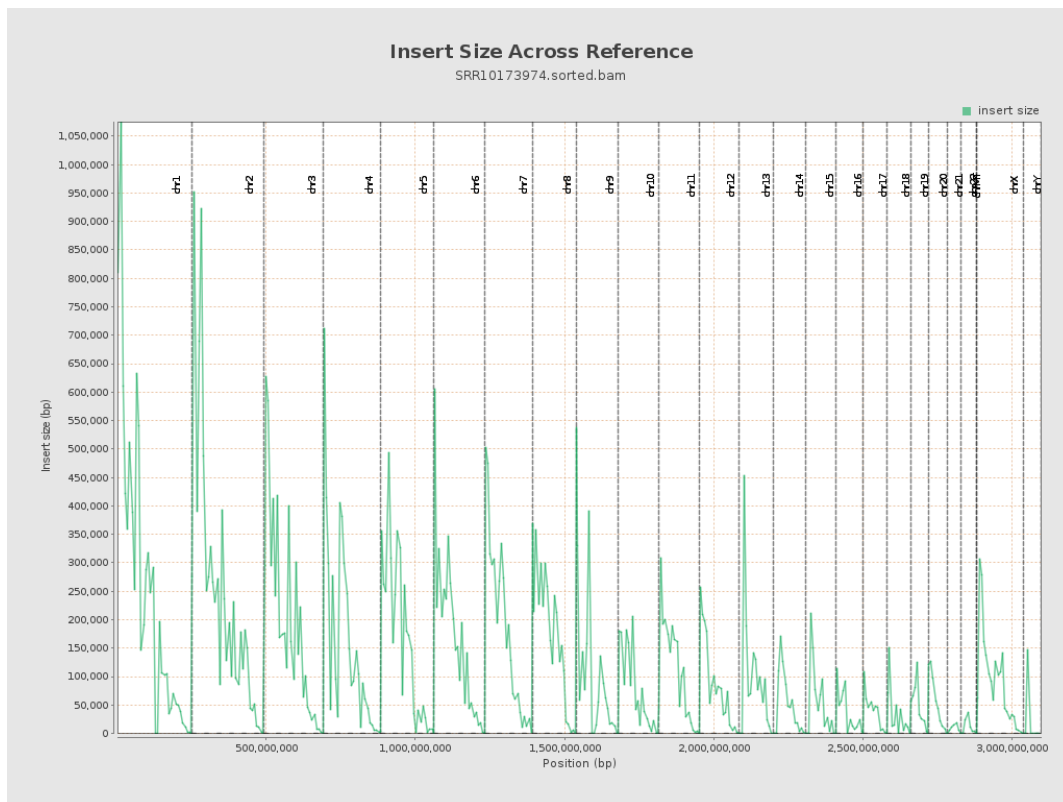
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

