

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 03:34:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174062.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_SRR10174062 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174062_1.fastq.gz SRR10174062_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 03:34:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174062.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,534,522
Mapped reads	1,500,582 / 97.79%
Unmapped reads	33,940 / 2.21%
Mapped paired reads	1,500,582 / 97.79%
Mapped reads, first in pair	749,833 / 48.86%
Mapped reads, second in pair	750,749 / 48.92%
Mapped reads, both in pair	1,477,664 / 96.29%
Mapped reads, singletons	22,918 / 1.49%
Secondary alignments	0
Supplementary alignments	145,071 / 9.45%
Read min/max/mean length	30 / 133 / 128.08
Duplicated reads (estimated)	1,179,868 / 76.89%
Duplication rate	65.88%
Clipped reads	608,038 / 39.62%

2.2. ACGT Content

Number/percentage of A's	53,570,767 / 30.07%
Number/percentage of C's	34,957,648 / 19.62%
Number/percentage of T's	53,470,647 / 30.01%
Number/percentage of G's	36,149,712 / 20.29%
Number/percentage of N's	2,036 / 0%

GC Percentage	39.91%
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2.3. Coverage

Mean	0.0576
Standard Deviation	1.0298

2.4. Mapping Quality

Mean Mapping Quality	52.8
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2.5. Insert size

Mean	843,921.43
Standard Deviation	8,598,435.83
P25/Median/P75	145 / 202 / 292

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	1,751,632
Insertions	17,785
Mapped reads with at least one insertion	1.15%
Deletions	36,396
Mapped reads with at least one deletion	2.37%
Homopolymer indels	43.83%

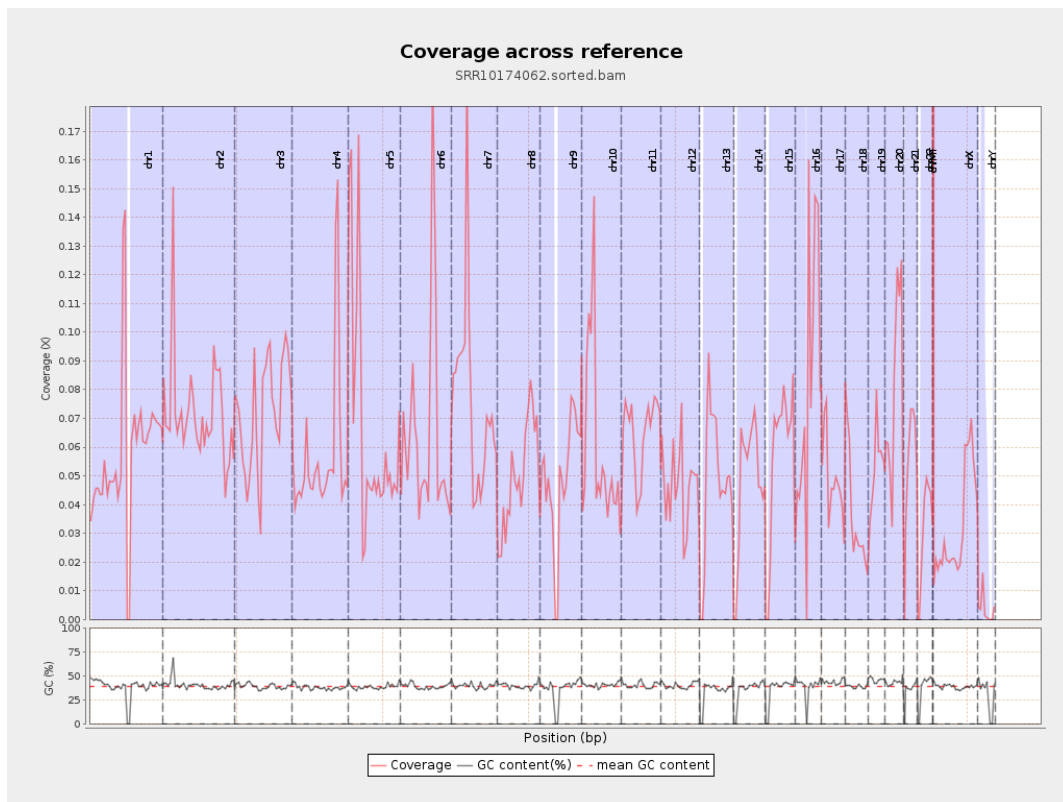
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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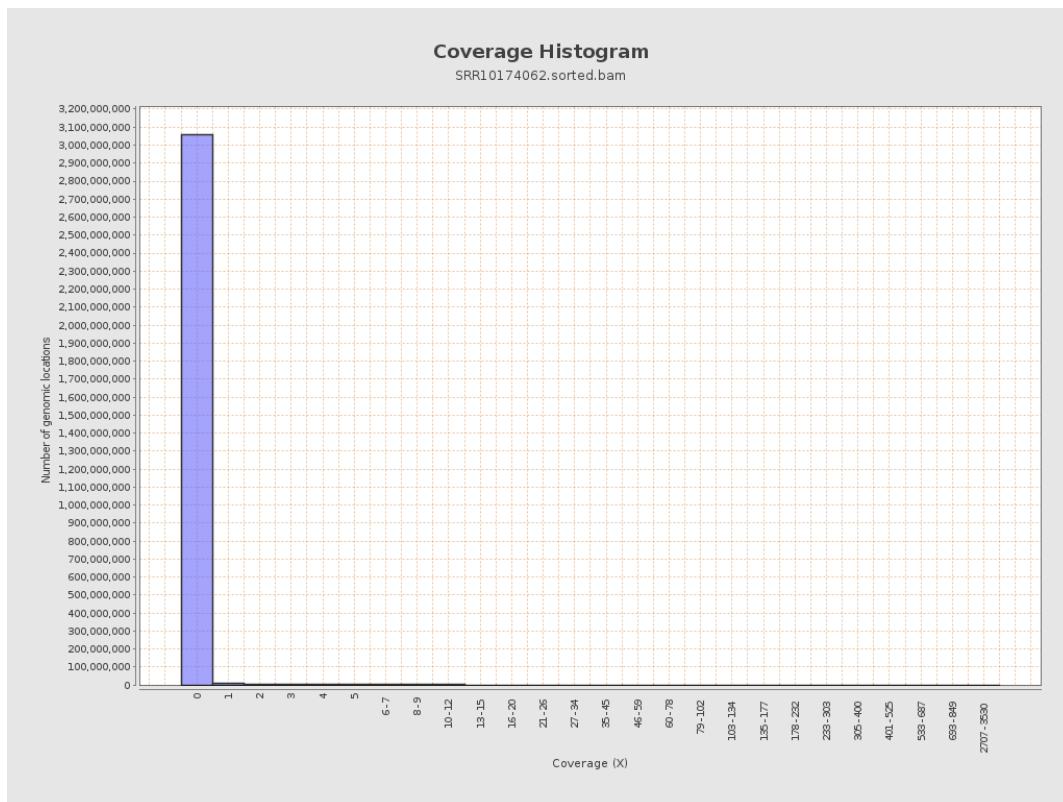
		bases	coverage	deviation
chr1	249250621	14466051	0.058	0.8651
chr2	243199373	17495087	0.0719	2.5597
chr3	198022430	14292698	0.0722	0.7898
chr4	191154276	10898815	0.057	0.7395
chr5	180915260	12120990	0.067	0.766
chr6	171115067	10896489	0.0637	0.7523
chr7	159138663	12069155	0.0758	1.0345
chr8	146364022	7364916	0.0503	0.6794
chr9	141213431	7000359	0.0496	0.7065
chr10	135534747	8020172	0.0592	1.0363
chr11	135006516	8707175	0.0645	0.7487
chr12	133851895	6319998	0.0472	0.6331
chr13	115169878	5581023	0.0485	0.656
chr14	107349540	5241551	0.0488	0.6457
chr15	102531392	5763125	0.0562	0.6916
chr16	90354753	7211645	0.0798	1.0011
chr17	81195210	4013500	0.0494	0.6861
chr18	78077248	2842129	0.0364	0.7002
chr19	59128983	3112808	0.0526	0.8467
chr20	63025520	5100233	0.0809	0.8282
chr21	48129895	2570960	0.0534	0.6781
chr22	51304566	1604853	0.0313	0.5041
chrMT	16571	307238	18.5407	19.6638
chrX	155270560	5020104	0.0323	0.5208

chrY	59373566	221701	0.0037	0.1974
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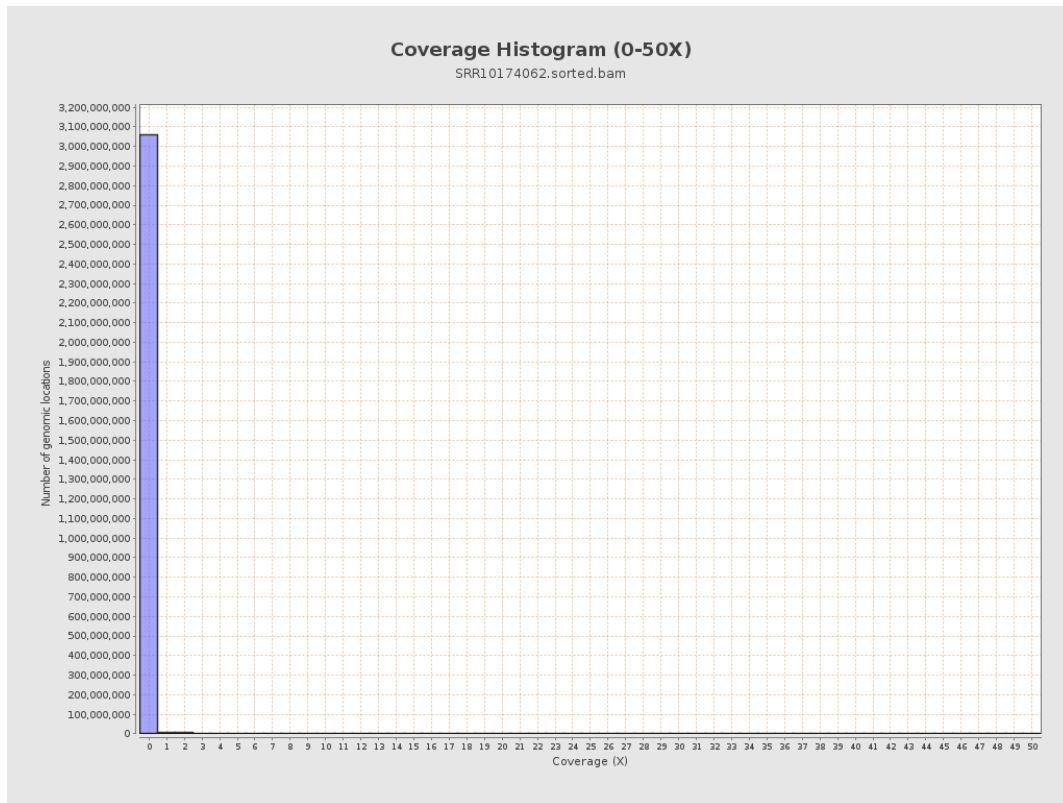
3. Results : Coverage across reference



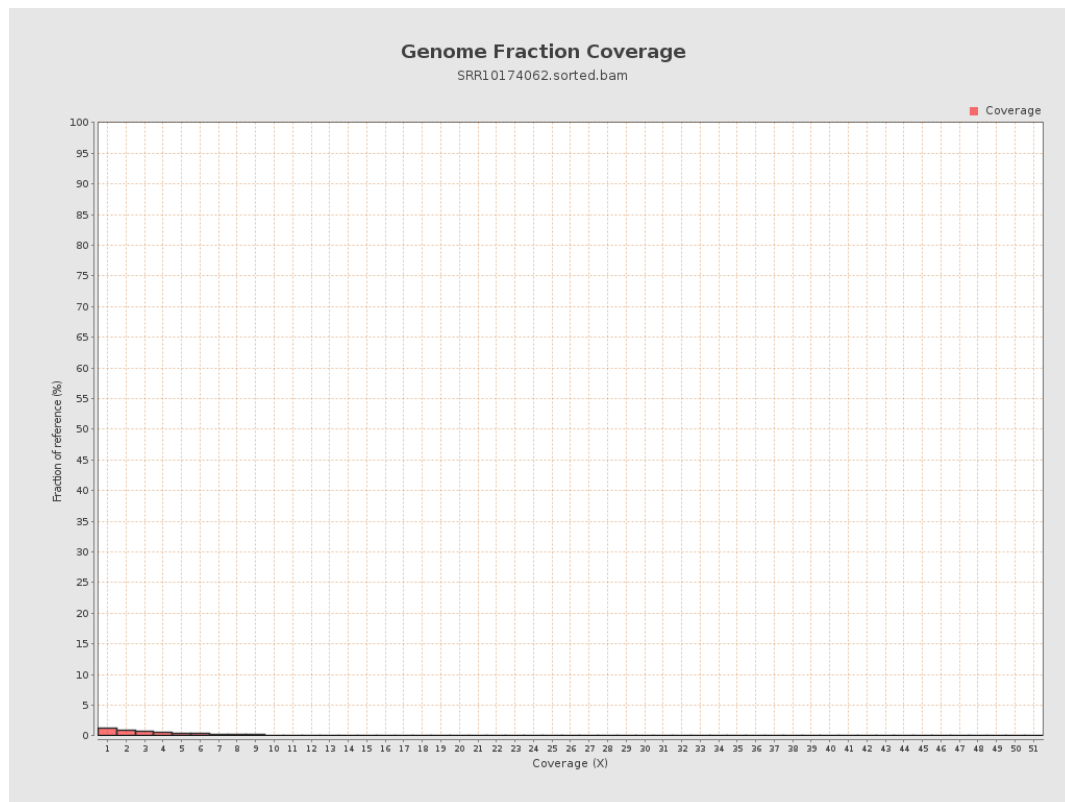
4. Results : Coverage Histogram



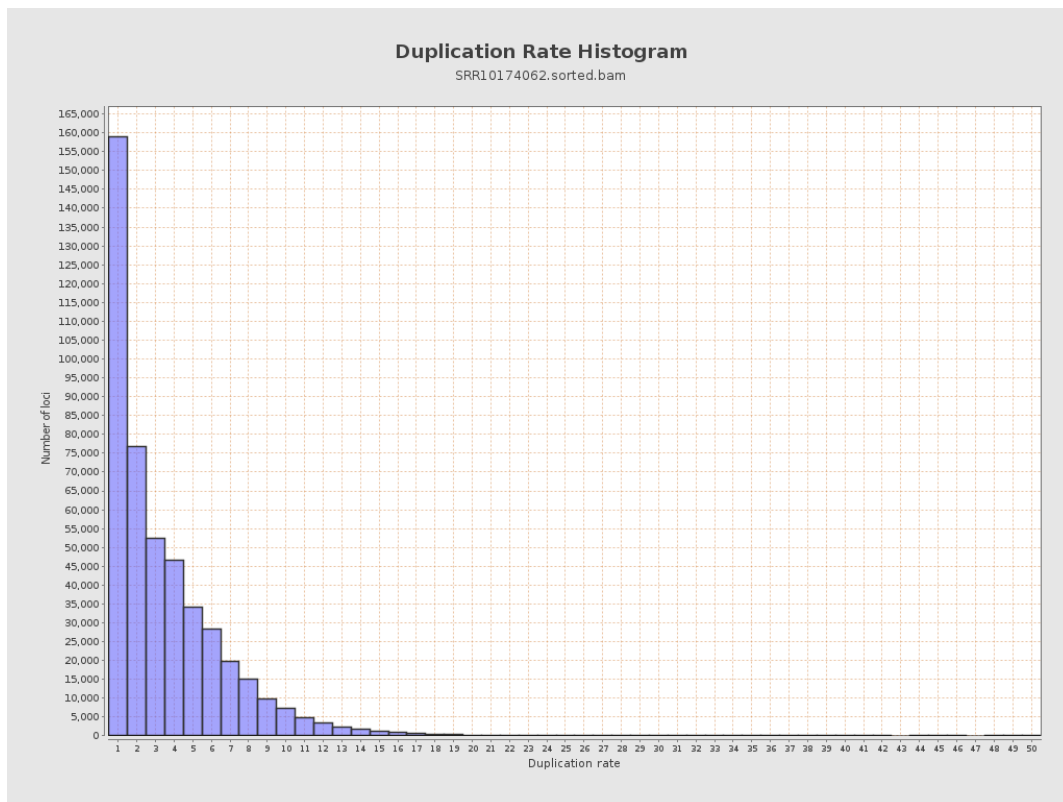
5. Results : Coverage Histogram (0-50X)



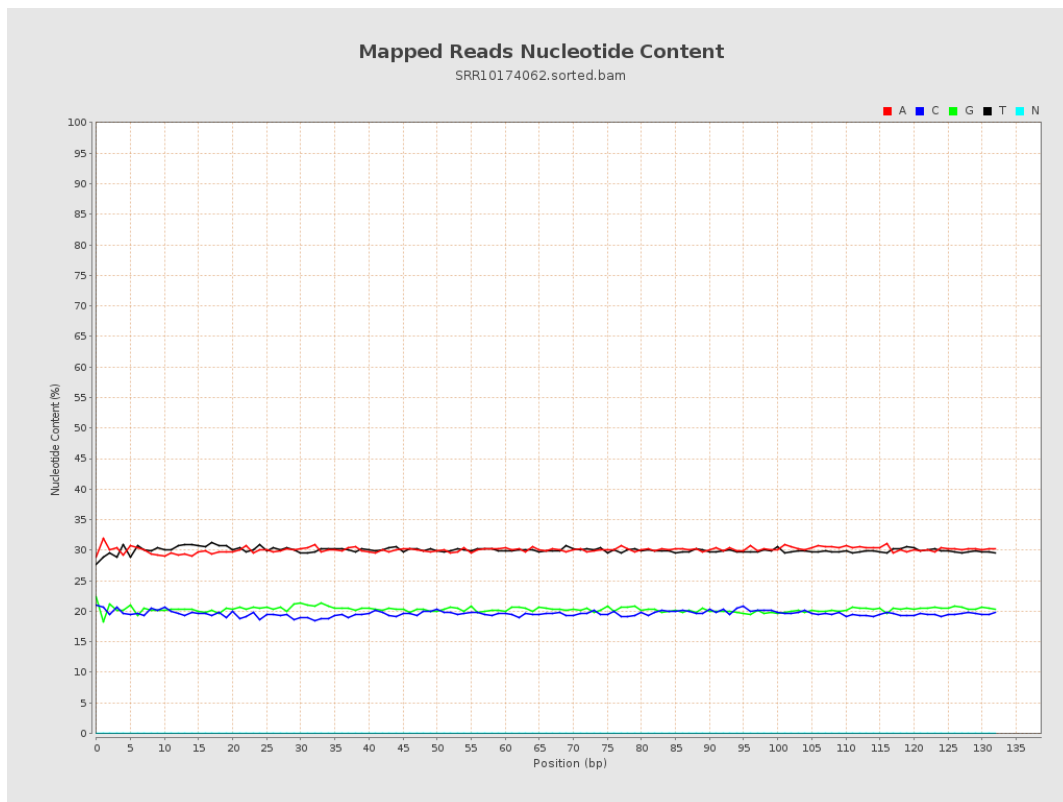
6. Results : Genome Fraction Coverage



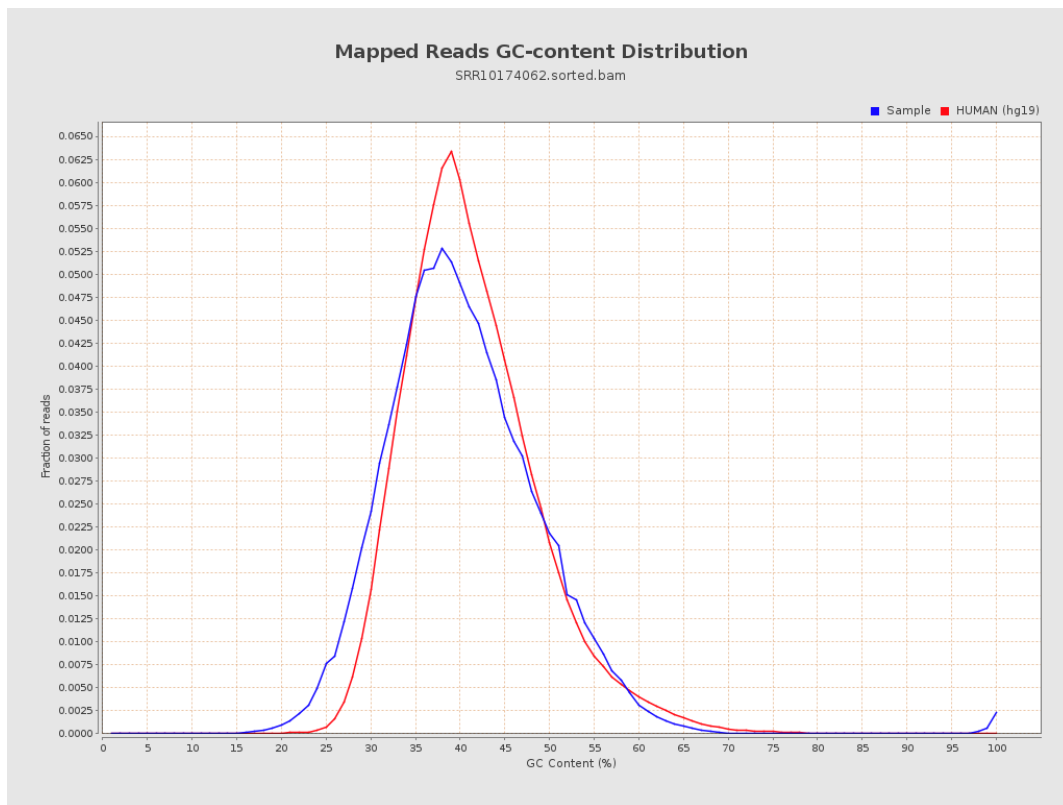
7. Results : Duplication Rate Histogram



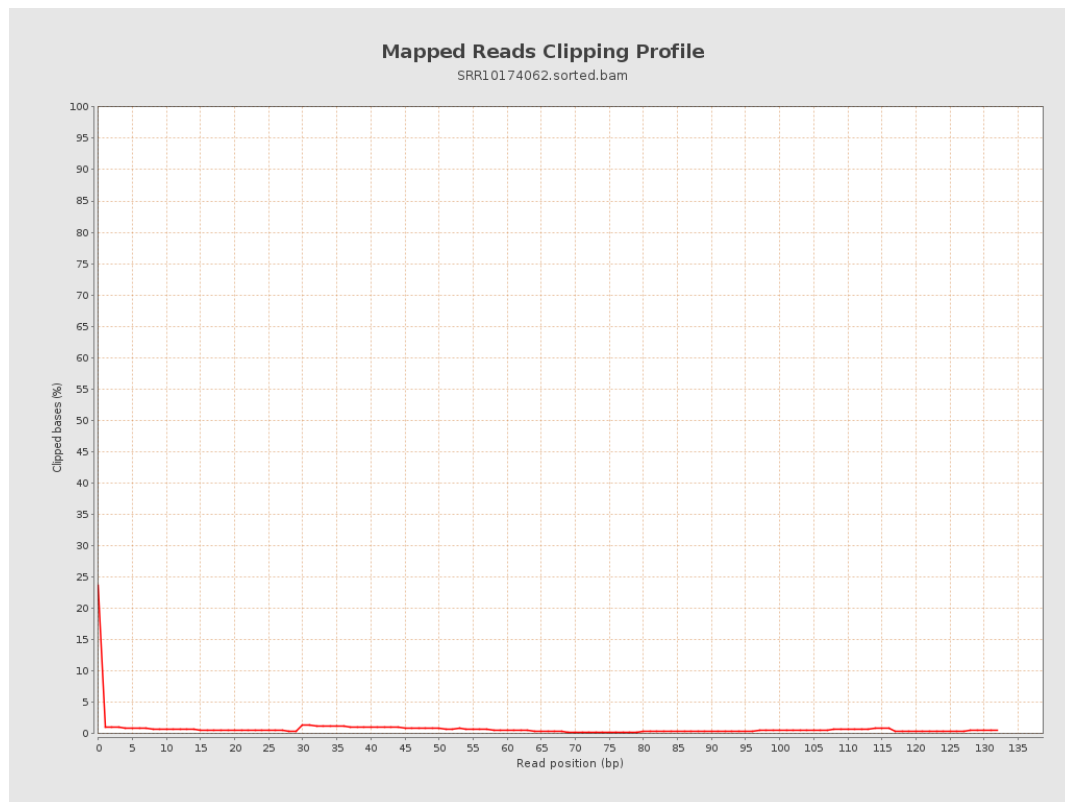
8. Results : Mapped Reads Nucleotide Content



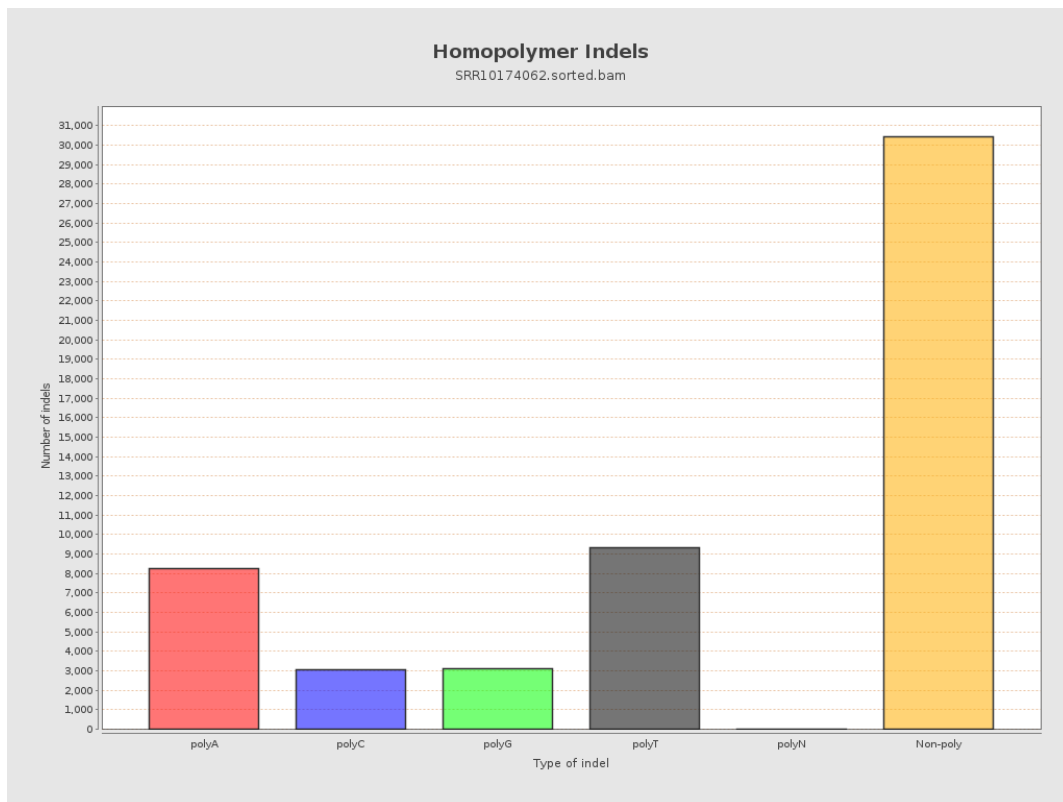
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



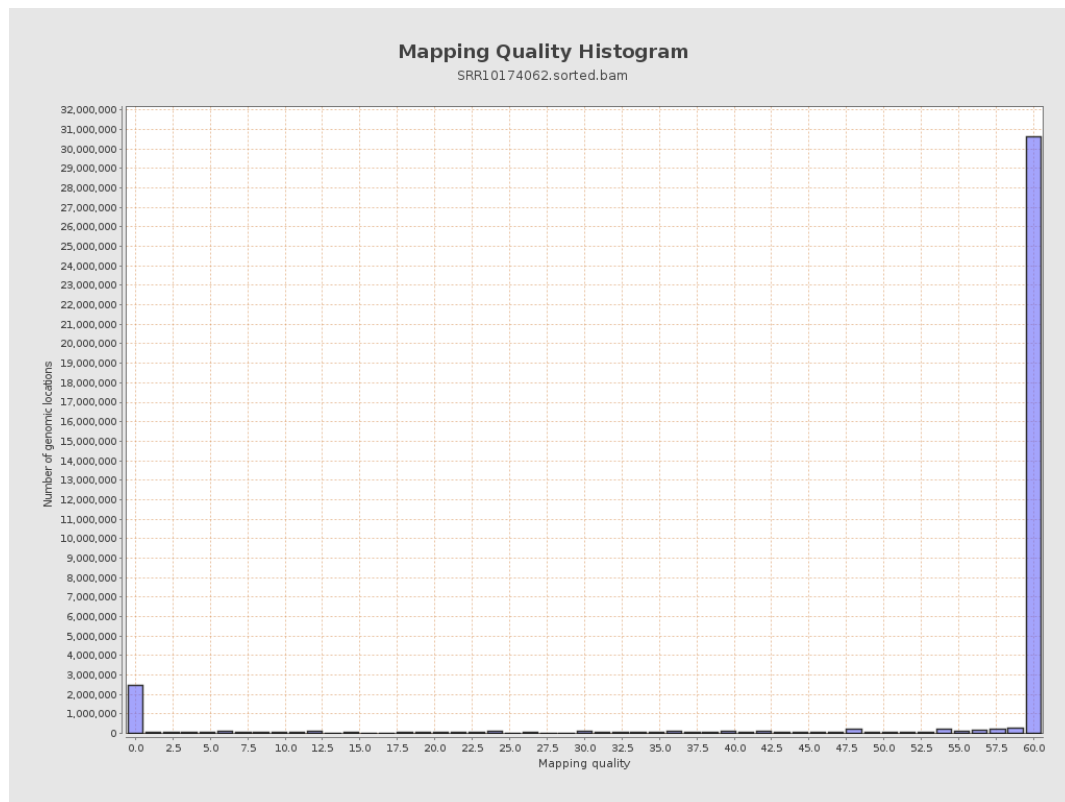
11. Results : Homopolymer Indels



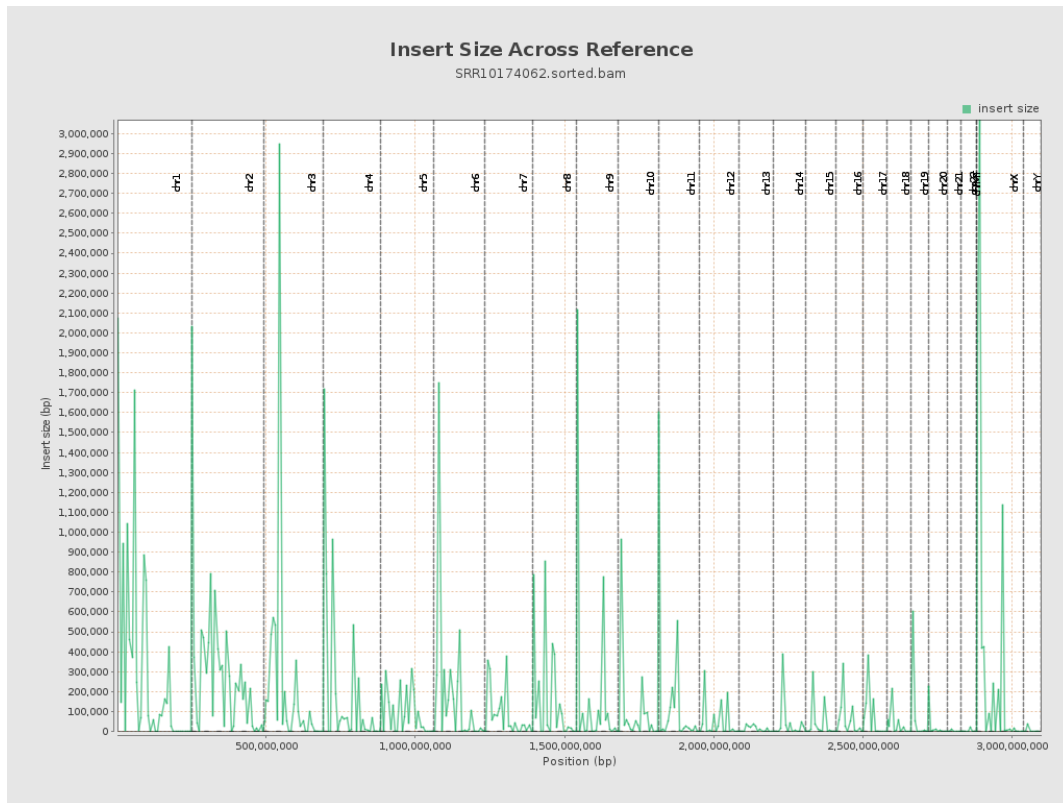
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

