

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 13:58:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173962.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_SRR10173962 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173962_1.fastq.gz SRR10173962_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 13:58:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173962.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,453,602
Mapped reads	1,415,088 / 97.35%
Unmapped reads	38,514 / 2.65%
Mapped paired reads	1,415,088 / 97.35%
Mapped reads, first in pair	707,735 / 48.69%
Mapped reads, second in pair	707,353 / 48.66%
Mapped reads, both in pair	1,390,662 / 95.67%
Mapped reads, singletons	24,426 / 1.68%
Secondary alignments	0
Supplementary alignments	144,372 / 9.93%
Read min/max/mean length	30 / 133 / 128.38
Duplicated reads (estimated)	1,060,550 / 72.96%
Duplication rate	61.66%
Clipped reads	574,550 / 39.53%

2.2. ACGT Content

Number/percentage of A's	50,732,819 / 30.3%
Number/percentage of C's	32,497,584 / 19.41%
Number/percentage of T's	50,495,689 / 30.16%
Number/percentage of G's	33,709,792 / 20.13%
Number/percentage of N's	1,969 / 0%

GC Percentage	39.54%
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2.3. Coverage

Mean	0.0541
Standard Deviation	0.9633

2.4. Mapping Quality

Mean Mapping Quality	52.88
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2.5. Insert size

Mean	1,086,897.22
Standard Deviation	9,441,832.9
P25/Median/P75	145 / 200 / 285

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	1,793,724
Insertions	19,609
Mapped reads with at least one insertion	1.33%
Deletions	39,814
Mapped reads with at least one deletion	2.75%
Homopolymer indels	42.28%

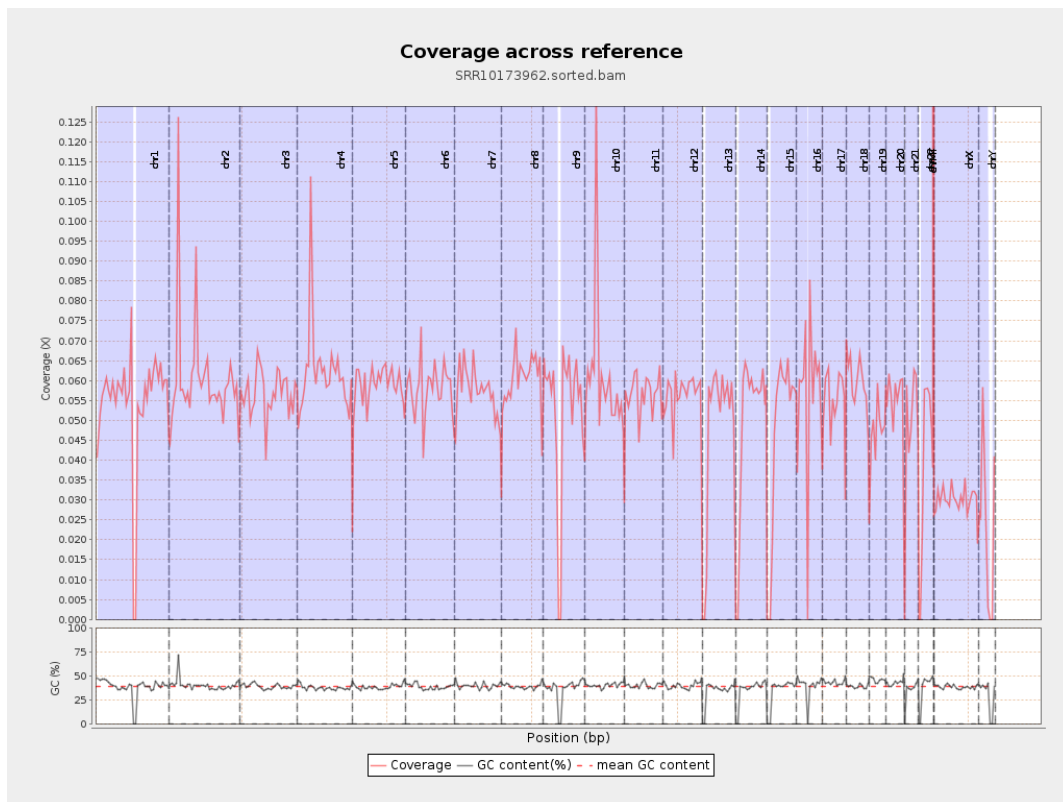
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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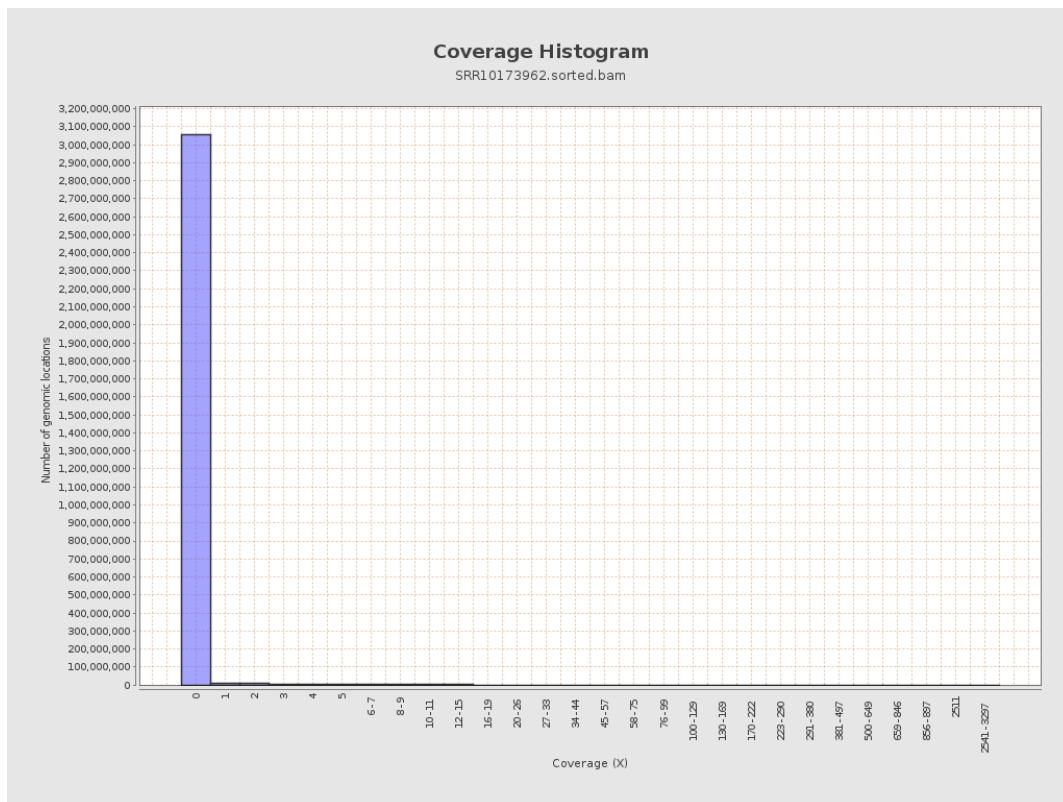
		bases	coverage	deviation
chr1	249250621	13584480	0.0545	0.8246
chr2	243199373	14750516	0.0607	2.3896
chr3	198022430	11244364	0.0568	0.664
chr4	191154276	11848050	0.062	0.8048
chr5	180915260	10654973	0.0589	0.6773
chr6	171115067	9920945	0.058	0.7067
chr7	159138663	9201004	0.0578	0.7358
chr8	146364022	8864553	0.0606	0.8157
chr9	141213431	7365352	0.0522	0.7728
chr10	135534747	8268272	0.061	0.9499
chr11	135006516	7589984	0.0562	0.6583
chr12	133851895	7539240	0.0563	0.6647
chr13	115169878	5422806	0.0471	0.6131
chr14	107349540	5309372	0.0495	0.6241
chr15	102531392	4846945	0.0473	0.6
chr16	90354753	5118605	0.0567	0.725
chr17	81195210	4421749	0.0545	0.6575
chr18	78077248	4692736	0.0601	0.9103
chr19	59128983	2834496	0.0479	0.6644
chr20	63025520	3483982	0.0553	0.6771
chr21	48129895	2322350	0.0483	0.7215
chr22	51304566	1950994	0.038	0.5419
chrMT	16571	282538	17.0501	16.8197
chrX	155270560	4694140	0.0302	0.4809

chrY	59373566	1322325	0.0223	0.5355
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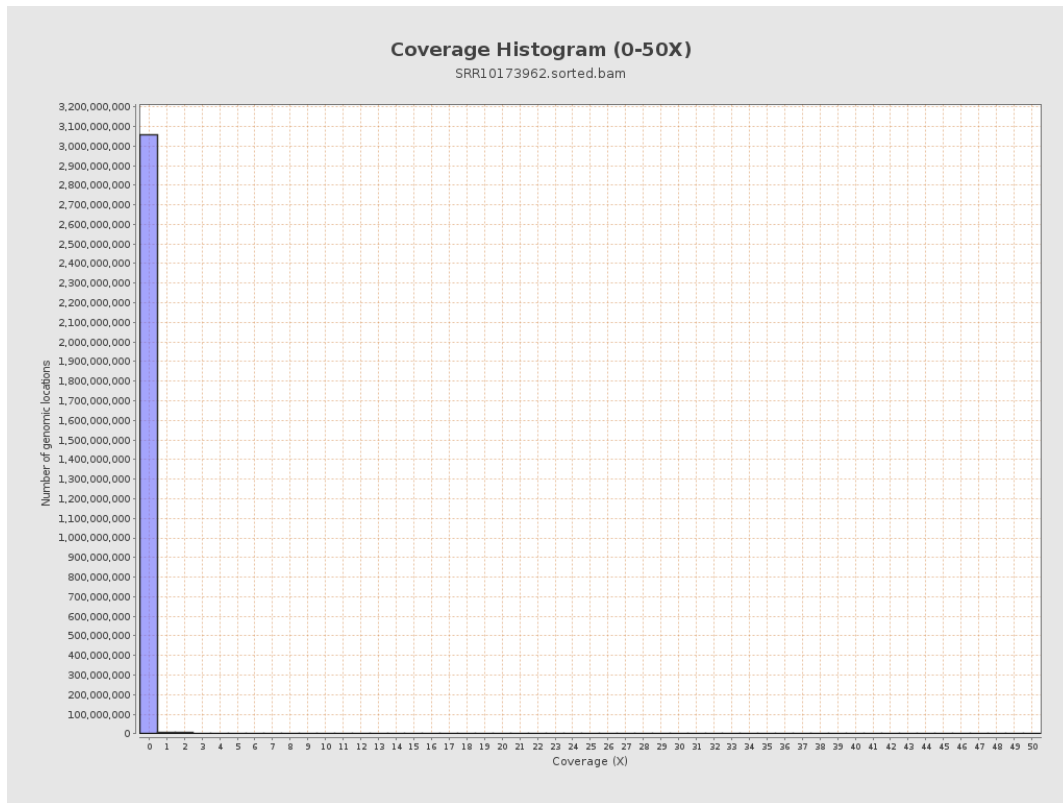
3. Results : Coverage across reference



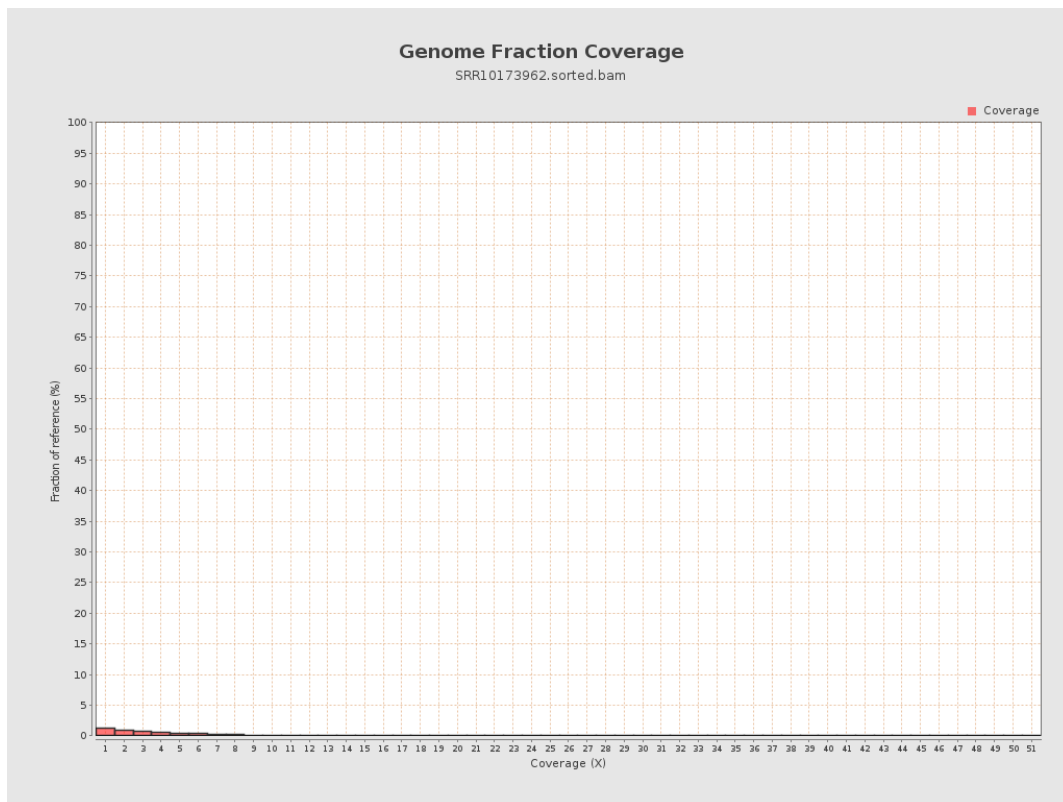
4. Results : Coverage Histogram



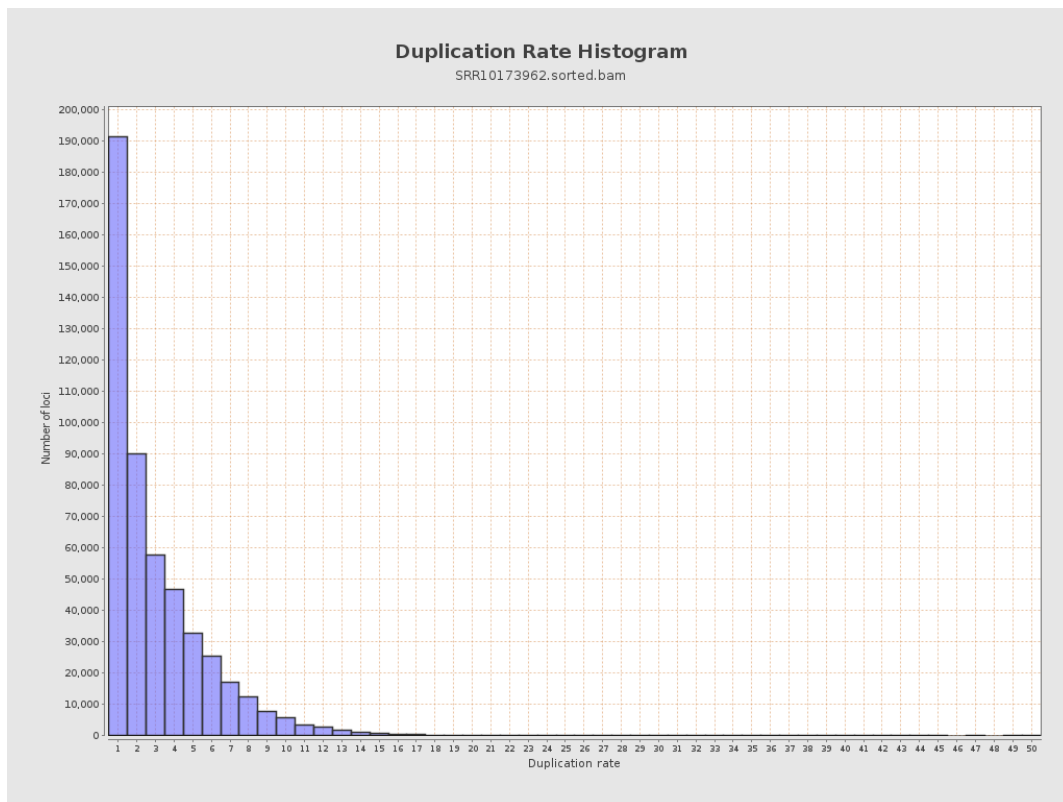
5. Results : Coverage Histogram (0-50X)



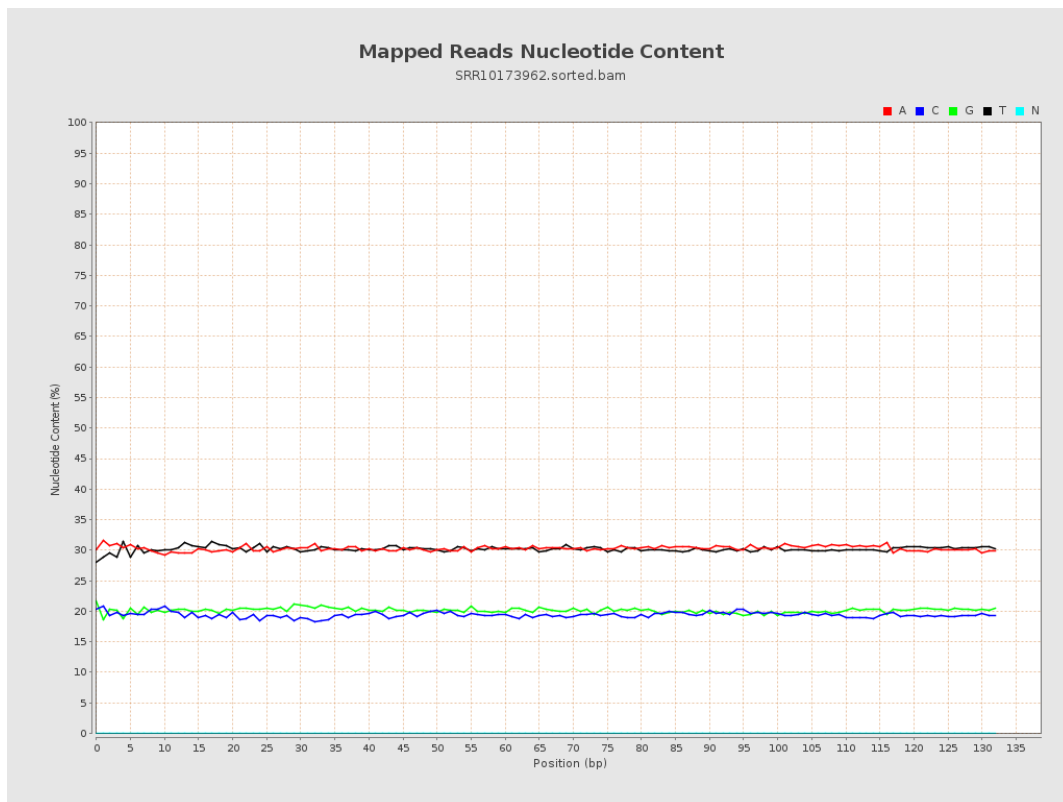
6. Results : Genome Fraction Coverage



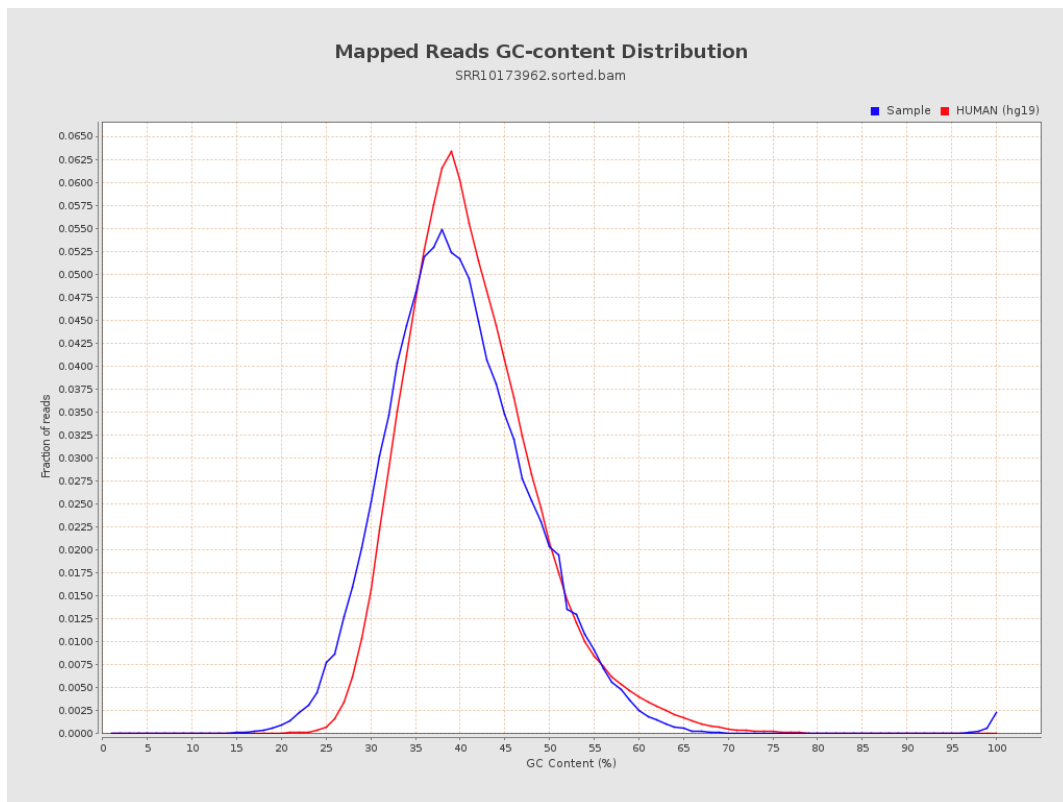
7. Results : Duplication Rate Histogram



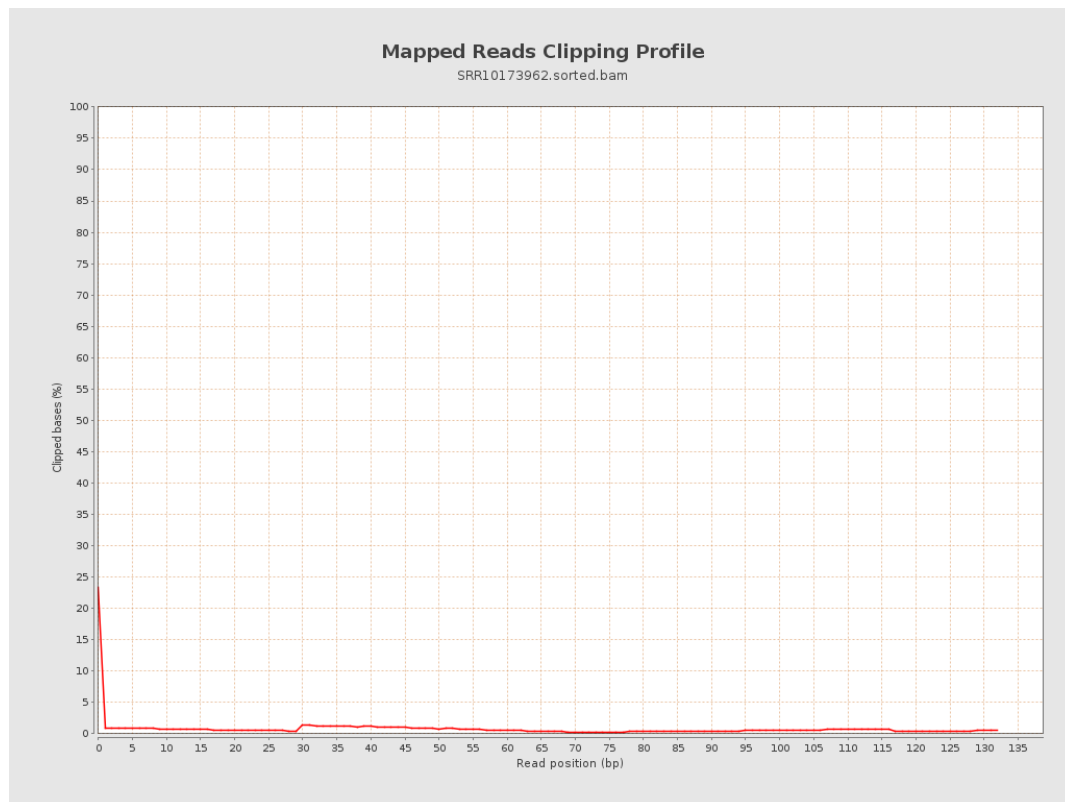
8. Results : Mapped Reads Nucleotide Content



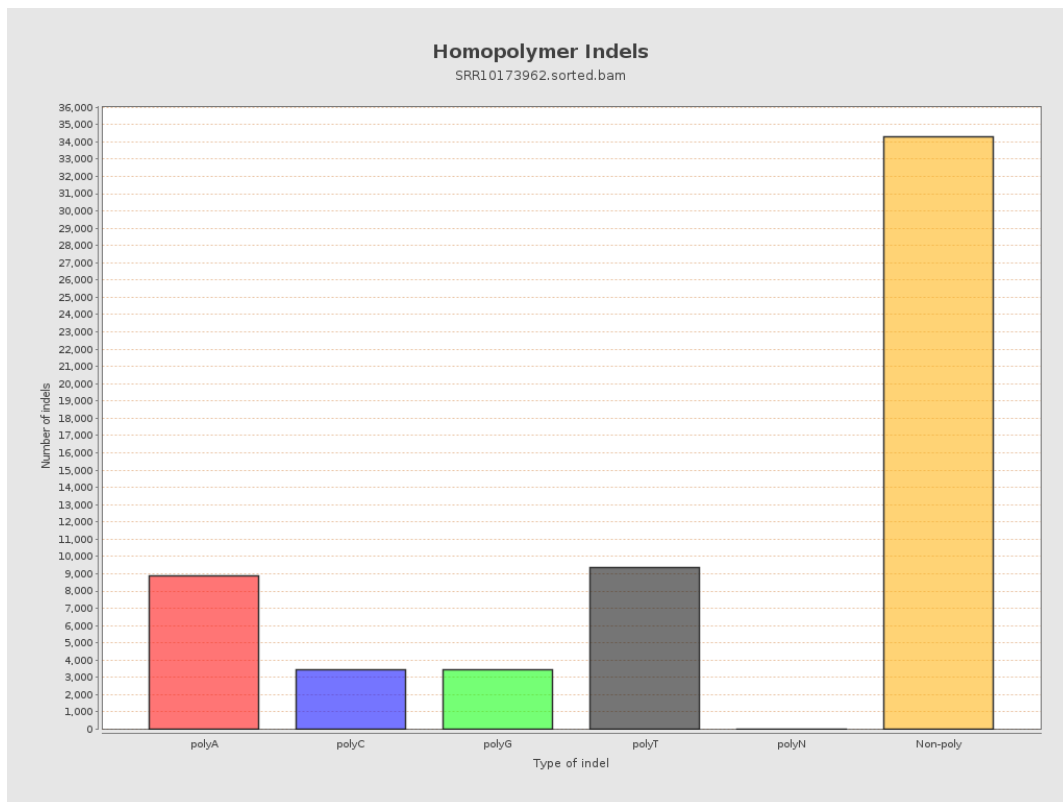
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



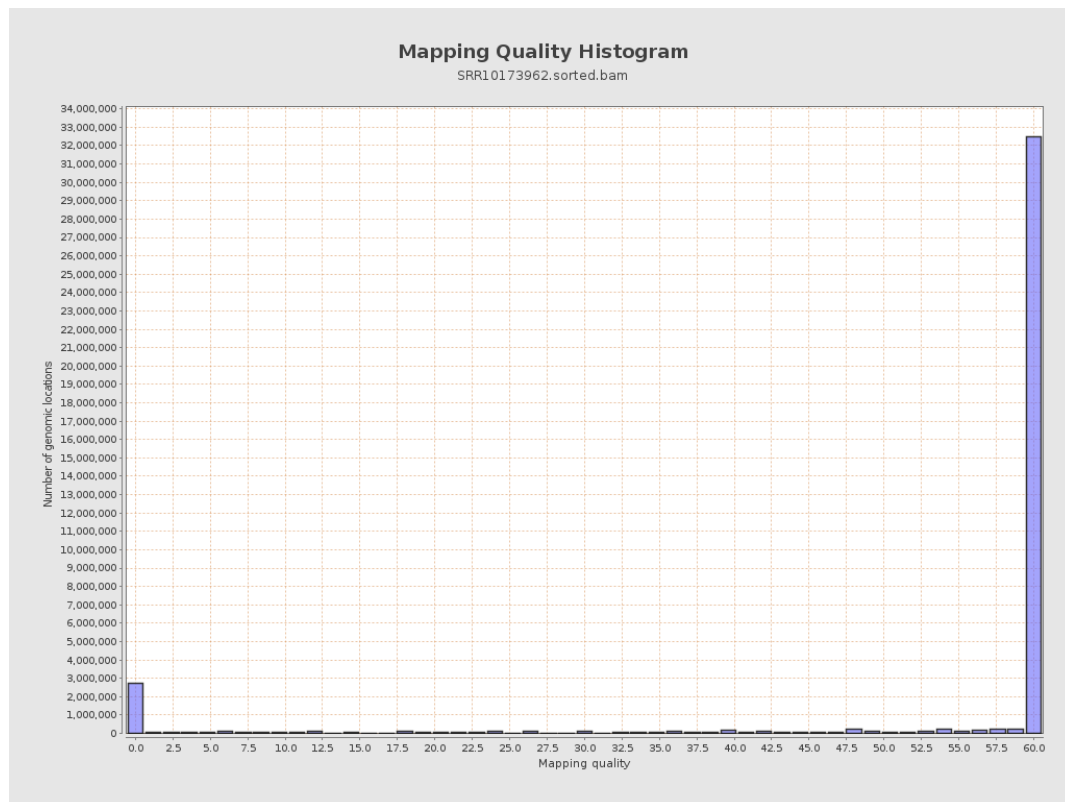
11. Results : Homopolymer Indels



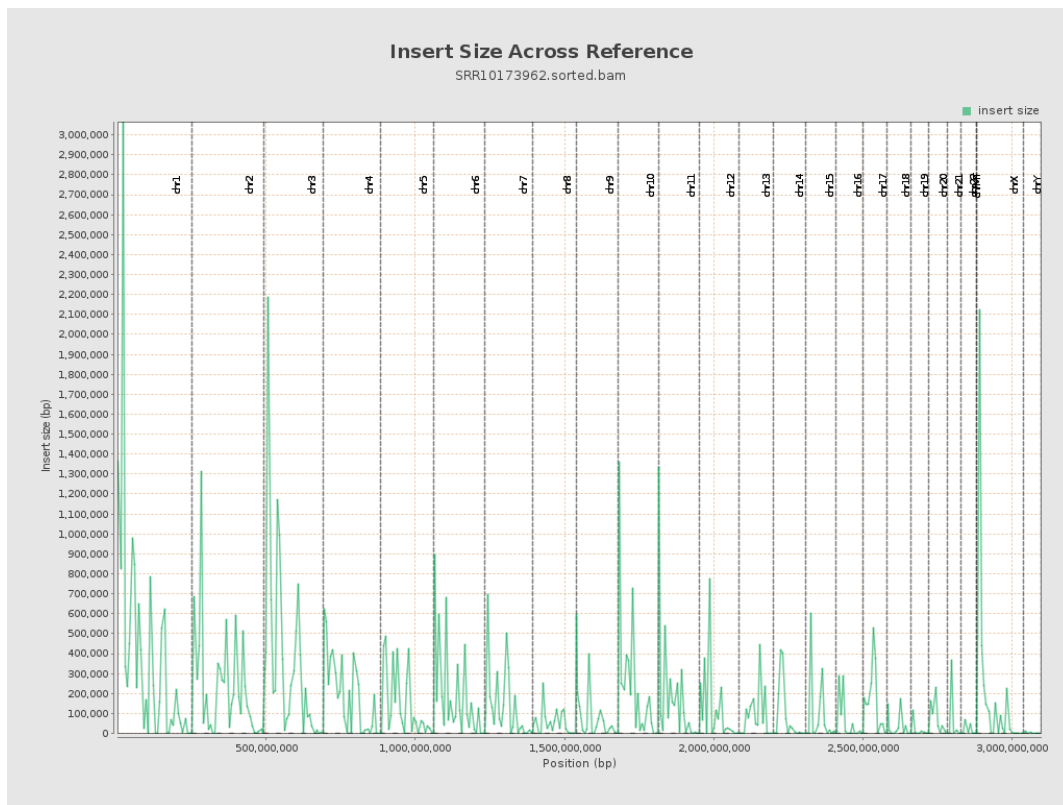
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

