

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:42:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173862.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_SRR10173862 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173862_1.fastq.gz SRR10173862_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:42:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173862.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,826,566
Mapped reads	4,708,206 / 97.55%
Unmapped reads	118,360 / 2.45%
Mapped paired reads	4,708,206 / 97.55%
Mapped reads, first in pair	2,355,781 / 48.81%
Mapped reads, second in pair	2,352,425 / 48.74%
Mapped reads, both in pair	4,632,654 / 95.98%
Mapped reads, singletons	75,552 / 1.57%
Secondary alignments	0
Supplementary alignments	436,705 / 9.05%
Read min/max/mean length	30 / 133 / 127.64
Duplicated reads (estimated)	3,667,741 / 75.99%
Duplication rate	65.17%
Clipped reads	1,908,335 / 39.54%

2.2. ACGT Content

Number/percentage of A's	166,605,301 / 30.03%
Number/percentage of C's	109,339,471 / 19.71%
Number/percentage of T's	166,002,488 / 29.92%
Number/percentage of G's	112,792,055 / 20.33%
Number/percentage of N's	6,138 / 0%

GC Percentage	40.04%
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2.3. Coverage

Mean	0.1793
Standard Deviation	2.5936

2.4. Mapping Quality

Mean Mapping Quality	52.76
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2.5. Insert size

Mean	801,599.95
Standard Deviation	8,099,634.93
P25/Median/P75	142 / 197 / 281

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	5,501,225
Insertions	58,153
Mapped reads with at least one insertion	1.19%
Deletions	123,287
Mapped reads with at least one deletion	2.55%
Homopolymer indels	43.36%

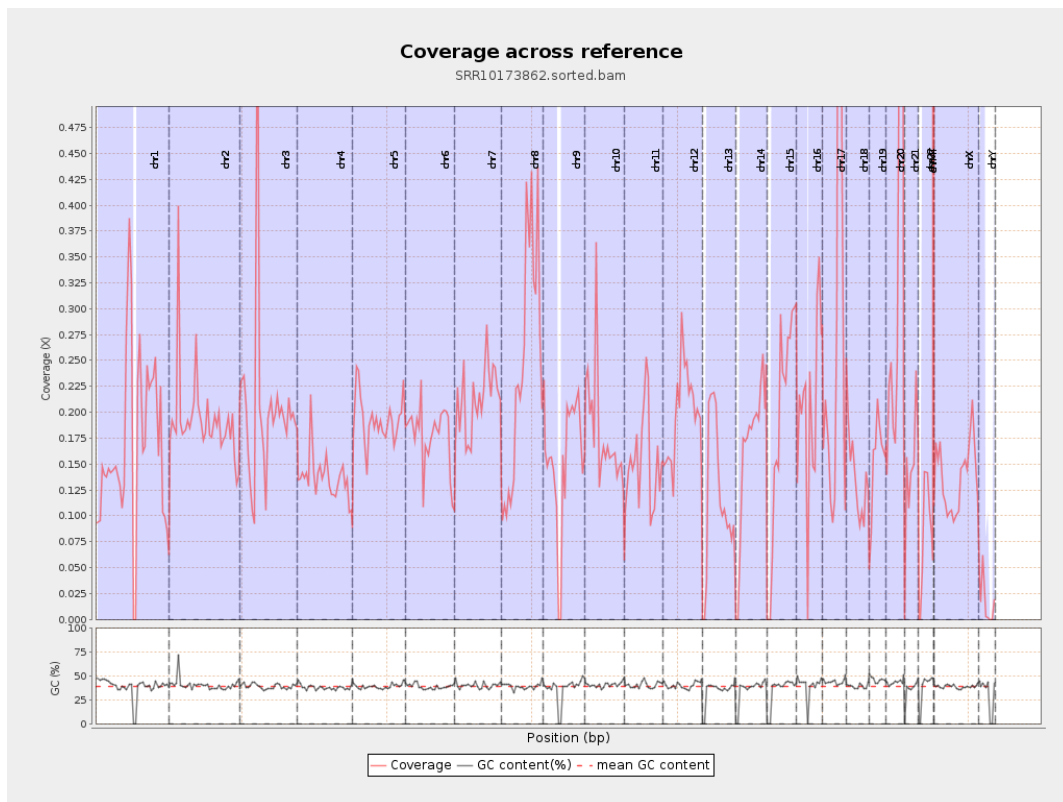
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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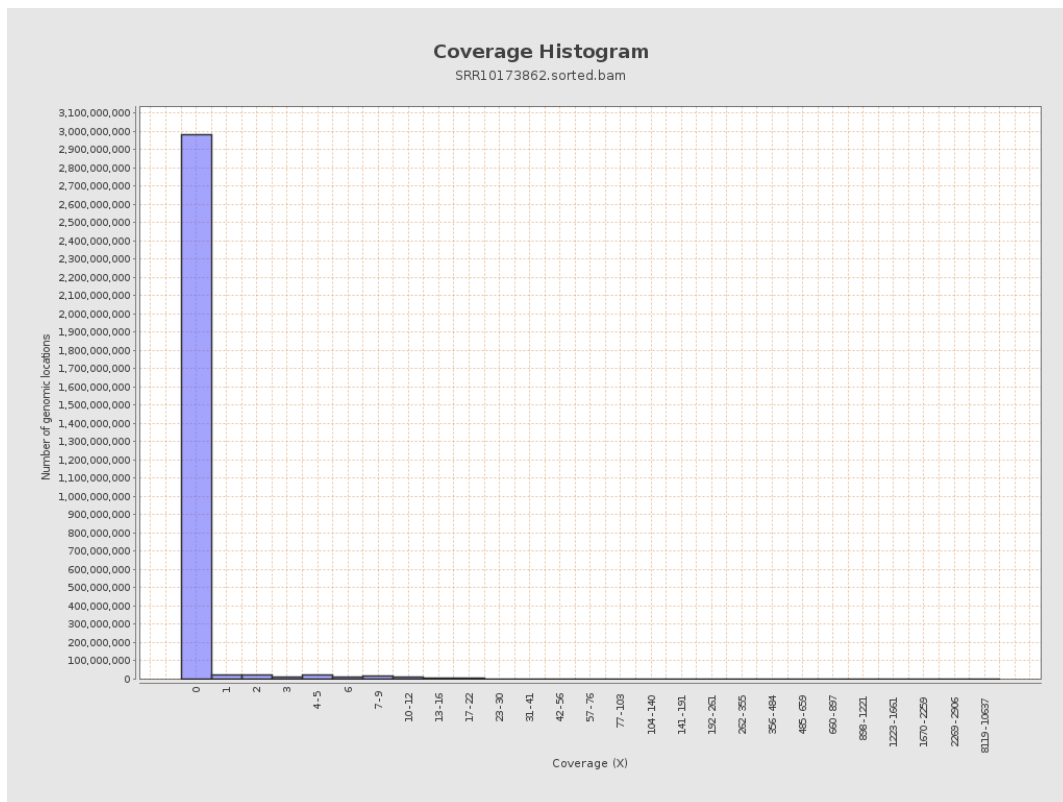
		bases	coverage	deviation
chr1	249250621	41724198	0.1674	1.9499
chr2	243199373	46940165	0.193	7.4896
chr3	198022430	39940468	0.2017	1.3406
chr4	191154276	26069666	0.1364	1.2807
chr5	180915260	34876058	0.1928	1.2791
chr6	171115067	30321396	0.1772	1.399
chr7	159138663	33986329	0.2136	1.8612
chr8	146364022	35440458	0.2421	2.1217
chr9	141213431	21398529	0.1515	1.3342
chr10	135534747	24351470	0.1797	2.5315
chr11	135006516	20509963	0.1519	1.1492
chr12	133851895	26577419	0.1986	1.3143
chr13	115169878	13332570	0.1158	0.9933
chr14	107349540	17518893	0.1632	1.1741
chr15	102531392	19518710	0.1904	1.2777
chr16	90354753	18814118	0.2082	1.6555
chr17	81195210	23259398	0.2865	1.691
chr18	78077248	10770366	0.1379	1.9465
chr19	59128983	9299759	0.1573	1.5796
chr20	63025520	25296662	0.4014	2.0286
chr21	48129895	6991129	0.1453	1.1742
chr22	51304566	4135877	0.0806	0.7925
chrMT	16571	1691282	102.0628	77.7247
chrX	155270560	21311602	0.1373	1.0843

chrY	59373566	980140	0.0165	0.5978
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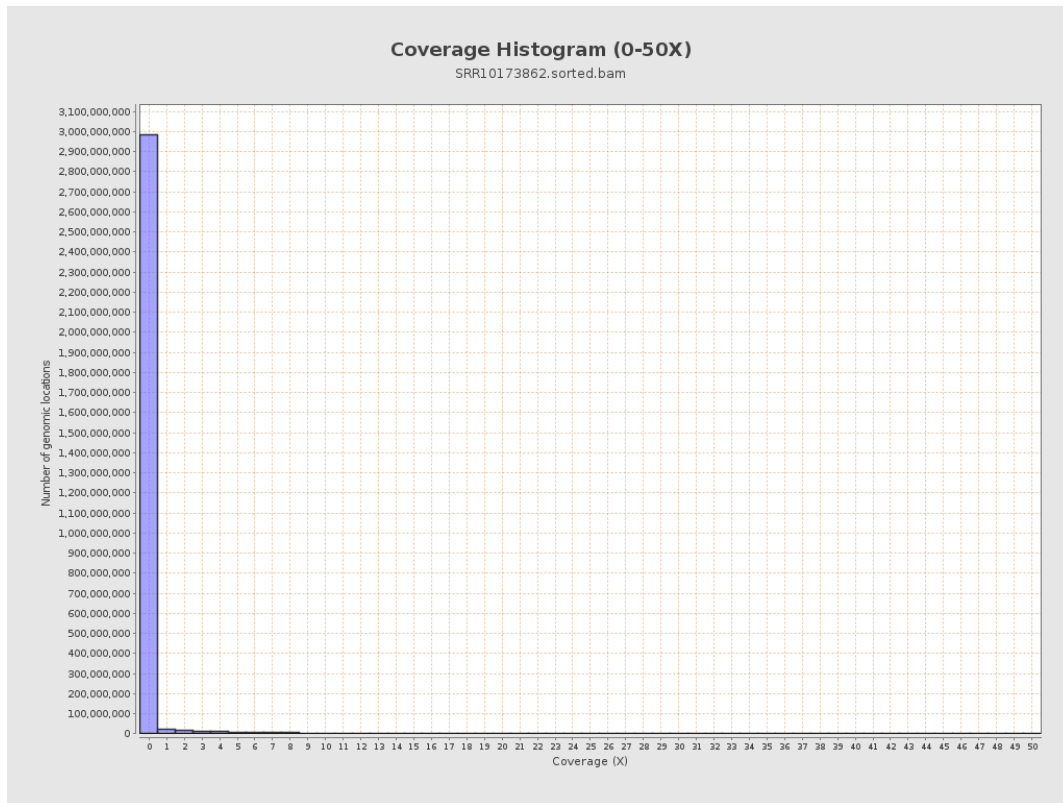
3. Results : Coverage across reference



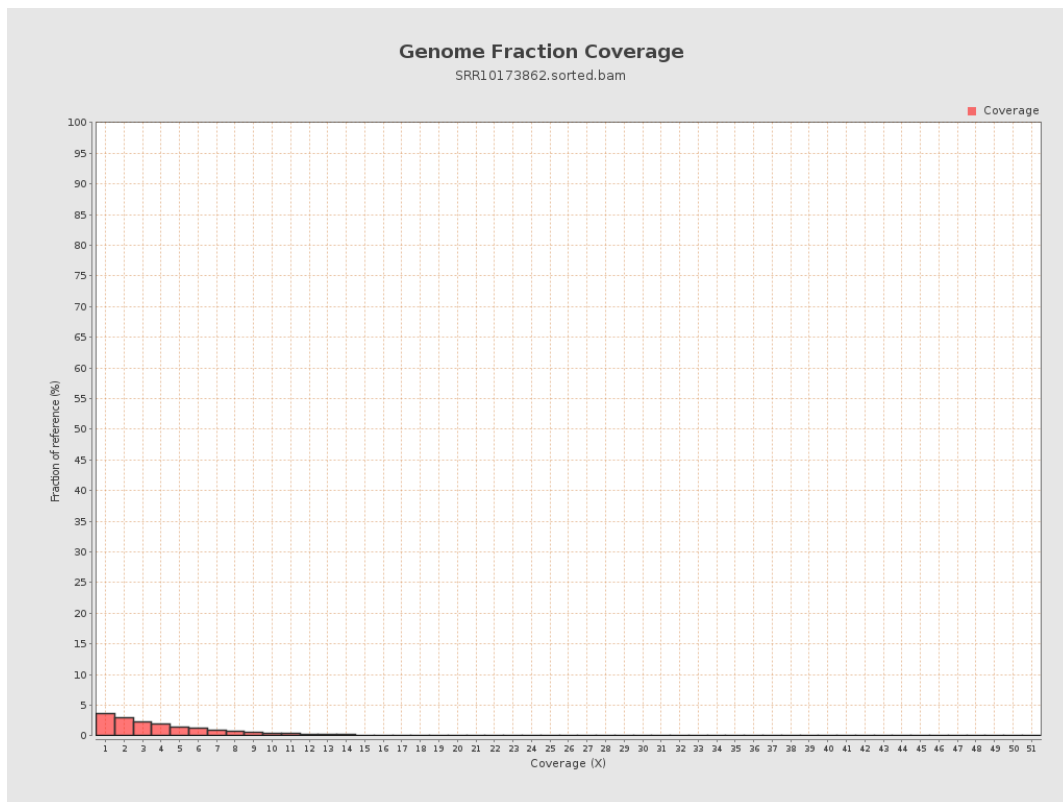
4. Results : Coverage Histogram



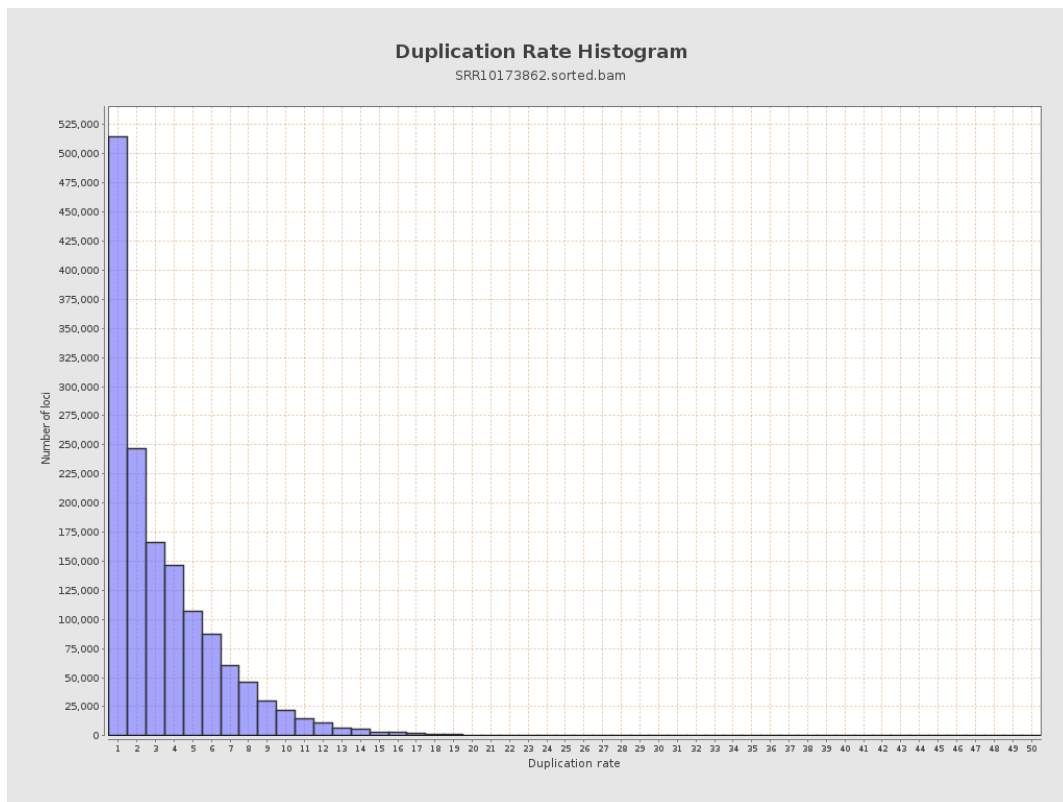
5. Results : Coverage Histogram (0-50X)



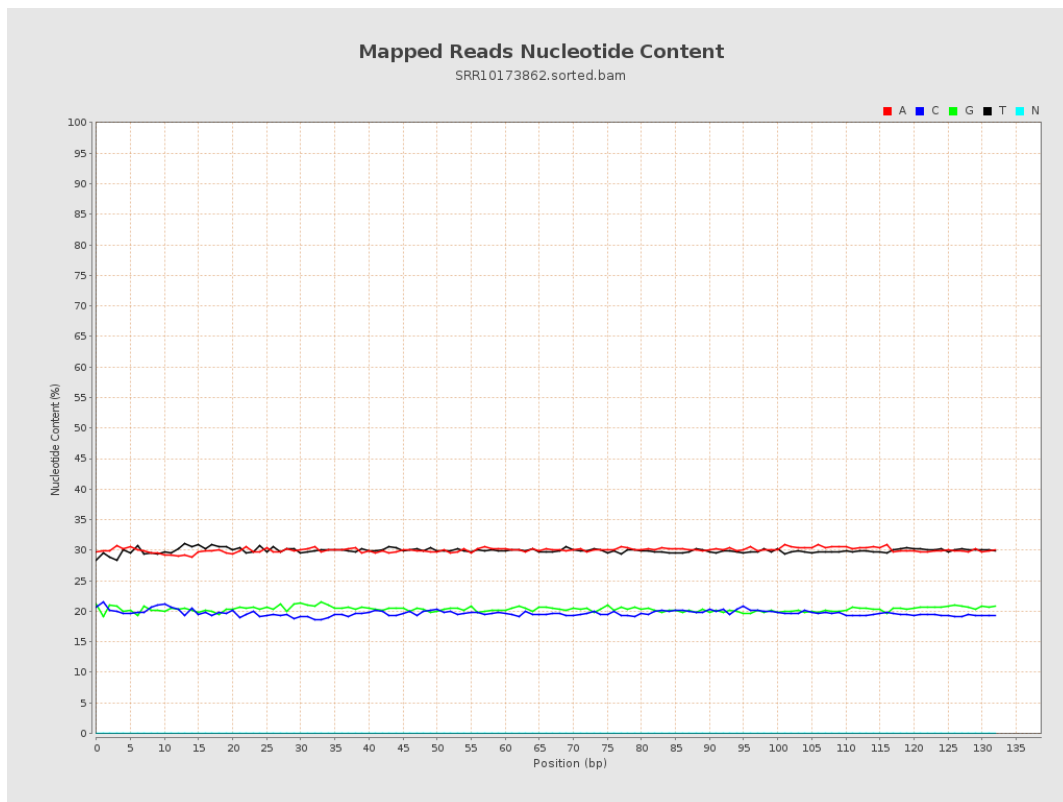
6. Results : Genome Fraction Coverage



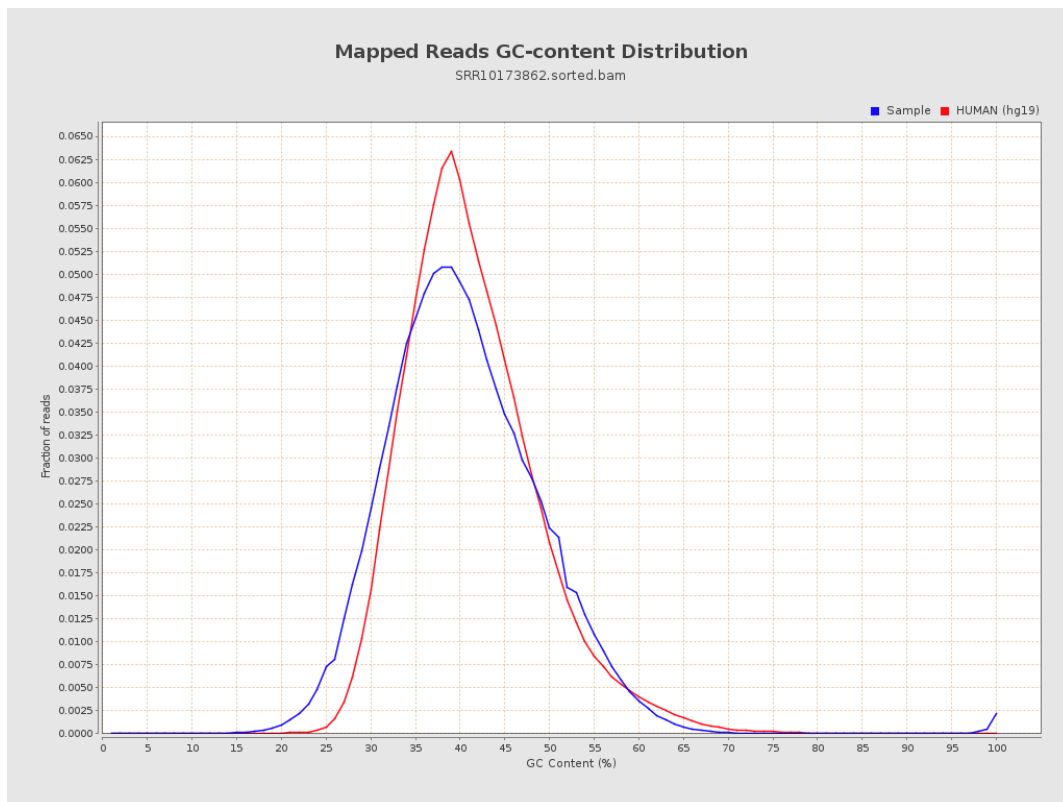
7. Results : Duplication Rate Histogram



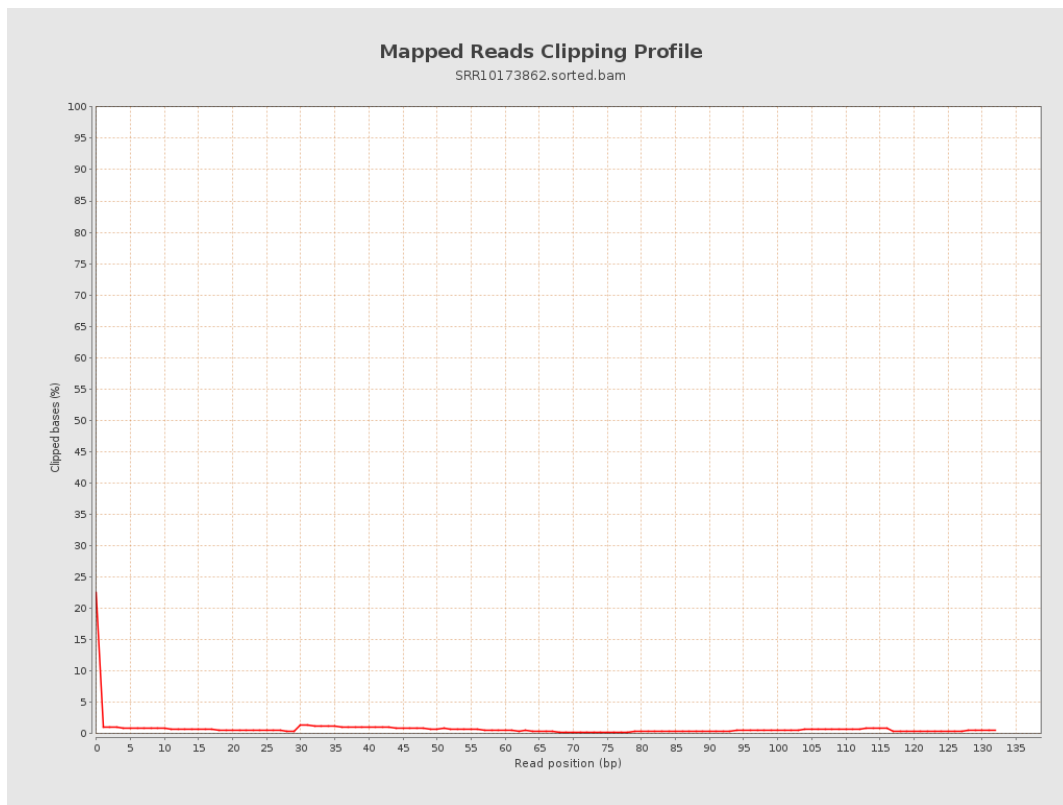
8. Results : Mapped Reads Nucleotide Content



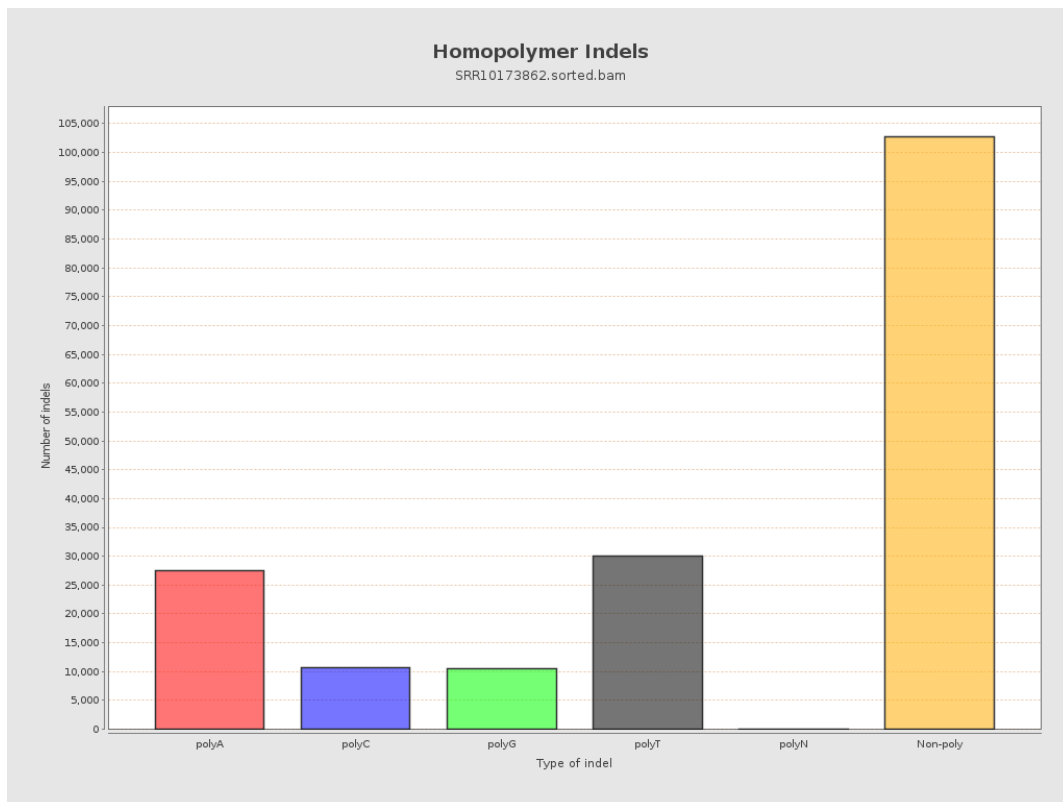
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



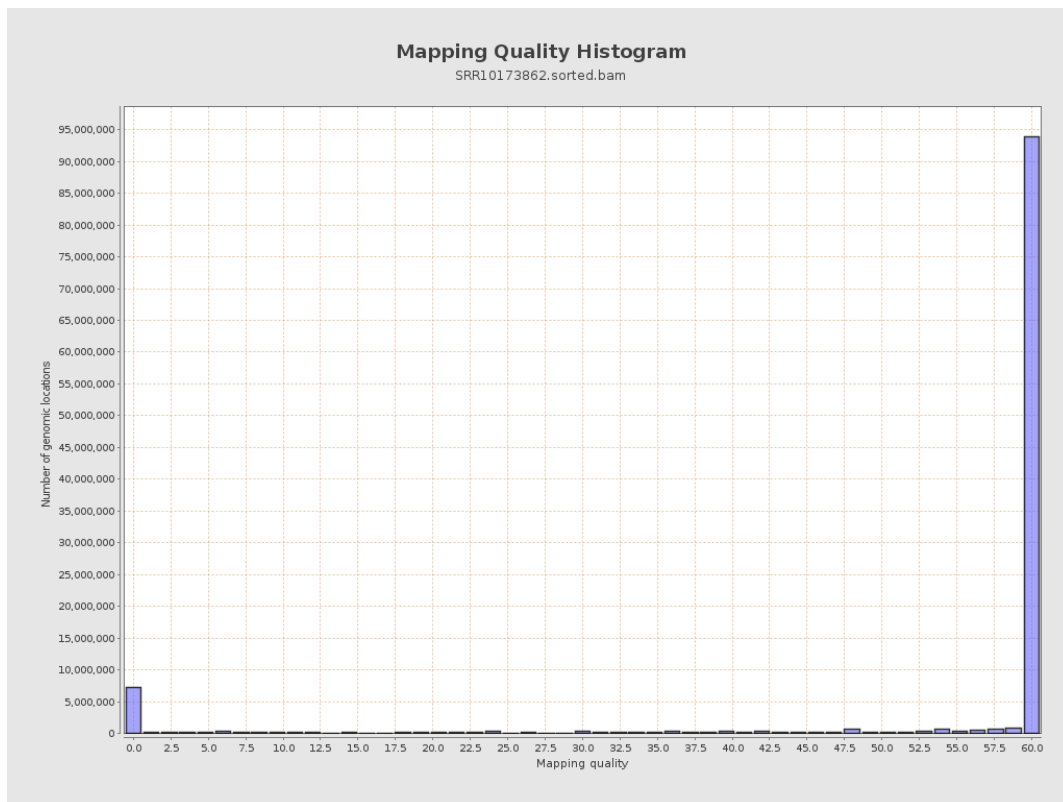
11. Results : Homopolymer Indels



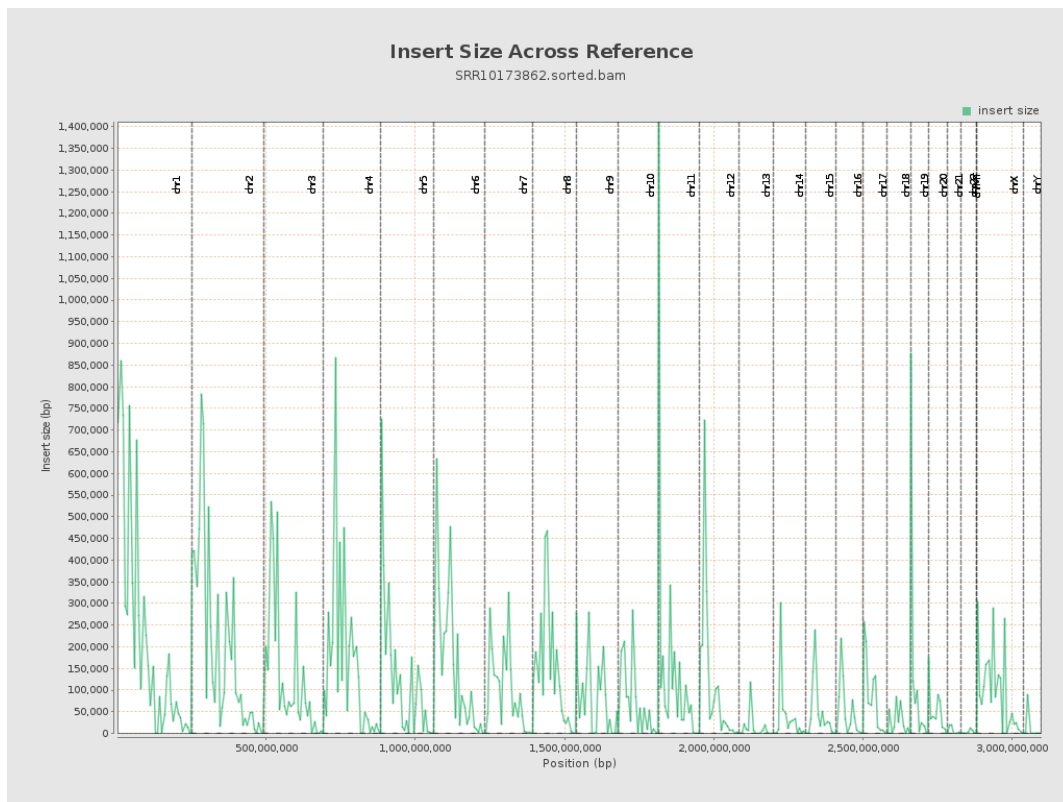
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

