

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 01:19:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174048.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_SRR10174048 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174048_1.fastq.gz SRR10174048_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 01:19:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174048.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,326,366
Mapped reads	4,206,404 / 97.23%
Unmapped reads	119,962 / 2.77%
Mapped paired reads	4,206,404 / 97.23%
Mapped reads, first in pair	2,100,809 / 48.56%
Mapped reads, second in pair	2,105,595 / 48.67%
Mapped reads, both in pair	4,120,978 / 95.25%
Mapped reads, singletons	85,426 / 1.97%
Secondary alignments	0
Supplementary alignments	536,441 / 12.4%
Read min/max/mean length	30 / 133 / 129.62
Duplicated reads (estimated)	3,209,970 / 74.2%
Duplication rate	63.58%
Clipped reads	1,944,198 / 44.94%

2.2. ACGT Content

Number/percentage of A's	148,062,756 / 29.8%
Number/percentage of C's	98,010,551 / 19.72%
Number/percentage of T's	148,357,978 / 29.86%
Number/percentage of G's	102,490,098 / 20.62%
Number/percentage of N's	6,135 / 0%

GC Percentage	40.35%
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2.3. Coverage

Mean	0.1606
Standard Deviation	2.4302

2.4. Mapping Quality

Mean Mapping Quality	52.42
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2.5. Insert size

Mean	1,147,930.57
Standard Deviation	9,852,037.13
P25/Median/P75	144 / 204 / 297

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	5,277,506
Insertions	53,190
Mapped reads with at least one insertion	1.22%
Deletions	142,167
Mapped reads with at least one deletion	3.3%
Homopolymer indels	41.23%

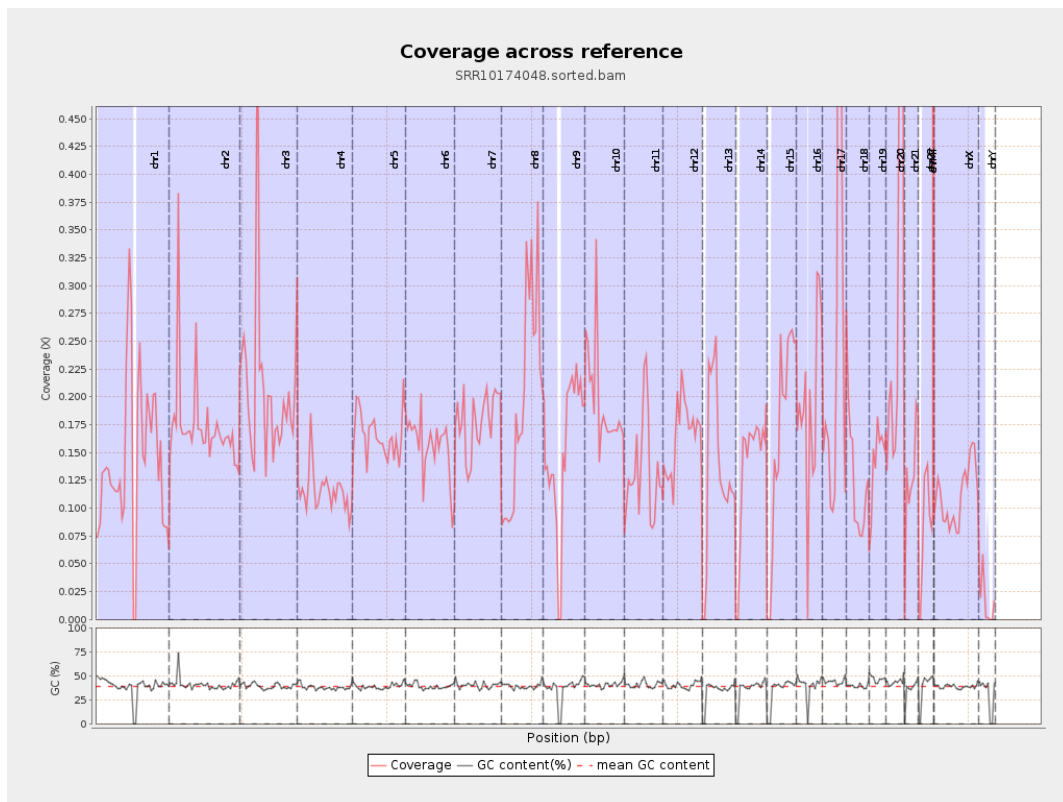
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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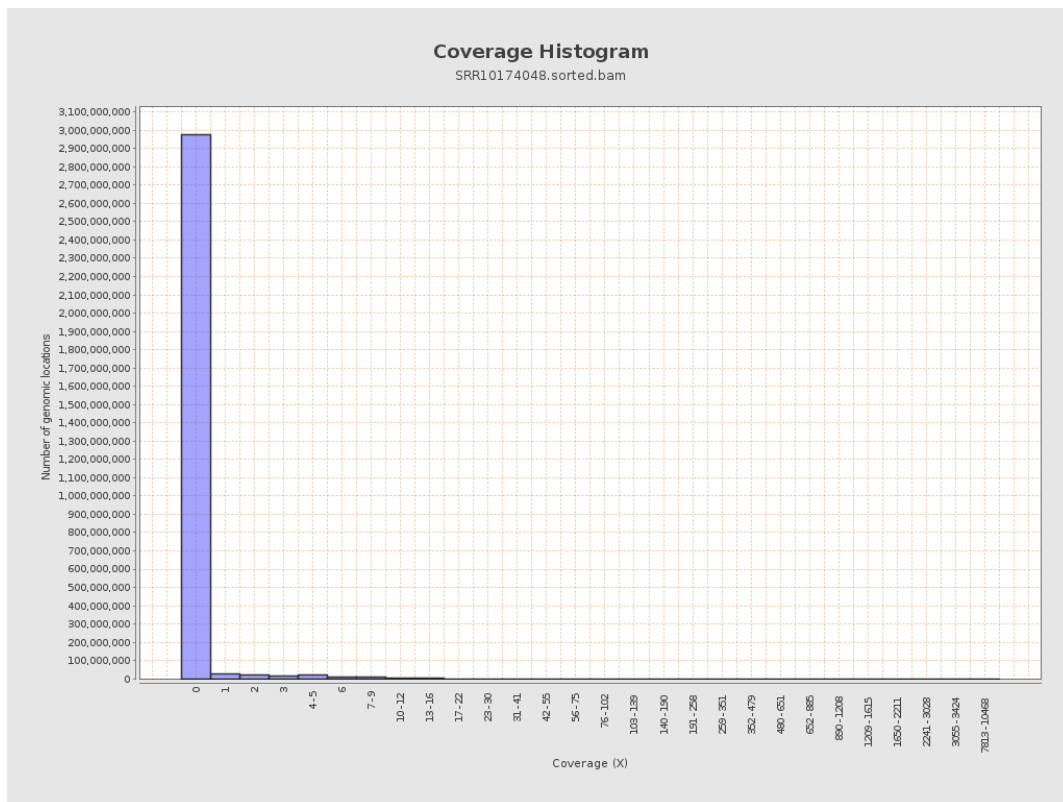
		bases	coverage	deviation
chr1	249250621	35424991	0.1421	1.6469
chr2	243199373	42382654	0.1743	7.3824
chr3	198022430	40271353	0.2034	1.2246
chr4	191154276	21948625	0.1148	1.0581
chr5	180915260	29991496	0.1658	1.0838
chr6	171115067	26640252	0.1557	1.2037
chr7	159138663	28501342	0.1791	1.5501
chr8	146364022	28647388	0.1957	1.4911
chr9	141213431	21191986	0.1501	1.2462
chr10	135534747	26400643	0.1948	2.0849
chr11	135006516	18064546	0.1338	0.99
chr12	133851895	22122196	0.1653	1.0917
chr13	115169878	15272249	0.1326	0.9829
chr14	107349540	14531709	0.1354	0.9863
chr15	102531392	17234478	0.1681	1.0882
chr16	90354753	17581613	0.1946	1.4611
chr17	81195210	21185041	0.2609	1.487
chr18	78077248	9778118	0.1252	1.6696
chr19	59128983	8512974	0.144	1.3075
chr20	63025520	21946668	0.3482	1.7098
chr21	48129895	6165923	0.1281	0.9983
chr22	51304566	4024075	0.0784	0.7155
chrMT	16571	1197791	72.2824	55.5102
chrX	155270560	17322896	0.1116	0.8889

chrY	59373566	911648	0.0154	0.5823
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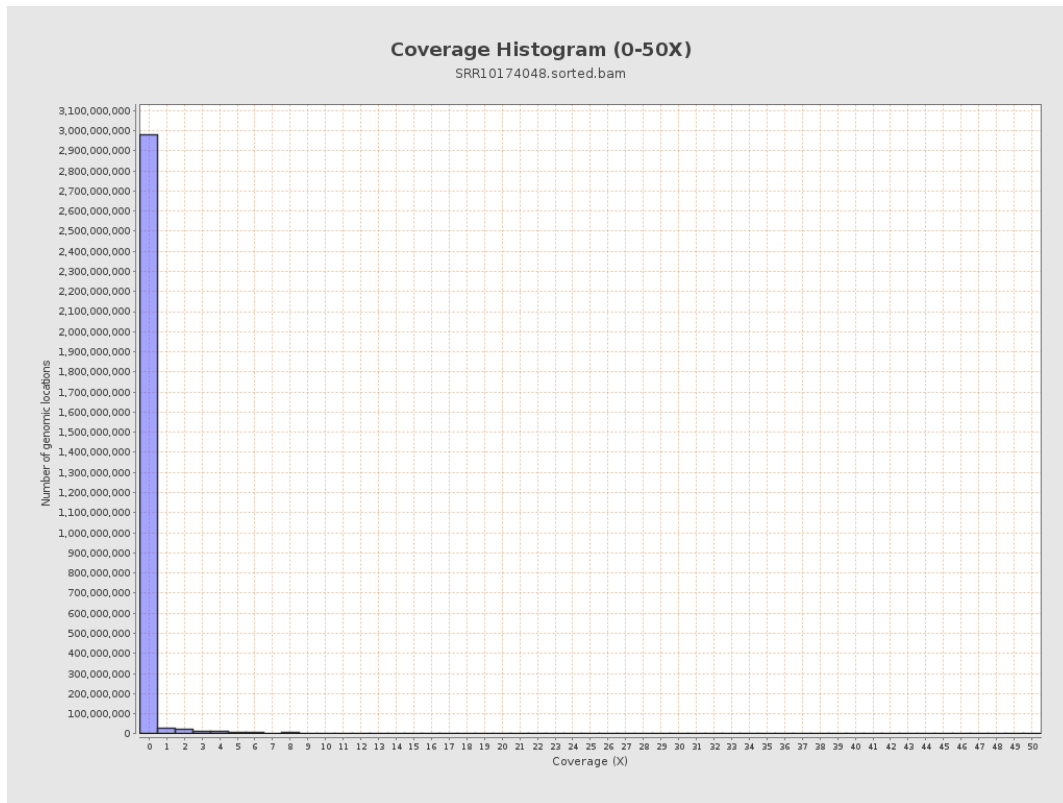
3. Results : Coverage across reference



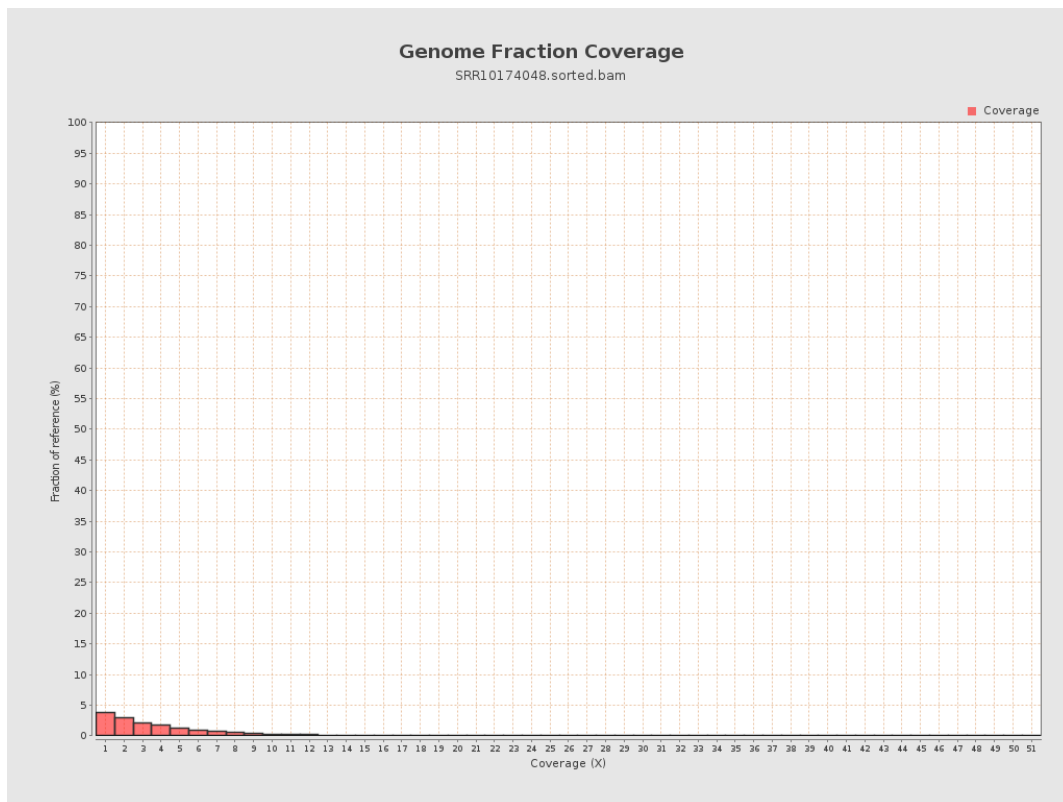
4. Results : Coverage Histogram



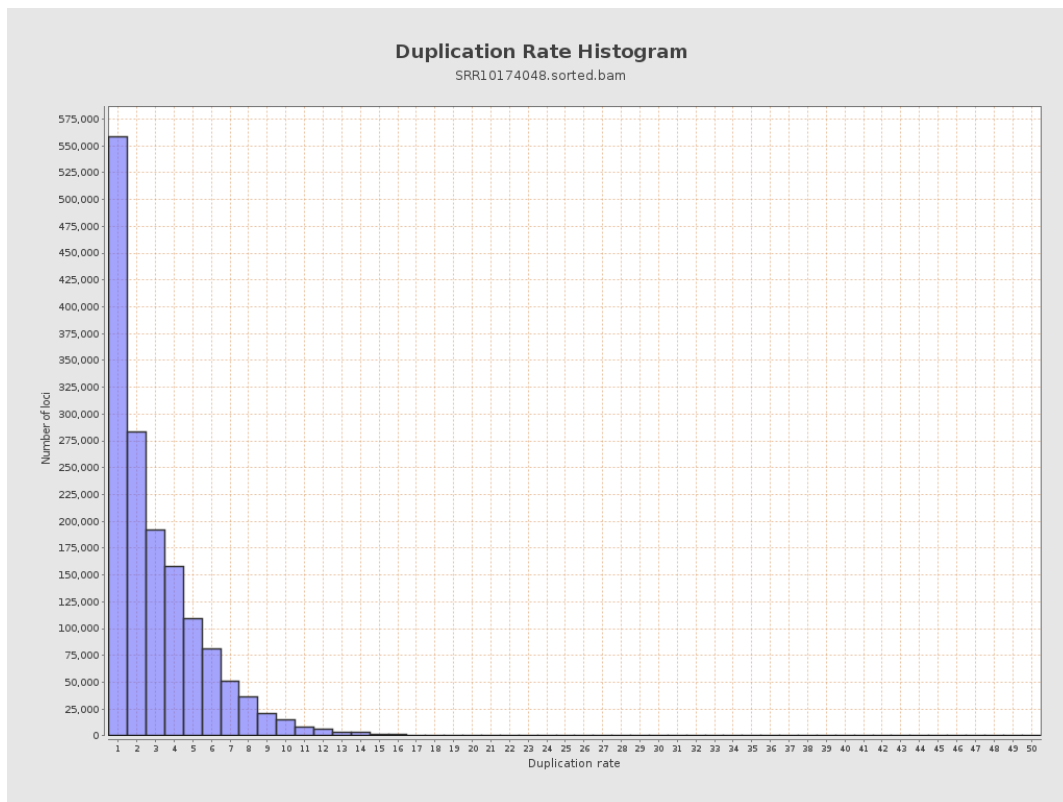
5. Results : Coverage Histogram (0-50X)



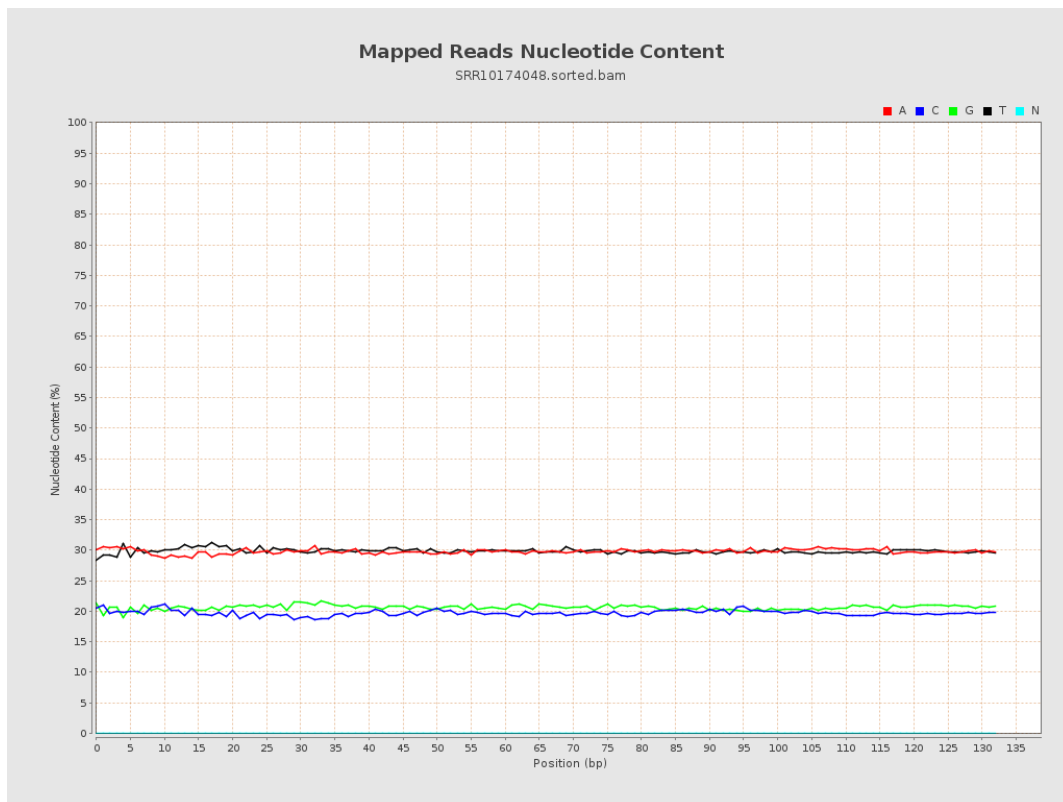
6. Results : Genome Fraction Coverage



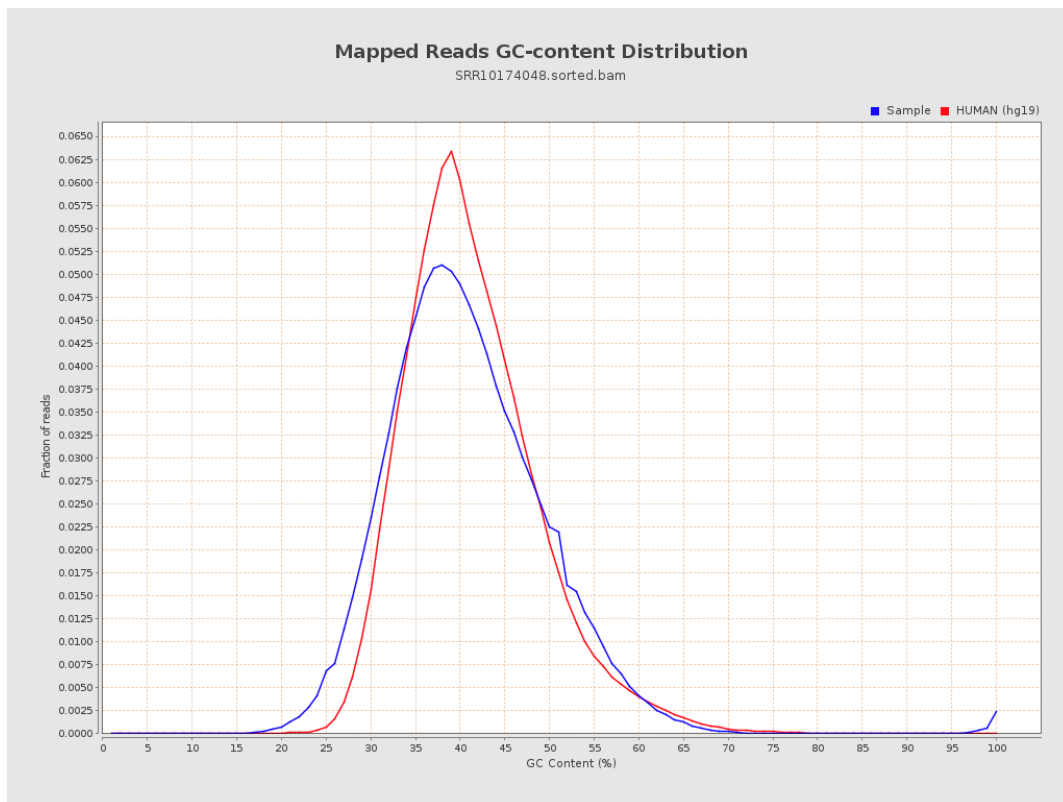
7. Results : Duplication Rate Histogram



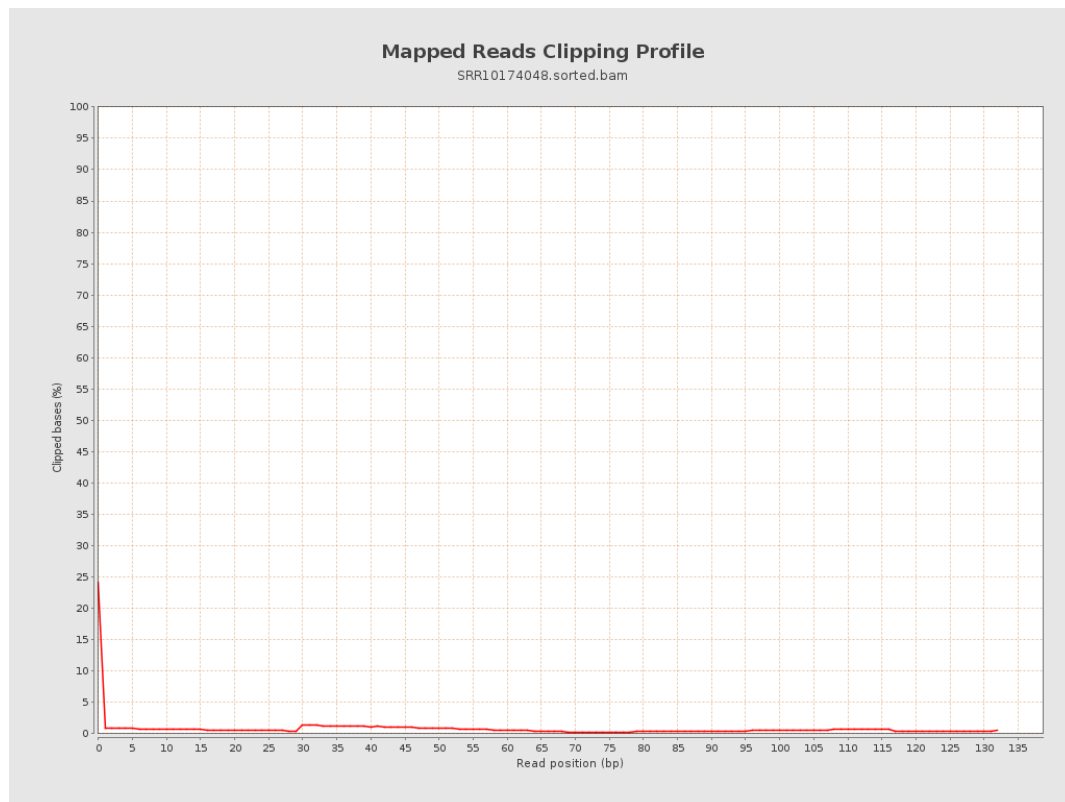
8. Results : Mapped Reads Nucleotide Content



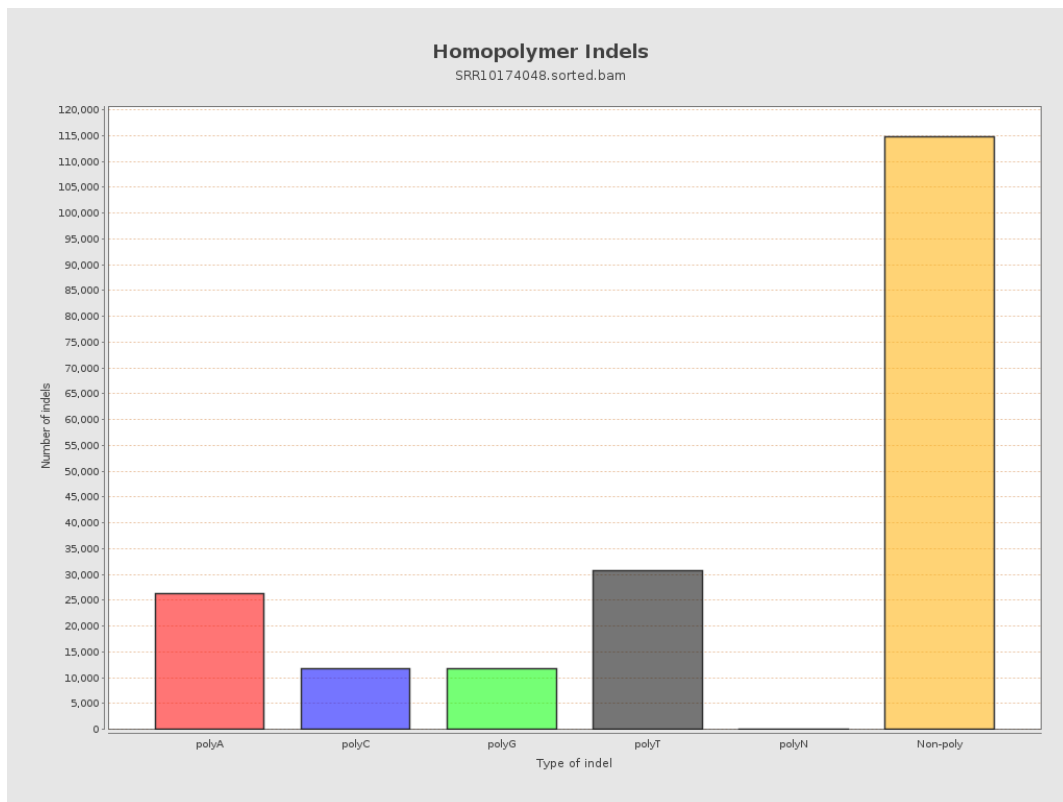
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



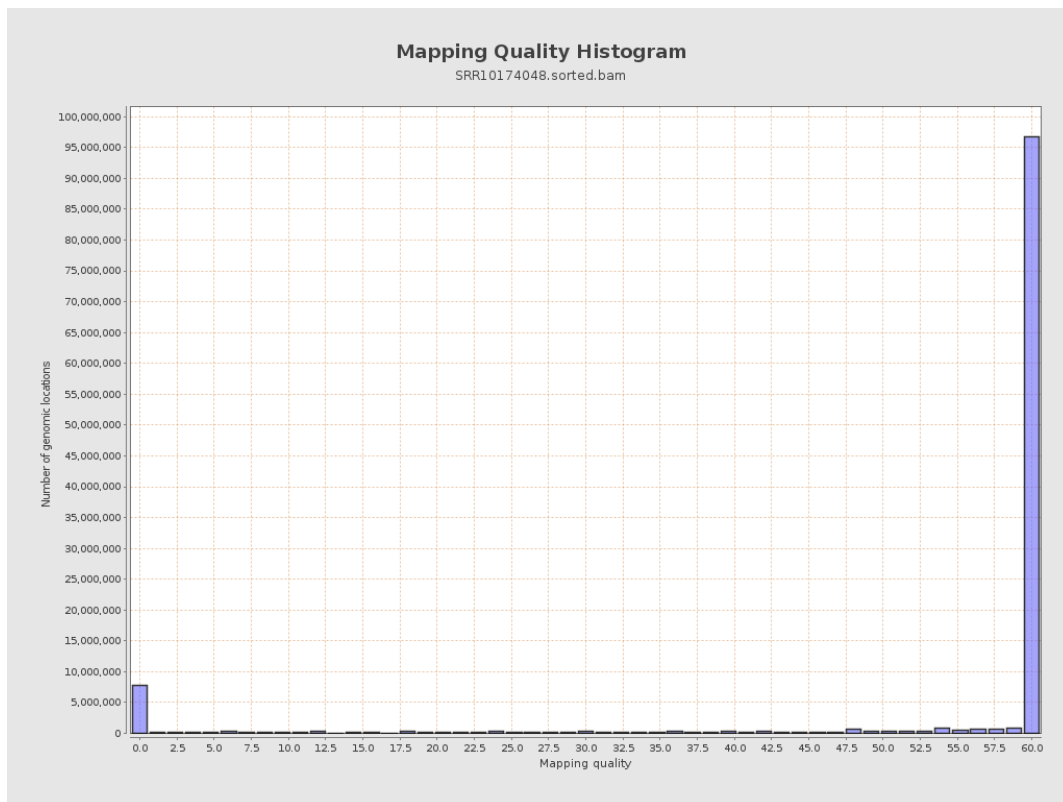
11. Results : Homopolymer Indels



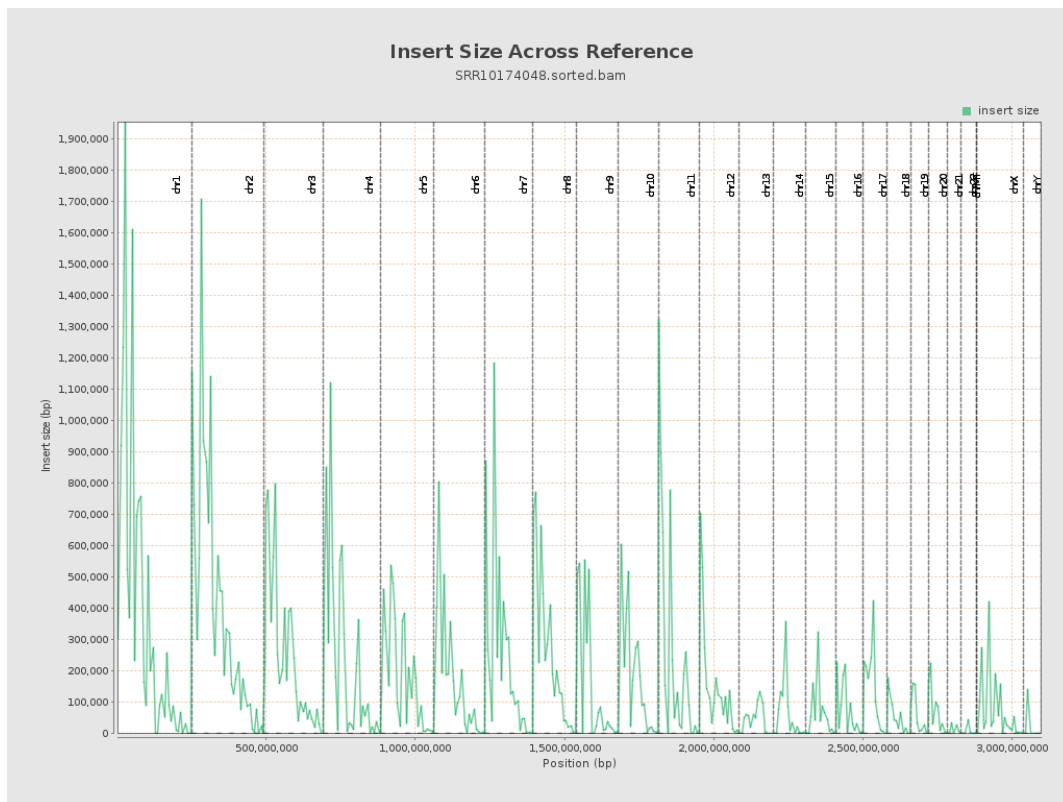
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

