

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 22:11:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174022.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_SRR10174022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174022_1.fastq.gz SRR10174022_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 22:11:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,862,550
Mapped reads	2,782,375 / 97.2%
Unmapped reads	80,175 / 2.8%
Mapped paired reads	2,782,375 / 97.2%
Mapped reads, first in pair	1,394,471 / 48.71%
Mapped reads, second in pair	1,387,904 / 48.48%
Mapped reads, both in pair	2,729,346 / 95.35%
Mapped reads, singletons	53,029 / 1.85%
Secondary alignments	0
Supplementary alignments	285,511 / 9.97%
Read min/max/mean length	30 / 133 / 127.94
Duplicated reads (estimated)	2,141,868 / 74.82%
Duplication rate	64.36%
Clipped reads	1,194,073 / 41.71%

2.2. ACGT Content

Number/percentage of A's	98,412,918 / 30.14%
Number/percentage of C's	63,838,427 / 19.55%
Number/percentage of T's	98,092,590 / 30.04%
Number/percentage of G's	66,190,231 / 20.27%
Number/percentage of N's	4,235 / 0%

GC Percentage	39.82%
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2.3. Coverage

Mean	0.1055
Standard Deviation	1.7135

2.4. Mapping Quality

Mean Mapping Quality	52.67
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2.5. Insert size

Mean	866,512.97
Standard Deviation	9,001,937.84
P25/Median/P75	139 / 194 / 280

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	3,369,705
Insertions	33,067
Mapped reads with at least one insertion	1.15%
Deletions	72,747
Mapped reads with at least one deletion	2.55%
Homopolymer indels	43.25%

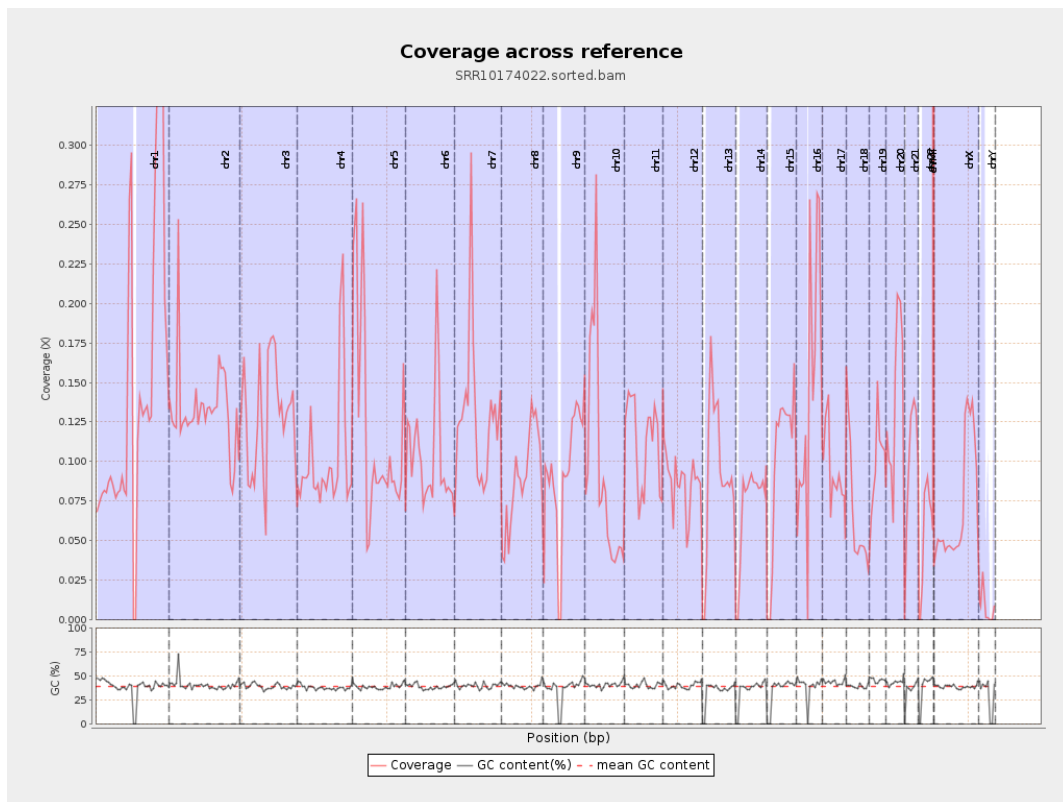
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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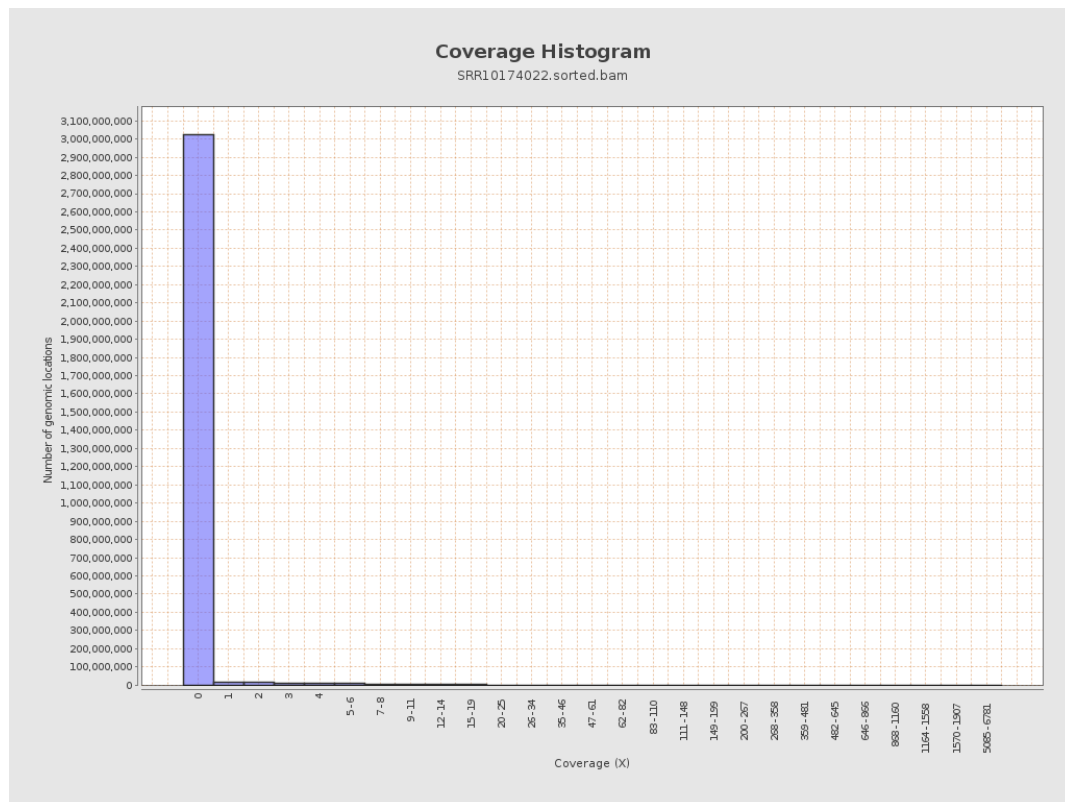
		bases	coverage	deviation
chr1	249250621	35889388	0.144	1.4947
chr2	243199373	32233147	0.1325	4.7788
chr3	198022430	25422641	0.1284	1.0326
chr4	191154276	19048880	0.0997	1.0103
chr5	180915260	21734040	0.1201	0.9917
chr6	171115067	17733741	0.1036	0.9386
chr7	159138663	20541428	0.1291	1.4346
chr8	146364022	13126600	0.0897	0.9704
chr9	141213431	13145014	0.0931	0.9573
chr10	135534747	12767422	0.0942	1.7704
chr11	135006516	15099870	0.1118	0.9744
chr12	133851895	11500176	0.0859	0.8328
chr13	115169878	10516207	0.0913	0.8686
chr14	107349540	7598885	0.0708	0.7596
chr15	102531392	10324108	0.1007	0.8886
chr16	90354753	12990011	0.1438	1.3803
chr17	81195210	7456837	0.0918	0.9036
chr18	78077248	5228042	0.067	1.1867
chr19	59128983	5855920	0.099	1.4066
chr20	63025520	8693497	0.1379	1.0538
chr21	48129895	4800894	0.0997	0.9106
chr22	51304566	2720159	0.053	0.6279
chrMT	16571	863428	52.1048	45.3324
chrX	155270560	10989844	0.0708	0.7606

chrY	59373566	439645	0.0074	0.3446
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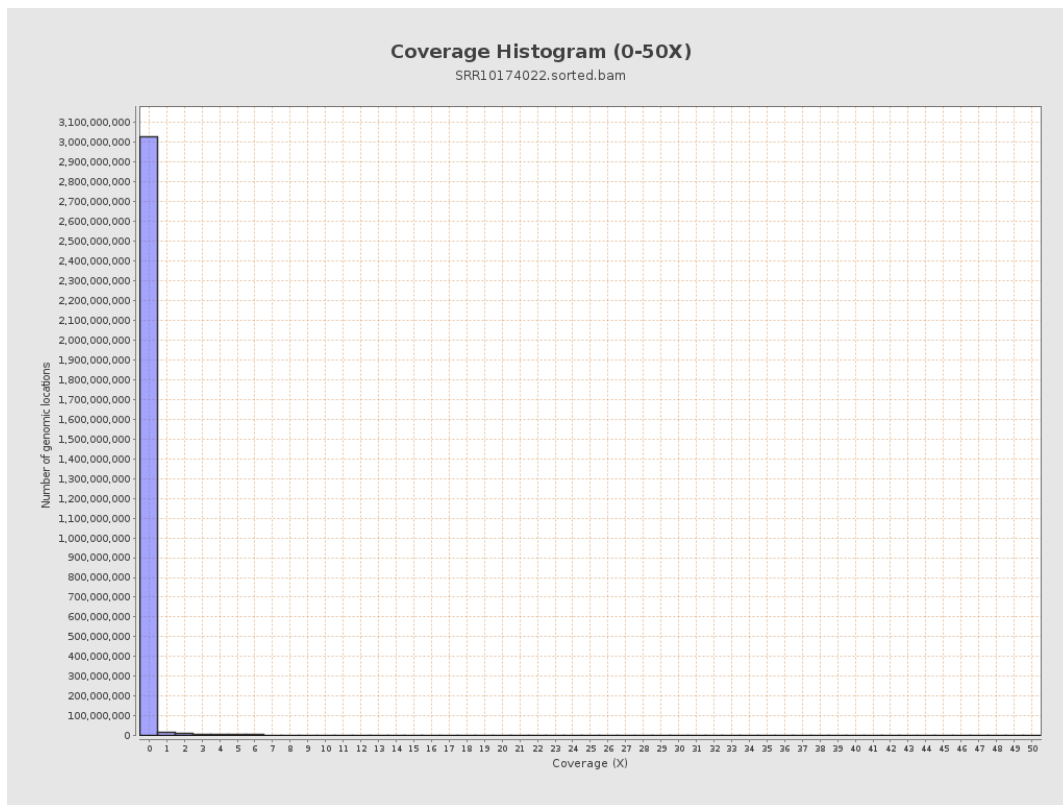
3. Results : Coverage across reference



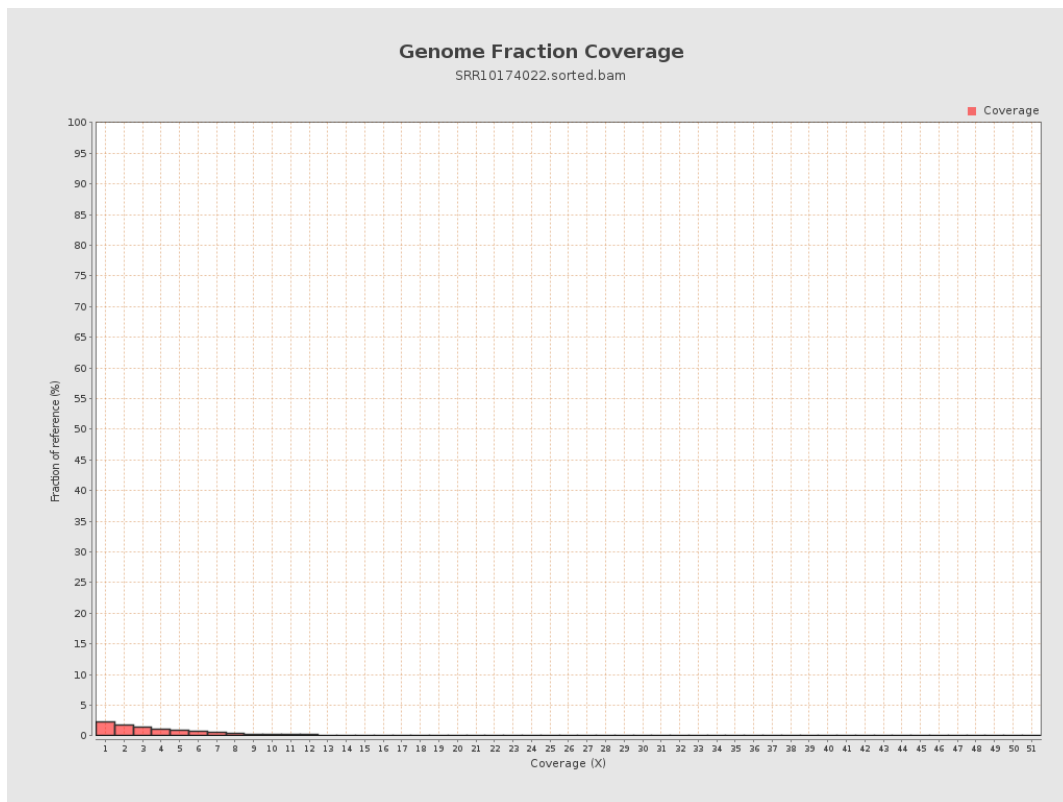
4. Results : Coverage Histogram



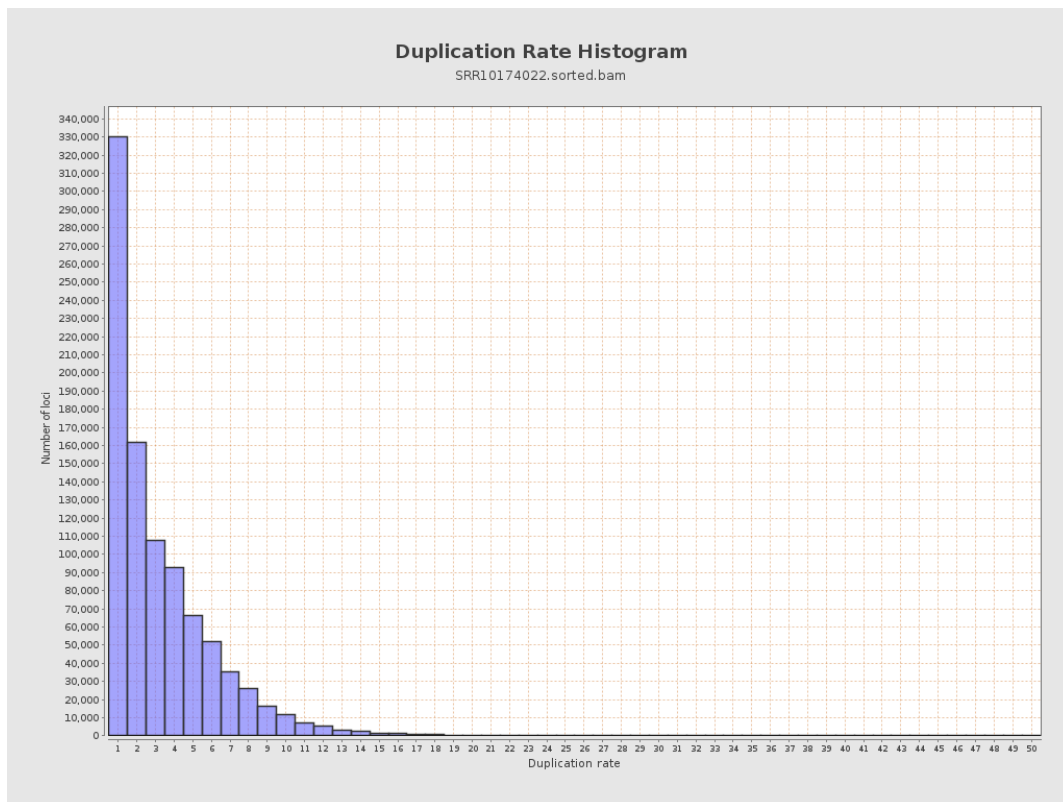
5. Results : Coverage Histogram (0-50X)



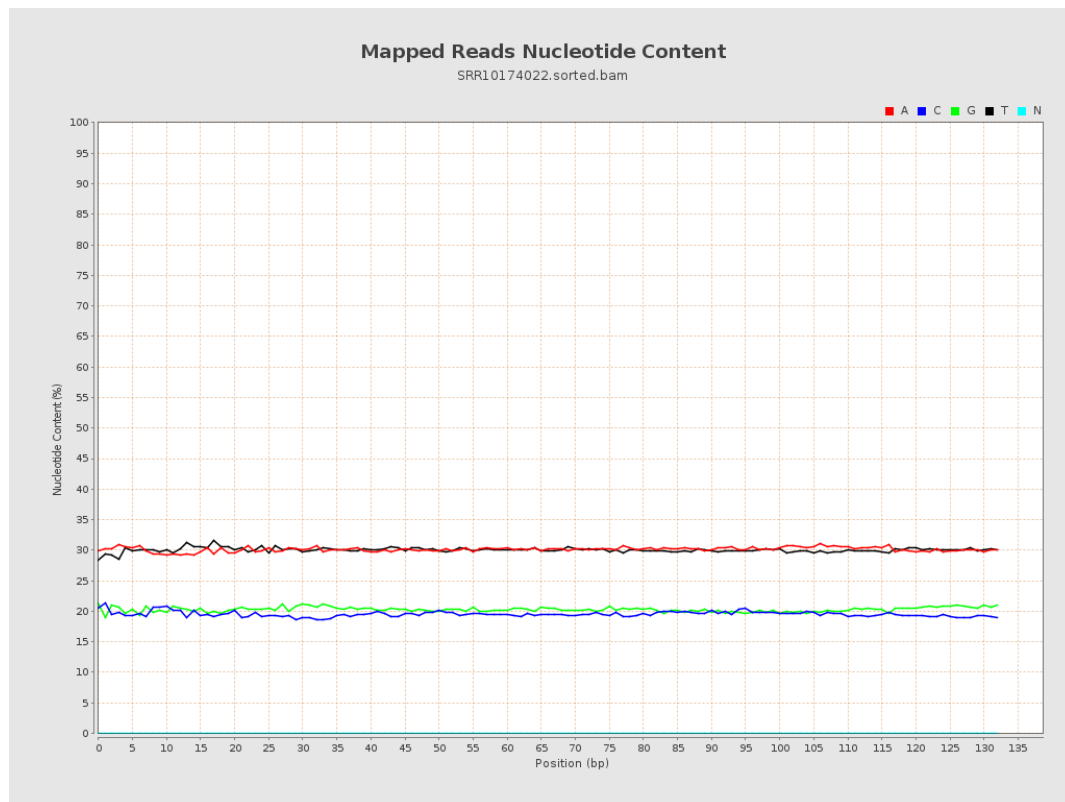
6. Results : Genome Fraction Coverage



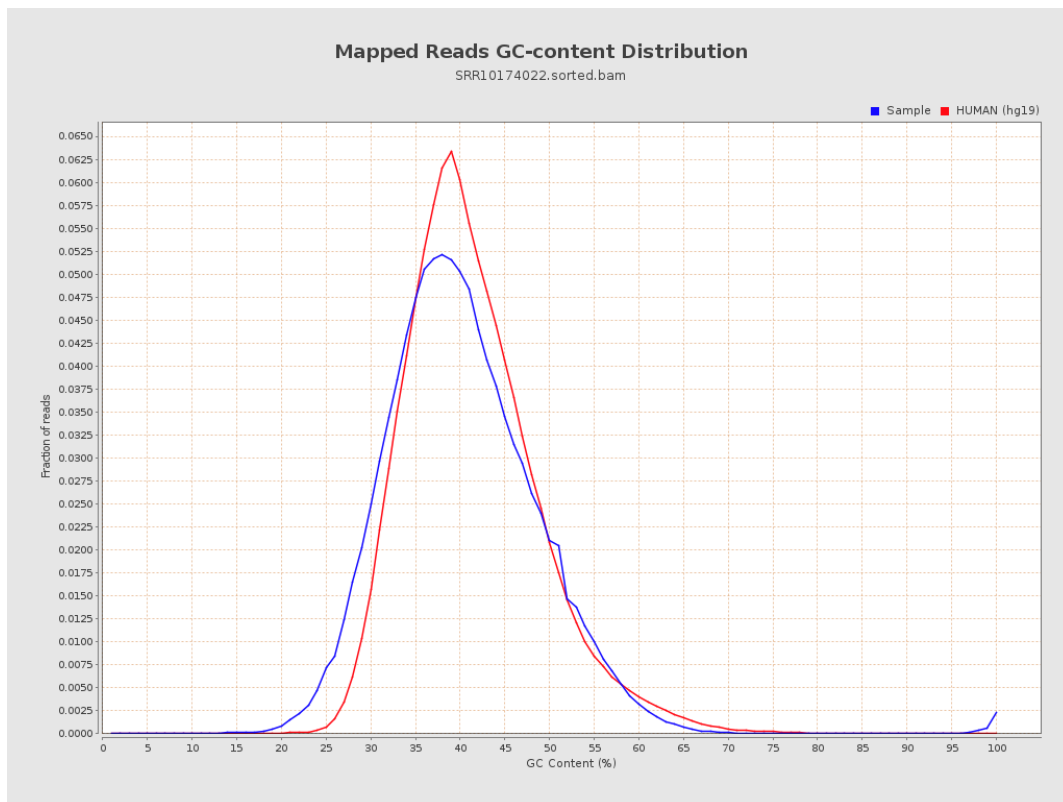
7. Results : Duplication Rate Histogram



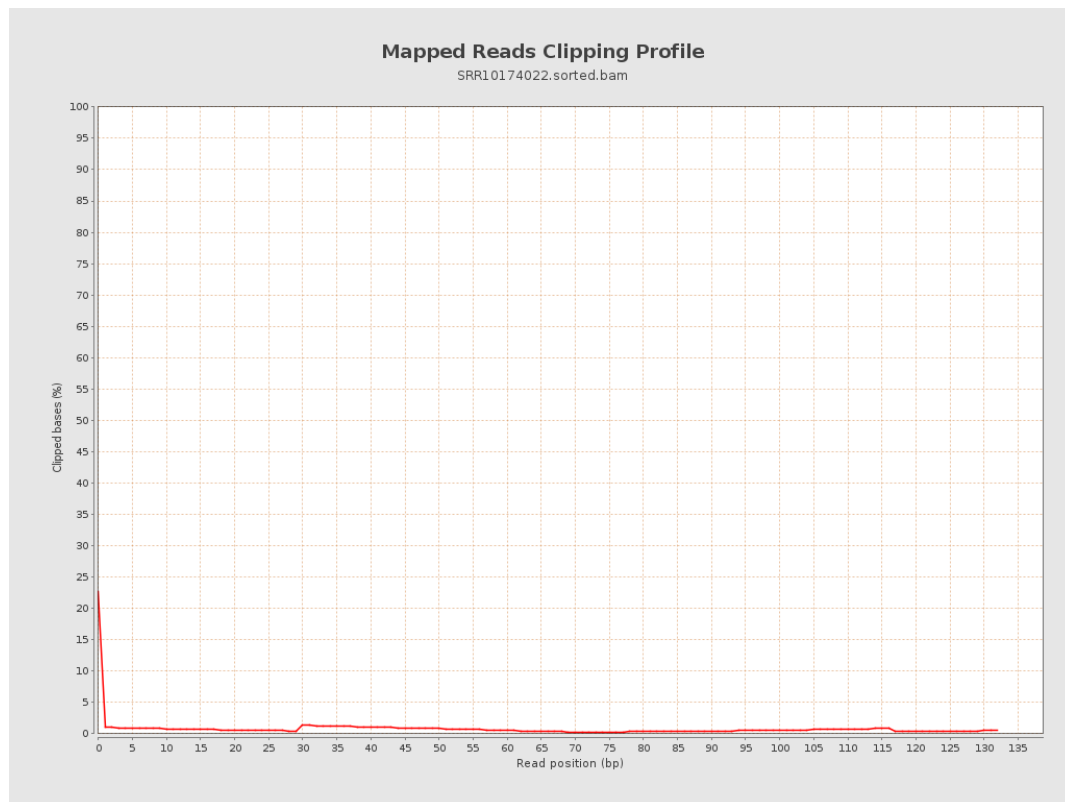
8. Results : Mapped Reads Nucleotide Content



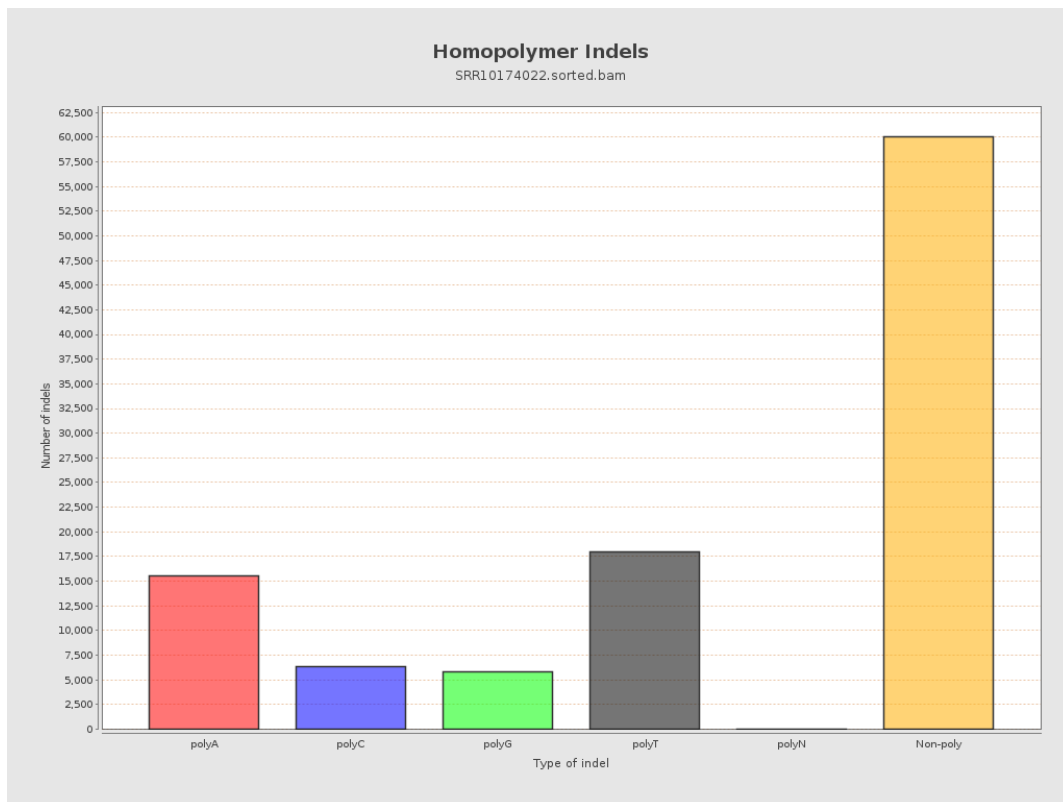
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



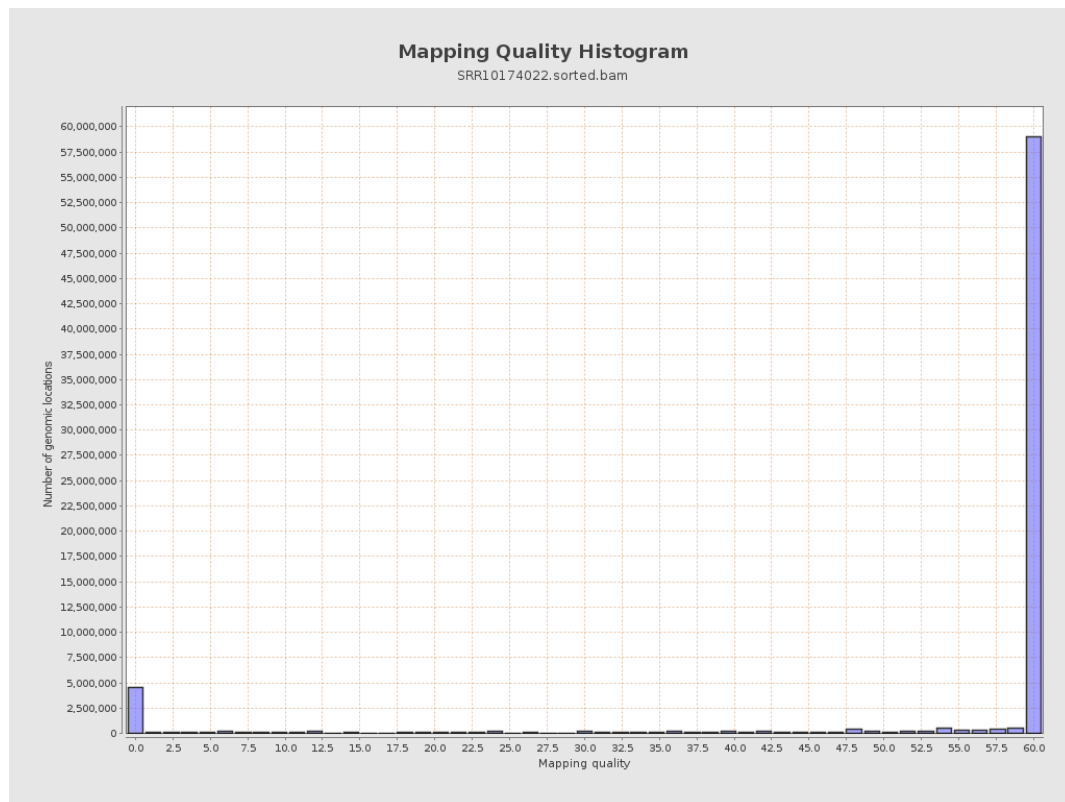
11. Results : Homopolymer Indels



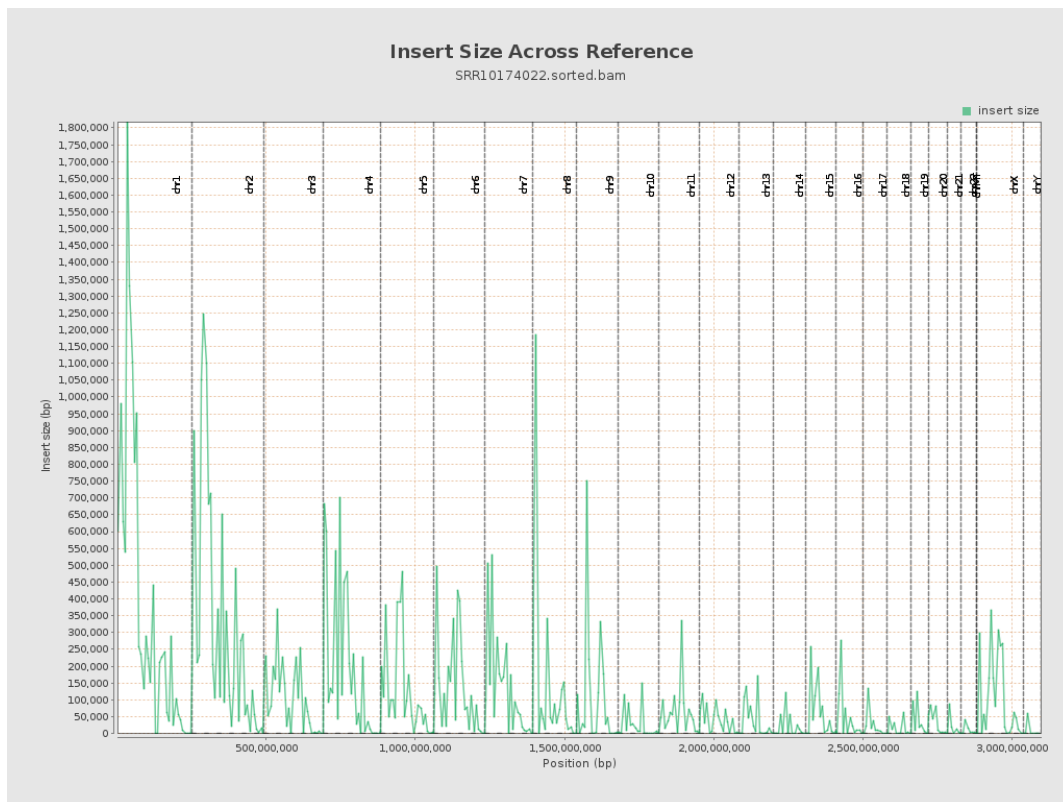
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

