

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 23:48:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174037.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_SRR10174037 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174037_1.fastq.gz SRR10174037_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 23:48:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174037.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,653,110
Mapped reads	3,577,020 / 97.92%
Unmapped reads	76,090 / 2.08%
Mapped paired reads	3,577,020 / 97.92%
Mapped reads, first in pair	1,790,202 / 49%
Mapped reads, second in pair	1,786,818 / 48.91%
Mapped reads, both in pair	3,529,890 / 96.63%
Mapped reads, singletons	47,130 / 1.29%
Secondary alignments	0
Supplementary alignments	335,063 / 9.17%
Read min/max/mean length	30 / 133 / 127.45
Duplicated reads (estimated)	2,633,038 / 72.08%
Duplication rate	63.07%
Clipped reads	1,344,126 / 36.79%

2.2. ACGT Content

Number/percentage of A's	128,684,417 / 30.38%
Number/percentage of C's	82,090,271 / 19.38%
Number/percentage of T's	128,214,518 / 30.27%
Number/percentage of G's	84,608,393 / 19.97%
Number/percentage of N's	5,225 / 0%

GC Percentage	39.35%
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2.3. Coverage

Mean	0.1369
Standard Deviation	1.9332

2.4. Mapping Quality

Mean Mapping Quality	52.96
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2.5. Insert size

Mean	634,590.46
Standard Deviation	7,271,154.56
P25/Median/P75	137 / 187 / 262

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	4,010,610
Insertions	41,863
Mapped reads with at least one insertion	1.14%
Deletions	89,762
Mapped reads with at least one deletion	2.45%
Homopolymer indels	43.36%

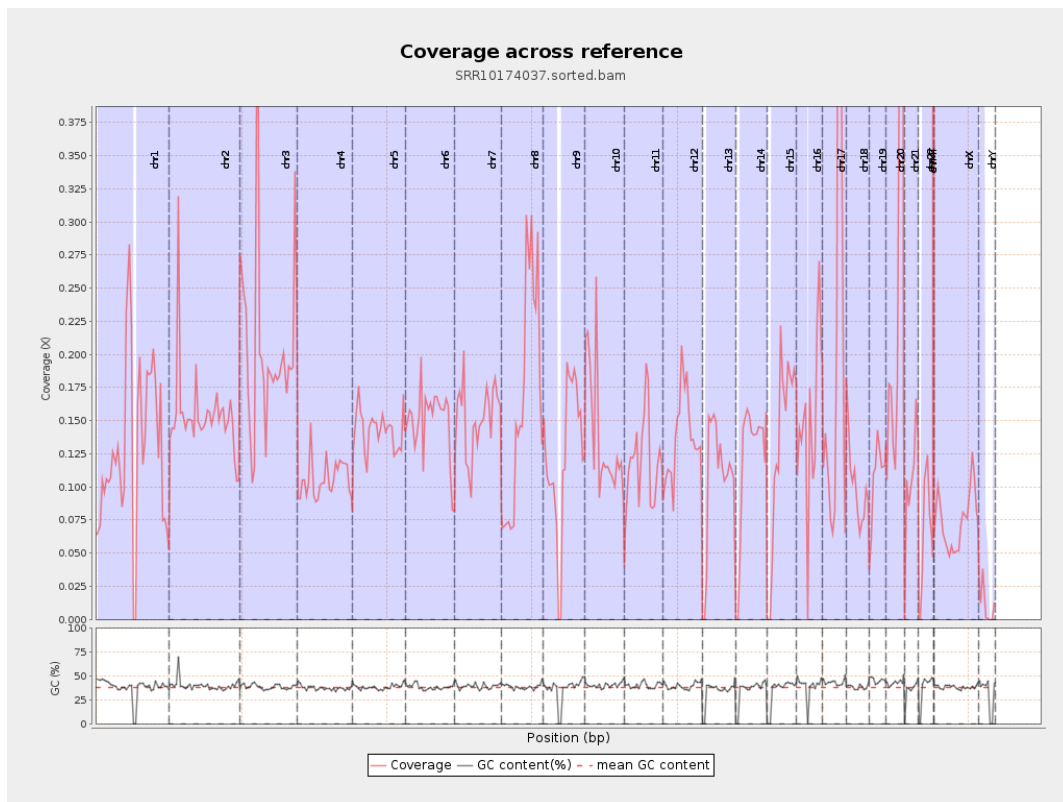
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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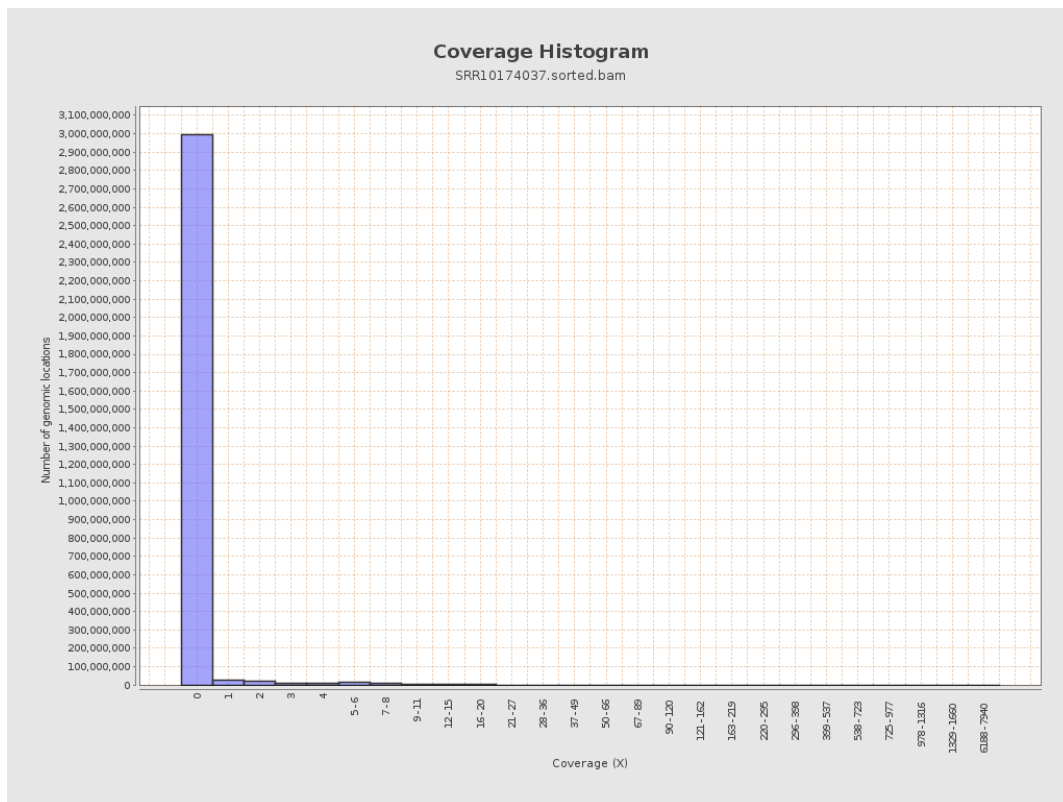
		bases	coverage	deviation
chr1	249250621	32089018	0.1287	1.3467
chr2	243199373	37571342	0.1545	5.608
chr3	198022430	40317561	0.2036	1.2629
chr4	191154276	20219927	0.1058	0.985
chr5	180915260	25821595	0.1427	1.0371
chr6	171115067	25633465	0.1498	1.2037
chr7	159138663	24282132	0.1526	1.307
chr8	146364022	24187010	0.1653	1.2752
chr9	141213431	17276455	0.1223	1.0883
chr10	135534747	18680639	0.1378	1.79
chr11	135006516	16140173	0.1196	0.9608
chr12	133851895	18285997	0.1366	1.0239
chr13	115169878	12092935	0.105	0.9002
chr14	107349540	12772779	0.119	0.9528
chr15	102531392	13553375	0.1322	0.9928
chr16	90354753	13670421	0.1513	1.2633
chr17	81195210	17122729	0.2109	1.3446
chr18	78077248	7855337	0.1006	1.2451
chr19	59128983	6478784	0.1096	1.0623
chr20	63025520	18484272	0.2933	1.6035
chr21	48129895	5119034	0.1064	0.8986
chr22	51304566	3256616	0.0635	0.6538
chrMT	16571	712577	43.0014	37.143
chrX	155270560	11593453	0.0747	0.7491

chrY	59373566	606138	0.0102	0.3882
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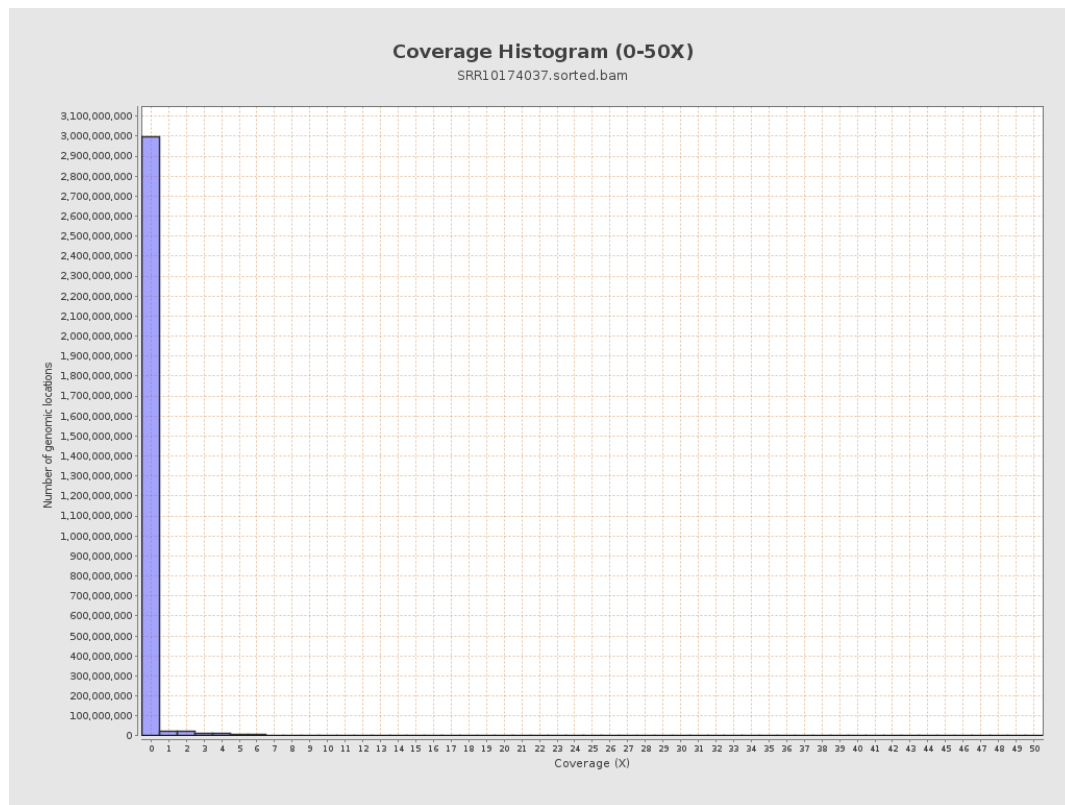
3. Results : Coverage across reference



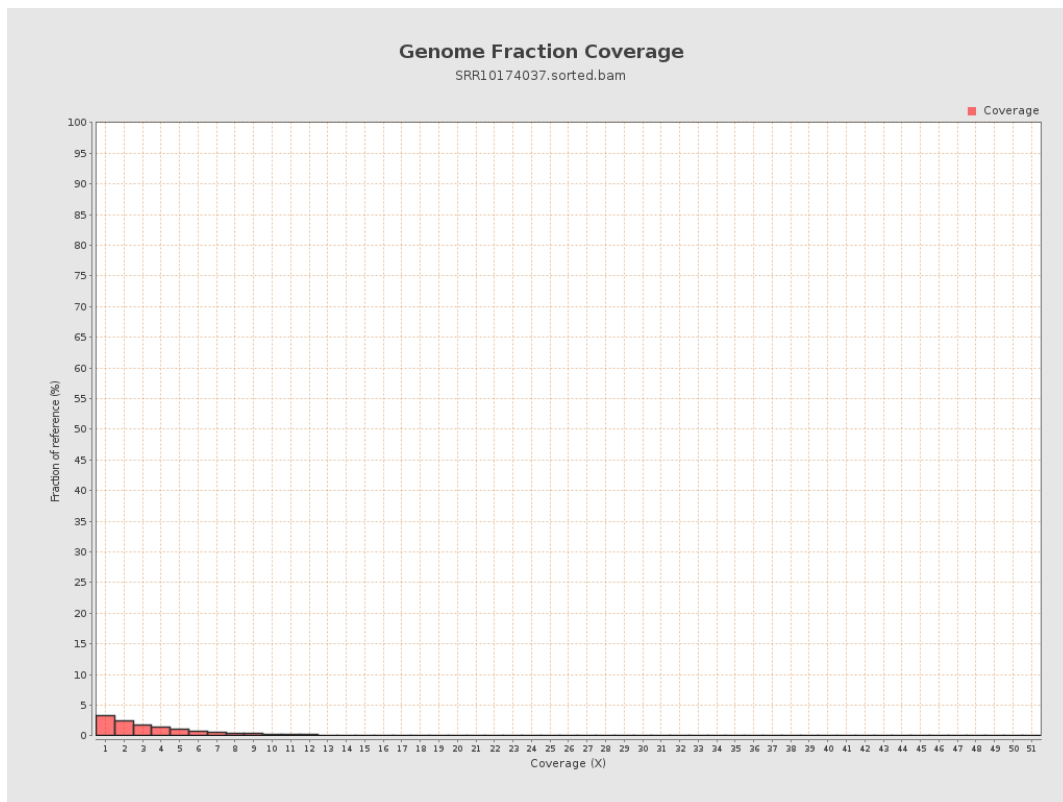
4. Results : Coverage Histogram



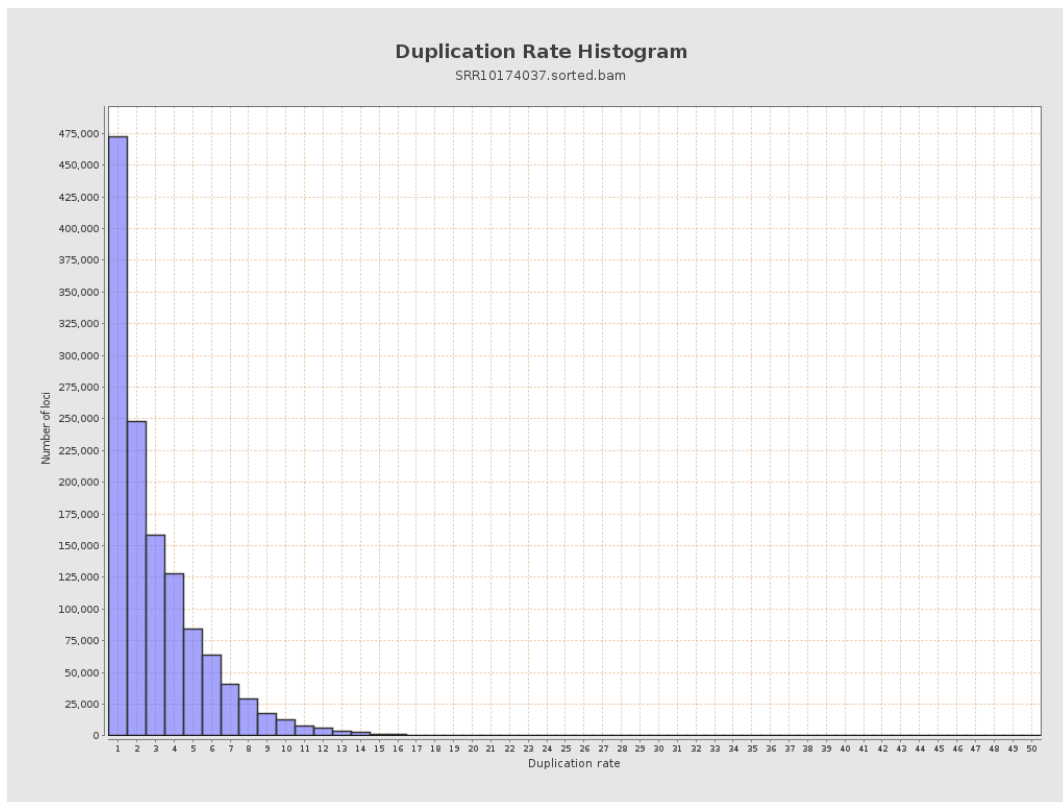
5. Results : Coverage Histogram (0-50X)



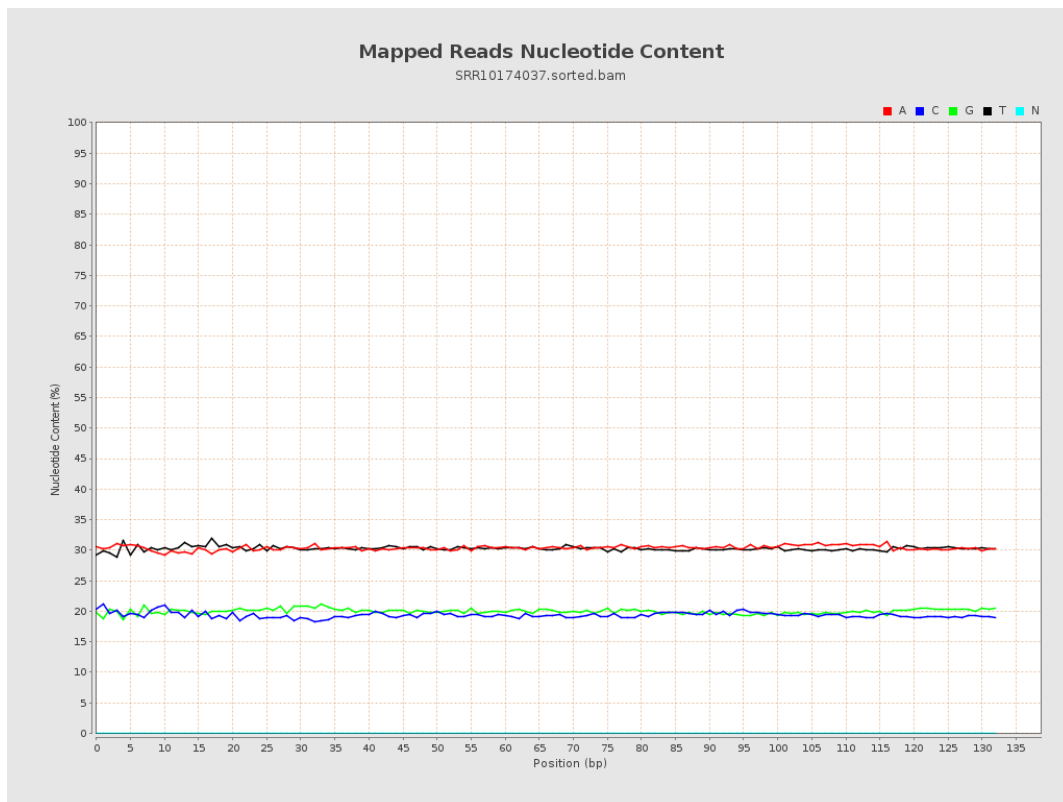
6. Results : Genome Fraction Coverage



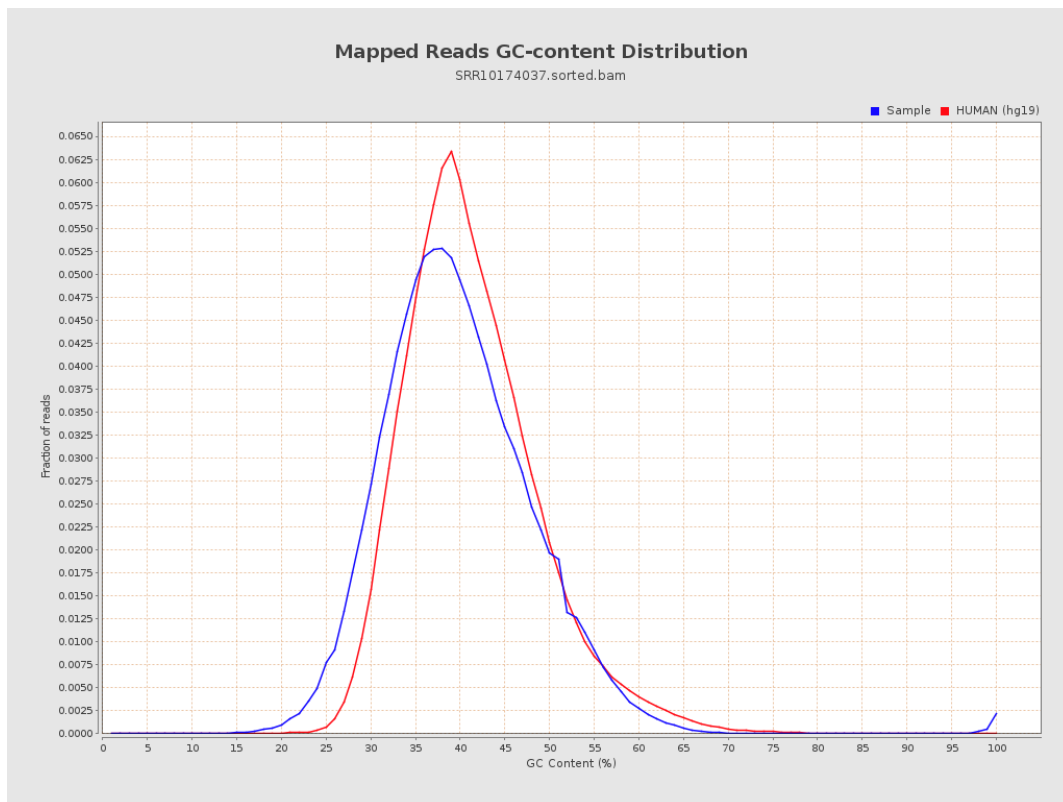
7. Results : Duplication Rate Histogram



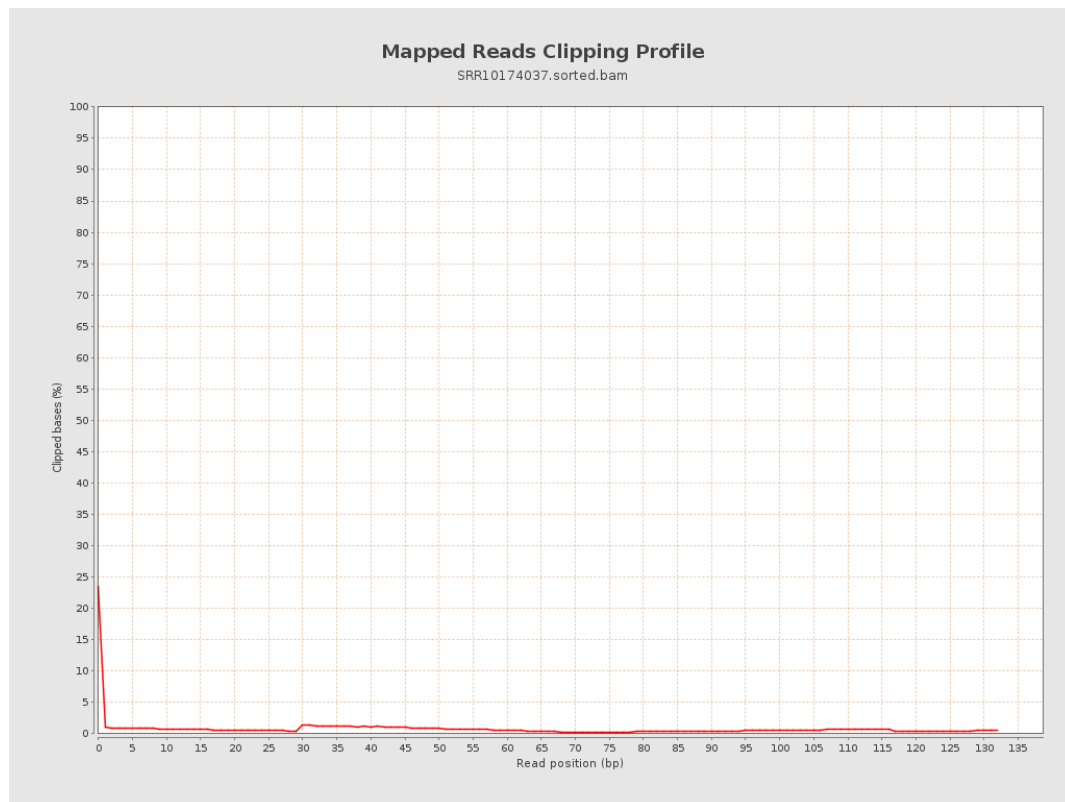
8. Results : Mapped Reads Nucleotide Content



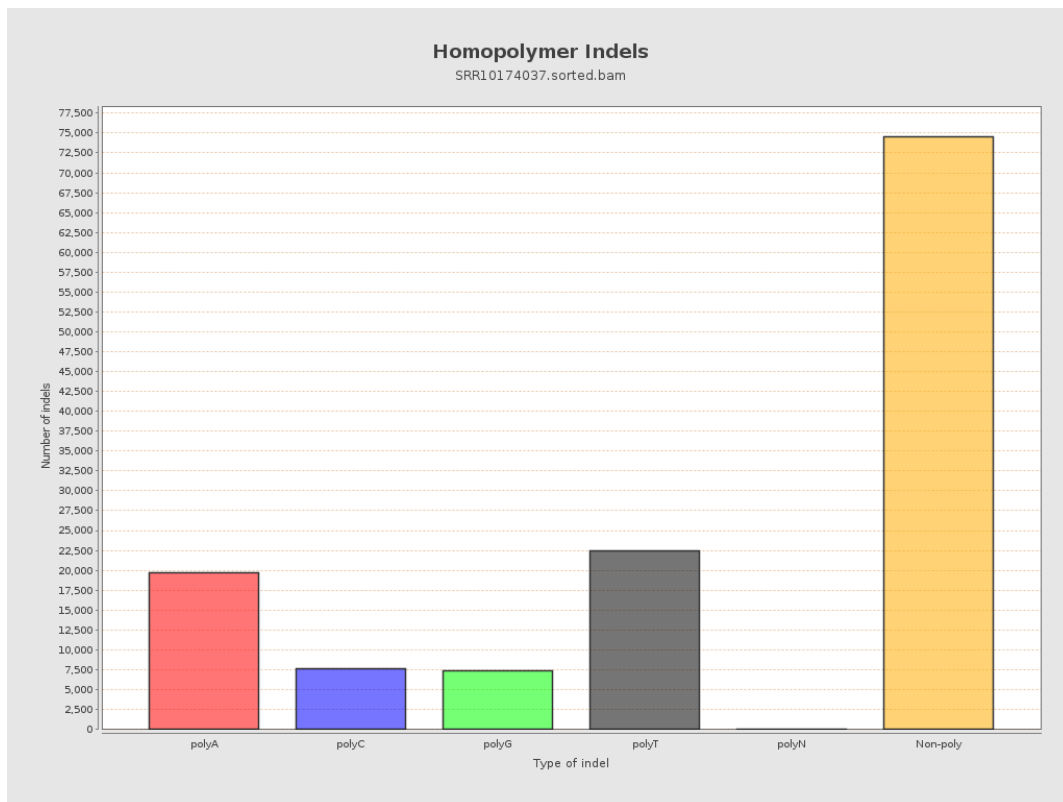
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



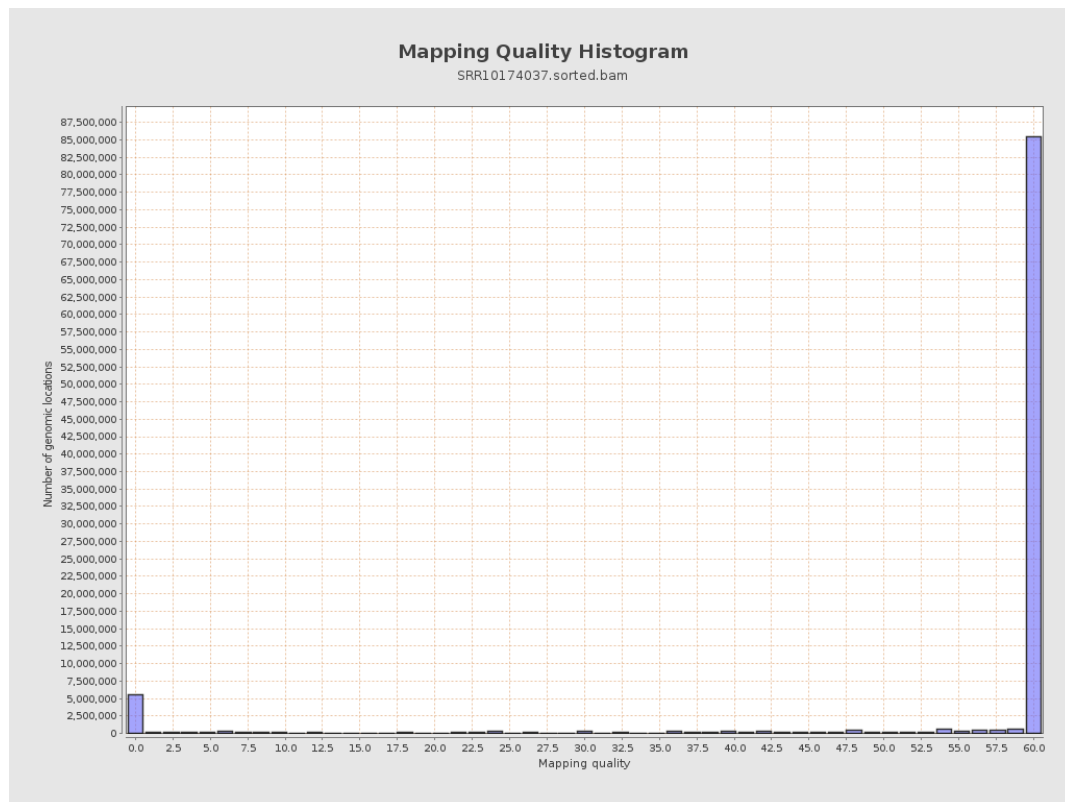
11. Results : Homopolymer Indels



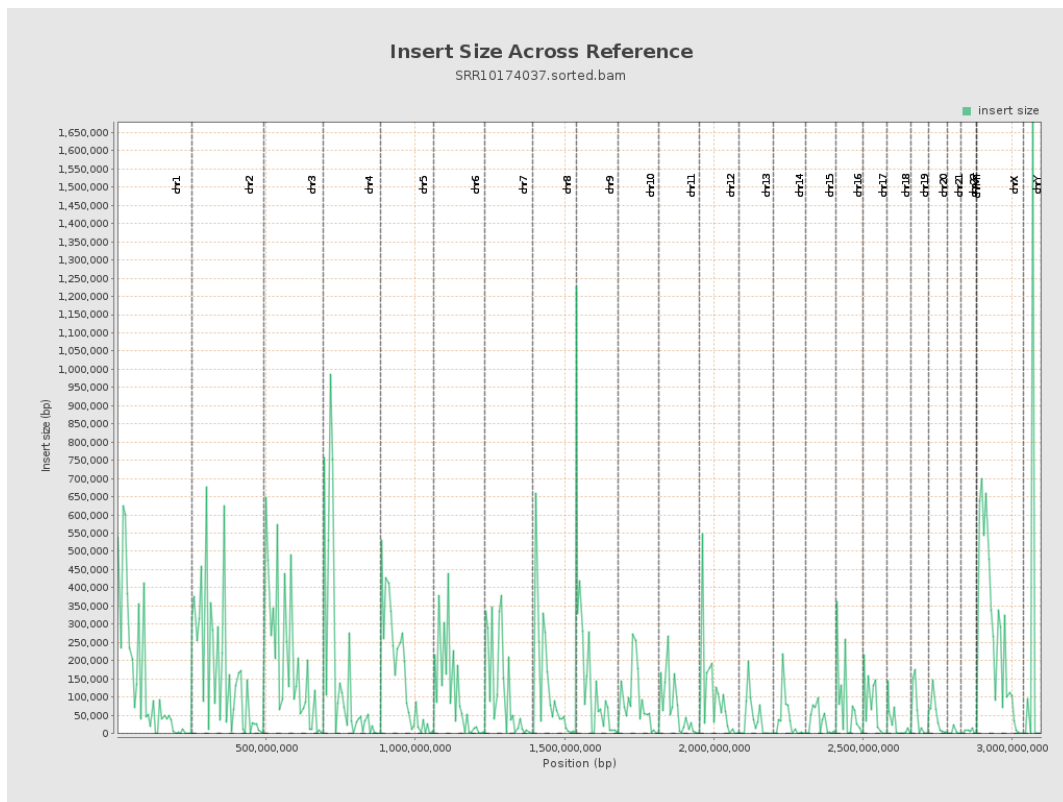
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

