

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:27:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173881.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_SRR10173881 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173881_1.fastq.gz SRR10173881_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:27:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173881.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,181,378
Mapped reads	6,023,737 / 97.45%
Unmapped reads	157,641 / 2.55%
Mapped paired reads	6,023,737 / 97.45%
Mapped reads, first in pair	3,014,088 / 48.76%
Mapped reads, second in pair	3,009,649 / 48.69%
Mapped reads, both in pair	5,919,382 / 95.76%
Mapped reads, singletons	104,355 / 1.69%
Secondary alignments	0
Supplementary alignments	580,261 / 9.39%
Read min/max/mean length	30 / 133 / 127.81
Duplicated reads (estimated)	4,619,098 / 74.73%
Duplication rate	64.54%
Clipped reads	2,355,193 / 38.1%

2.2. ACGT Content

Number/percentage of A's	214,920,067 / 30.21%
Number/percentage of C's	138,693,571 / 19.49%
Number/percentage of T's	214,554,793 / 30.16%
Number/percentage of G's	143,309,984 / 20.14%
Number/percentage of N's	7,752 / 0%

GC Percentage	39.64%
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2.3. Coverage

Mean	0.23
Standard Deviation	3.3012

2.4. Mapping Quality

Mean Mapping Quality	52.82
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2.5. Insert size

Mean	728,826.26
Standard Deviation	7,855,048.09
P25/Median/P75	141 / 193 / 273

2.6. Mismatches and indels

General error rate	1%
Mismatches	6,971,077
Insertions	71,570
Mapped reads with at least one insertion	1.15%
Deletions	161,315
Mapped reads with at least one deletion	2.61%
Homopolymer indels	42.83%

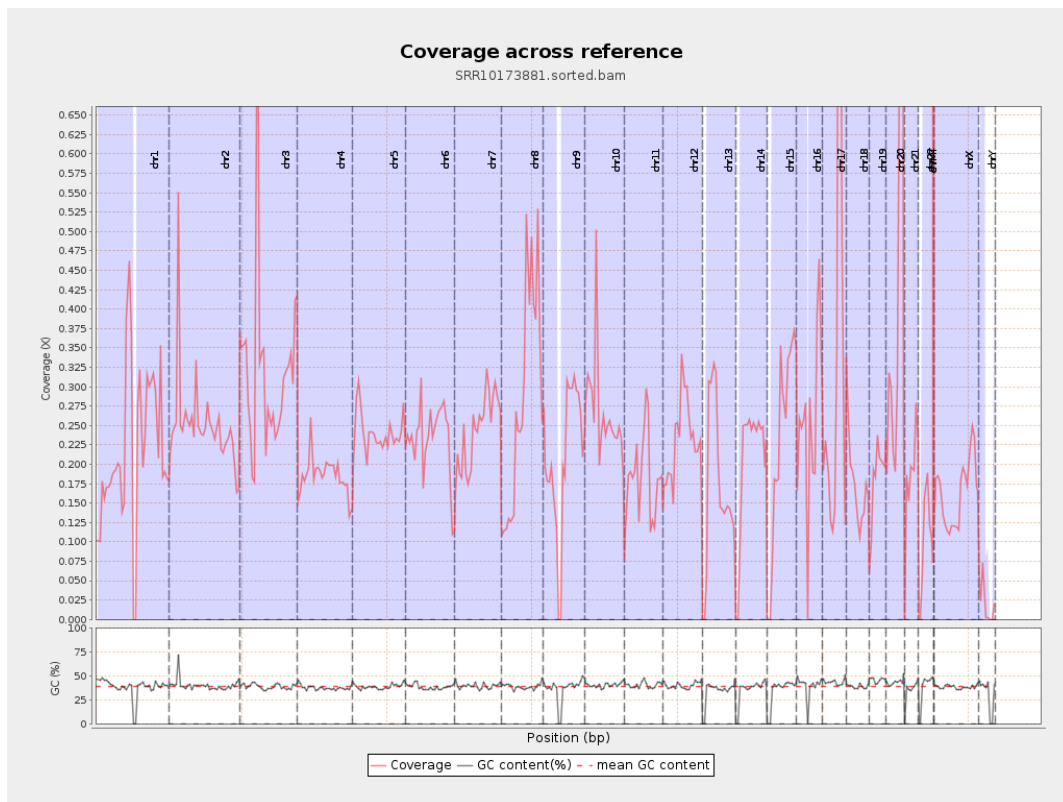
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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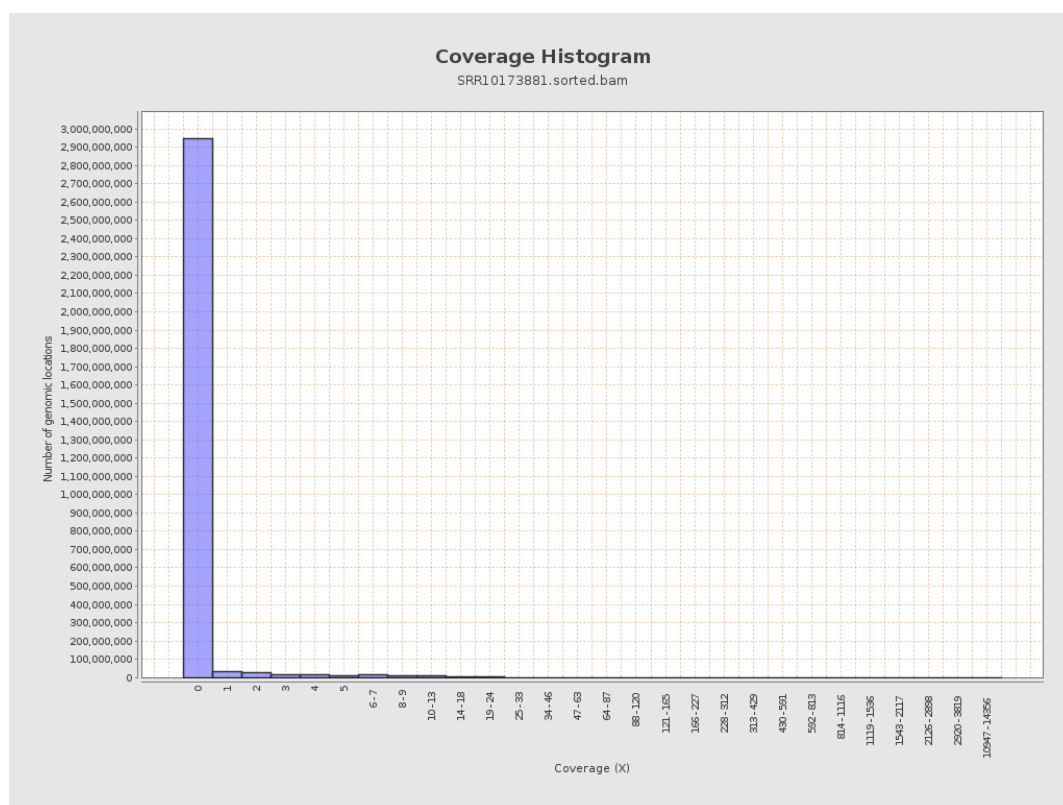
		bases	coverage	deviation
chr1	249250621	54573742	0.219	1.9934
chr2	243199373	61075321	0.2511	10.0441
chr3	198022430	62637881	0.3163	1.663
chr4	191154276	35336247	0.1849	1.423
chr5	180915260	43486142	0.2404	1.4185
chr6	171115067	39950013	0.2335	1.6145
chr7	159138663	39016215	0.2452	2.0048
chr8	146364022	41689536	0.2848	2.0727
chr9	141213431	29079097	0.2059	1.5709
chr10	135534747	36227651	0.2673	3.2072
chr11	135006516	24695209	0.1829	1.2528
chr12	133851895	30956102	0.2313	1.3844
chr13	115169878	19419992	0.1686	1.1977
chr14	107349540	21824899	0.2033	1.3073
chr15	102531392	23704648	0.2312	1.3784
chr16	90354753	23394789	0.2589	1.8659
chr17	81195210	27027727	0.3329	1.8728
chr18	78077248	13621904	0.1745	2.3083
chr19	59128983	10883687	0.1841	1.6379
chr20	63025520	30541287	0.4846	2.2449
chr21	48129895	8928491	0.1855	1.3007
chr22	51304566	5031674	0.0981	0.8585
chrMT	16571	2386730	144.0305	119.5302
chrX	155270560	25262232	0.1627	1.1628

chrY	59373566	1132202	0.0191	0.7027
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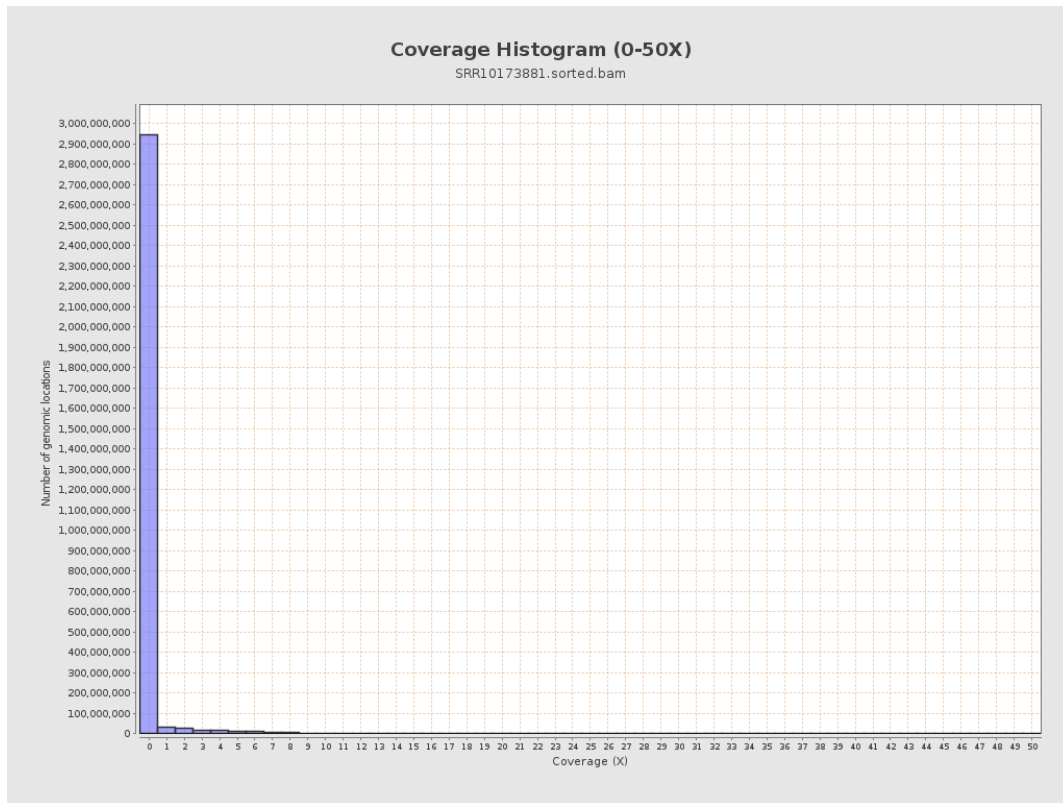
3. Results : Coverage across reference



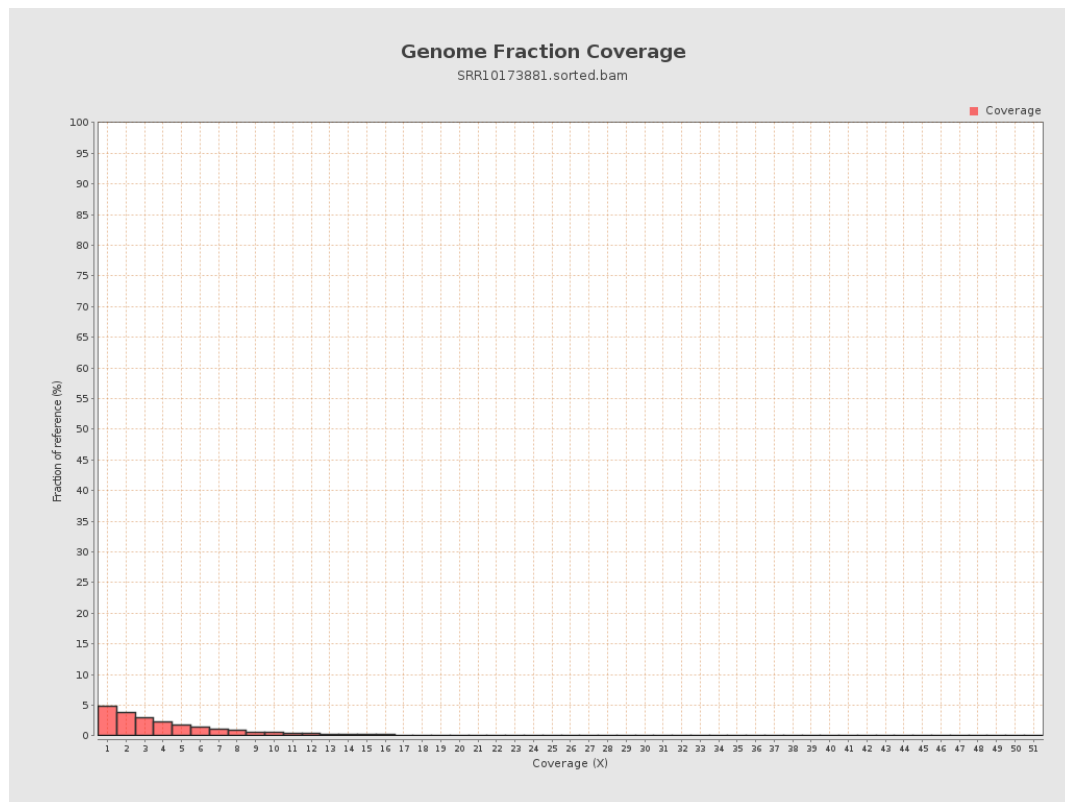
4. Results : Coverage Histogram



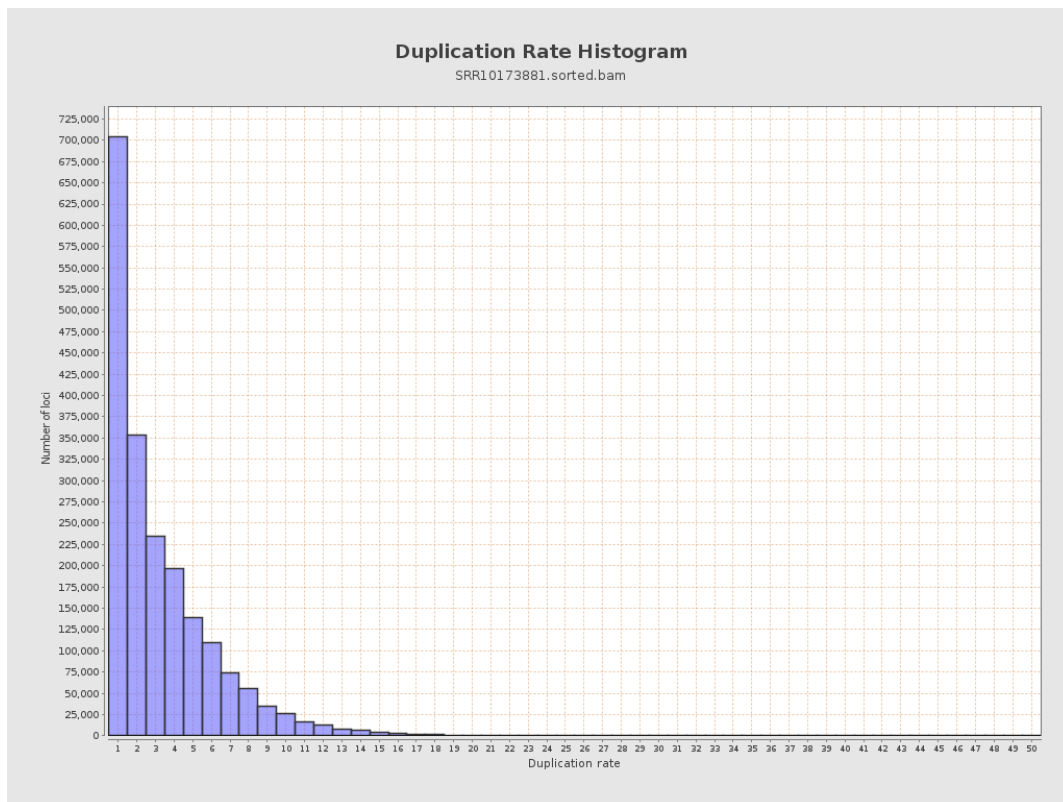
5. Results : Coverage Histogram (0-50X)



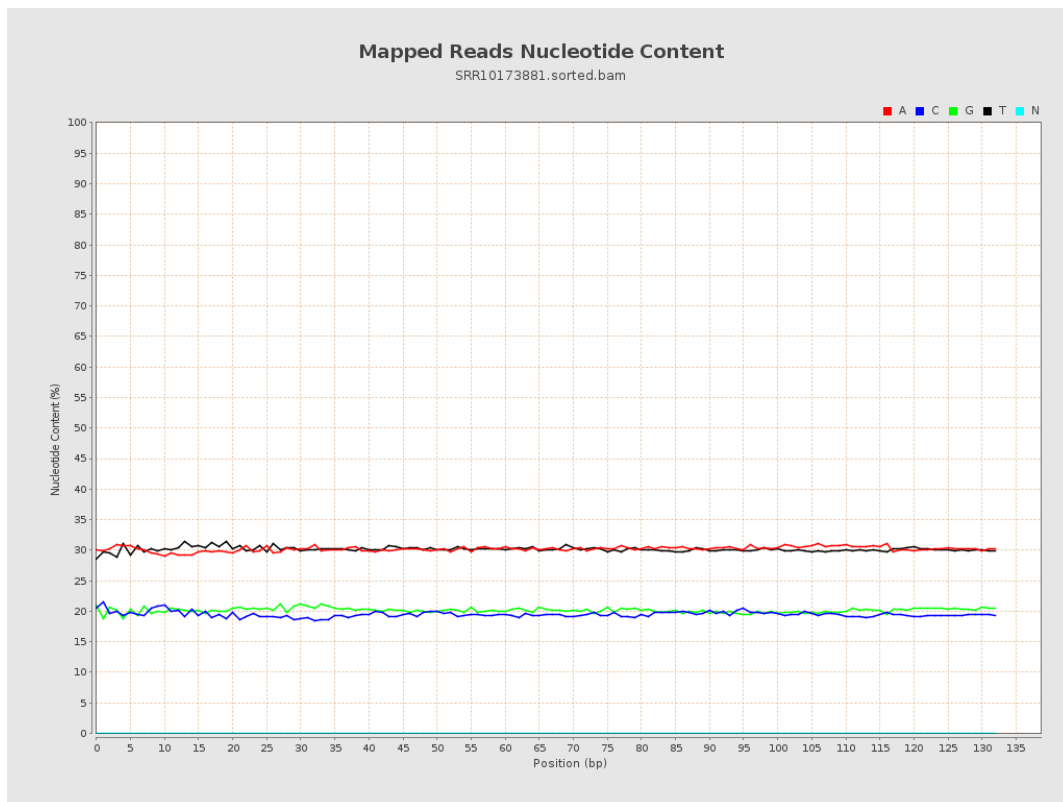
6. Results : Genome Fraction Coverage



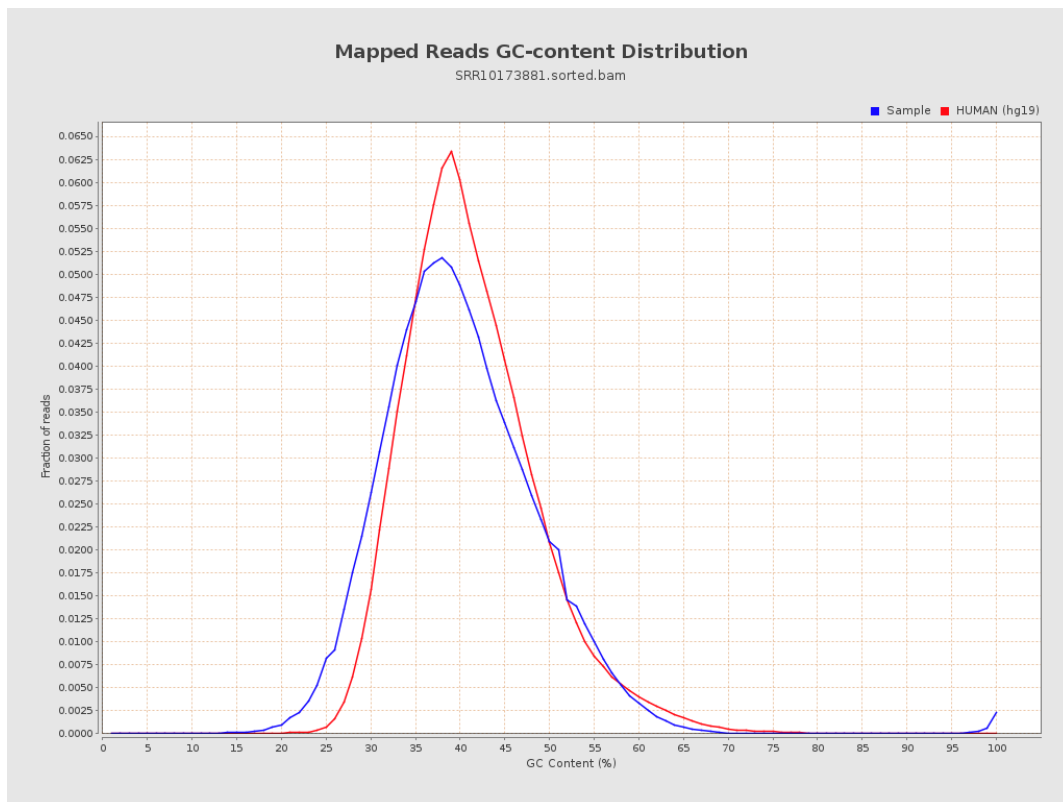
7. Results : Duplication Rate Histogram



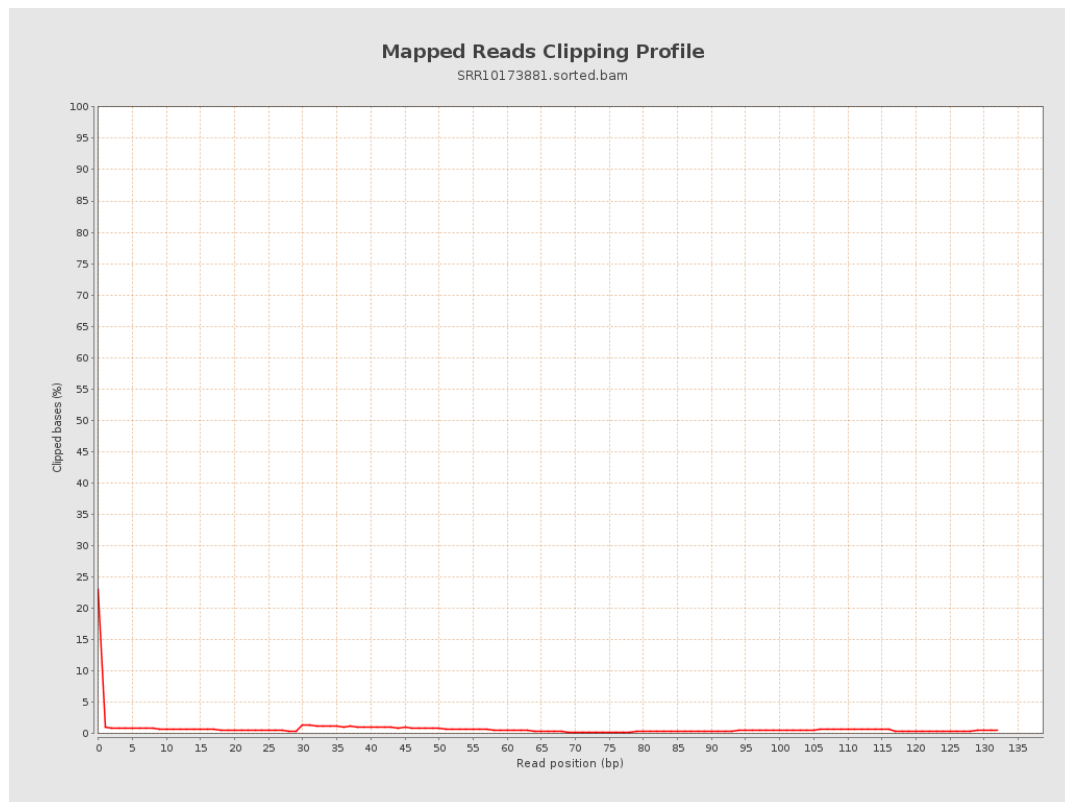
8. Results : Mapped Reads Nucleotide Content



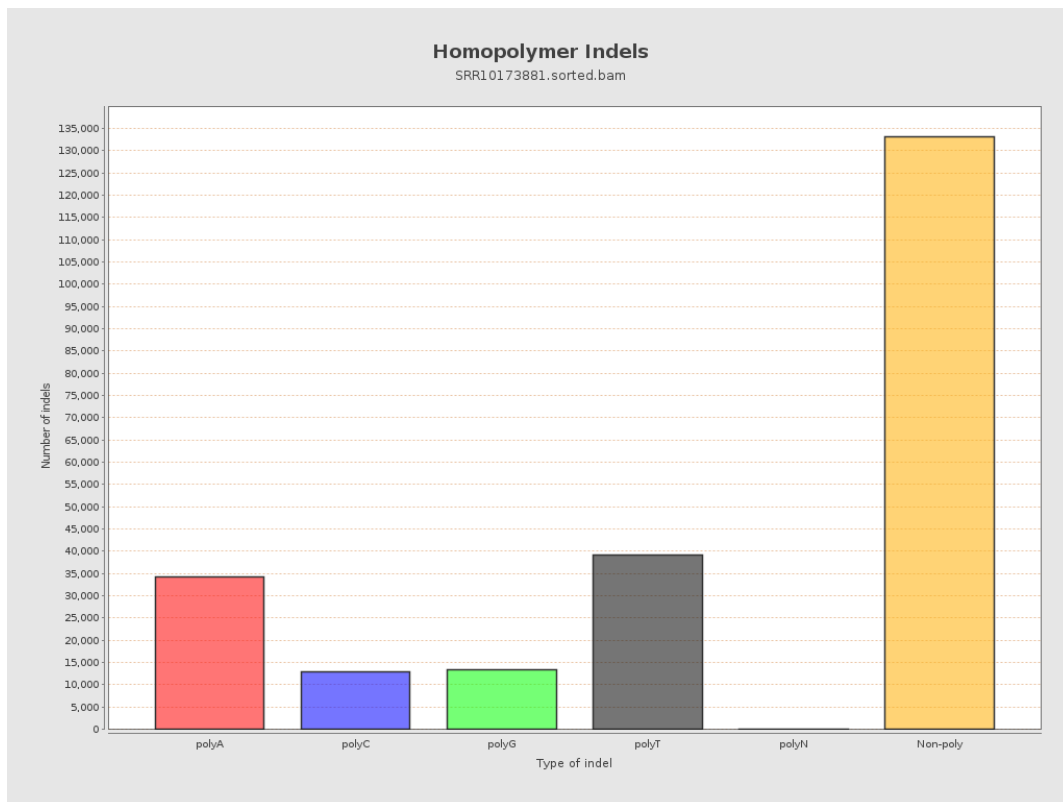
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



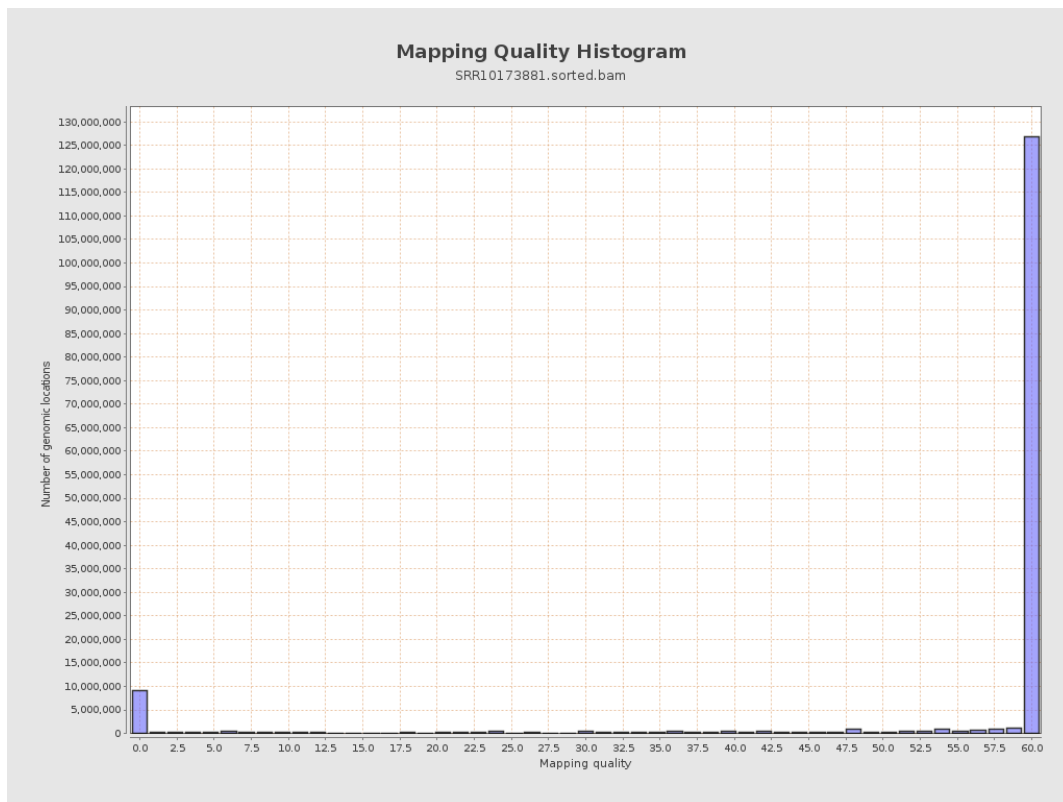
11. Results : Homopolymer Indels



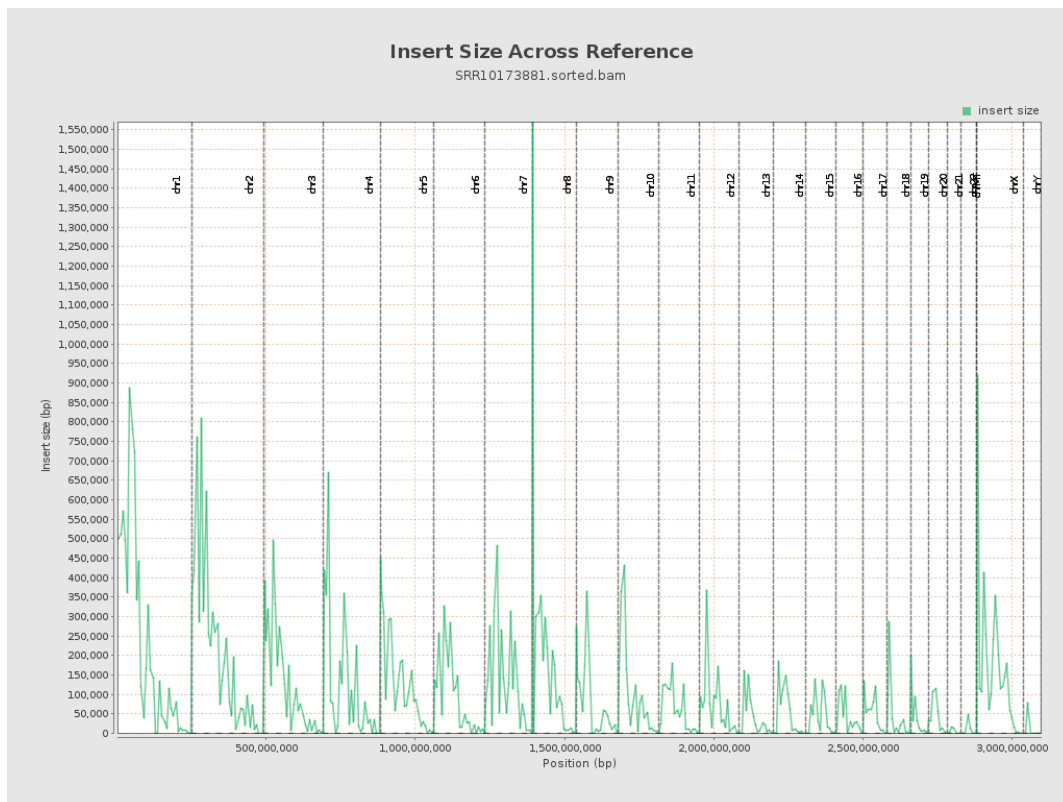
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

