

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/03 07:41:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438251.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_SRR8438251 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438251_1.fastq.gz SRR8438251_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 03 07:41:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438251.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	830,067,144
Mapped reads	825,707,878 / 99.47%
Unmapped reads	4,359,266 / 0.53%
Mapped paired reads	825,707,878 / 99.47%
Mapped reads, first in pair	413,095,292 / 49.77%
Mapped reads, second in pair	412,612,586 / 49.71%
Mapped reads, both in pair	822,908,678 / 99.14%
Mapped reads, singletons	2,799,200 / 0.34%
Secondary alignments	0
Supplementary alignments	21,592,174 / 2.6%
Read min/max/mean length	30 / 149 / 143.14
Duplicated reads (estimated)	346,701,740 / 41.77%
Duplication rate	36.79%
Clipped reads	112,735,270 / 13.58%

2.2. ACGT Content

Number/percentage of A's	35,688,081,537 / 30.53%
Number/percentage of C's	22,362,507,051 / 19.13%
Number/percentage of T's	33,568,710,007 / 28.72%
Number/percentage of G's	25,279,151,721 / 21.62%
Number/percentage of N's	215,692 / 0%

GC Percentage	40.75%
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2.3. Coverage

Mean	37.7738
Standard Deviation	95.9459

2.4. Mapping Quality

Mean Mapping Quality	54.33
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2.5. Insert size

Mean	114,267.31
Standard Deviation	3,300,191.02
P25/Median/P75	392 / 466 / 587

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	627,489,132
Insertions	15,520,269
Mapped reads with at least one insertion	1.84%
Deletions	13,728,931
Mapped reads with at least one deletion	1.62%
Homopolymer indels	48.3%

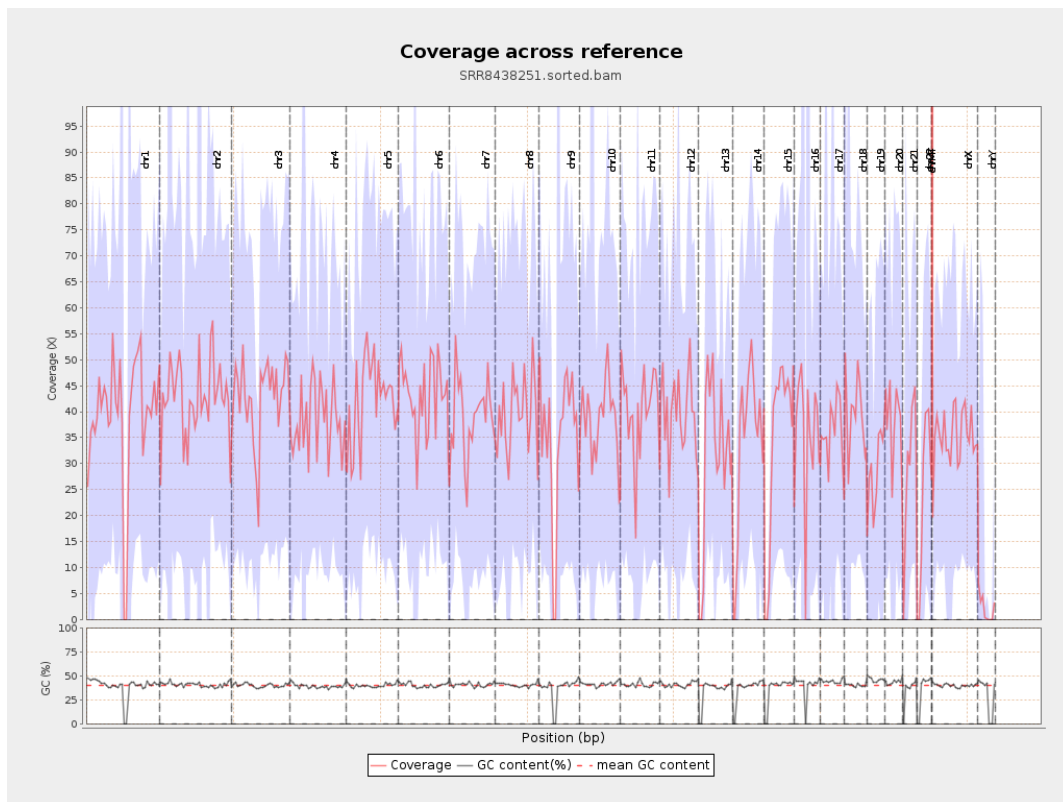
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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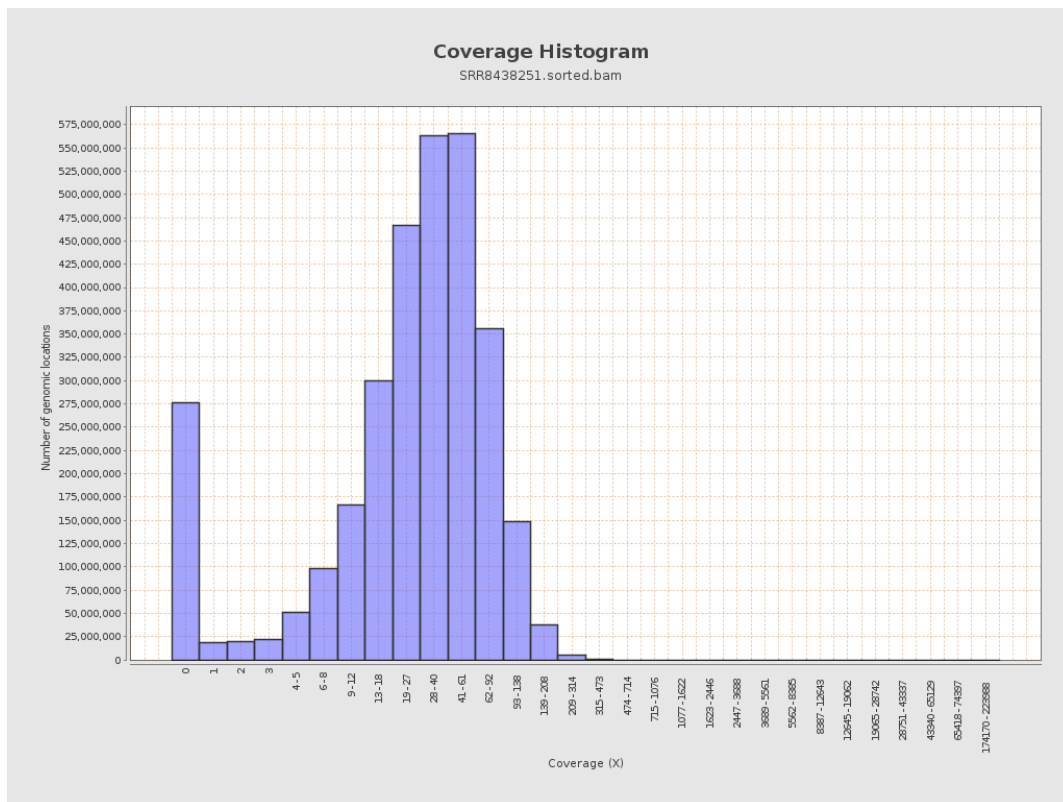
		bases	coverage	deviation
chr1	249250621	9821259466	39.4031	43.122
chr2	243199373	10400900094	42.767	173.4859
chr3	198022430	8500469045	42.9268	32.6269
chr4	191154276	7394817254	38.6851	35.7374
chr5	180915260	7641021306	42.2354	33.4983
chr6	171115067	7408943066	43.298	36.8558
chr7	159138663	6188657465	38.8885	33.1631
chr8	146364022	5809001039	39.6887	33.7949
chr9	141213431	4858318342	34.4041	47.5591
chr10	135534747	5279043992	38.9497	62.0398
chr11	135006516	5479327183	40.5856	36.4114
chr12	133851895	5337550947	39.8765	33.618
chr13	115169878	3610633006	31.3505	30.828
chr14	107349540	3646837030	33.9716	34.3775
chr15	102531392	3461167457	33.7571	34.1314
chr16	90354753	3190183623	35.3073	102.6122
chr17	81195210	2931408688	36.1032	48.6352
chr18	78077248	3114981349	39.8961	52.6899
chr19	59128983	1716130052	29.0235	34.1589
chr20	63025520	2387004862	37.8736	35.2416
chr21	48129895	1446254443	30.049	42.1195
chr22	51304566	1242278993	24.2138	32.1295
chrMT	16571	482798699	29,135.1577	10,882.4143
chrX	155270560	5461943197	35.1769	28.3037

chrY	59373566	125206075	2.1088	33.8524
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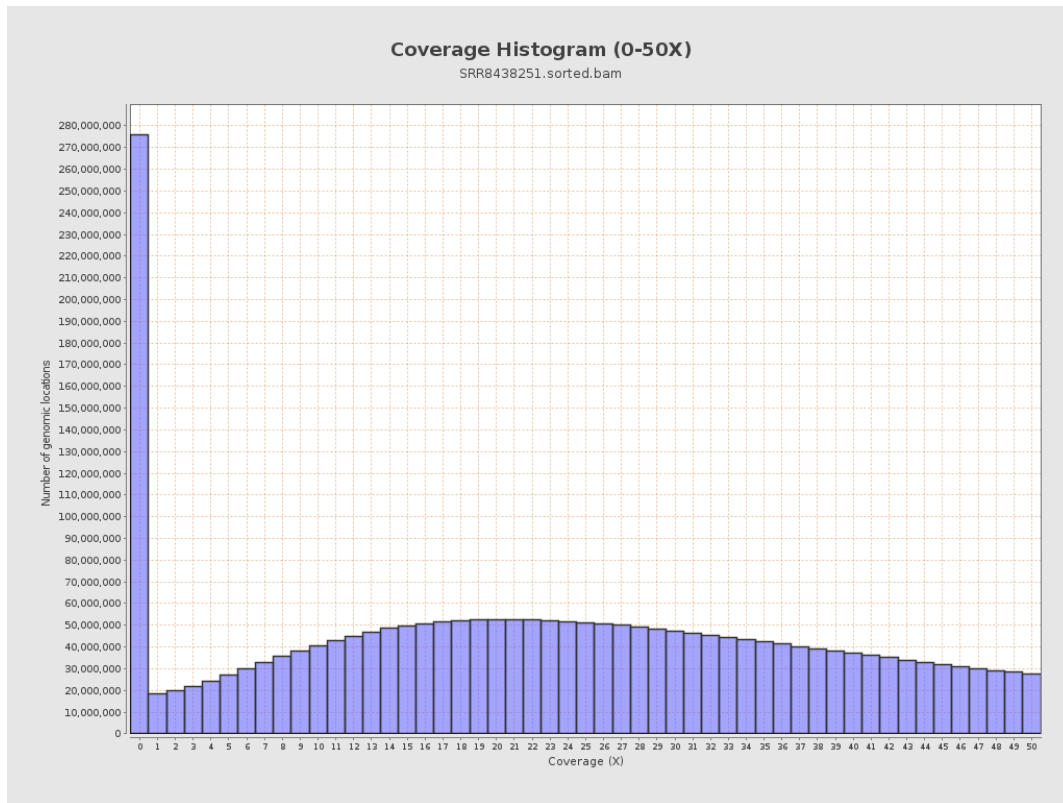
3. Results : Coverage across reference



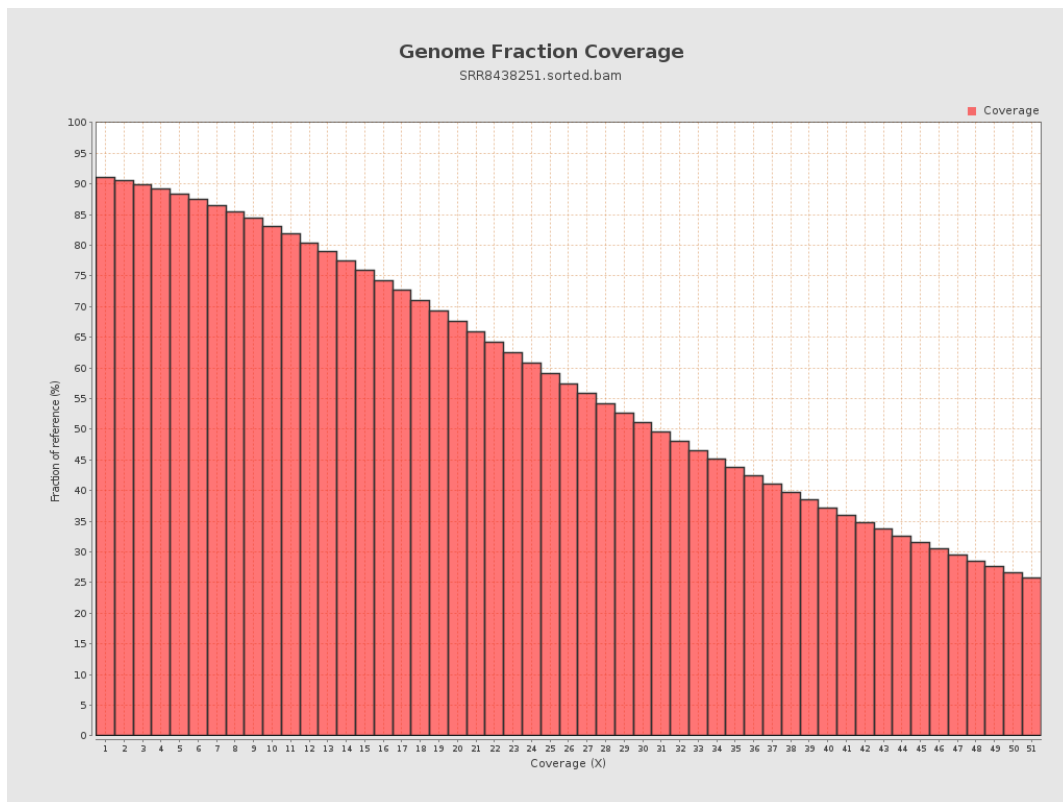
4. Results : Coverage Histogram



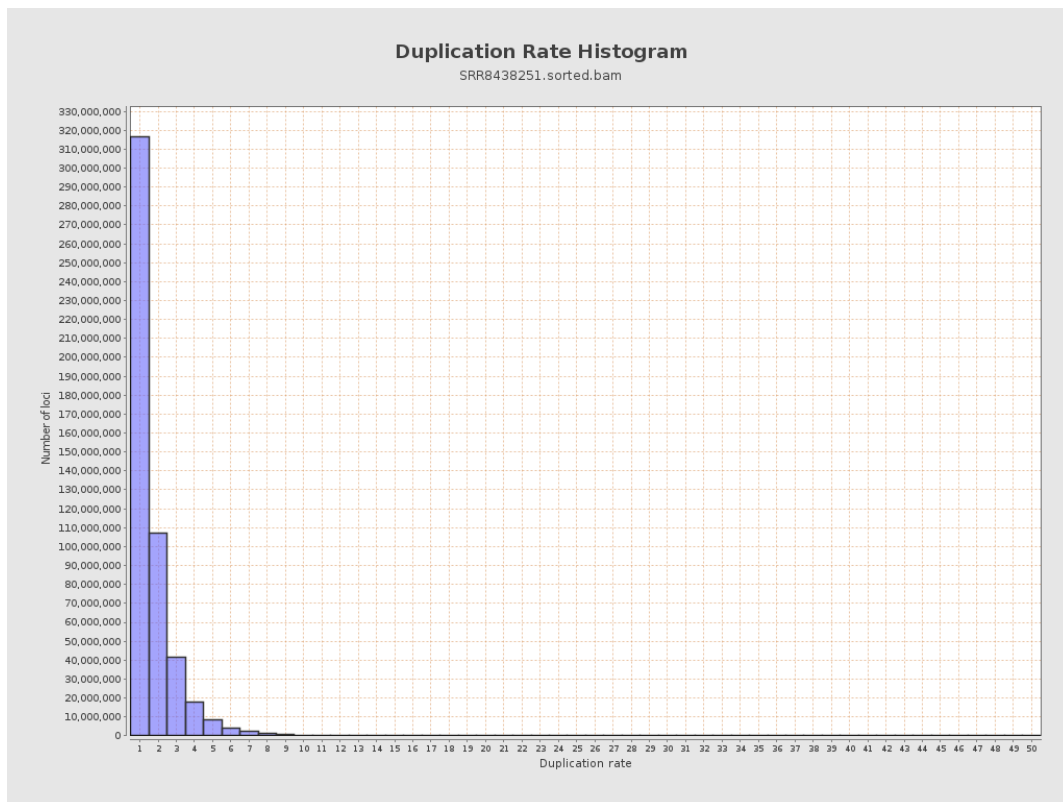
5. Results : Coverage Histogram (0-50X)



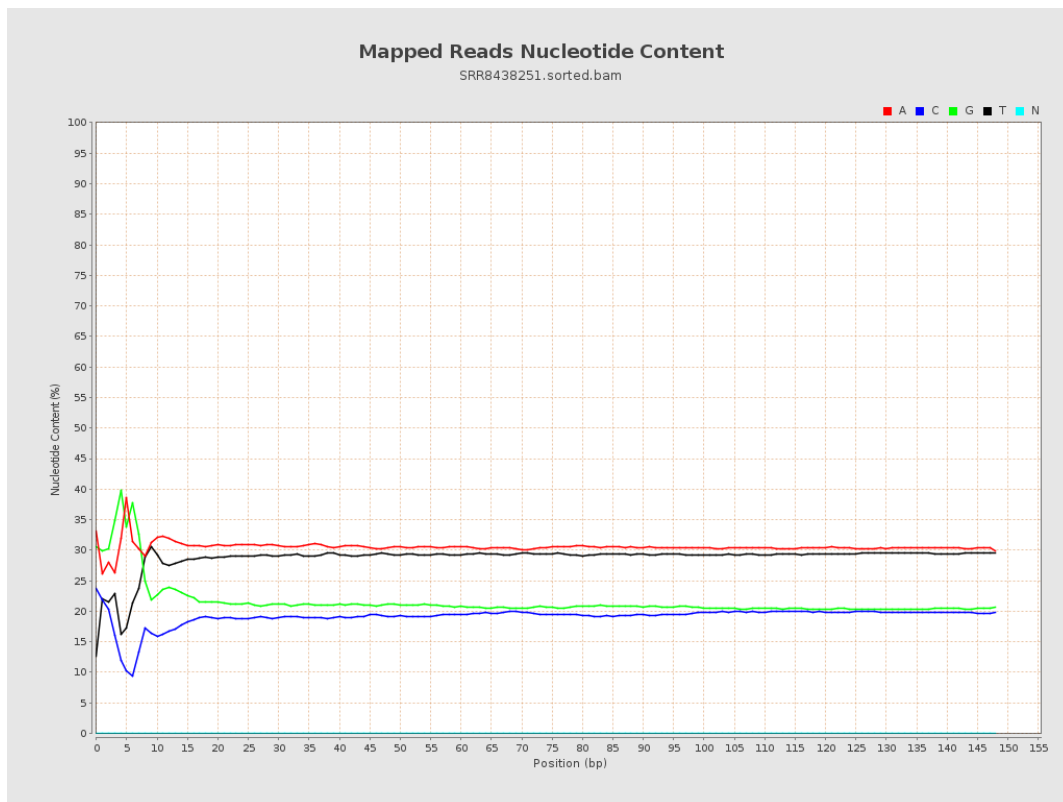
6. Results : Genome Fraction Coverage



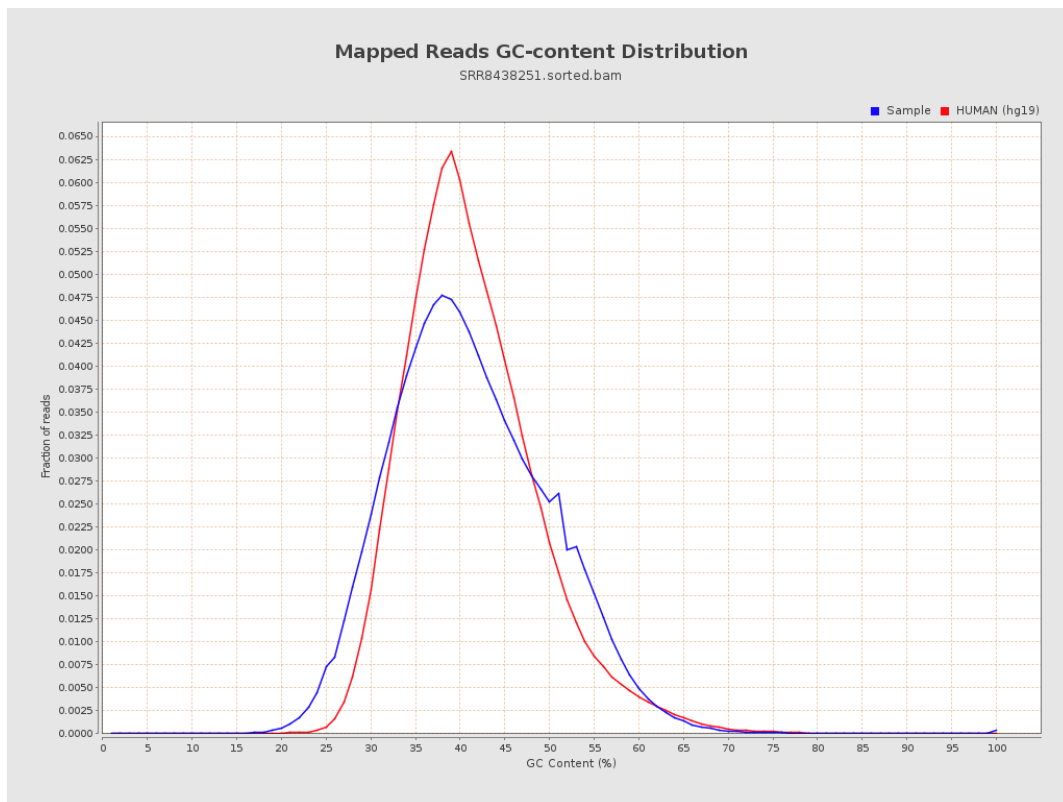
7. Results : Duplication Rate Histogram



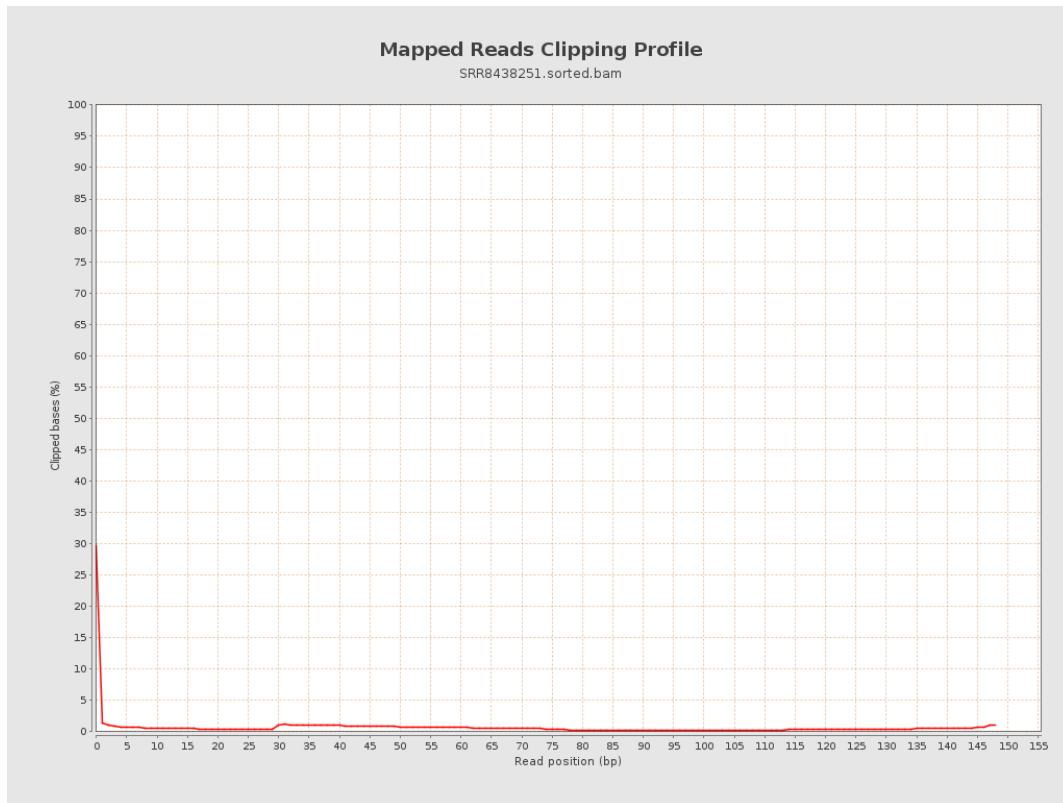
8. Results : Mapped Reads Nucleotide Content



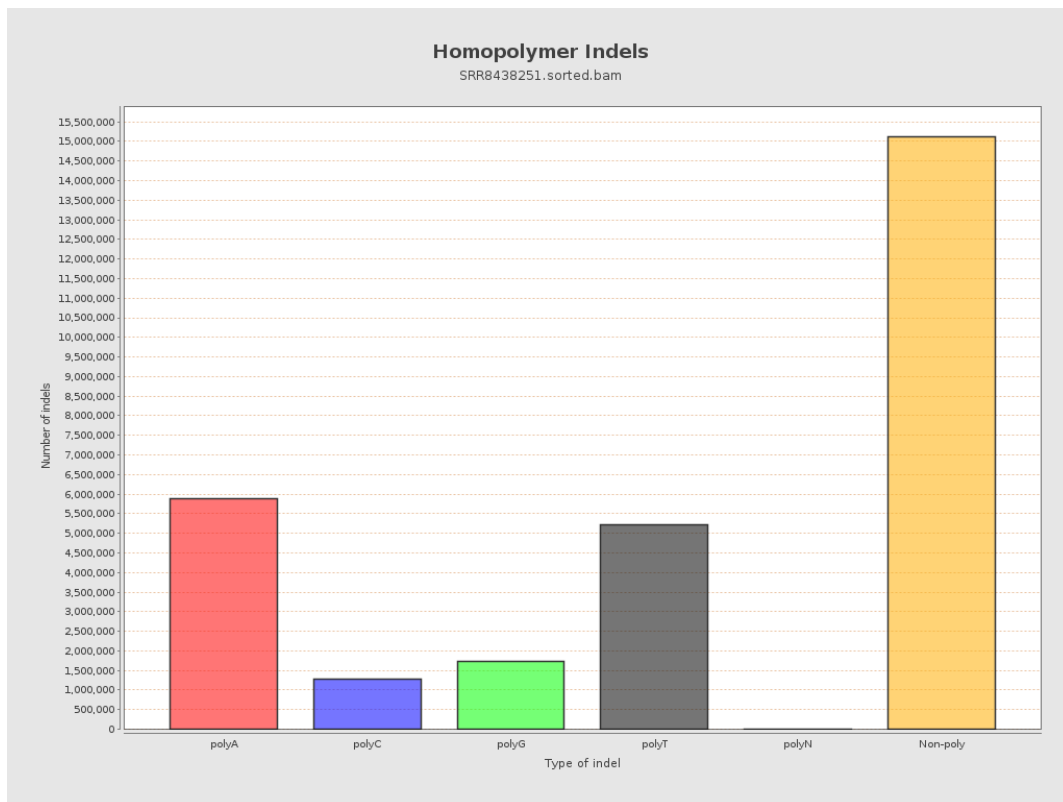
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



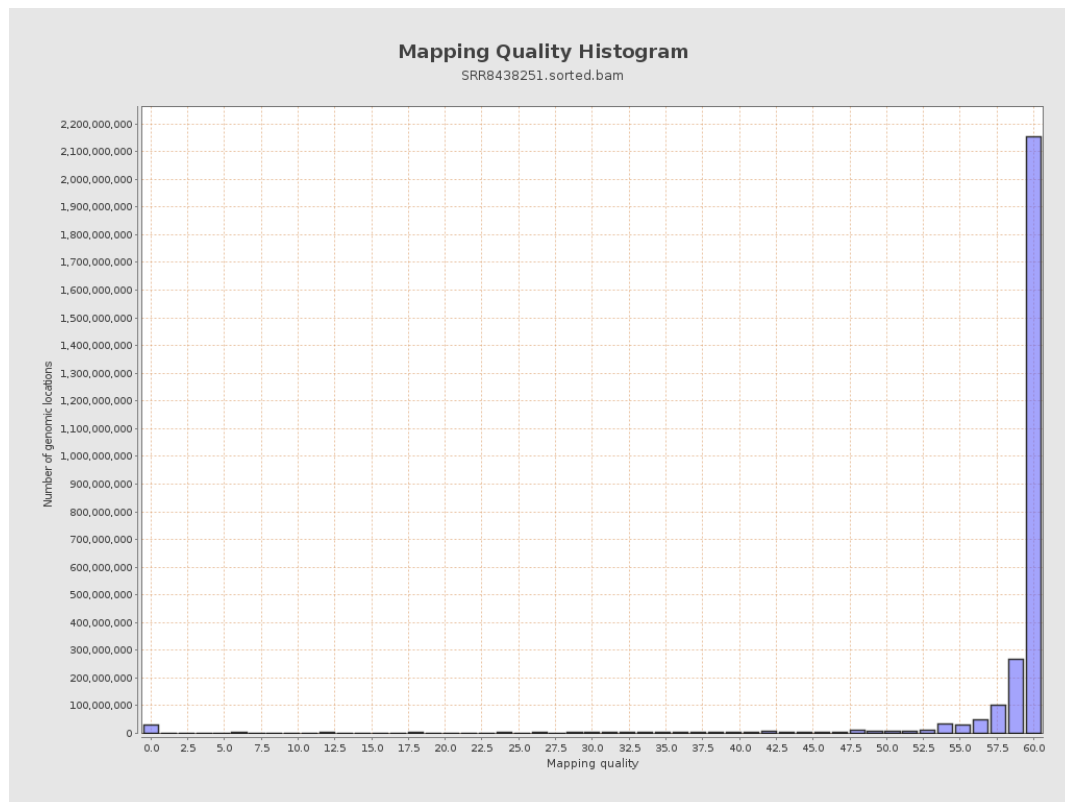
11. Results : Homopolymer Indels



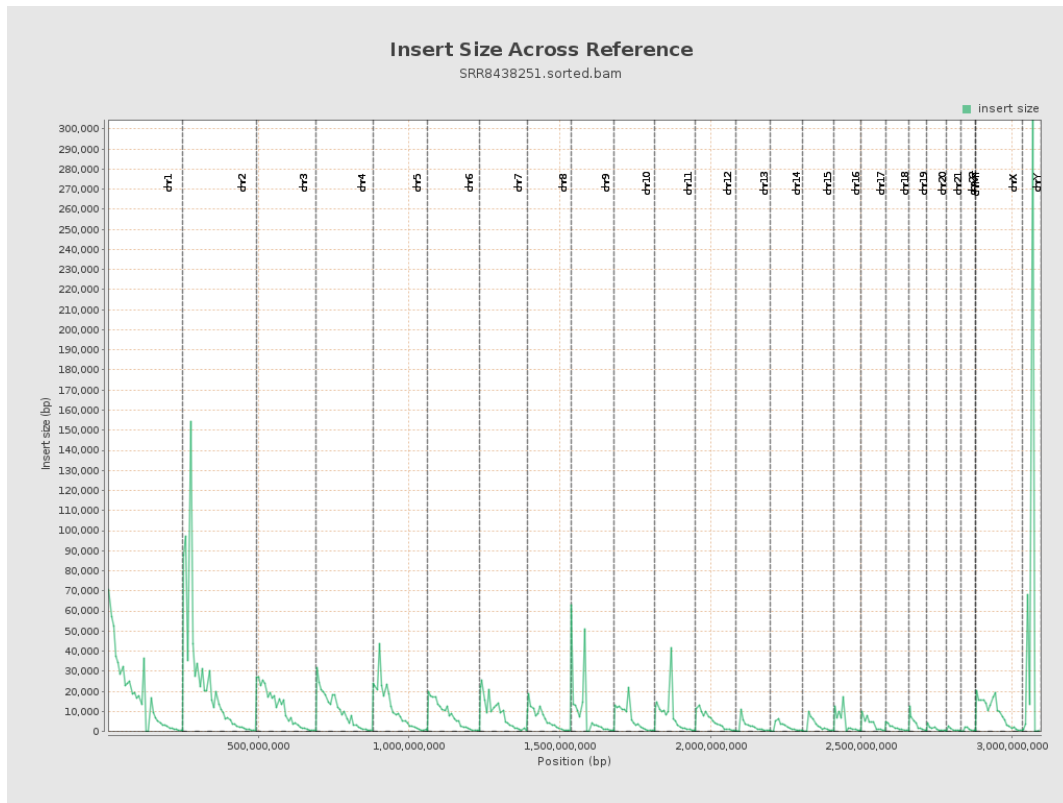
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

