

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 02:06:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777251.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_SRR1777251 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777251_1.fastq.gz SRR1777251_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 02:06:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777251.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,336,476
Mapped reads	12,102,847 / 98.11%
Unmapped reads	233,629 / 1.89%
Mapped paired reads	12,102,847 / 98.11%
Mapped reads, first in pair	6,057,387 / 49.1%
Mapped reads, second in pair	6,045,460 / 49%
Mapped reads, both in pair	12,042,166 / 97.61%
Mapped reads, singletons	60,681 / 0.49%
Secondary alignments	0
Supplementary alignments	629,074 / 5.1%
Read min/max/mean length	30 / 101 / 103.06
Duplicated reads (estimated)	1,558,381 / 12.63%
Duplication rate	6.41%
Clipped reads	3,691,775 / 29.93%

2.2. ACGT Content

Number/percentage of A's	347,507,409 / 29.9%
Number/percentage of C's	234,100,872 / 20.14%
Number/percentage of T's	339,458,499 / 29.21%
Number/percentage of G's	241,120,337 / 20.75%
Number/percentage of N's	25,697 / 0%

GC Percentage	40.89%
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2.3. Coverage

Mean	0.3756
Standard Deviation	18.1042

2.4. Mapping Quality

Mean Mapping Quality	53.22
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2.5. Insert size

Mean	253,338.46
Standard Deviation	3,732,915.92
P25/Median/P75	116 / 162 / 227

2.6. Mismatches and indels

General error rate	0.45%
Mismatches	4,598,472
Insertions	339,006
Mapped reads with at least one insertion	2.69%
Deletions	223,301
Mapped reads with at least one deletion	1.7%
Homopolymer indels	38.83%

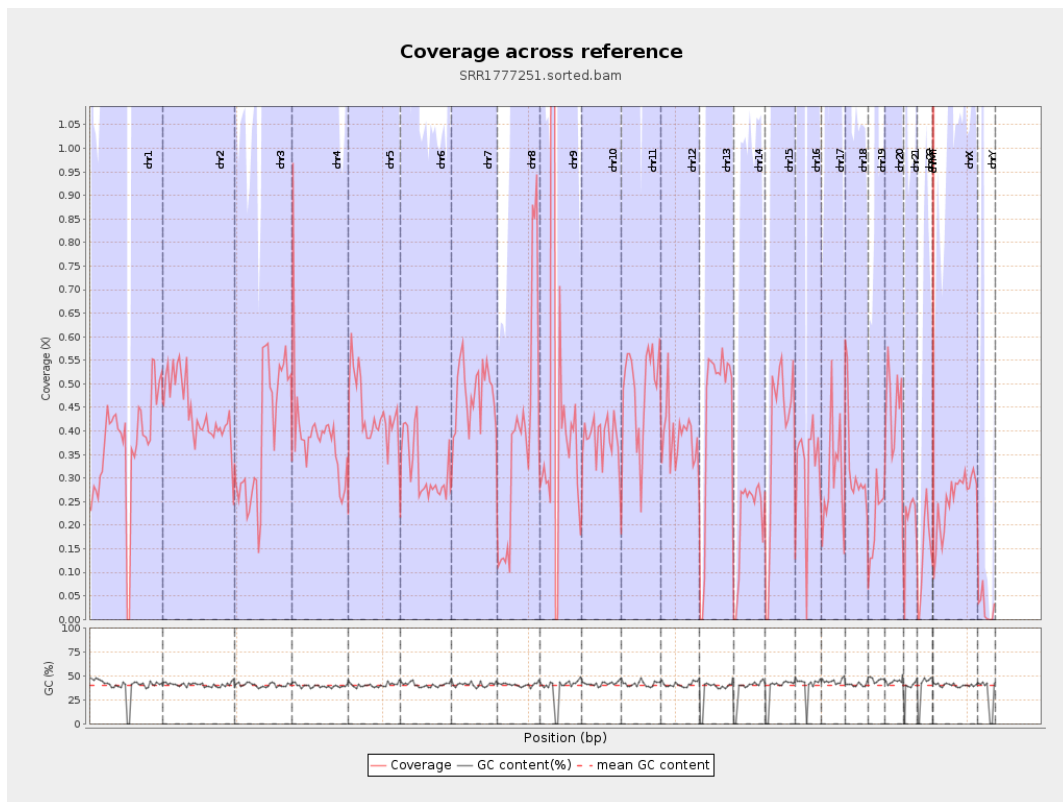
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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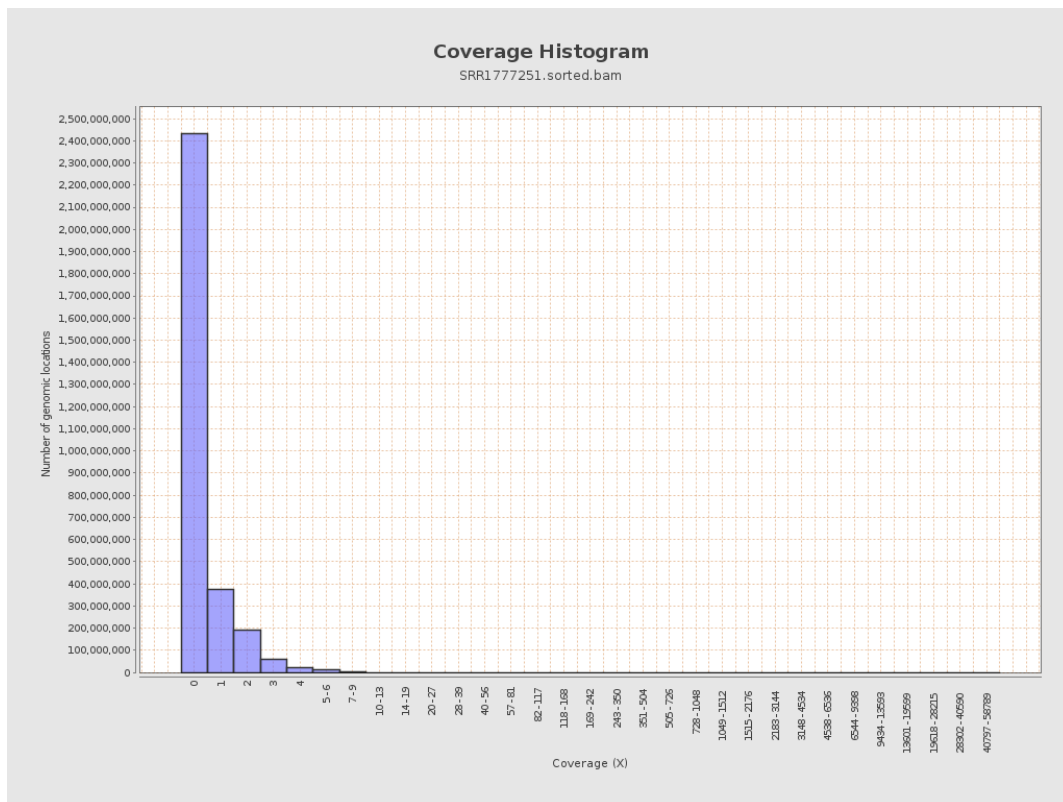
		bases	coverage	deviation
chr1	249250621	92668117	0.3718	1.8718
chr2	243199373	107342897	0.4414	1.1635
chr3	198022430	77617797	0.392	0.8646
chr4	191154276	74596139	0.3902	12.9084
chr5	180915260	78503877	0.4339	0.9015
chr6	171115067	54546060	0.3188	1.0453
chr7	159138663	75582743	0.4749	1.2413
chr8	146364022	57235183	0.391	0.9379
chr9	141213431	78980076	0.5593	83.1993
chr10	135534747	52053642	0.3841	1.6989
chr11	135006516	66071526	0.4894	1.2451
chr12	133851895	51827544	0.3872	0.8527
chr13	115169878	50449446	0.438	0.918
chr14	107349540	22922684	0.2135	0.6449
chr15	102531392	40509906	0.3951	0.8778
chr16	90354753	28842951	0.3192	1.1371
chr17	81195210	24488263	0.3016	1.0202
chr18	78077248	25240639	0.3233	1.6183
chr19	59128983	12461357	0.2107	1.3143
chr20	63025520	28281643	0.4487	0.9394
chr21	48129895	9955769	0.2069	0.7956
chr22	51304566	7298702	0.1423	0.5171
chrMT	16571	5000840	301.7826	66.9931
chrX	155270560	38910224	0.2506	0.7252

chrY	59373566	1478322	0.0249	0.6325
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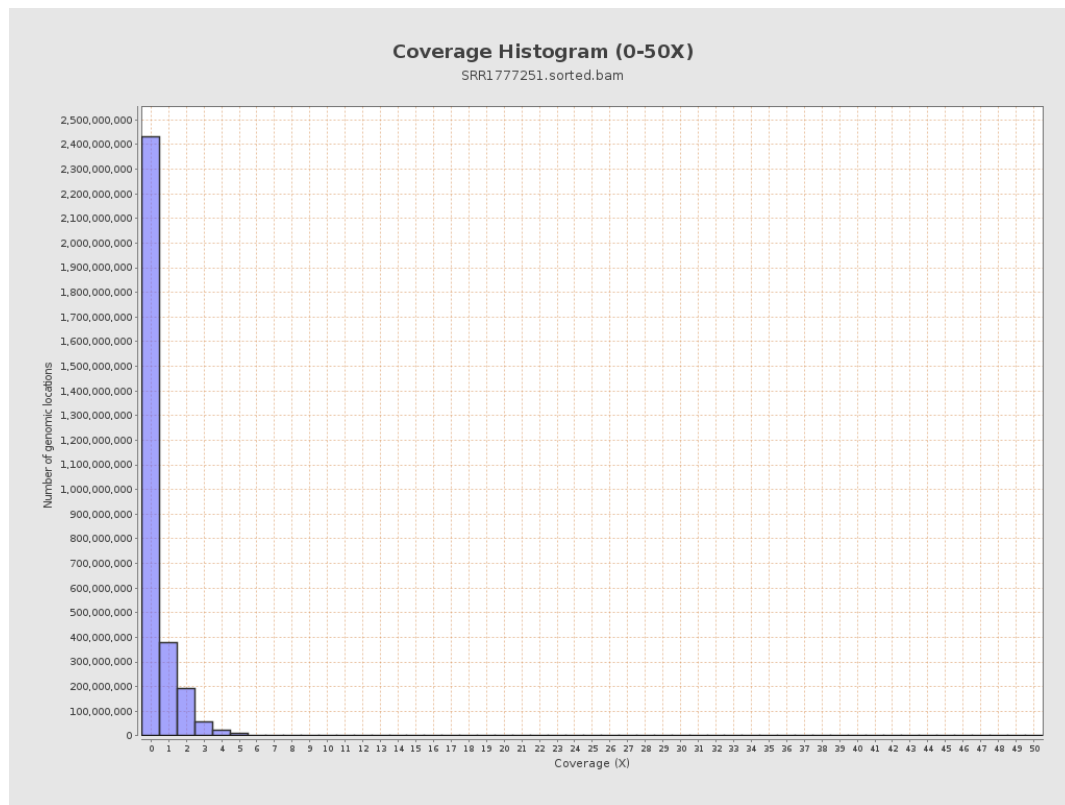
3. Results : Coverage across reference



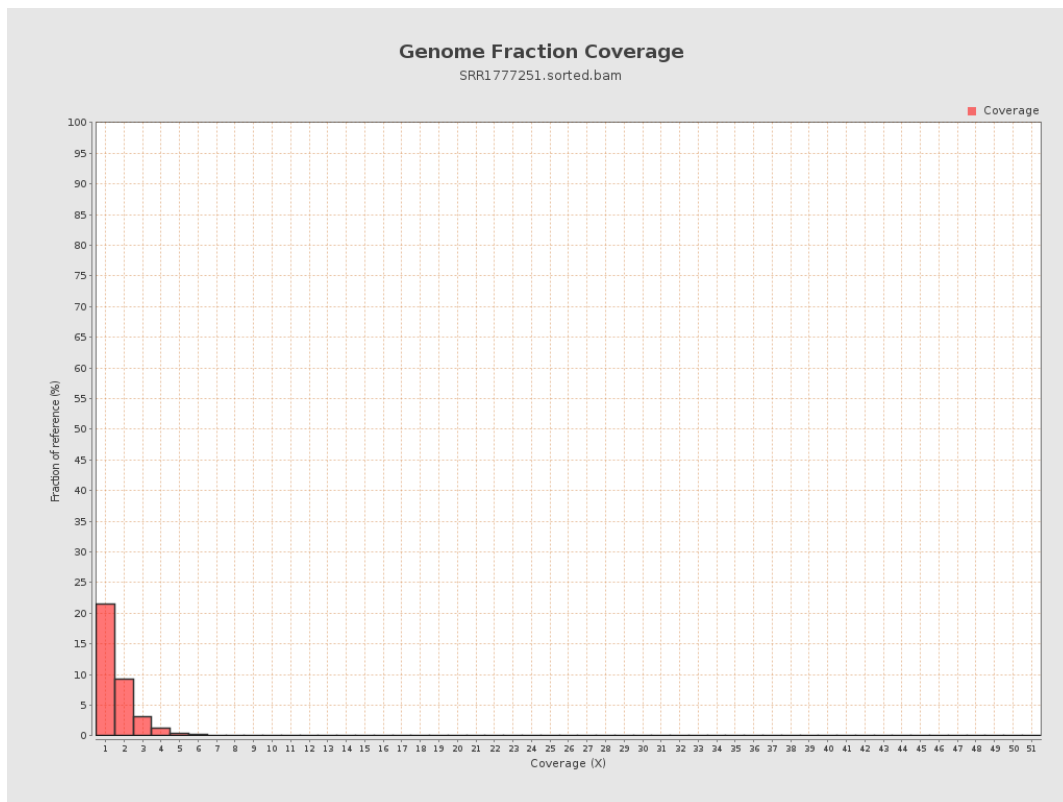
4. Results : Coverage Histogram



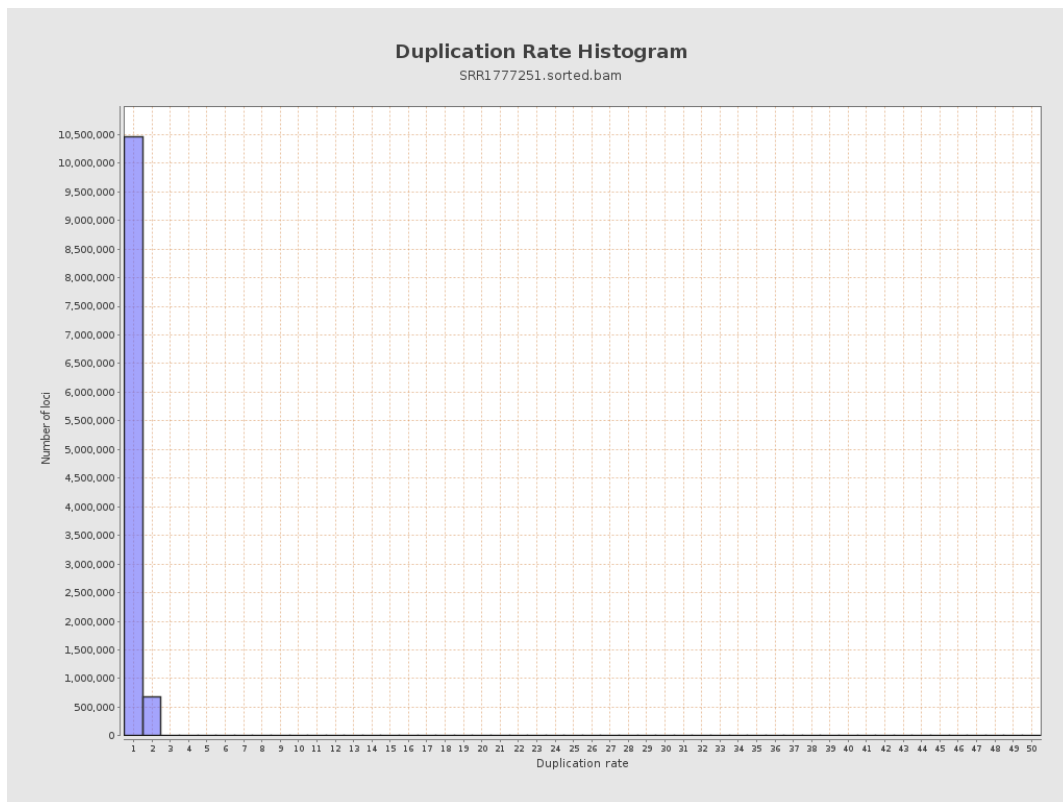
5. Results : Coverage Histogram (0-50X)



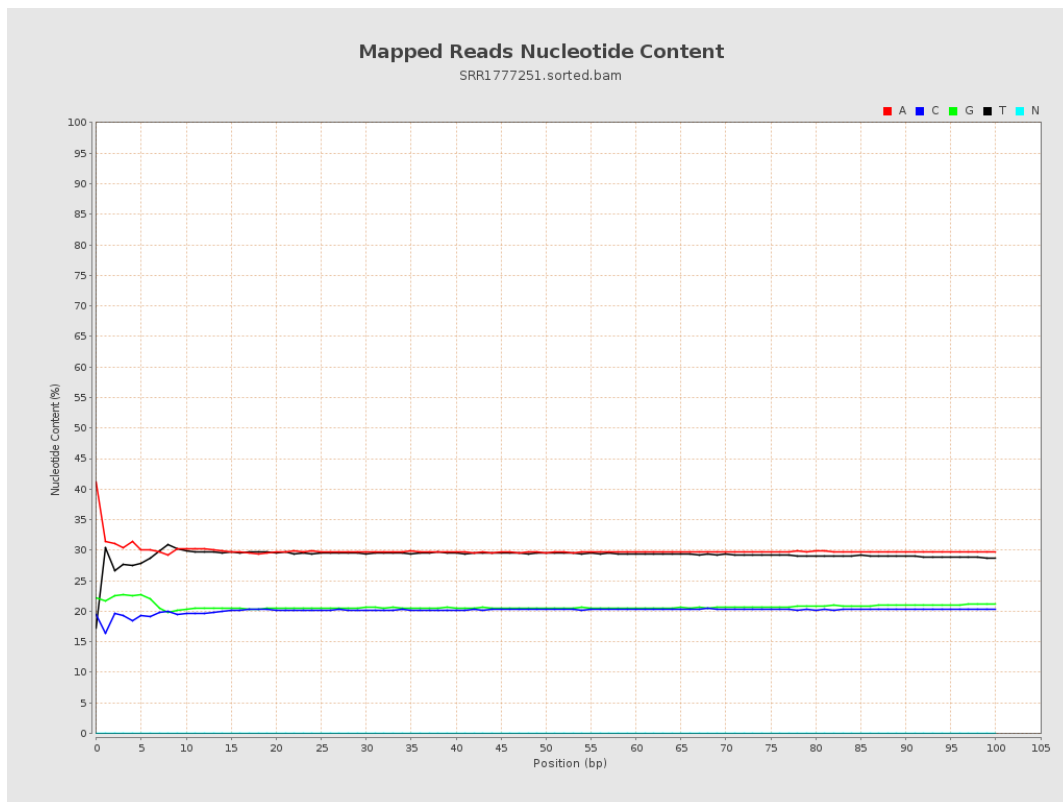
6. Results : Genome Fraction Coverage



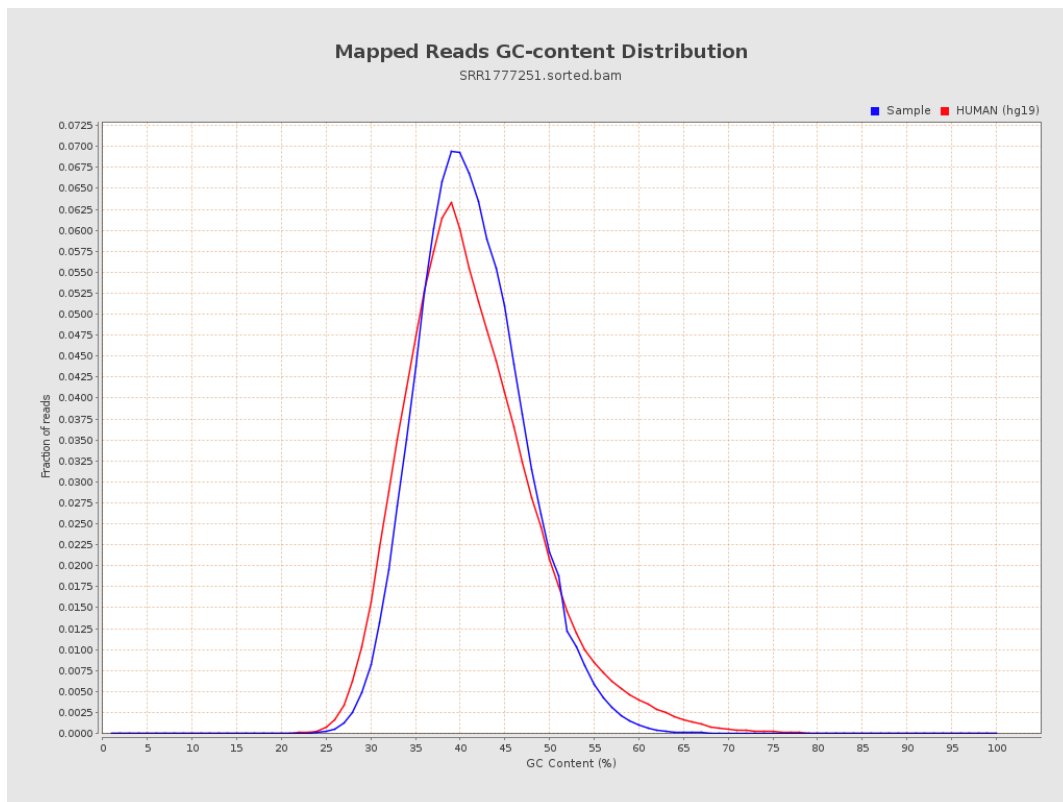
7. Results : Duplication Rate Histogram



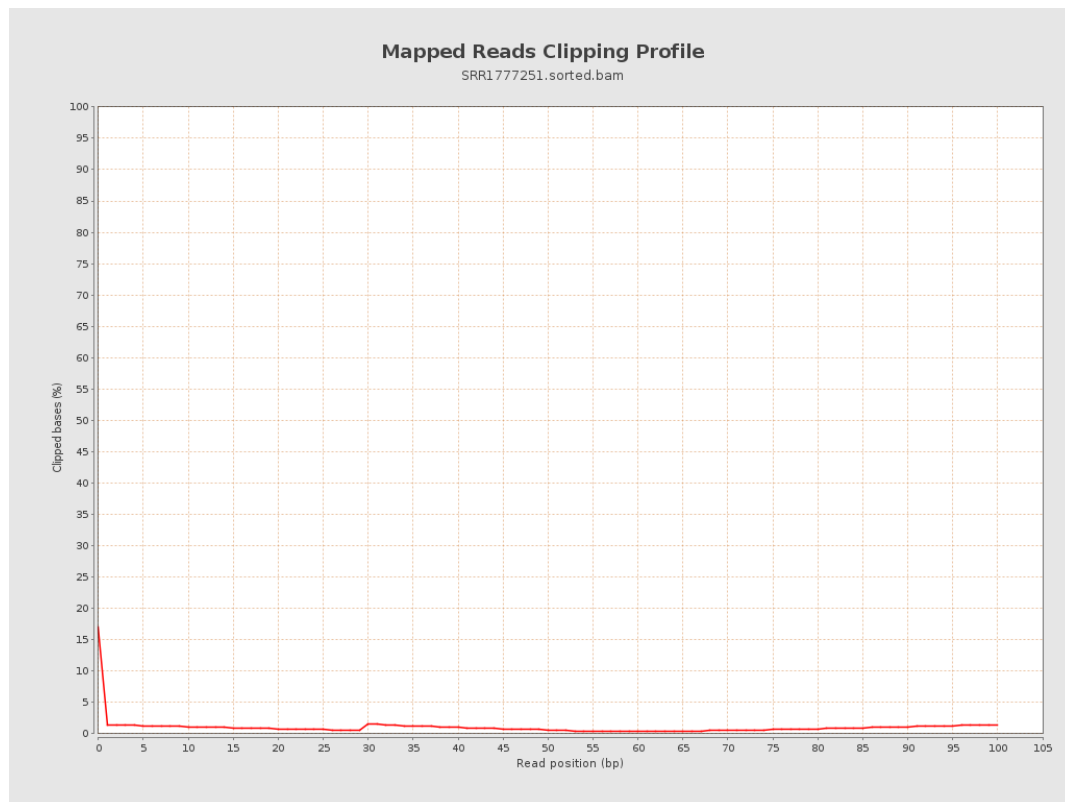
8. Results : Mapped Reads Nucleotide Content



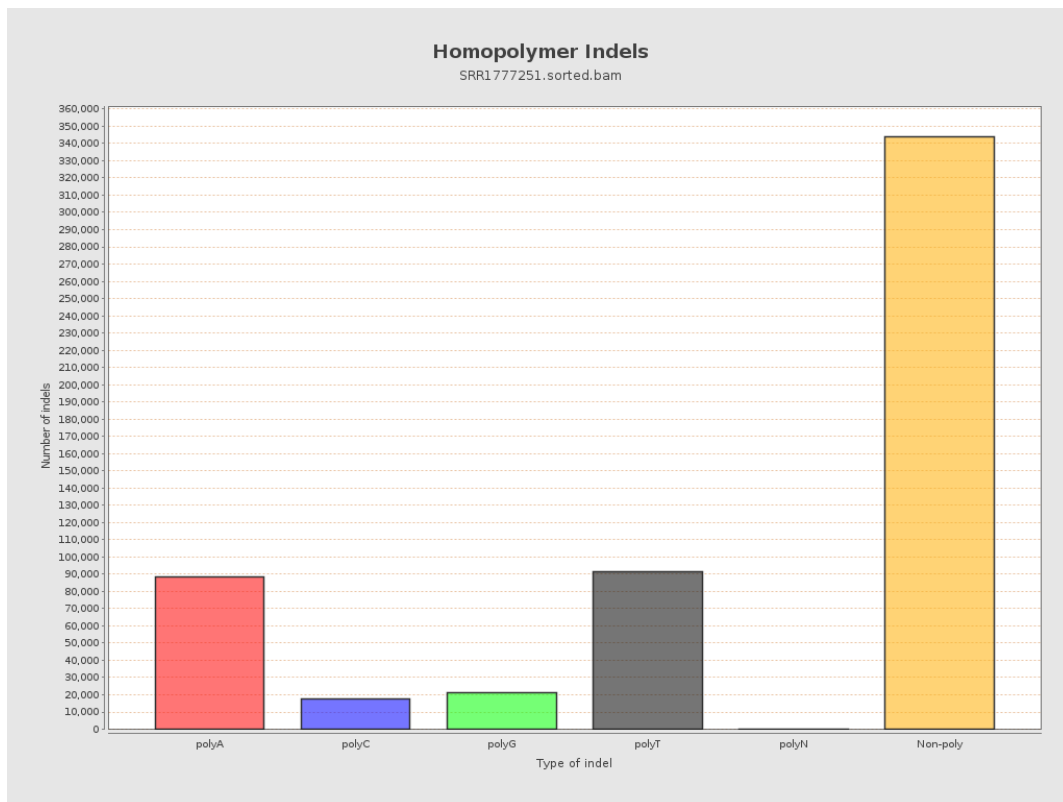
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



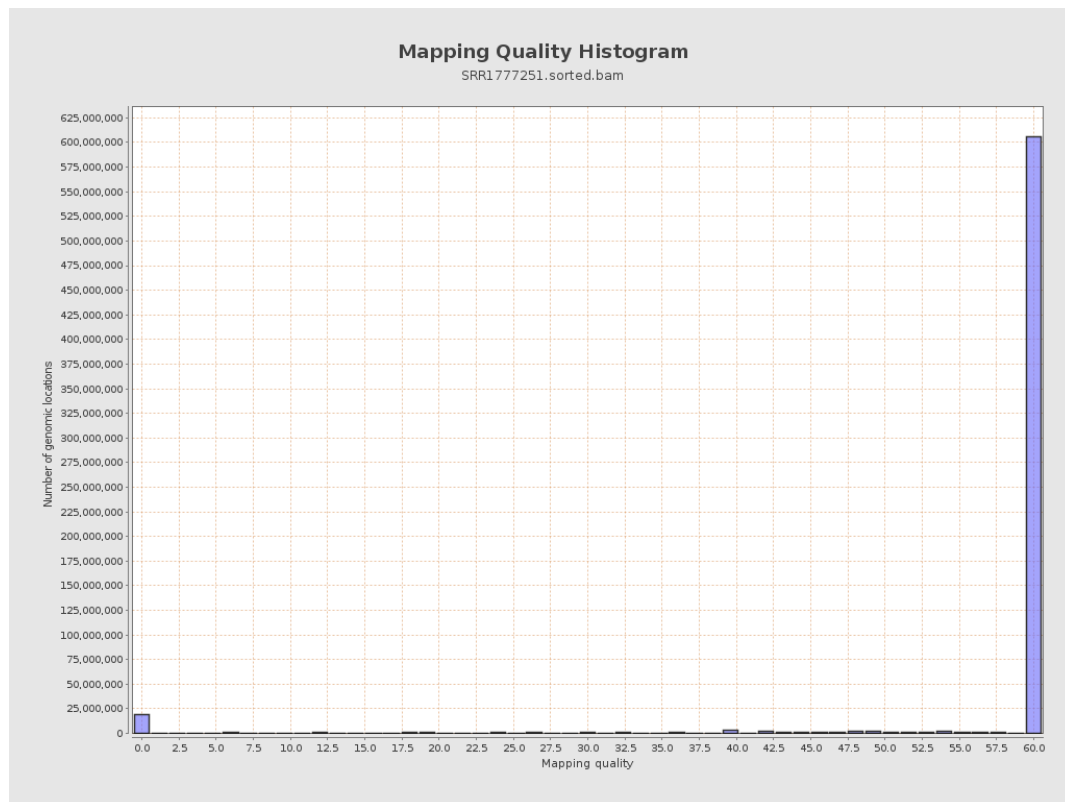
11. Results : Homopolymer Indels



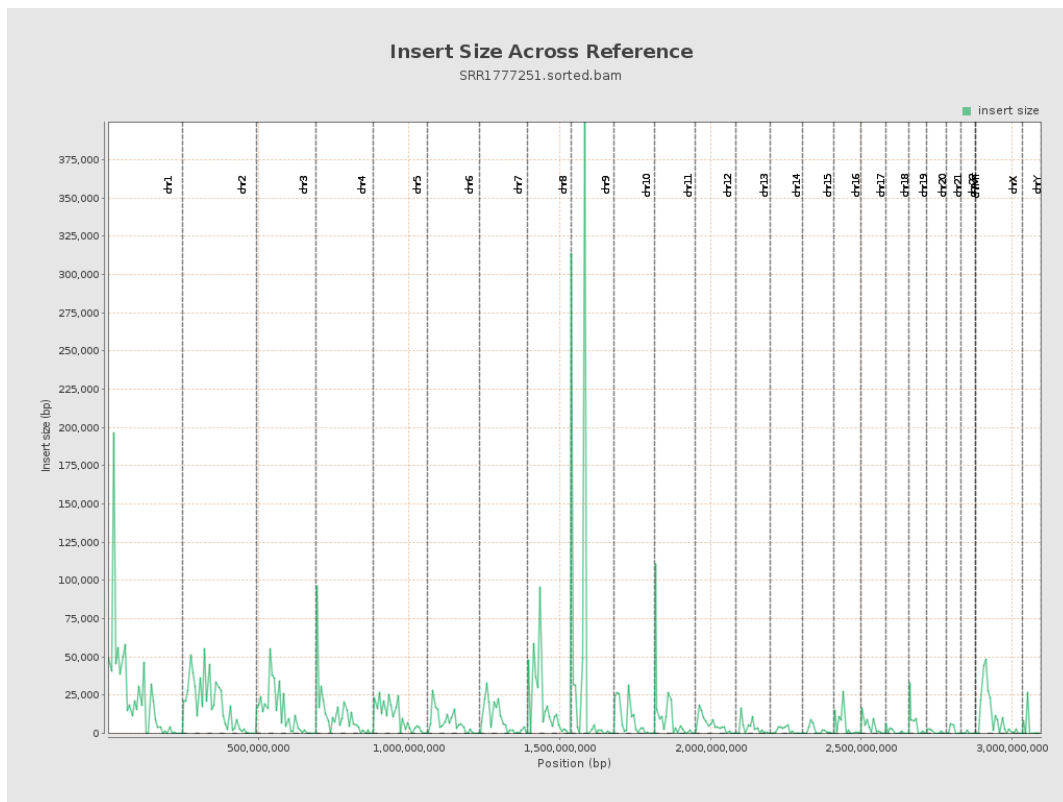
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

