

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 09:51:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777281.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_SRR1777281 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777281_1.fastq.gz SRR1777281_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 09:51:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777281.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,526,294
Mapped reads	10,810,290 / 93.79%
Unmapped reads	716,004 / 6.21%
Mapped paired reads	10,810,290 / 93.79%
Mapped reads, first in pair	5,424,811 / 47.06%
Mapped reads, second in pair	5,385,479 / 46.72%
Mapped reads, both in pair	10,572,700 / 91.73%
Mapped reads, singletons	237,590 / 2.06%
Secondary alignments	0
Supplementary alignments	1,084,432 / 9.41%
Read min/max/mean length	30 / 101 / 104.64
Duplicated reads (estimated)	4,879,491 / 42.33%
Duplication rate	8.49%
Clipped reads	5,575,953 / 48.38%

2.2. ACGT Content

Number/percentage of A's	275,013,287 / 28.33%
Number/percentage of C's	211,179,973 / 21.75%
Number/percentage of T's	269,587,017 / 27.77%
Number/percentage of G's	215,099,291 / 22.15%
Number/percentage of N's	17,036 / 0%

GC Percentage	43.91%
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2.3. Coverage

Mean	0.315
Standard Deviation	51.8271

2.4. Mapping Quality

Mean Mapping Quality	48.98
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2.5. Insert size

Mean	634,675.71
Standard Deviation	7,858,513.87
P25/Median/P75	102 / 153 / 217

2.6. Mismatches and indels

General error rate	1.96%
Mismatches	15,397,896
Insertions	1,069,233
Mapped reads with at least one insertion	8.67%
Deletions	1,043,156
Mapped reads with at least one deletion	8.61%
Homopolymer indels	22.06%

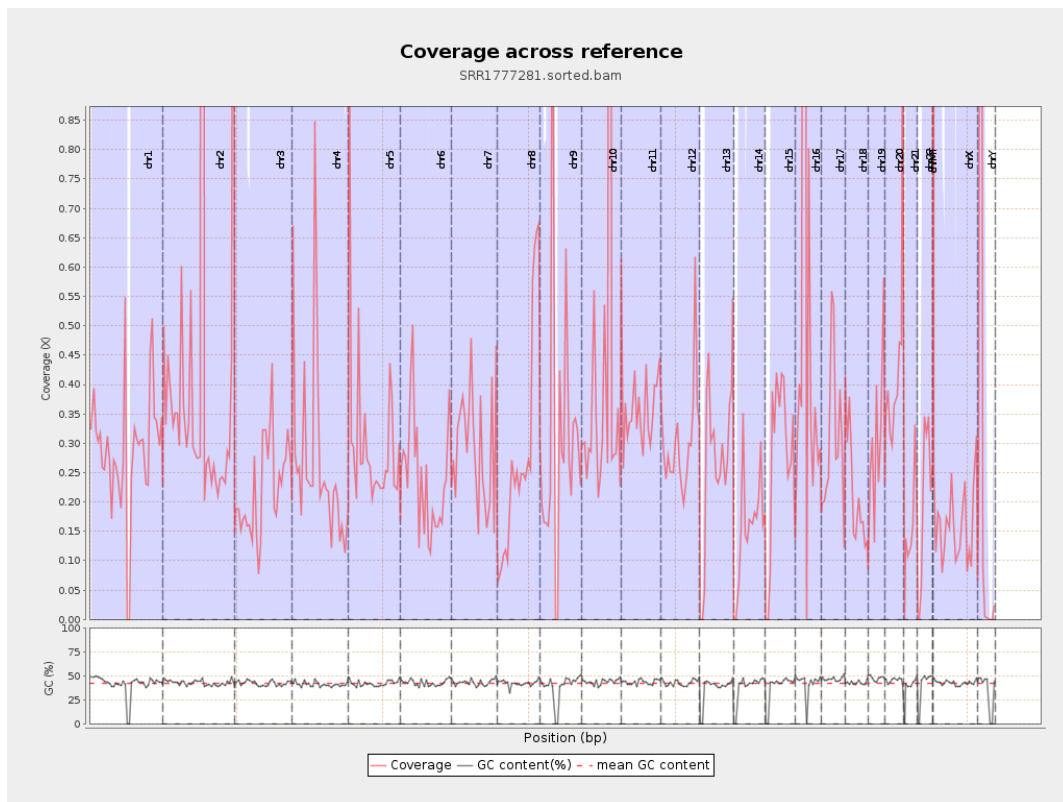
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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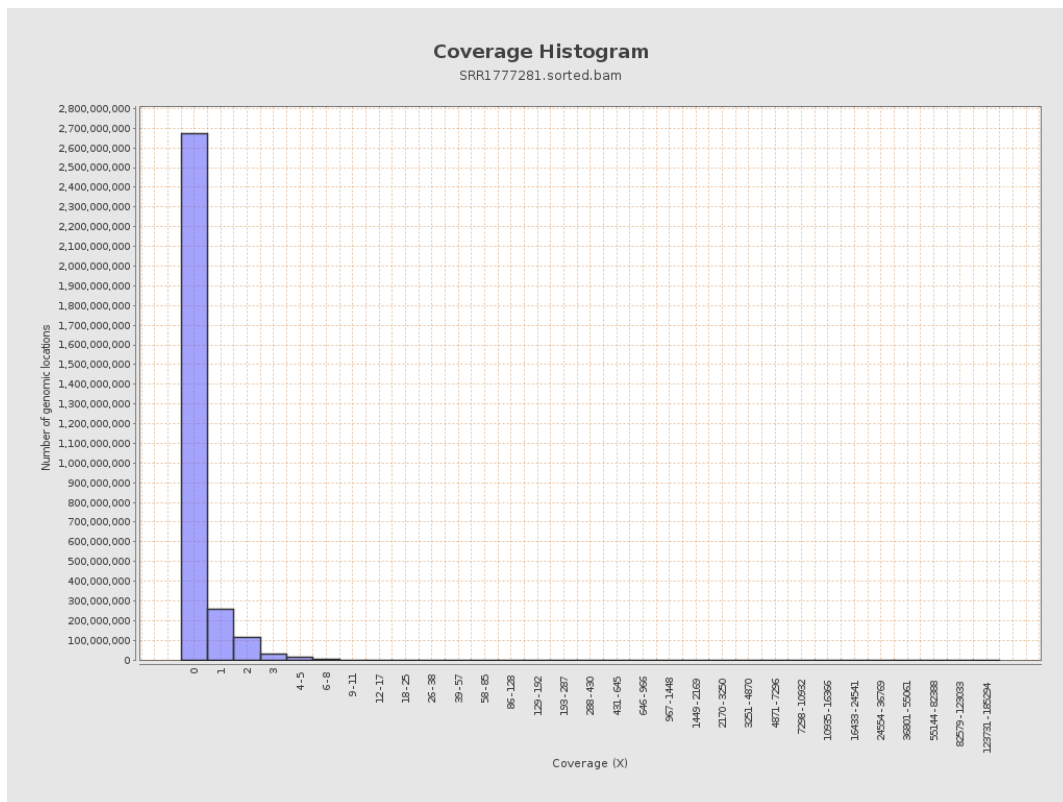
		bases	coverage	deviation
chr1	249250621	71924192	0.2886	16.8395
chr2	243199373	148149723	0.6092	127.0332
chr3	198022430	44224858	0.2233	7.0455
chr4	191154276	50637419	0.2649	26.7822
chr5	180915260	56461366	0.3121	24.9858
chr6	171115067	41508687	0.2426	22.8736
chr7	159138663	46667032	0.2932	23.19
chr8	146364022	41576819	0.2841	9.5079
chr9	141213431	42674908	0.3022	24.089
chr10	135534747	61542742	0.4541	121.2306
chr11	135006516	48153286	0.3567	16.1501
chr12	133851895	40654944	0.3037	8.988
chr13	115169878	30467202	0.2645	8.7709
chr14	107349540	17240174	0.1606	23.6511
chr15	102531392	28265619	0.2757	5.1836
chr16	90354753	50227518	0.5559	81.4458
chr17	81195210	25221148	0.3106	9.2983
chr18	78077248	16852337	0.2158	15.8177
chr19	59128983	17927922	0.3032	24.6362
chr20	63025520	26279469	0.417	19.1529
chr21	48129895	7466289	0.1551	5.4523
chr22	51304566	10449692	0.2037	13.8064
chrMT	16571	2226179	134.3419	28.4548
chrX	155270560	24807192	0.1598	12.263

chrY	59373566	23575749	0.3971	127.1746
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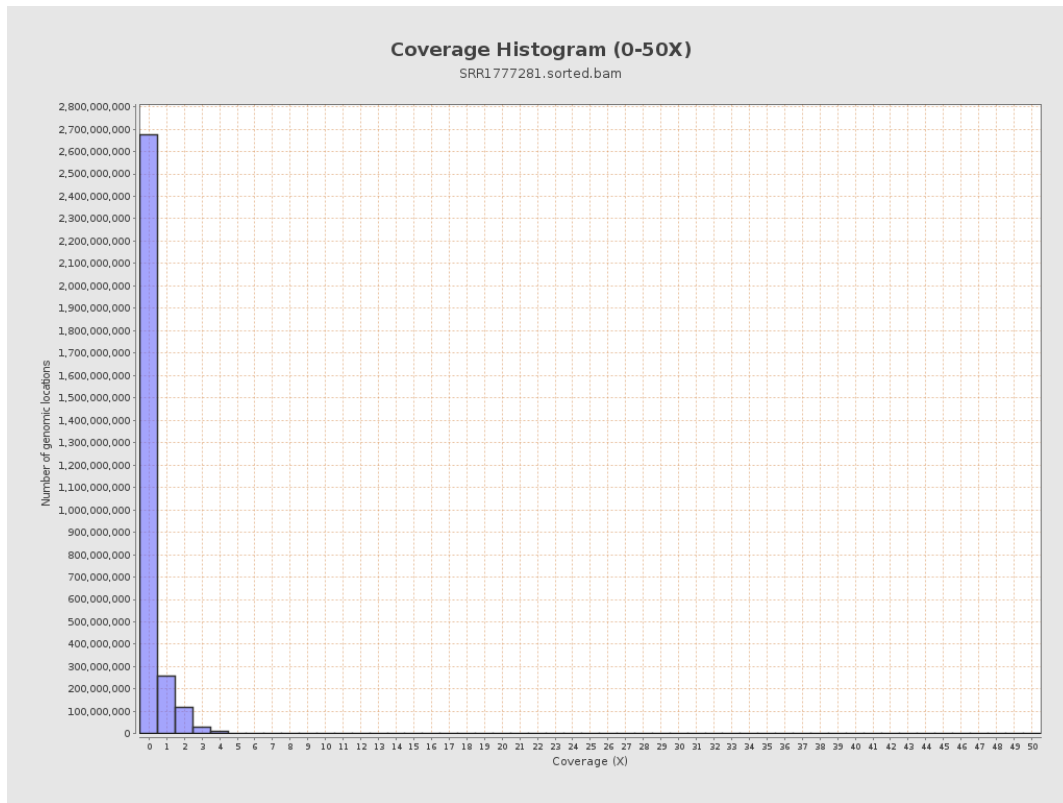
3. Results : Coverage across reference



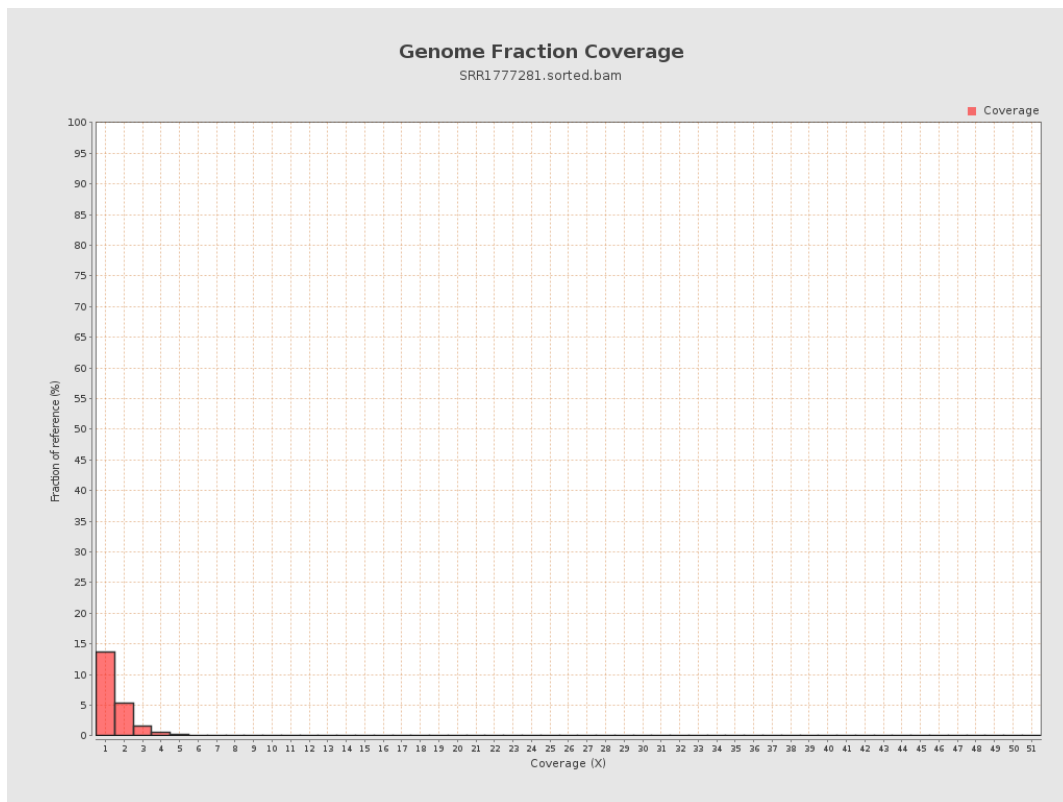
4. Results : Coverage Histogram



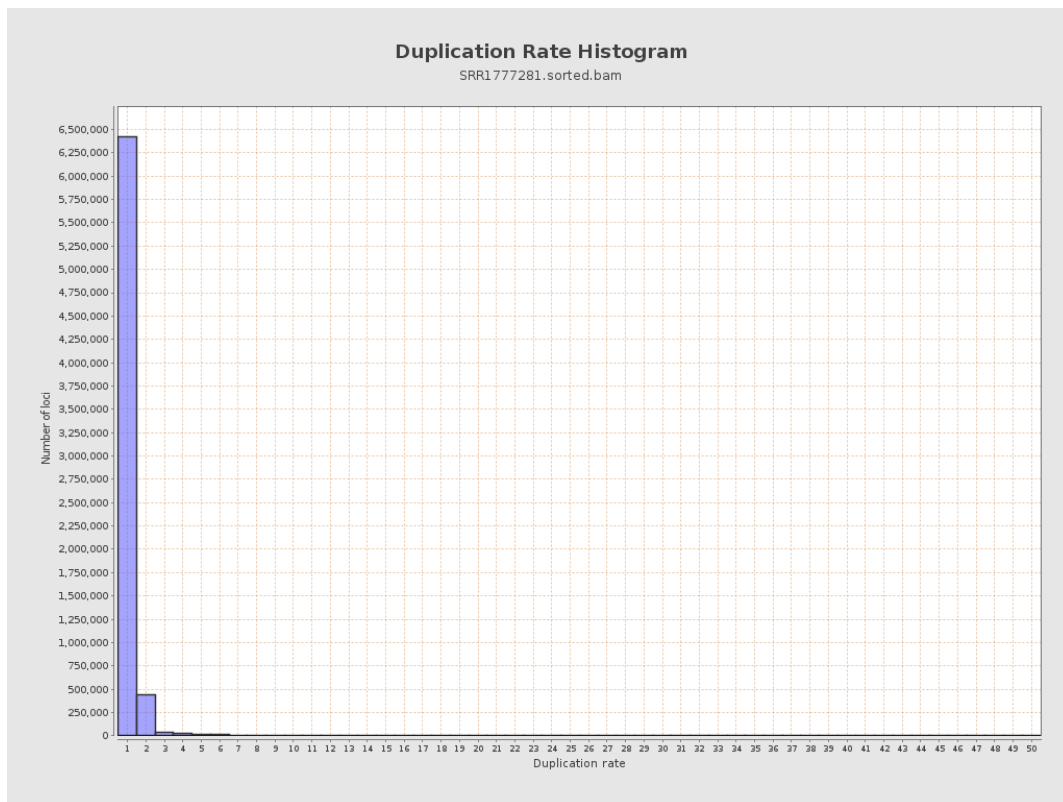
5. Results : Coverage Histogram (0-50X)



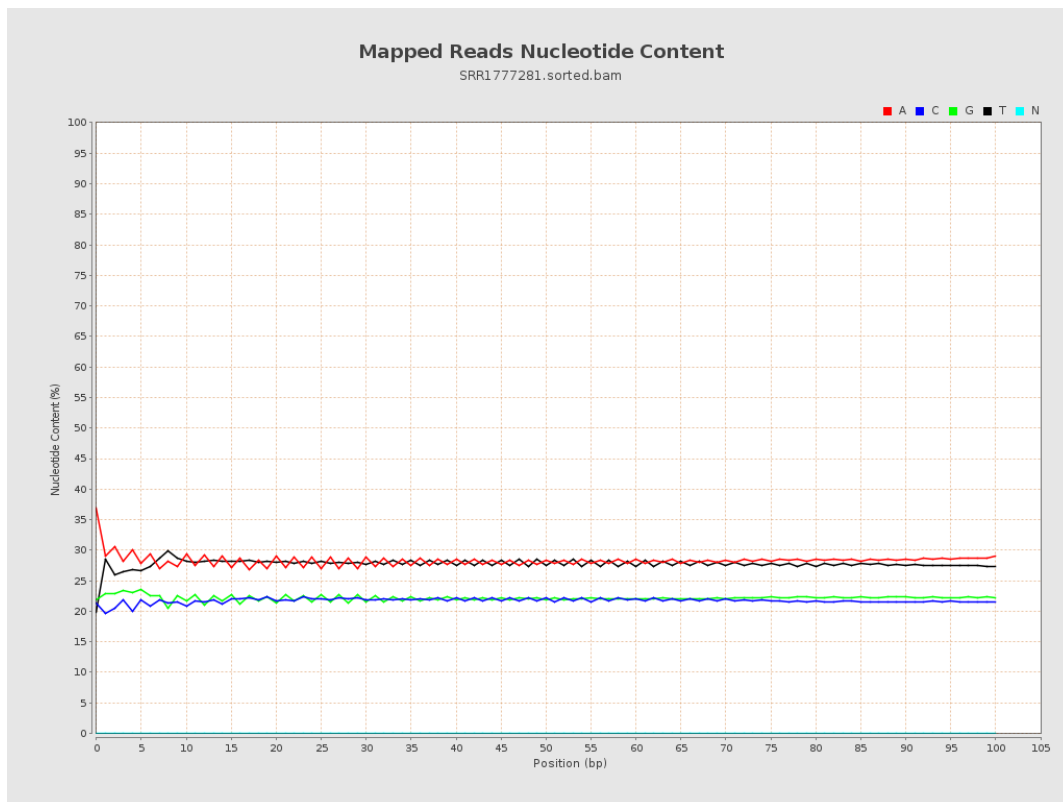
6. Results : Genome Fraction Coverage



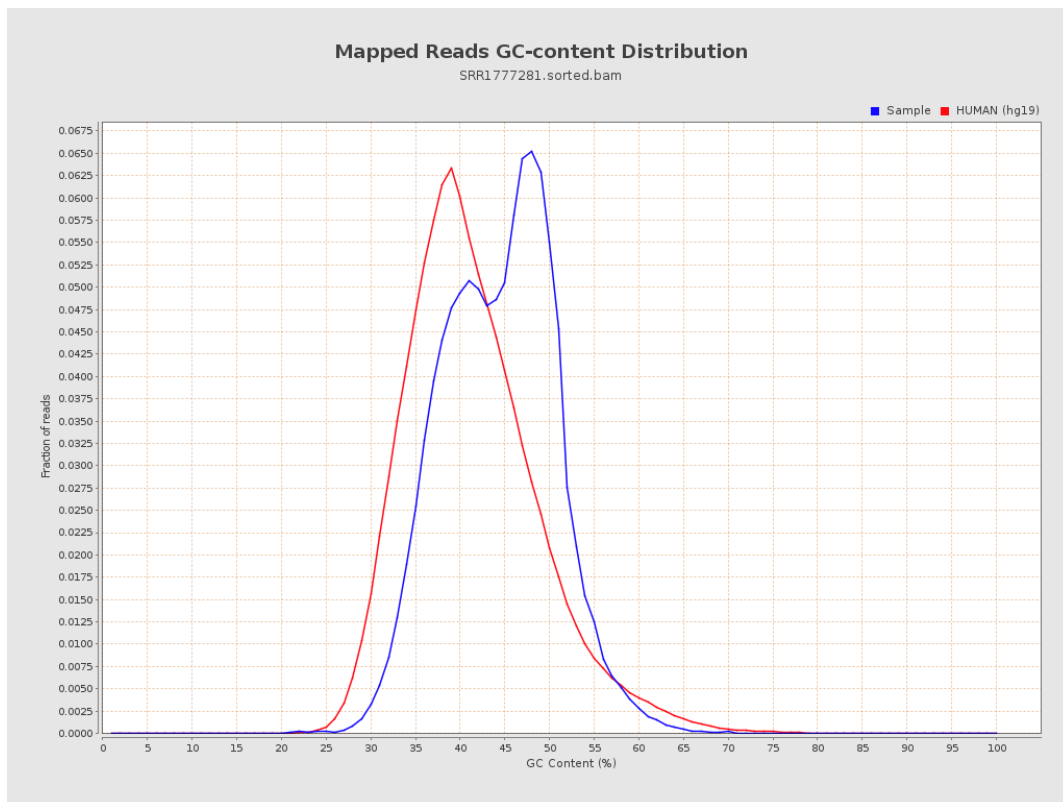
7. Results : Duplication Rate Histogram



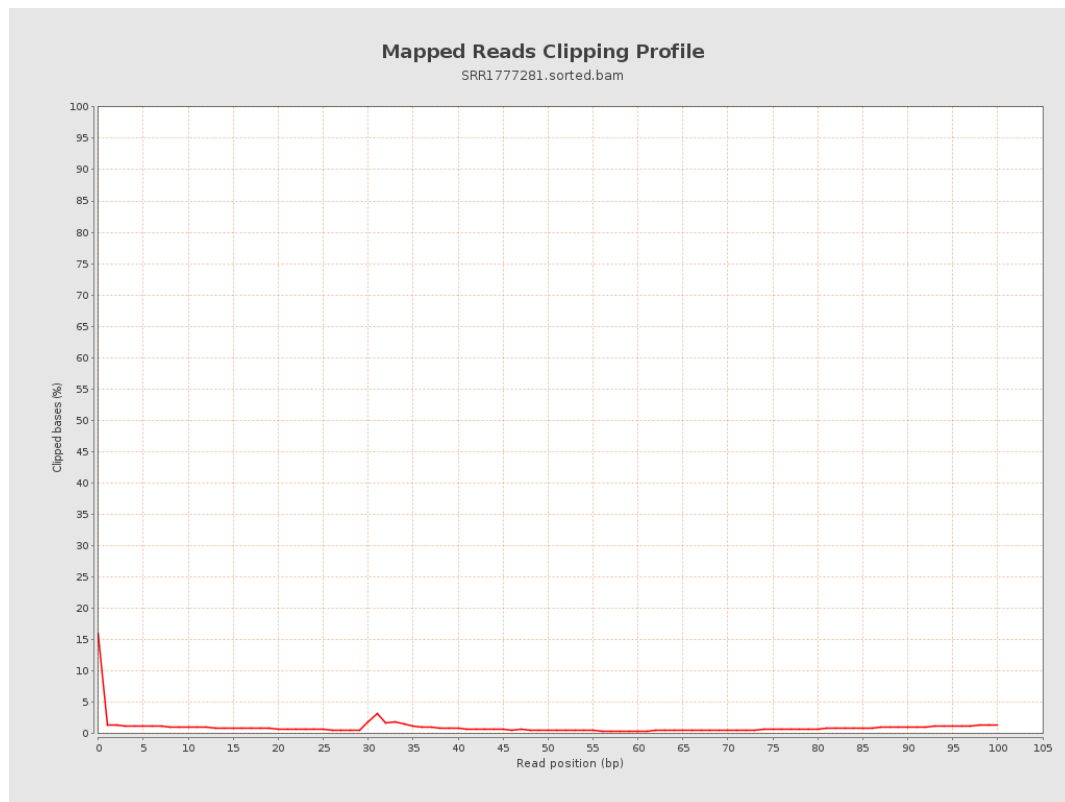
8. Results : Mapped Reads Nucleotide Content



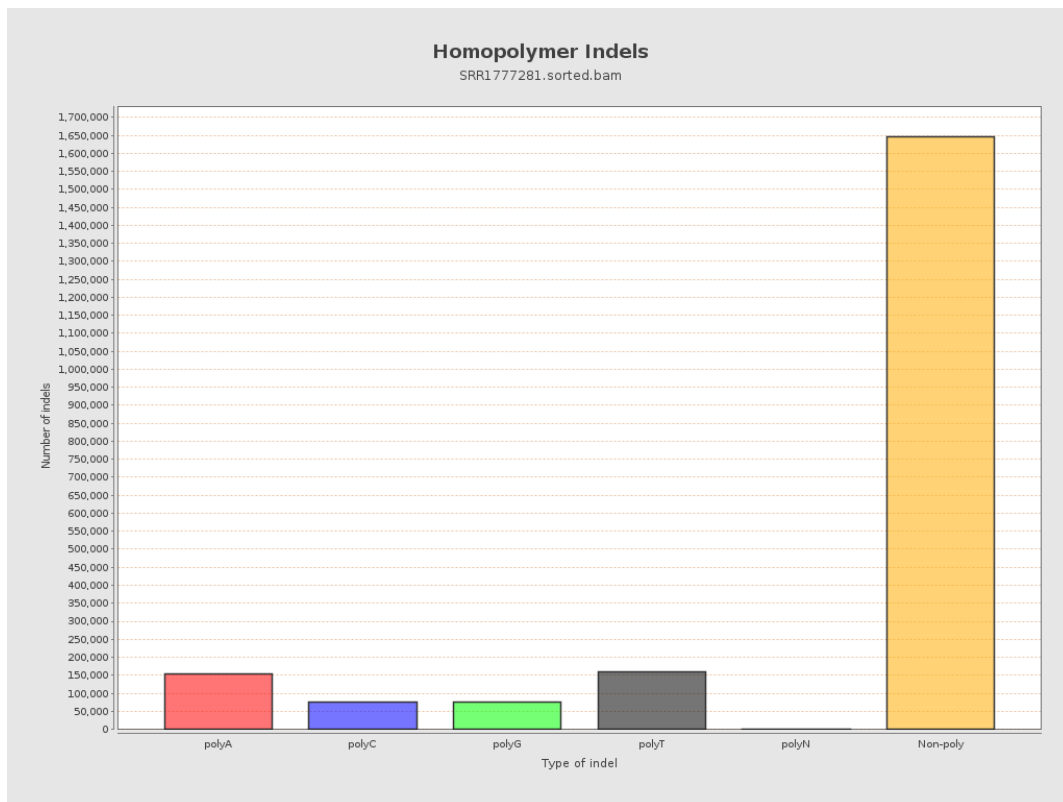
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



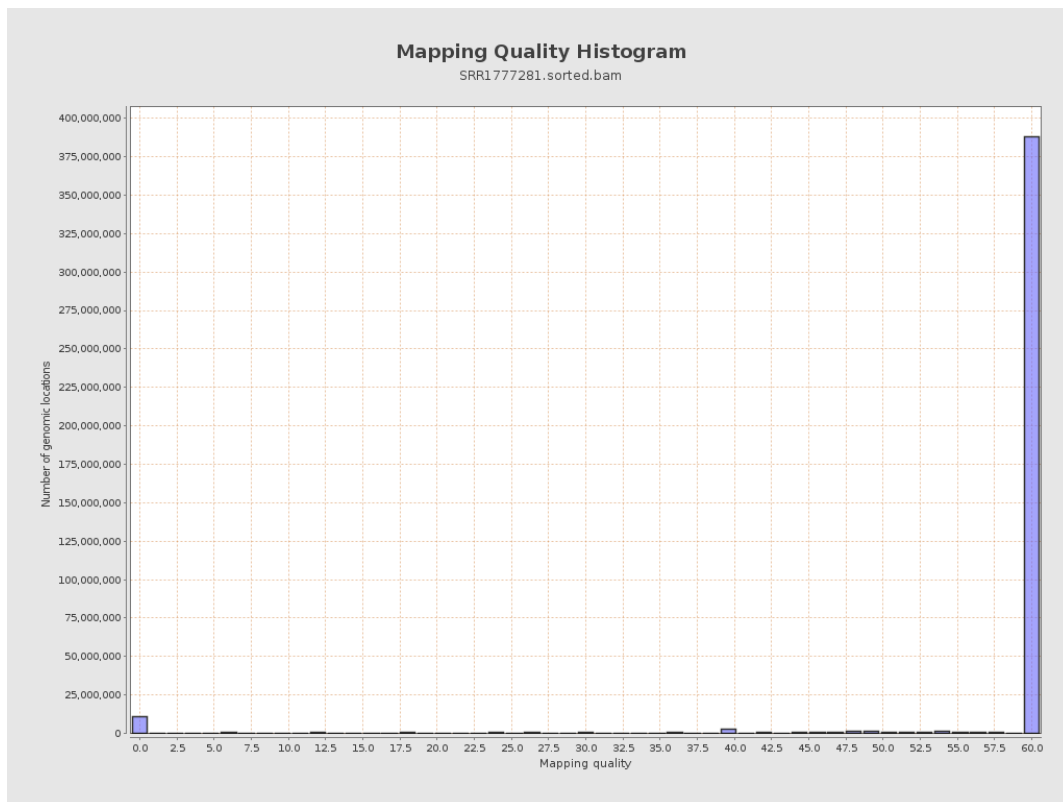
11. Results : Homopolymer Indels



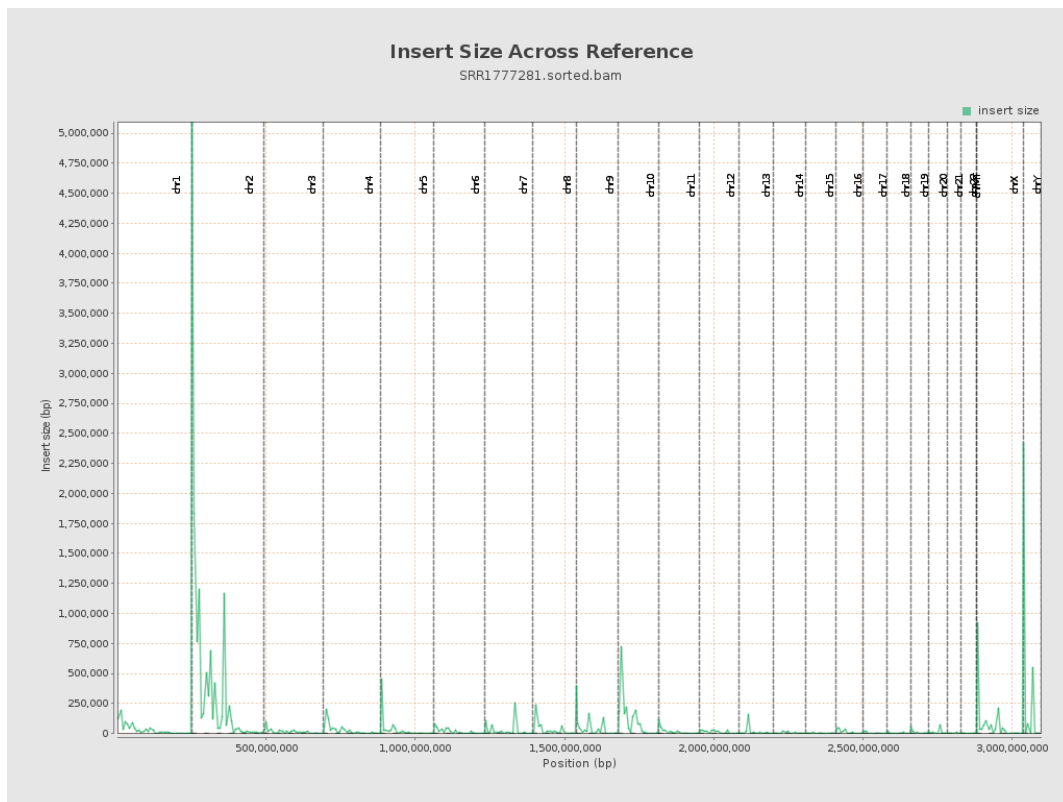
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

