

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 20:44:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777273.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_SRR1777273 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777273_1.fastq.gz SRR1777273_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 20:44:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777273.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	49,563,790
Mapped reads	49,396,956 / 99.66%
Unmapped reads	166,834 / 0.34%
Mapped paired reads	49,396,956 / 99.66%
Mapped reads, first in pair	24,699,705 / 49.83%
Mapped reads, second in pair	24,697,251 / 49.83%
Mapped reads, both in pair	49,338,710 / 99.55%
Mapped reads, singletons	58,246 / 0.12%
Secondary alignments	0
Supplementary alignments	1,576,556 / 3.18%
Read min/max/mean length	30 / 101 / 102.3
Duplicated reads (estimated)	20,866,442 / 42.1%
Duplication rate	35.44%
Clipped reads	5,743,909 / 11.59%

2.2. ACGT Content

Number/percentage of A's	1,384,382,587 / 27.94%
Number/percentage of C's	1,094,538,301 / 22.09%
Number/percentage of T's	1,375,820,590 / 27.76%
Number/percentage of G's	1,100,611,388 / 22.21%
Number/percentage of N's	185,511 / 0%

GC Percentage	44.3%
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2.3. Coverage

Mean	1.601
Standard Deviation	13.7134

2.4. Mapping Quality

Mean Mapping Quality	54.69
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2.5. Insert size

Mean	438,066.62
Standard Deviation	6,524,493.95
P25/Median/P75	184 / 232 / 291

2.6. Mismatches and indels

General error rate	0.25%
Mismatches	11,413,947
Insertions	843,276
Mapped reads with at least one insertion	1.68%
Deletions	333,431
Mapped reads with at least one deletion	0.67%
Homopolymer indels	52.3%

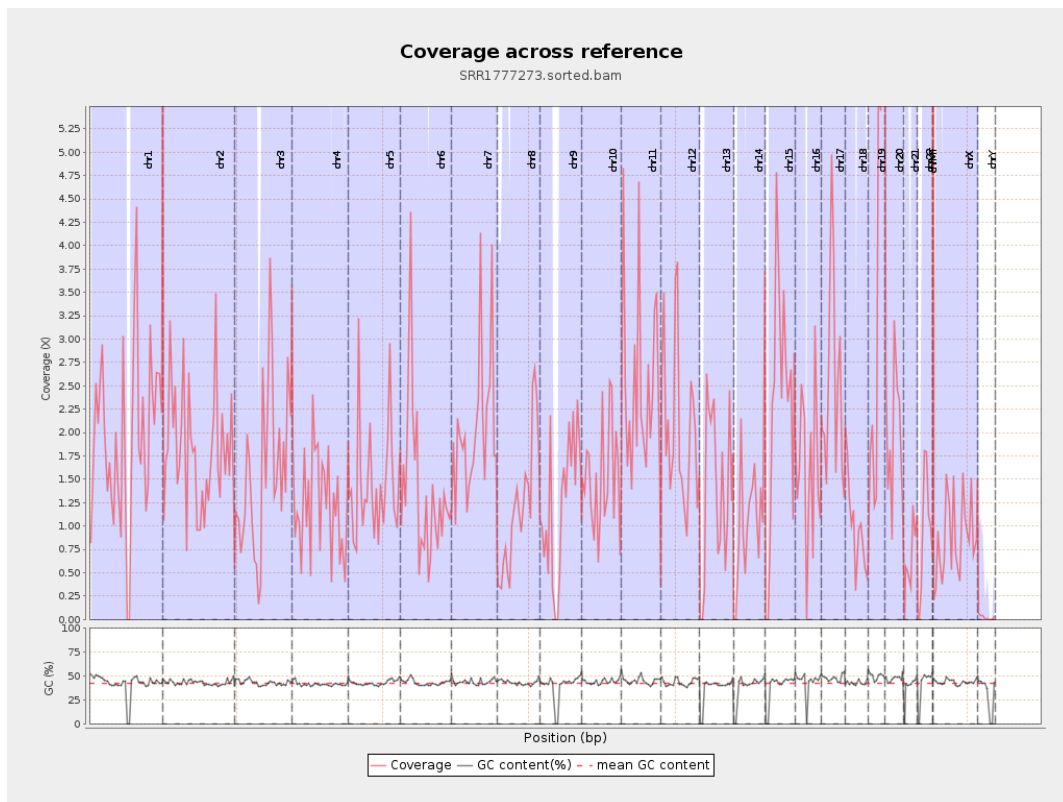
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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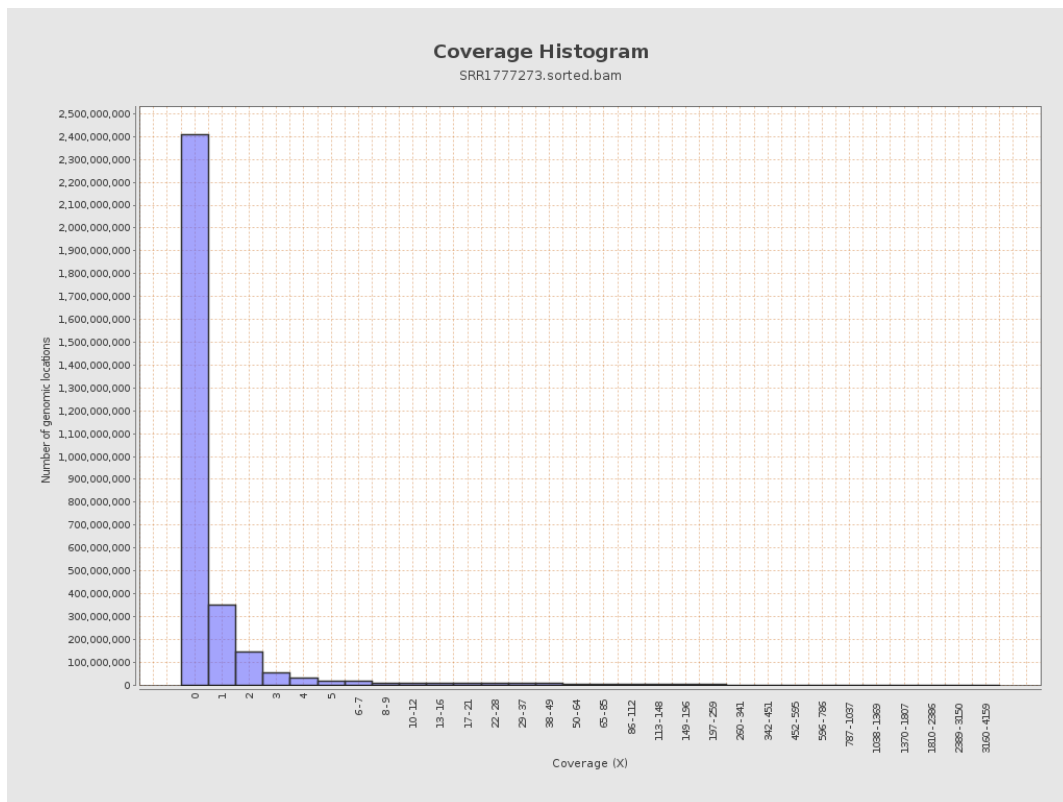
		bases	coverage	deviation
chr1	249250621	492845102	1.9773	15.8249
chr2	243199373	443047478	1.8217	14.3936
chr3	198022430	308837393	1.5596	13.5188
chr4	191154276	234405615	1.2263	11.3301
chr5	180915260	263784801	1.4581	12.2173
chr6	171115067	233389626	1.3639	11.9684
chr7	159138663	323739218	2.0343	16.6846
chr8	146364022	178571635	1.2201	12.0392
chr9	141213431	171220019	1.2125	11.223
chr10	135534747	207347494	1.5298	12.442
chr11	135006516	337975340	2.5034	19.0022
chr12	133851895	279408263	2.0874	15.9216
chr13	115169878	157331629	1.3661	13.7654
chr14	107349540	111241898	1.0363	9.4931
chr15	102531392	229436658	2.2377	17.546
chr16	90354753	142380043	1.5758	12.4822
chr17	81195210	204200792	2.5149	16.8917
chr18	78077248	78566610	1.0063	9.341
chr19	59128983	214672947	3.6306	22.0091
chr20	63025520	124757749	1.9795	14.658
chr21	48129895	32779967	0.6811	8.128
chr22	51304566	48130103	0.9381	8.869
chrMT	16571	1658322	100.0737	28.8894
chrX	155270560	135197807	0.8707	8.9425

chrY	59373566	1340344	0.0226	0.6168
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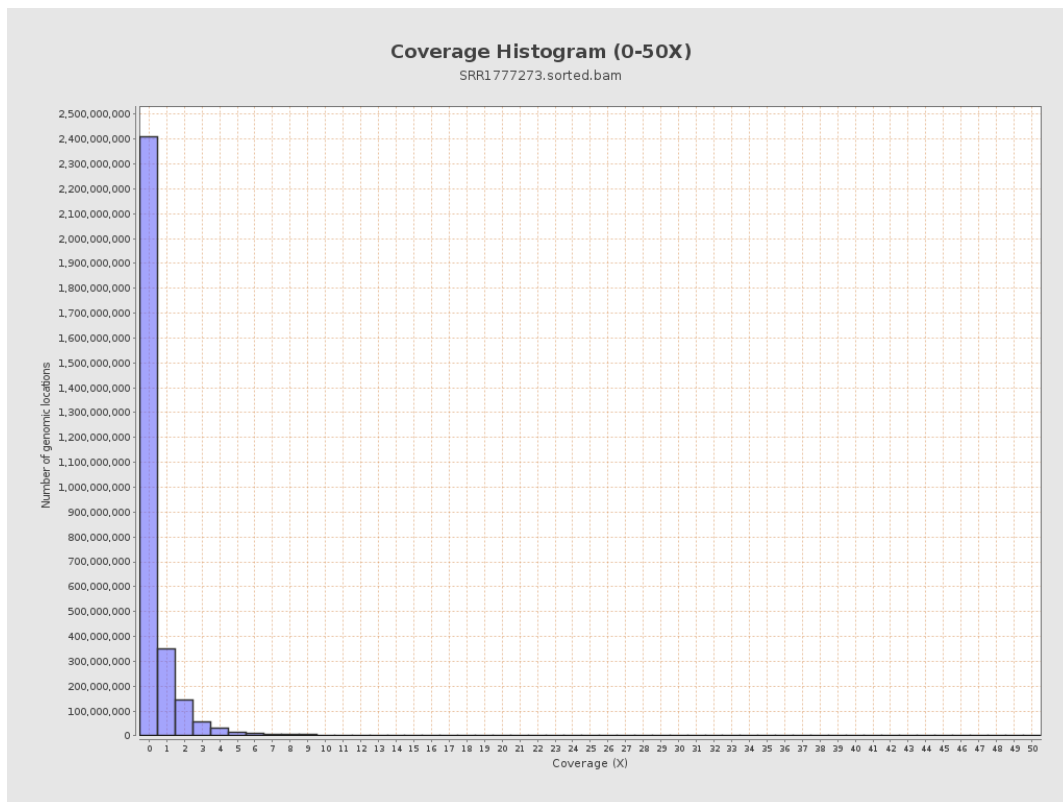
3. Results : Coverage across reference



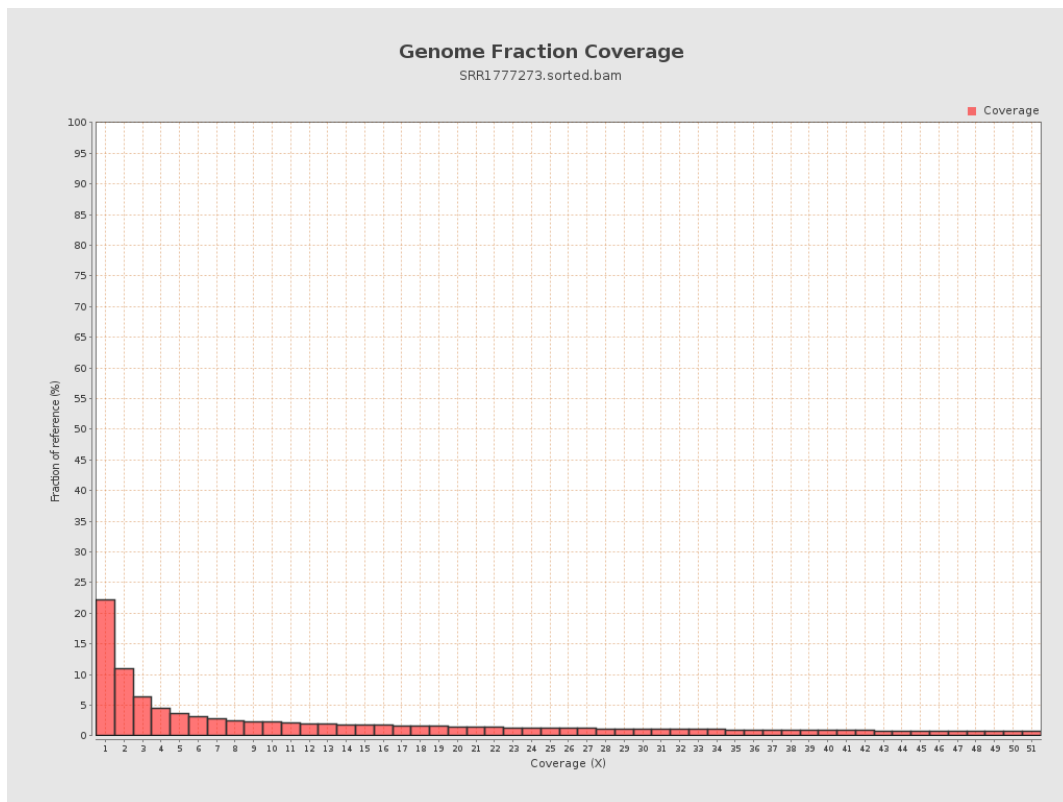
4. Results : Coverage Histogram



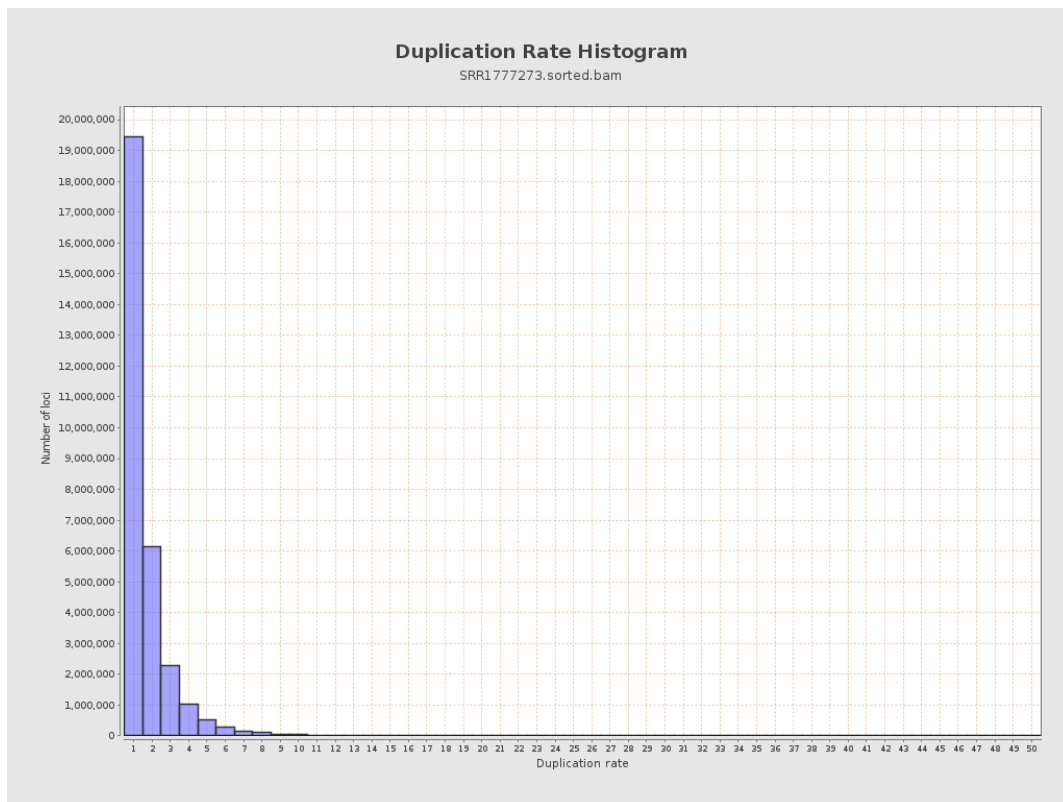
5. Results : Coverage Histogram (0-50X)



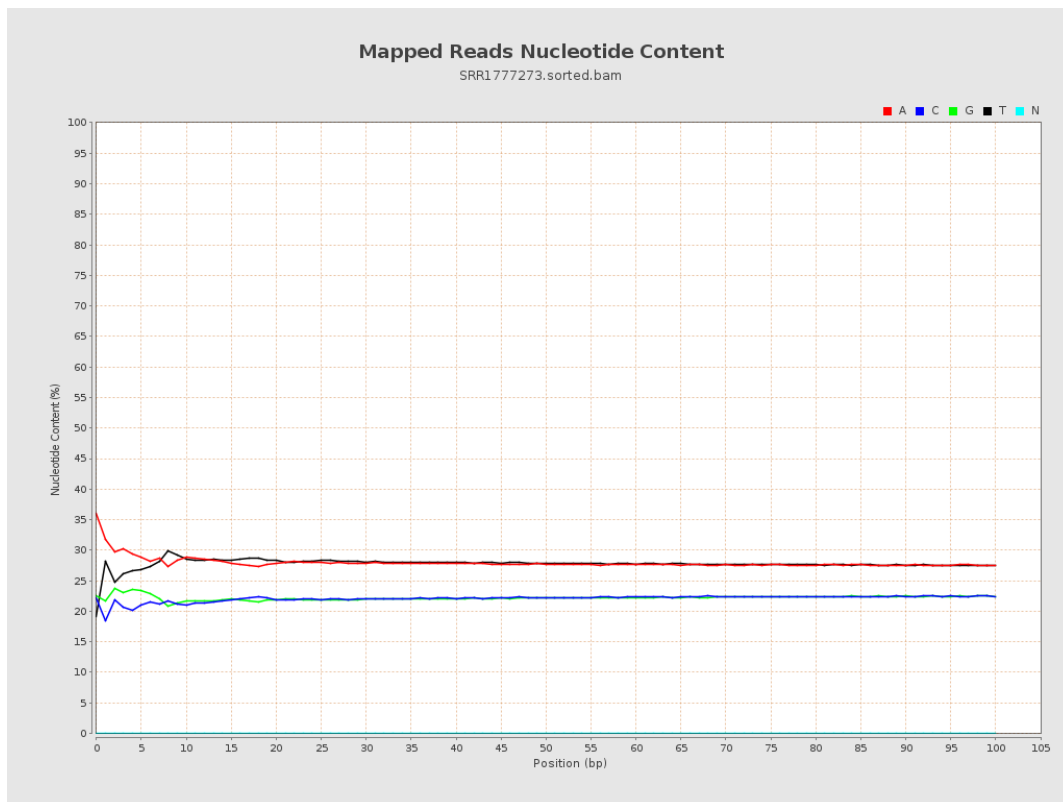
6. Results : Genome Fraction Coverage



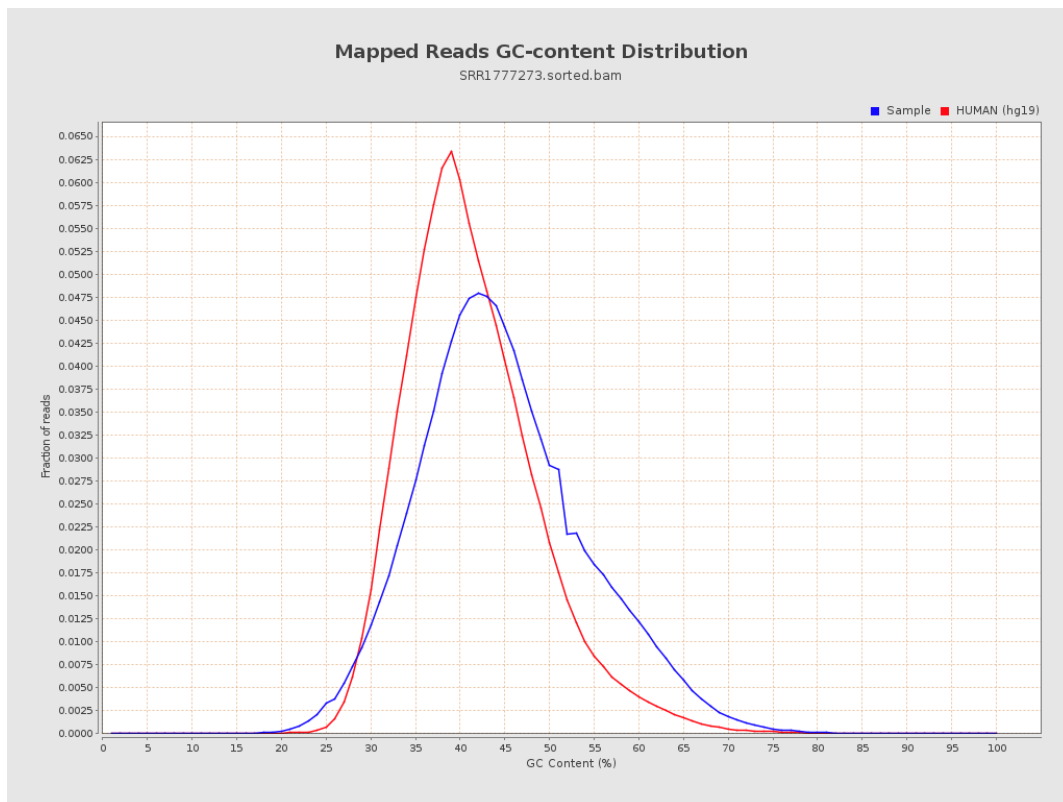
7. Results : Duplication Rate Histogram



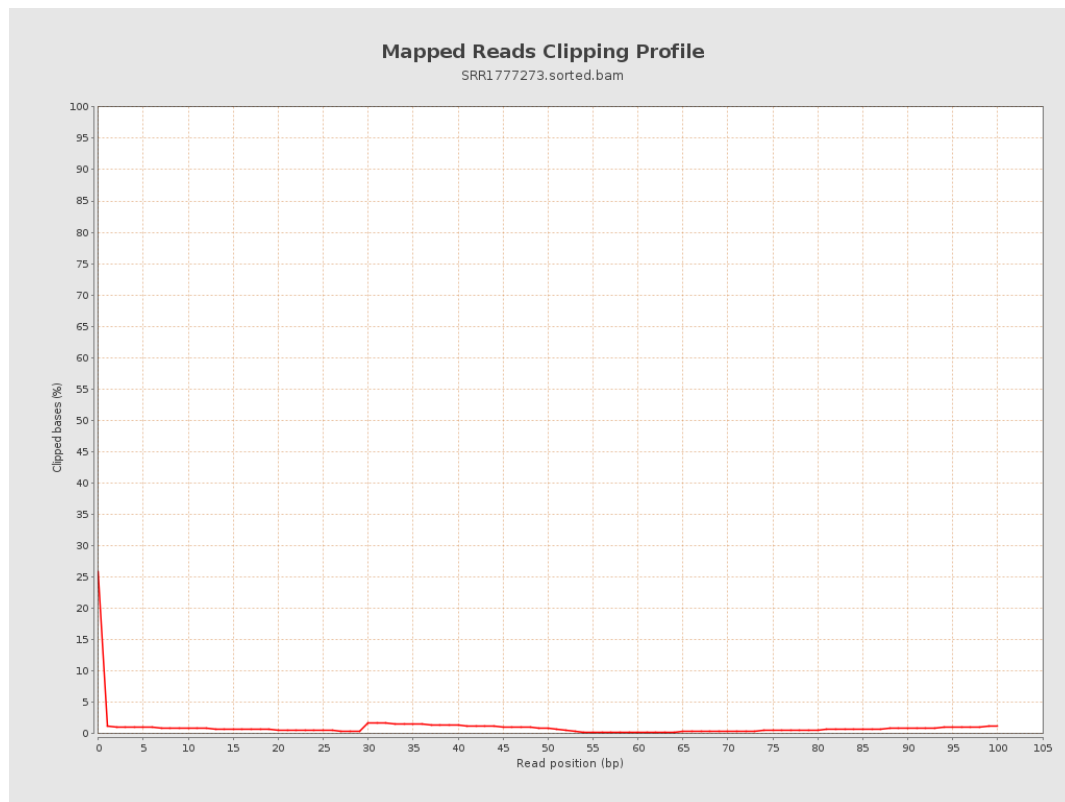
8. Results : Mapped Reads Nucleotide Content



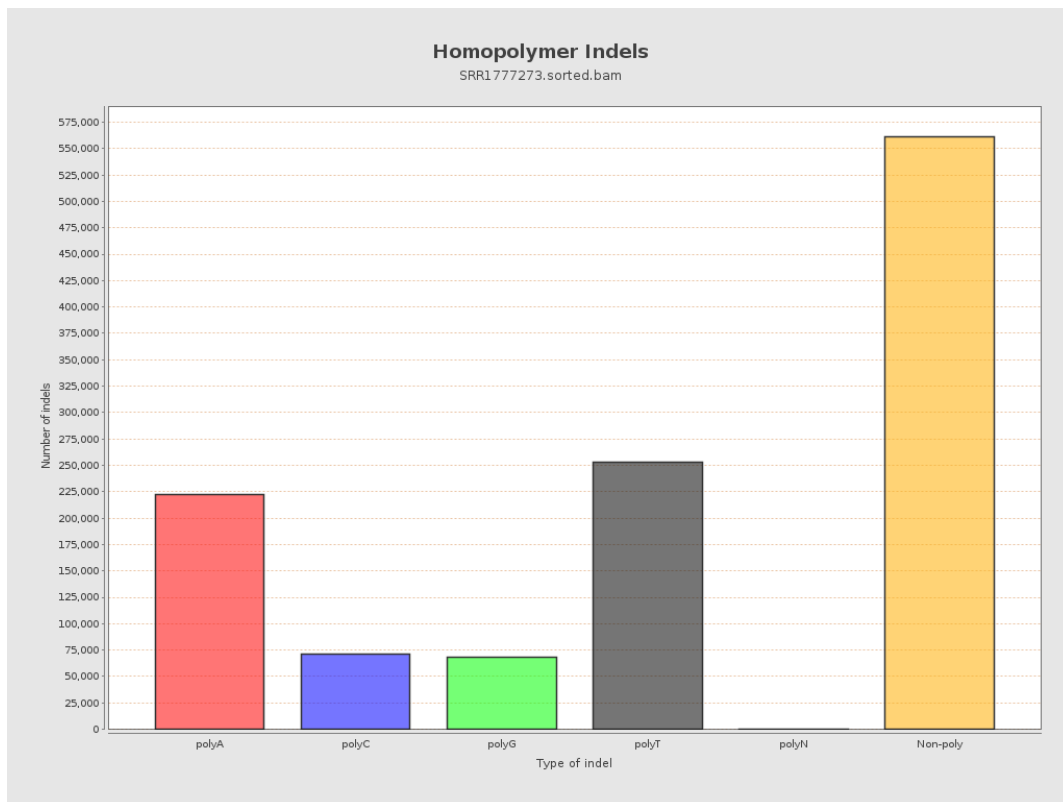
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



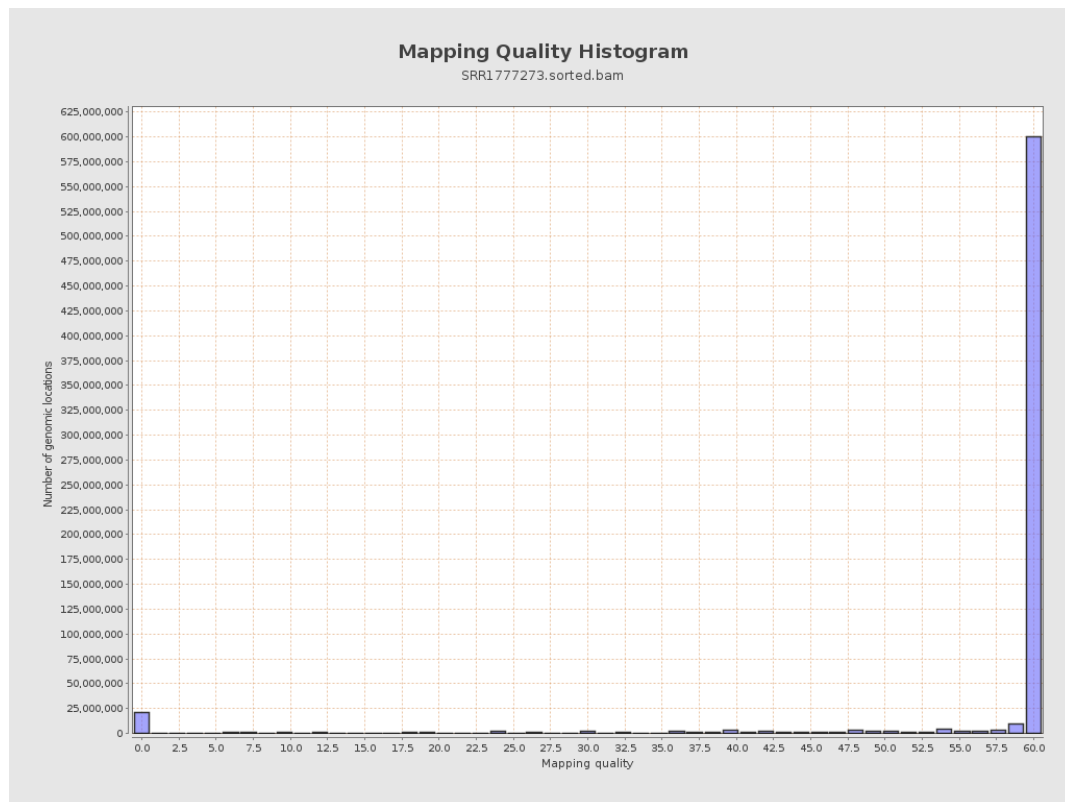
11. Results : Homopolymer Indels



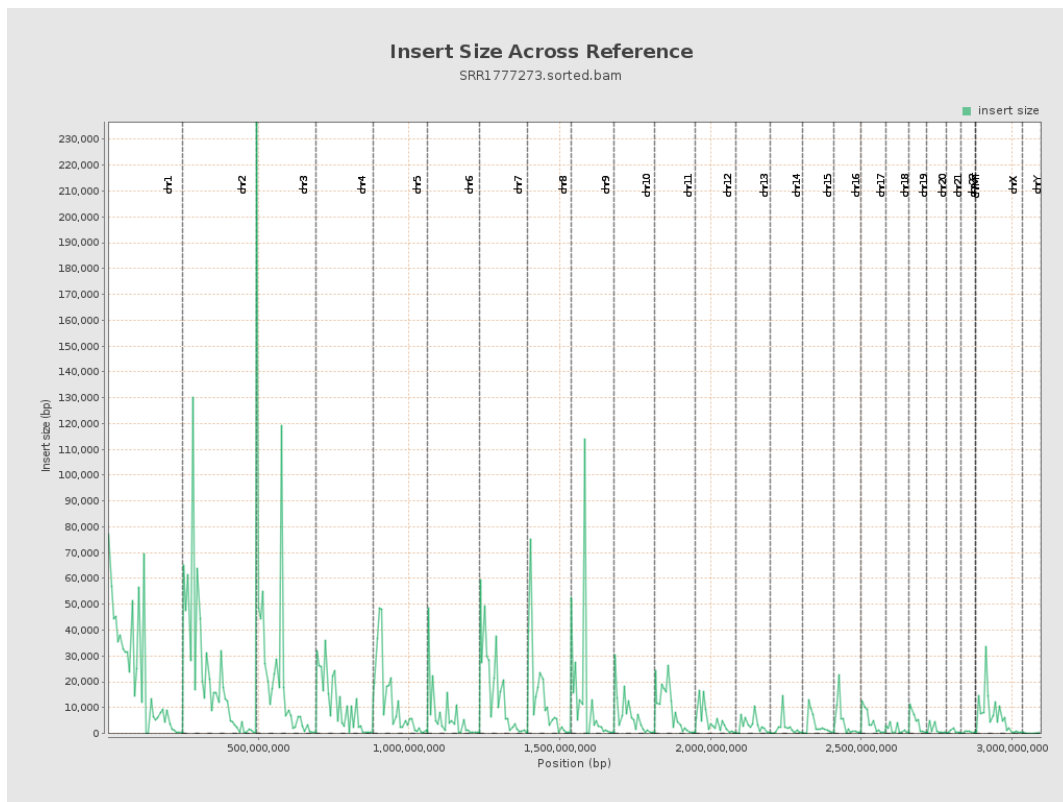
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

