

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 00:58:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777244.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_SRR1777244 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777244_1.fastq.gz SRR1777244_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 00:58:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777244.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	49,368,012
Mapped reads	49,144,711 / 99.55%
Unmapped reads	223,301 / 0.45%
Mapped paired reads	49,144,711 / 99.55%
Mapped reads, first in pair	24,571,227 / 49.77%
Mapped reads, second in pair	24,573,484 / 49.78%
Mapped reads, both in pair	49,078,168 / 99.41%
Mapped reads, singletons	66,543 / 0.13%
Secondary alignments	0
Supplementary alignments	672,757 / 1.36%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	21,530,294 / 43.61%
Duplication rate	41.5%
Clipped reads	3,149,864 / 6.38%

2.2. ACGT Content

Number/percentage of A's	1,241,244,774 / 25.16%
Number/percentage of C's	1,218,315,981 / 24.7%
Number/percentage of T's	1,229,831,562 / 24.93%
Number/percentage of G's	1,243,836,387 / 25.21%
Number/percentage of N's	60,526 / 0%

GC Percentage	49.91%
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2.3. Coverage

Mean	1.5938
Standard Deviation	10.7673

2.4. Mapping Quality

Mean Mapping Quality	54.33
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2.5. Insert size

Mean	674,390.04
Standard Deviation	8,288,431.93
P25/Median/P75	189 / 237 / 293

2.6. Mismatches and indels

General error rate	0.22%
Mismatches	10,074,384
Insertions	231,166
Mapped reads with at least one insertion	0.46%
Deletions	307,216
Mapped reads with at least one deletion	0.61%
Homopolymer indels	44.59%

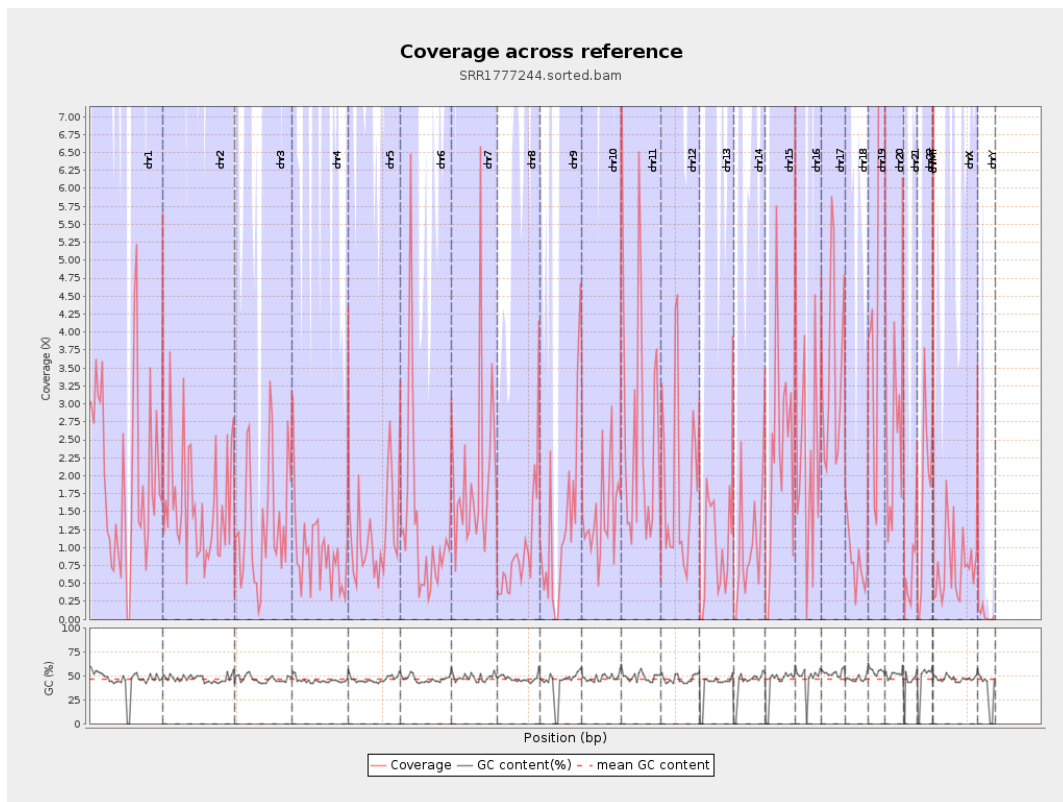
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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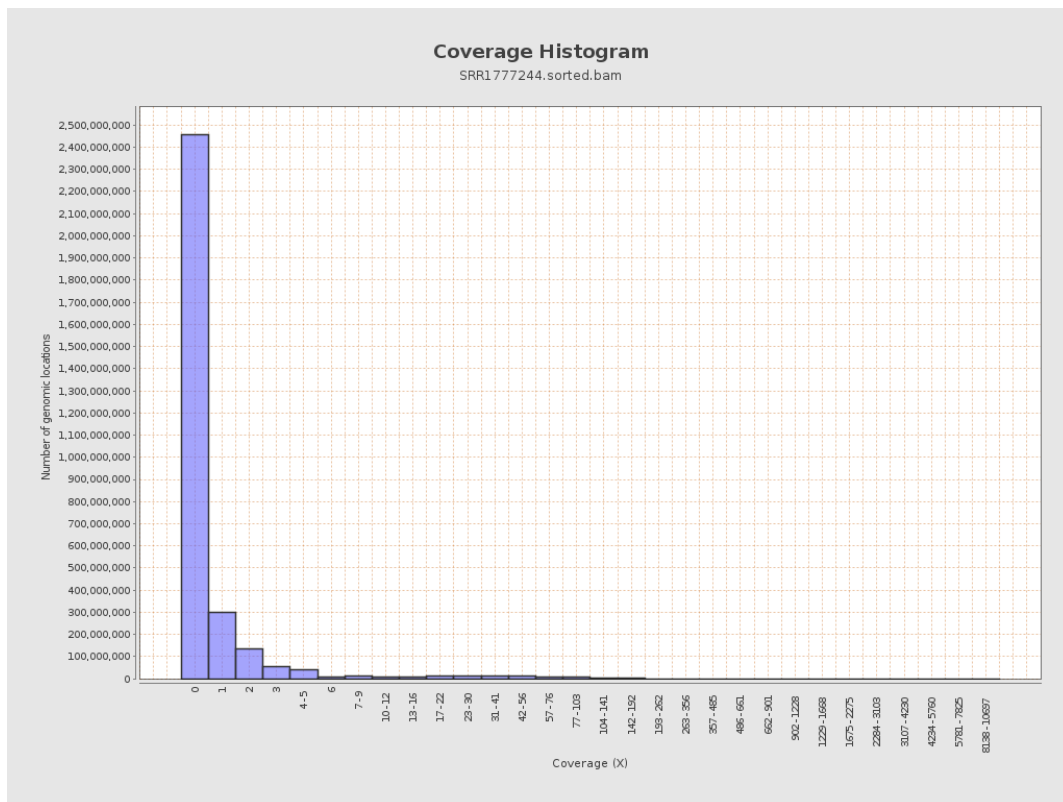
		bases	coverage	deviation
chr1	249250621	490724231	1.9688	12.4328
chr2	243199373	385836196	1.5865	10.1385
chr3	198022430	263225772	1.3293	8.9414
chr4	191154276	175275750	0.9169	6.8886
chr5	180915260	224690779	1.242	8.3174
chr6	171115067	213663282	1.2487	8.8684
chr7	159138663	317139551	1.9929	15.4065
chr8	146364022	148174283	1.0124	7.7819
chr9	141213431	183909968	1.3024	9.0452
chr10	135534747	199282483	1.4703	9.6379
chr11	135006516	356108963	2.6377	16.2121
chr12	133851895	258902191	1.9342	10.8602
chr13	115169878	117123971	1.017	8.4156
chr14	107349540	106447385	0.9916	6.5174
chr15	102531392	227692759	2.2207	13.7899
chr16	90354753	209623728	2.32	12.1866
chr17	81195210	274667725	3.3828	15.8689
chr18	78077248	63918521	0.8187	6.3034
chr19	59128983	307357381	5.1981	20.2821
chr20	63025520	159553041	2.5316	13.8901
chr21	48129895	36296531	0.7541	8.762
chr22	51304566	89184756	1.7383	10.1645
chrMT	16571	1133871	68.425	23.8183
chrX	155270560	120546722	0.7764	5.8747

chrY	59373566	3539577	0.0596	2.3921
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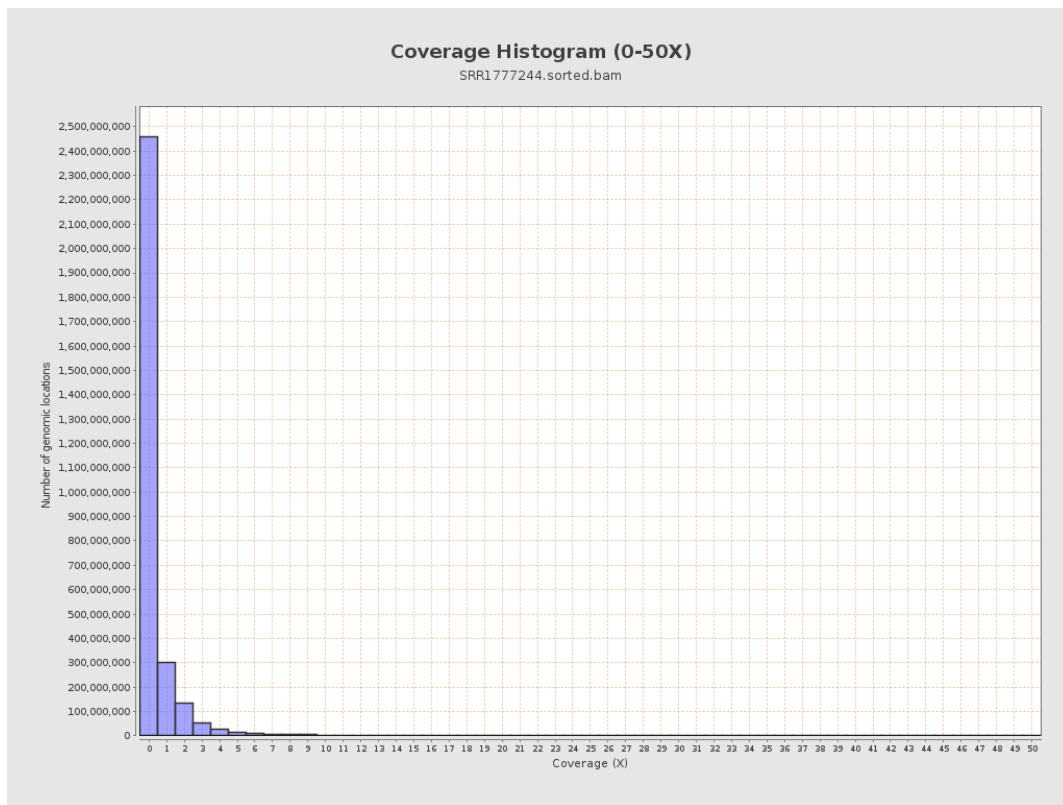
3. Results : Coverage across reference



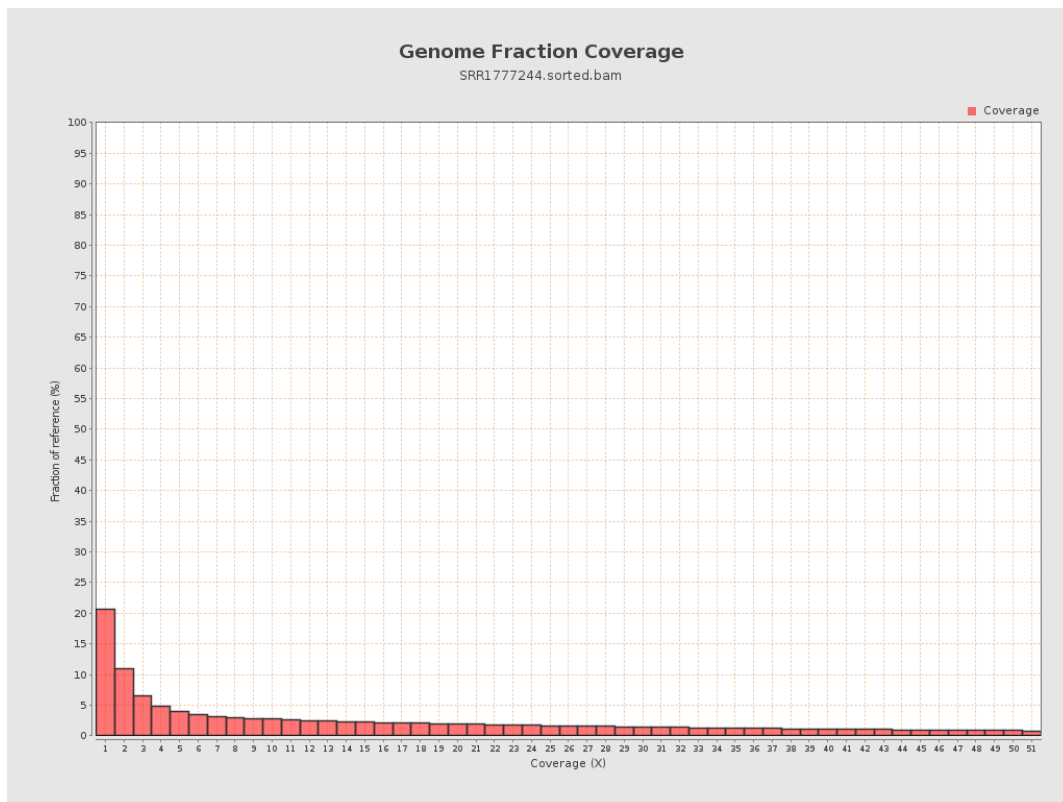
4. Results : Coverage Histogram



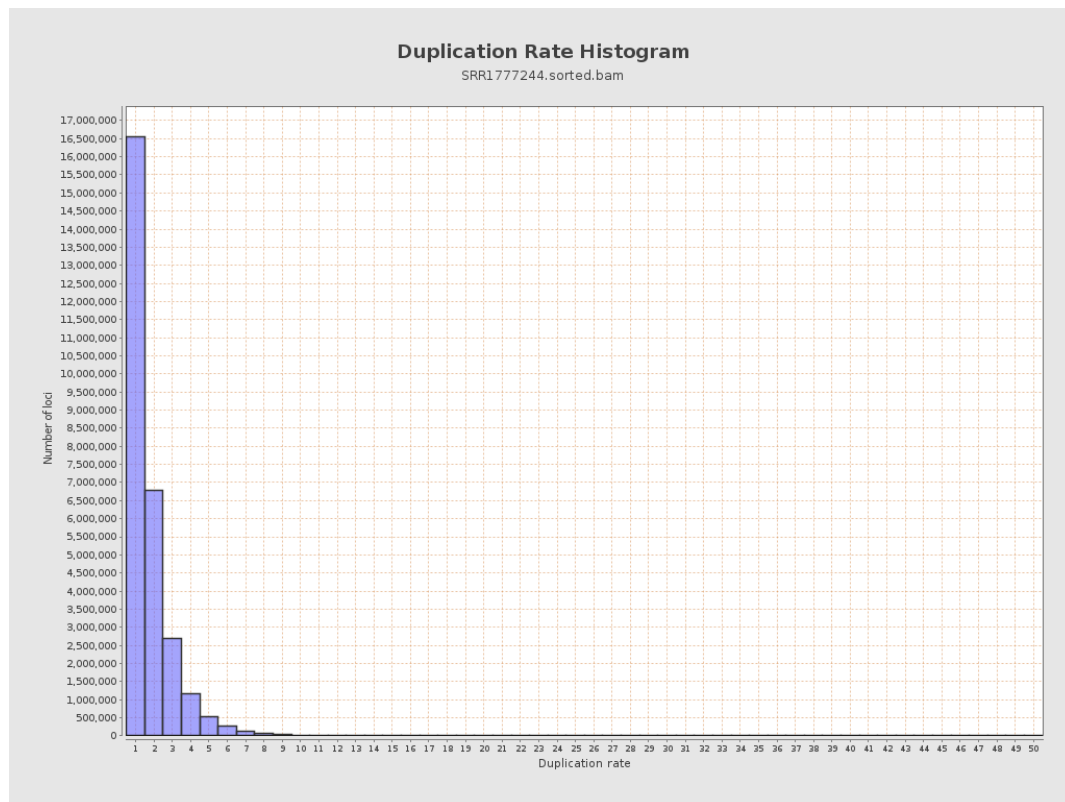
5. Results : Coverage Histogram (0-50X)



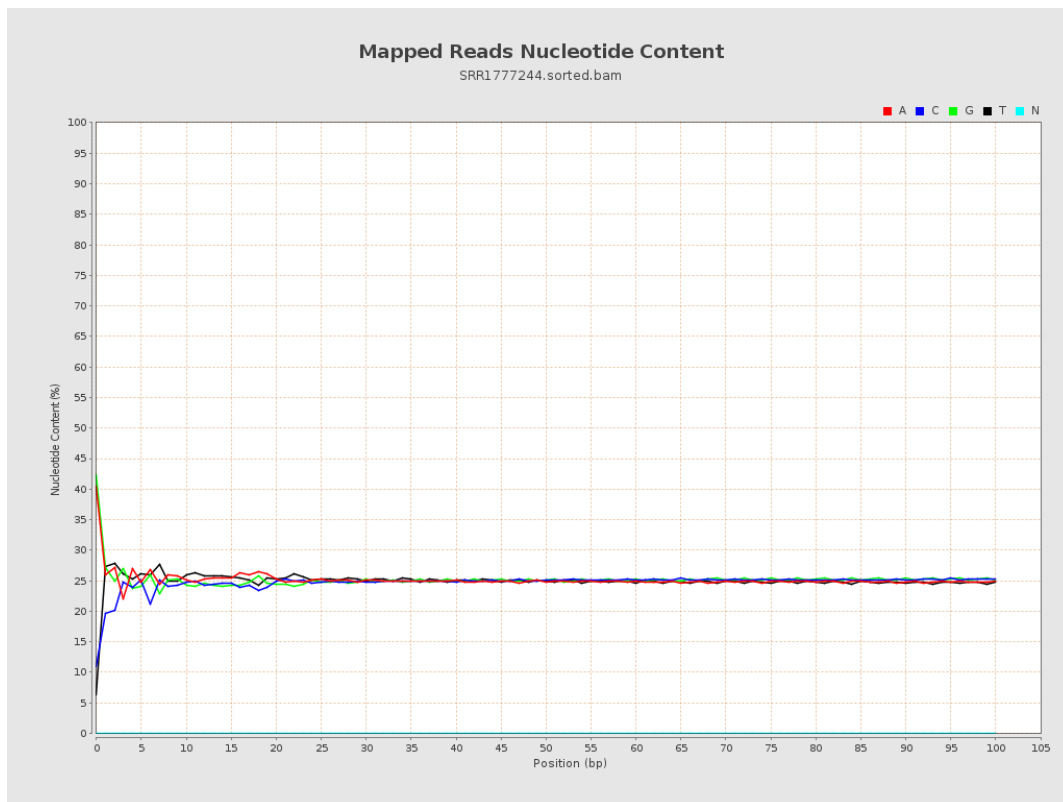
6. Results : Genome Fraction Coverage



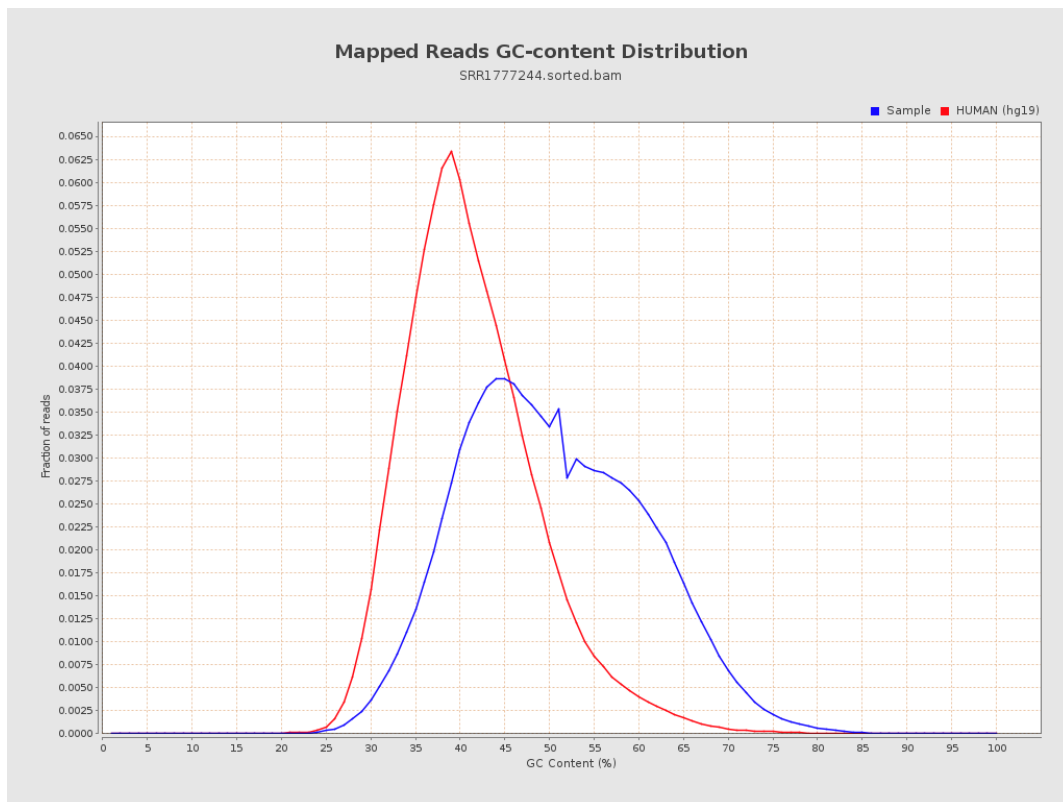
7. Results : Duplication Rate Histogram



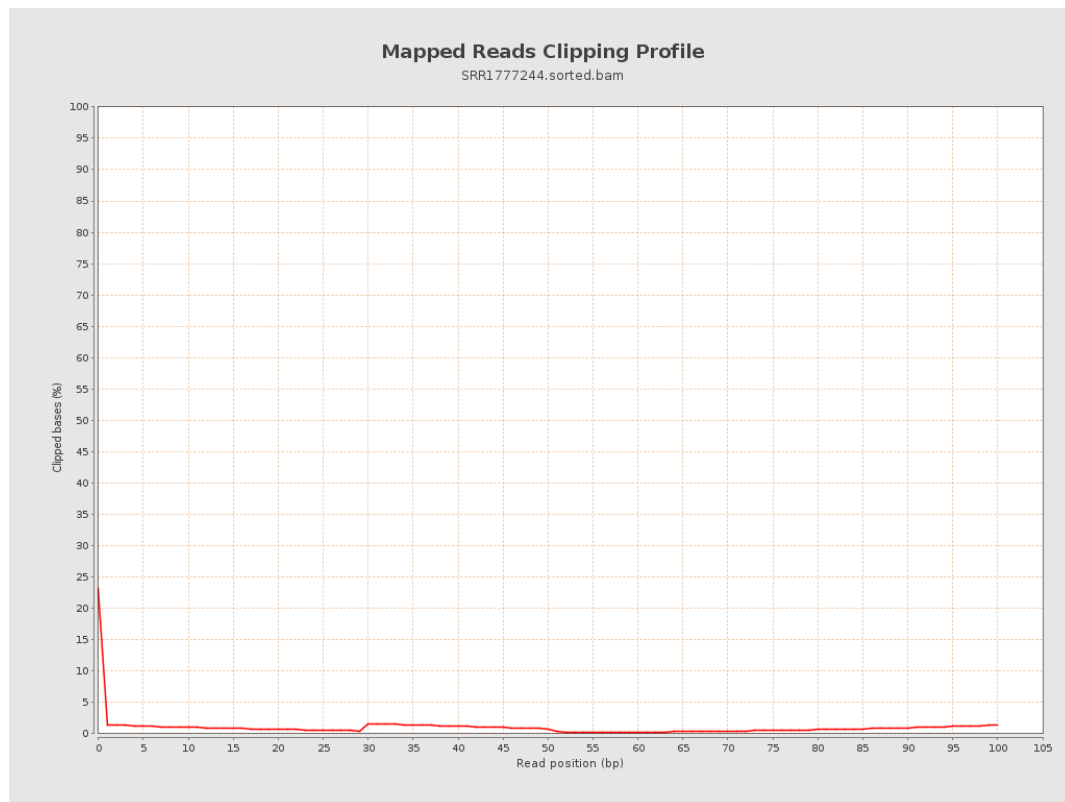
8. Results : Mapped Reads Nucleotide Content



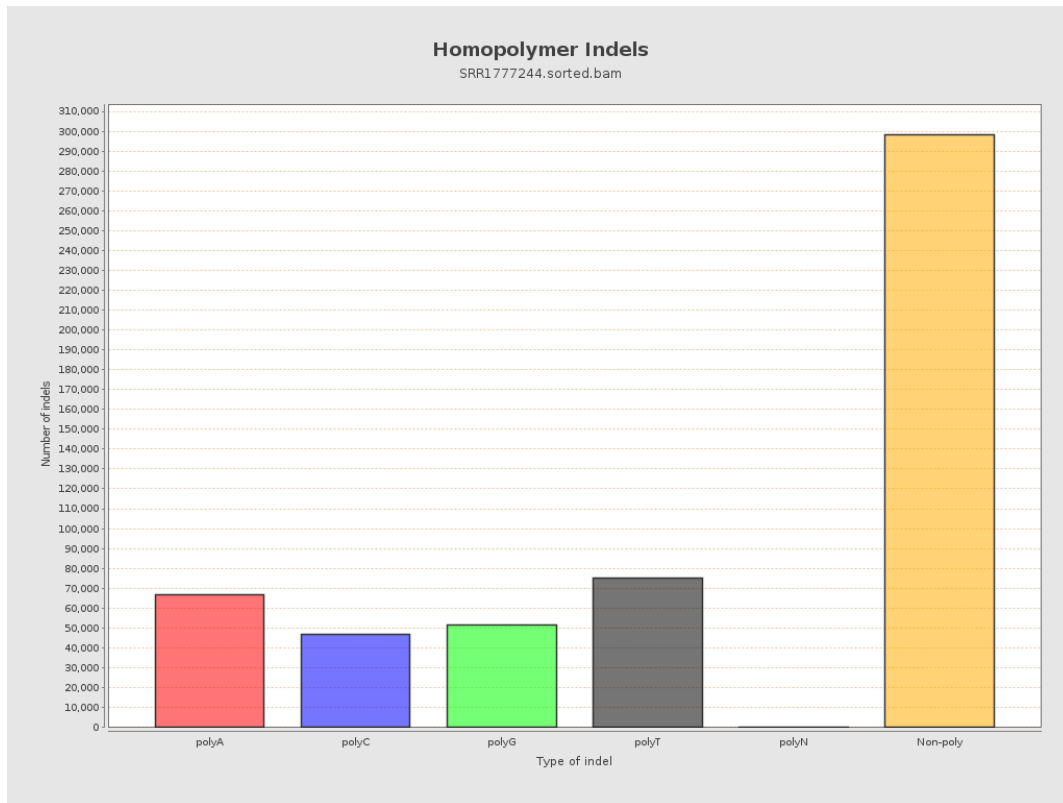
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



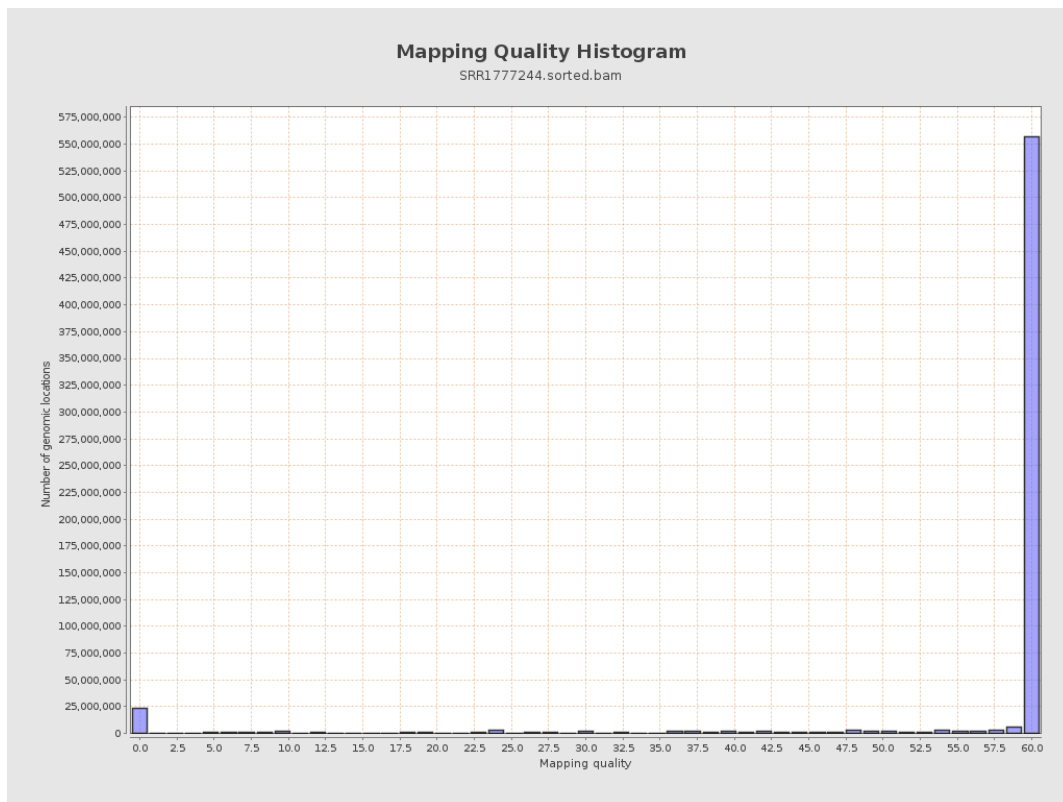
11. Results : Homopolymer Indels



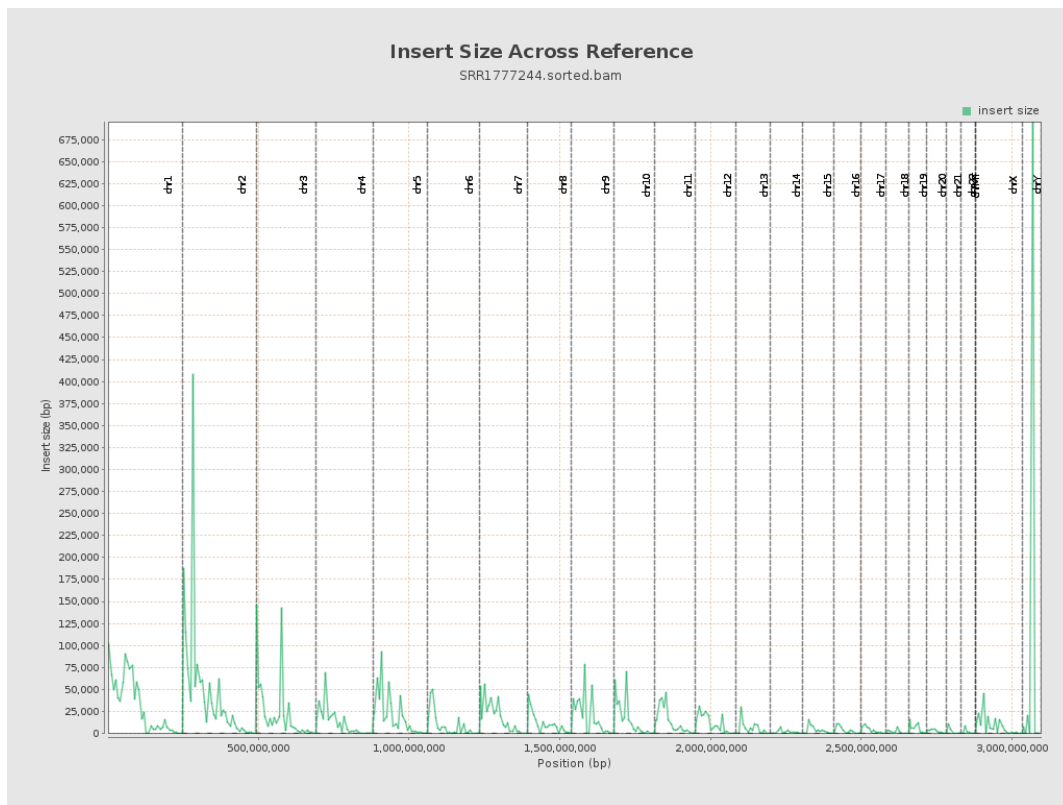
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

