

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 16:06:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173977.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_SRR10173977 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173977_1.fastq.gz SRR10173977_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 16:06:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173977.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,248,898
Mapped reads	5,139,055 / 97.91%
Unmapped reads	109,843 / 2.09%
Mapped paired reads	5,139,055 / 97.91%
Mapped reads, first in pair	2,571,801 / 49%
Mapped reads, second in pair	2,567,254 / 48.91%
Mapped reads, both in pair	5,072,456 / 96.64%
Mapped reads, singletons	66,599 / 1.27%
Secondary alignments	0
Supplementary alignments	626,402 / 11.93%
Read min/max/mean length	30 / 133 / 124.46
Duplicated reads (estimated)	3,879,752 / 73.92%
Duplication rate	62.11%
Clipped reads	2,691,797 / 51.28%

2.2. ACGT Content

Number/percentage of A's	173,372,063 / 30.09%
Number/percentage of C's	113,414,833 / 19.69%
Number/percentage of T's	171,818,974 / 29.82%
Number/percentage of G's	117,520,109 / 20.4%
Number/percentage of N's	4,483 / 0%

GC Percentage	40.08%
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2.3. Coverage

Mean	0.1862
Standard Deviation	3.2951

2.4. Mapping Quality

Mean Mapping Quality	52.7
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2.5. Insert size

Mean	975,078.96
Standard Deviation	8,586,963.38
P25/Median/P75	103 / 151 / 231

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	4,803,993
Insertions	65,844
Mapped reads with at least one insertion	1.23%
Deletions	157,402
Mapped reads with at least one deletion	2.99%
Homopolymer indels	40.91%

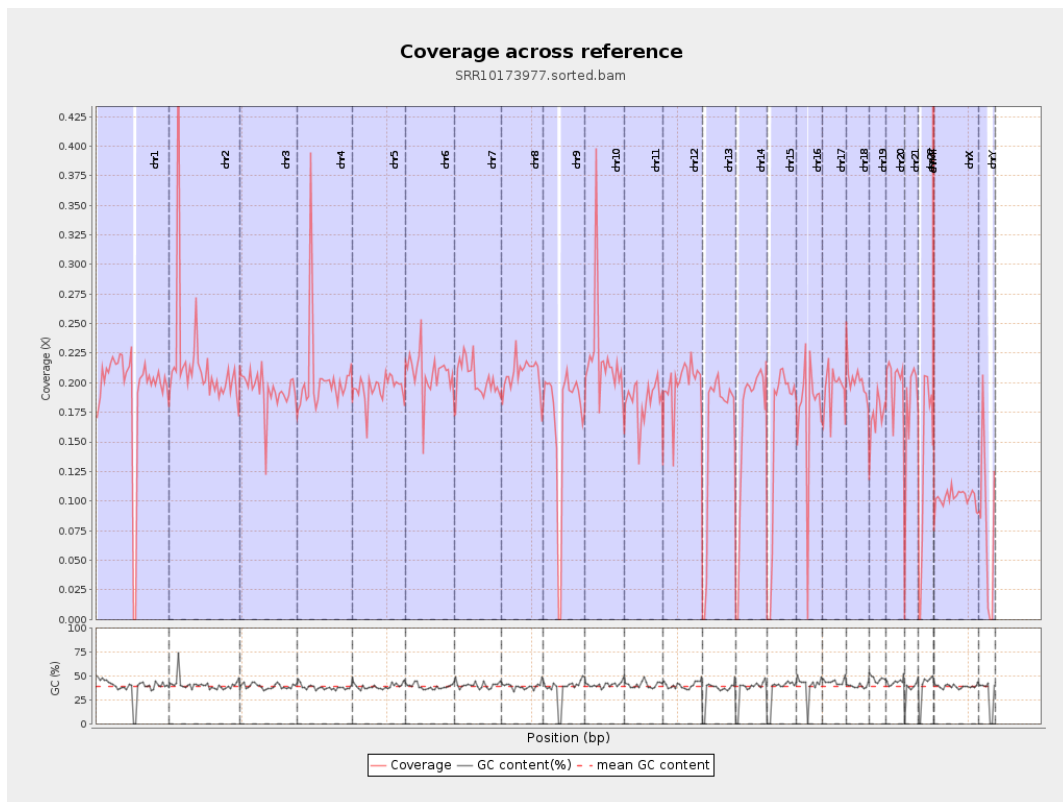
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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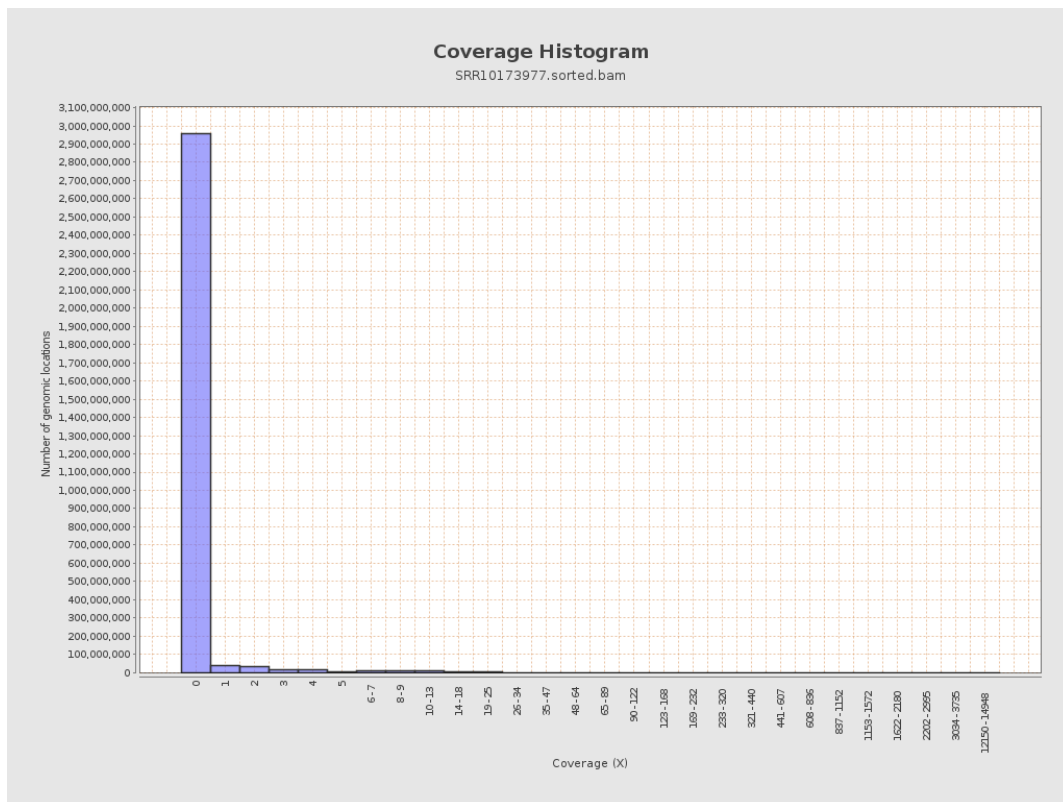
		bases	coverage	deviation
chr1	249250621	48227197	0.1935	1.7721
chr2	243199373	52488312	0.2158	10.4847
chr3	198022430	38385937	0.1938	1.2436
chr4	191154276	38856336	0.2033	1.8656
chr5	180915260	35322865	0.1952	1.2463
chr6	171115067	35540745	0.2077	1.445
chr7	159138663	32464479	0.204	1.6983
chr8	146364022	30264486	0.2068	2.3896
chr9	141213431	23984504	0.1698	1.4655
chr10	135534747	29897639	0.2206	2.1383
chr11	135006516	24977426	0.185	1.2395
chr12	133851895	26749862	0.1998	1.3051
chr13	115169878	18399098	0.1598	1.1259
chr14	107349540	17729525	0.1652	1.1511
chr15	102531392	16303924	0.159	1.15
chr16	90354753	15842929	0.1753	1.3565
chr17	81195210	15679619	0.1931	1.3069
chr18	78077248	15729317	0.2015	1.9899
chr19	59128983	10227020	0.173	1.3557
chr20	63025520	12679782	0.2012	1.3739
chr21	48129895	8385613	0.1742	1.559
chr22	51304566	6895958	0.1344	1.2621
chrMT	16571	1024702	61.8371	53.6447
chrX	155270560	15948812	0.1027	0.9002

chrY	59373566	4496375	0.0757	1.4629
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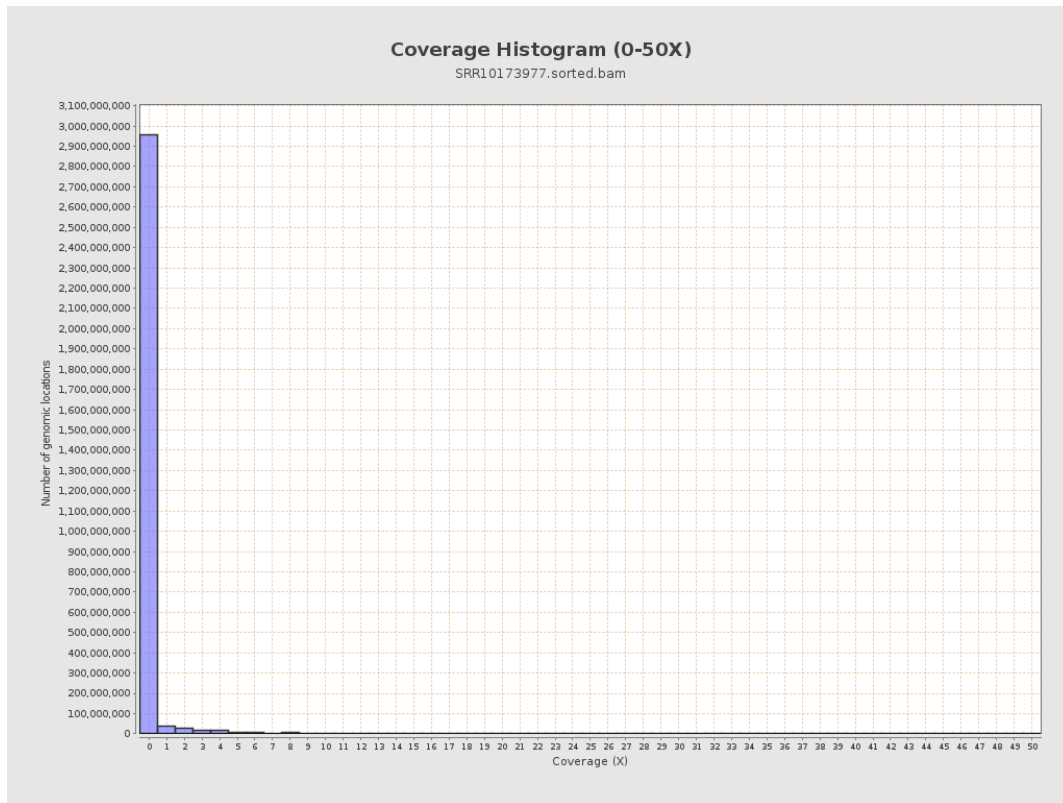
3. Results : Coverage across reference



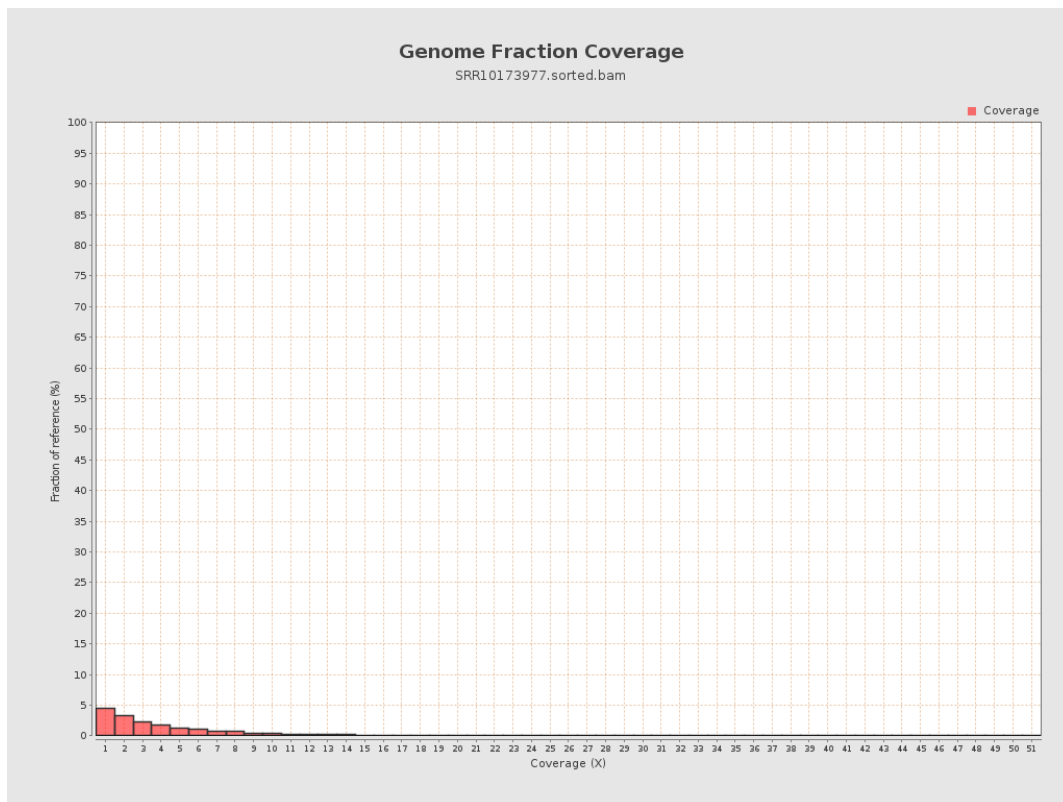
4. Results : Coverage Histogram



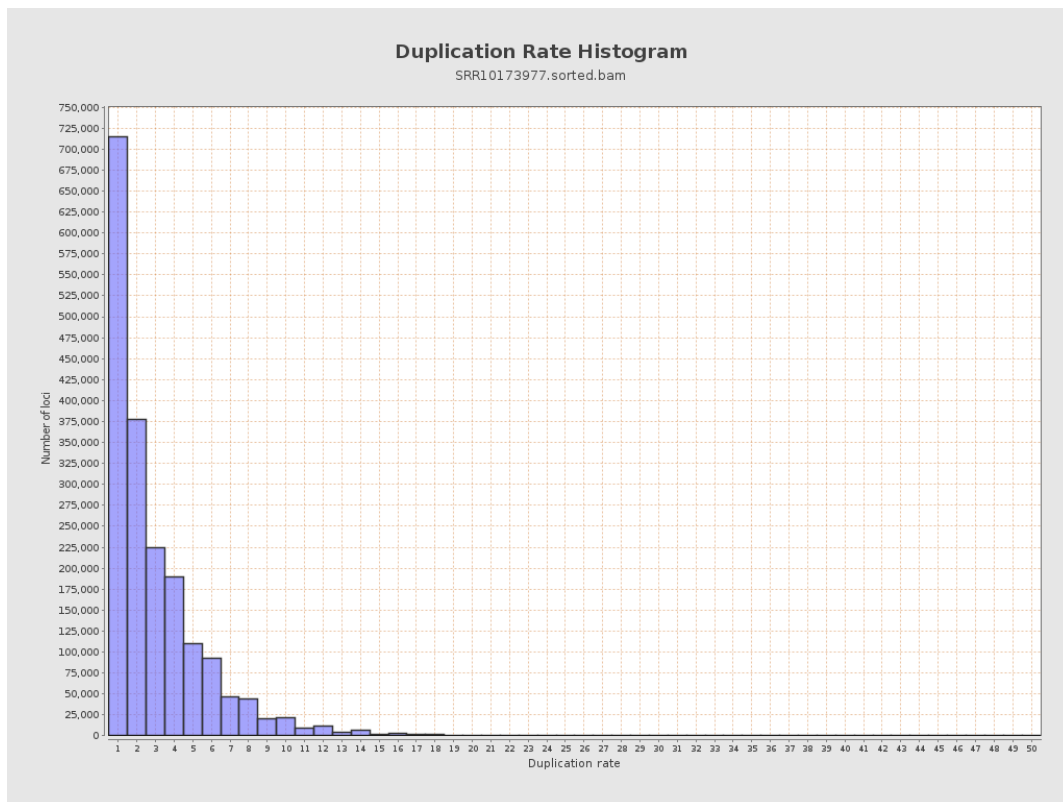
5. Results : Coverage Histogram (0-50X)



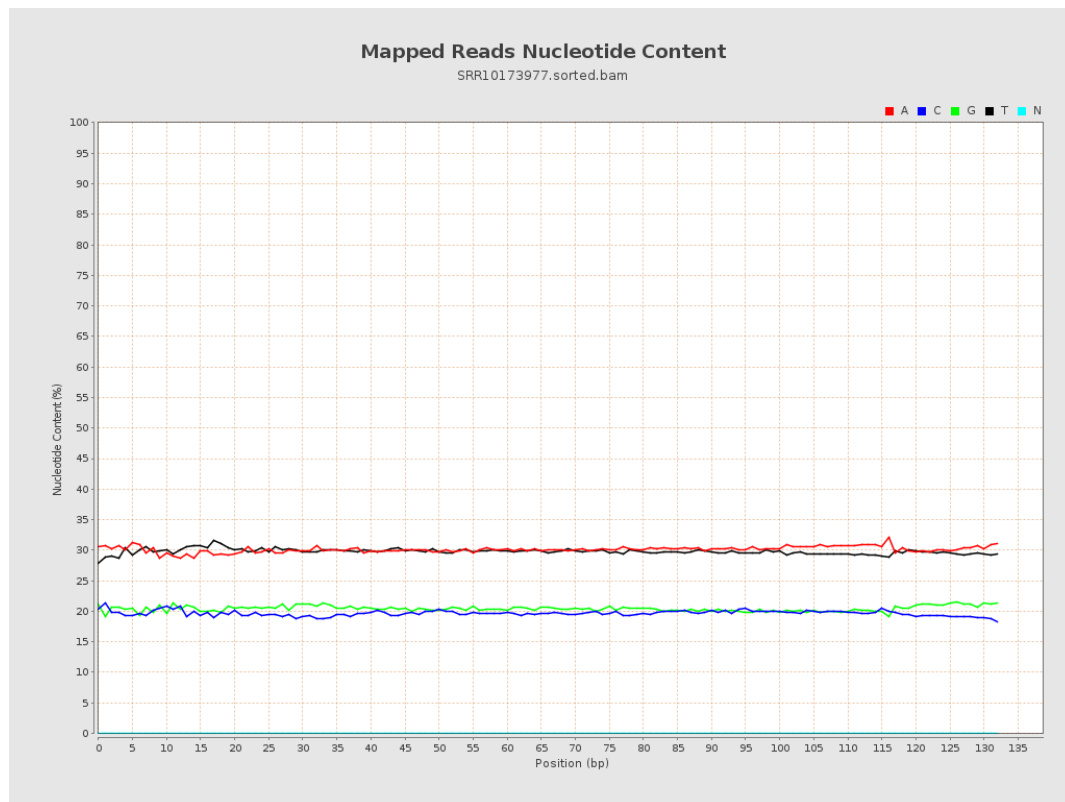
6. Results : Genome Fraction Coverage



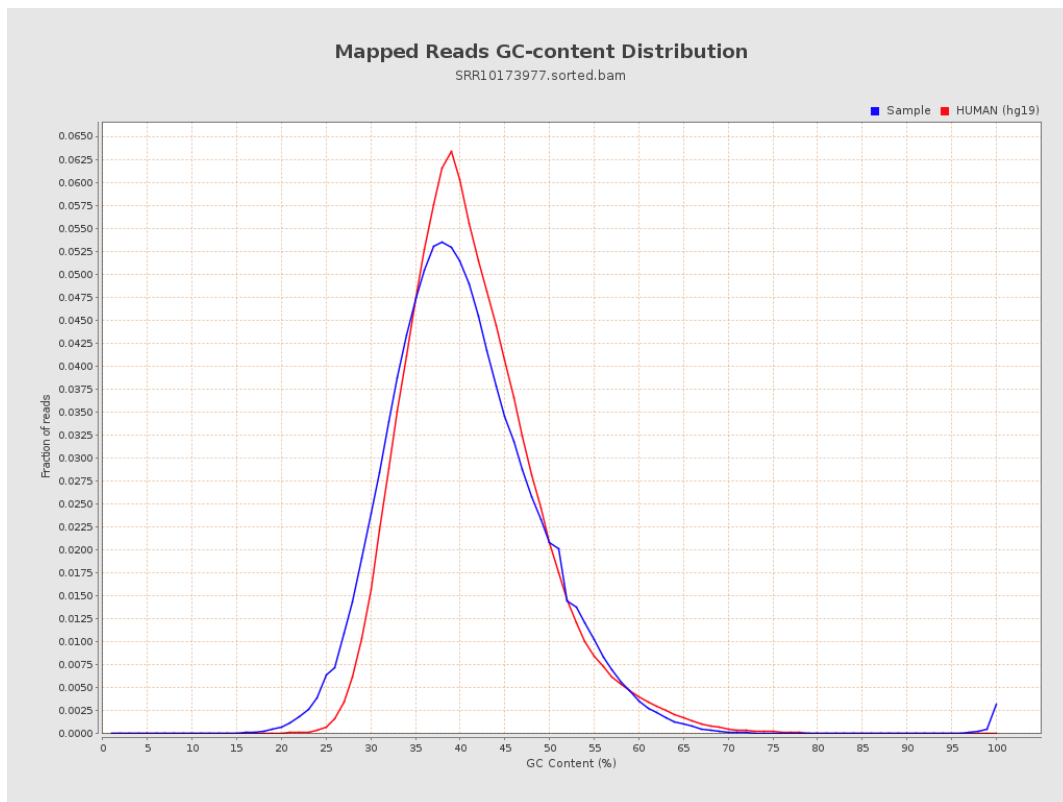
7. Results : Duplication Rate Histogram



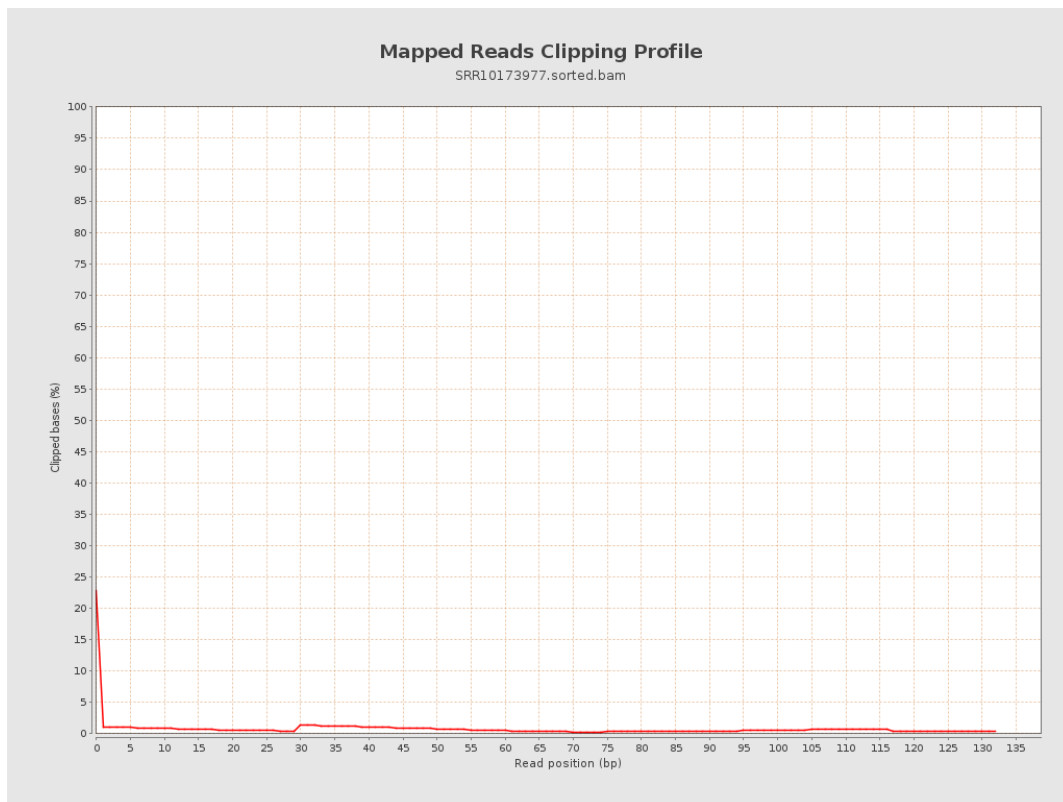
8. Results : Mapped Reads Nucleotide Content



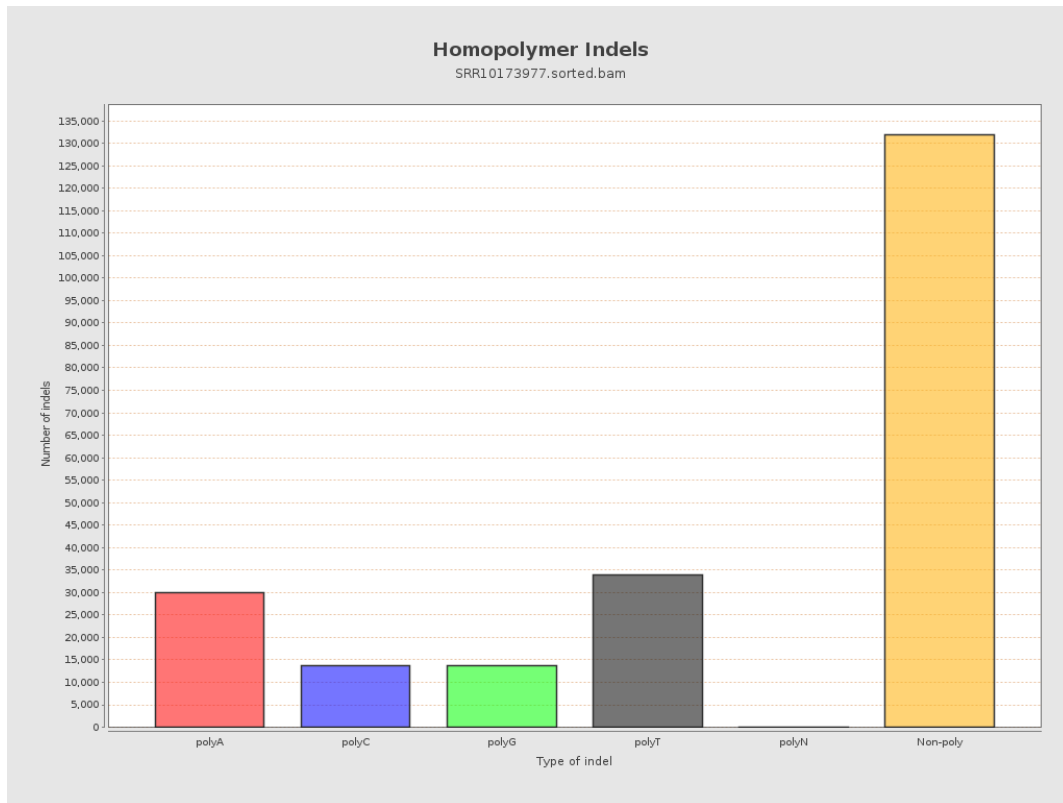
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



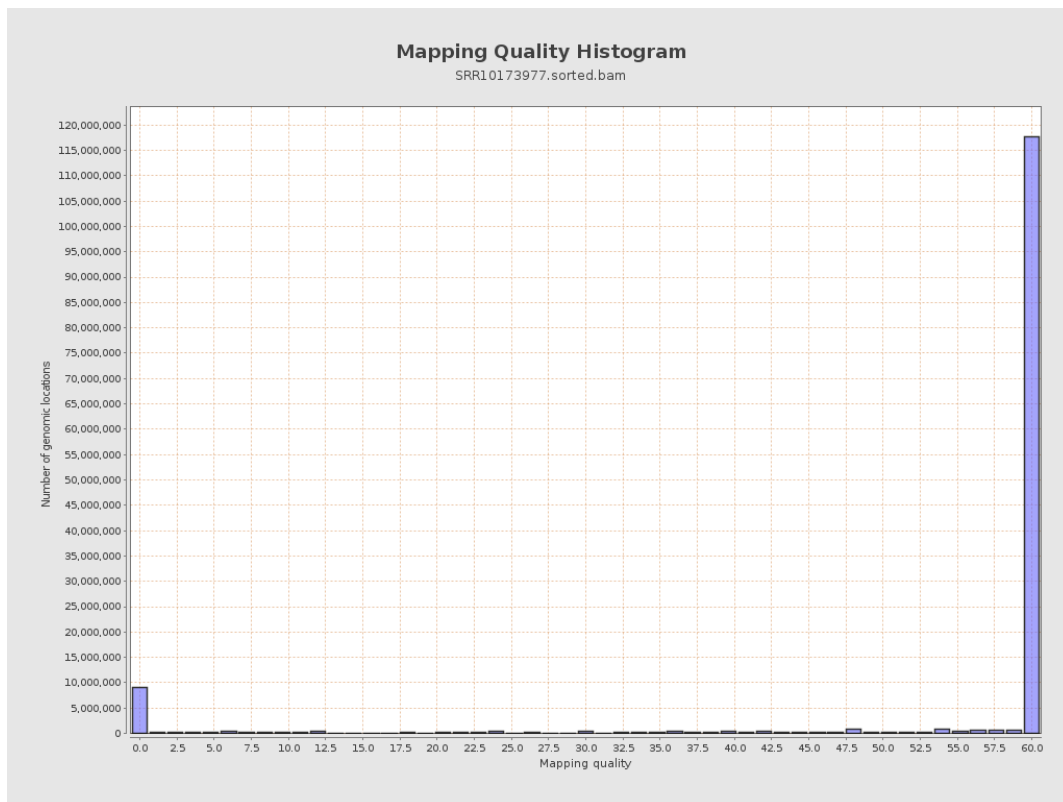
11. Results : Homopolymer Indels



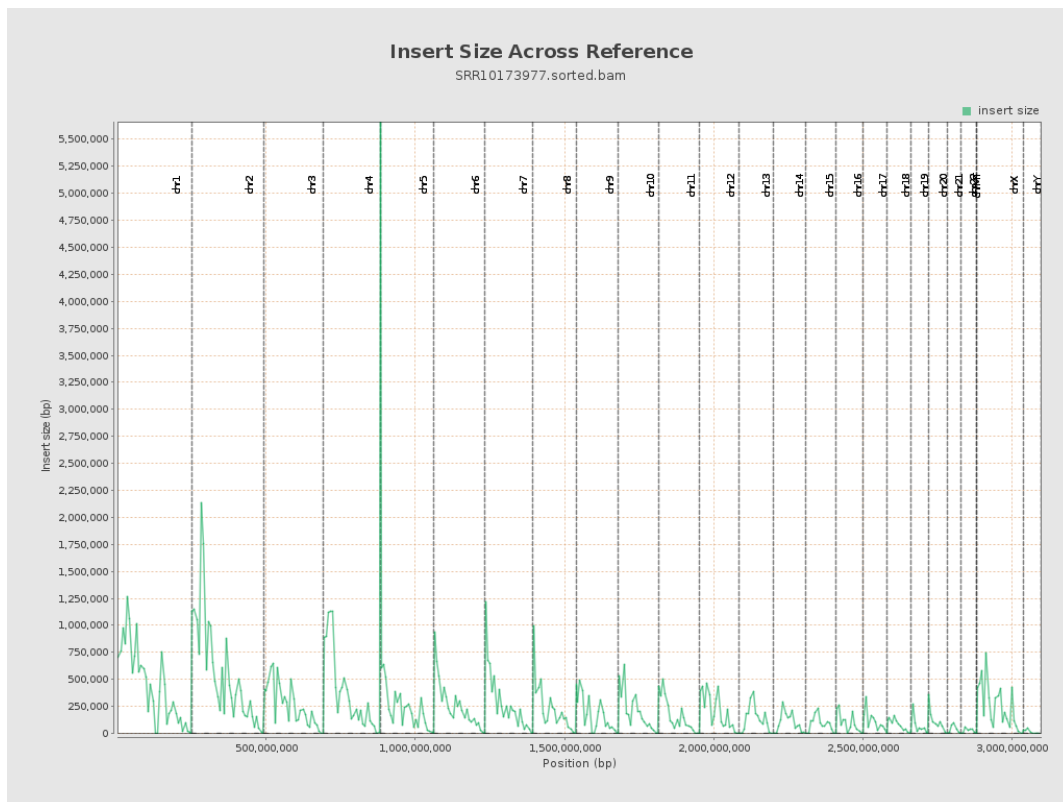
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

