

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 05:37:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174077.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_SRR10174077 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174077_1.fastq.gz SRR10174077_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 05:37:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174077.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,695,956
Mapped reads	1,666,355 / 98.25%
Unmapped reads	29,601 / 1.75%
Mapped paired reads	1,666,355 / 98.25%
Mapped reads, first in pair	832,965 / 49.11%
Mapped reads, second in pair	833,390 / 49.14%
Mapped reads, both in pair	1,648,600 / 97.21%
Mapped reads, singletons	17,755 / 1.05%
Secondary alignments	0
Supplementary alignments	210,060 / 12.39%
Read min/max/mean length	30 / 133 / 124.12
Duplicated reads (estimated)	1,250,157 / 73.71%
Duplication rate	60.79%
Clipped reads	851,581 / 50.21%

2.2. ACGT Content

Number/percentage of A's	56,506,086 / 30.18%
Number/percentage of C's	36,709,935 / 19.61%
Number/percentage of T's	56,034,602 / 29.93%
Number/percentage of G's	37,975,301 / 20.28%
Number/percentage of N's	1,634 / 0%

GC Percentage	39.89%
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2.3. Coverage

Mean	0.0605
Standard Deviation	1.2309

2.4. Mapping Quality

Mean Mapping Quality	52.71
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2.5. Insert size

Mean	935,389.79
Standard Deviation	9,087,271
P25/Median/P75	101 / 144 / 215

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	1,485,820
Insertions	20,213
Mapped reads with at least one insertion	1.17%
Deletions	49,625
Mapped reads with at least one deletion	2.91%
Homopolymer indels	41.64%

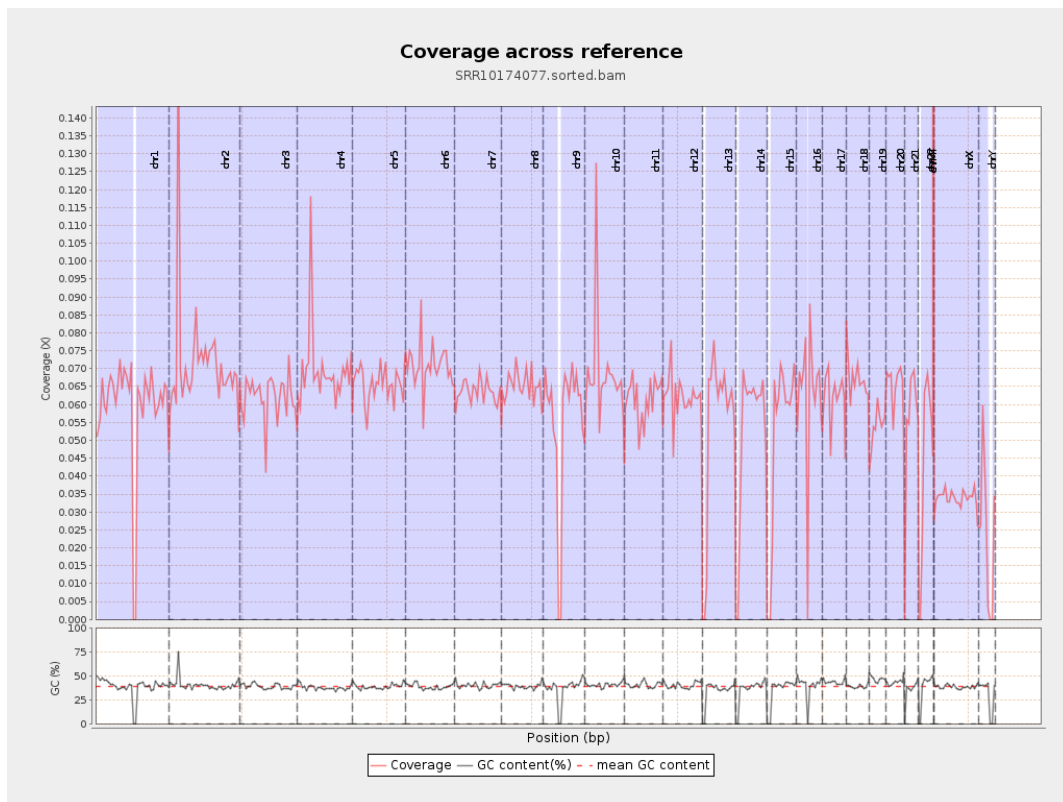
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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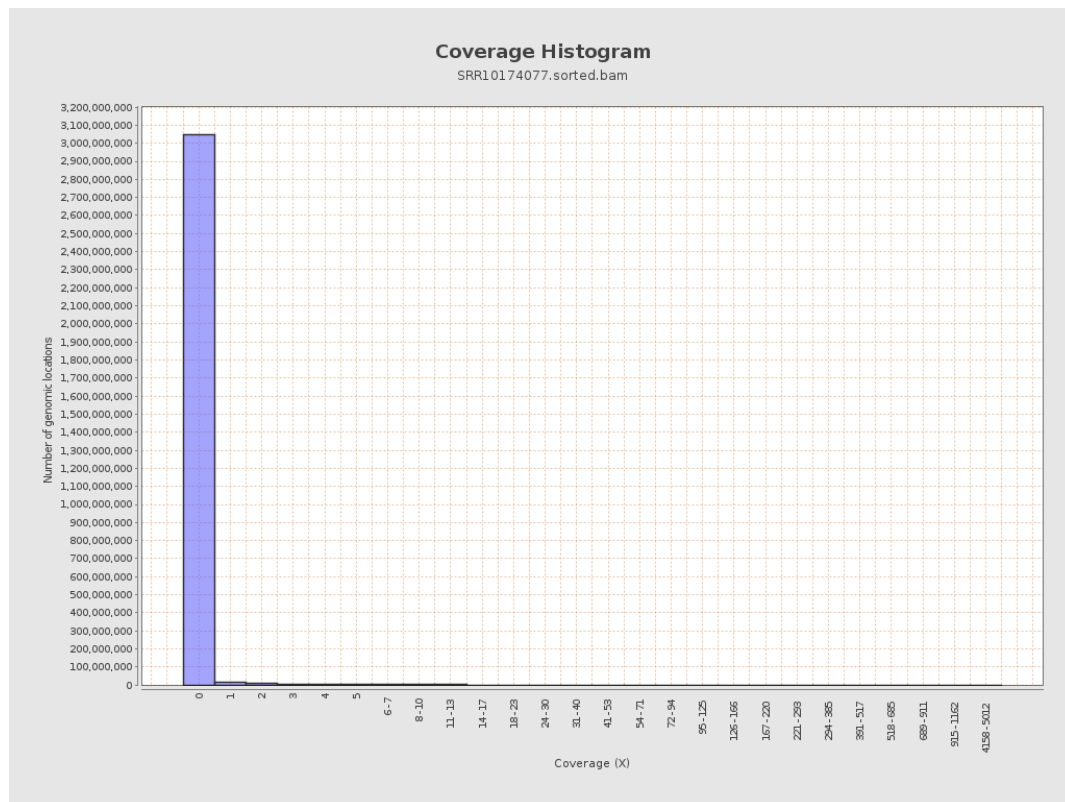
		bases	coverage	deviation
chr1	249250621	14855262	0.0596	0.7679
chr2	243199373	17533189	0.0721	3.5836
chr3	198022430	12314944	0.0622	0.7063
chr4	191154276	13258326	0.0694	0.8276
chr5	180915260	11845527	0.0655	0.7235
chr6	171115067	12134300	0.0709	0.7932
chr7	159138663	10153993	0.0638	0.7755
chr8	146364022	9545298	0.0652	0.9331
chr9	141213431	7833547	0.0555	0.7081
chr10	135534747	9303192	0.0686	0.9189
chr11	135006516	8270614	0.0613	0.7
chr12	133851895	8292872	0.062	0.7079
chr13	115169878	6231381	0.0541	0.6651
chr14	107349540	5656980	0.0527	0.6501
chr15	102531392	5309960	0.0518	0.6397
chr16	90354753	5604763	0.062	0.7532
chr17	81195210	4992382	0.0615	0.7086
chr18	78077248	5237339	0.0671	0.8278
chr19	59128983	3208441	0.0543	0.6392
chr20	63025520	4106780	0.0652	0.7209
chr21	48129895	2663359	0.0553	0.7211
chr22	51304566	2205559	0.043	0.6325
chrMT	16571	189250	11.4206	13.0823
chrX	155270560	5255804	0.0338	0.518

chrY	59373566	1340729	0.0226	0.4751
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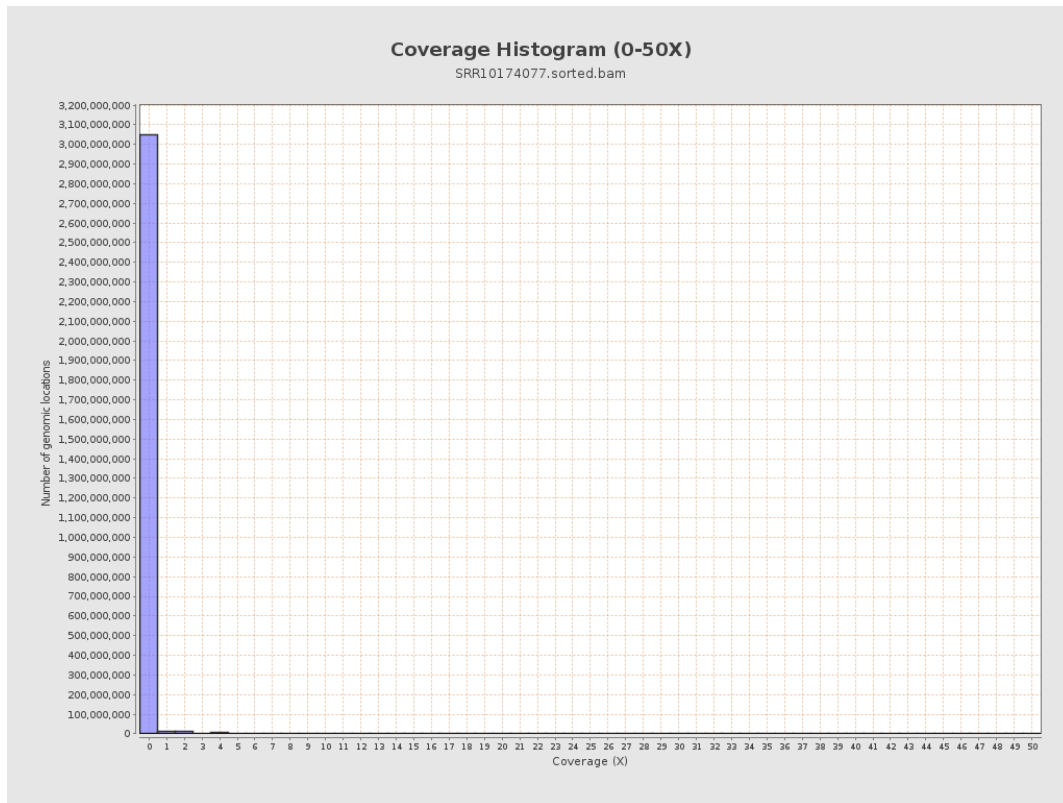
3. Results : Coverage across reference



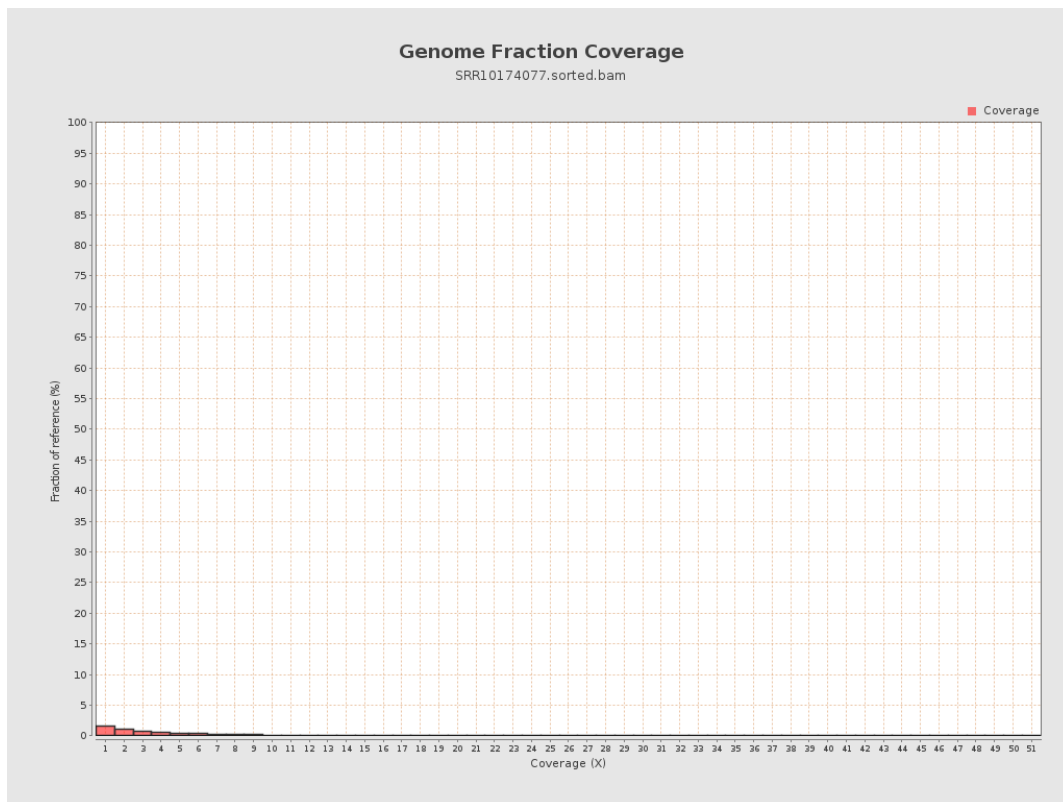
4. Results : Coverage Histogram



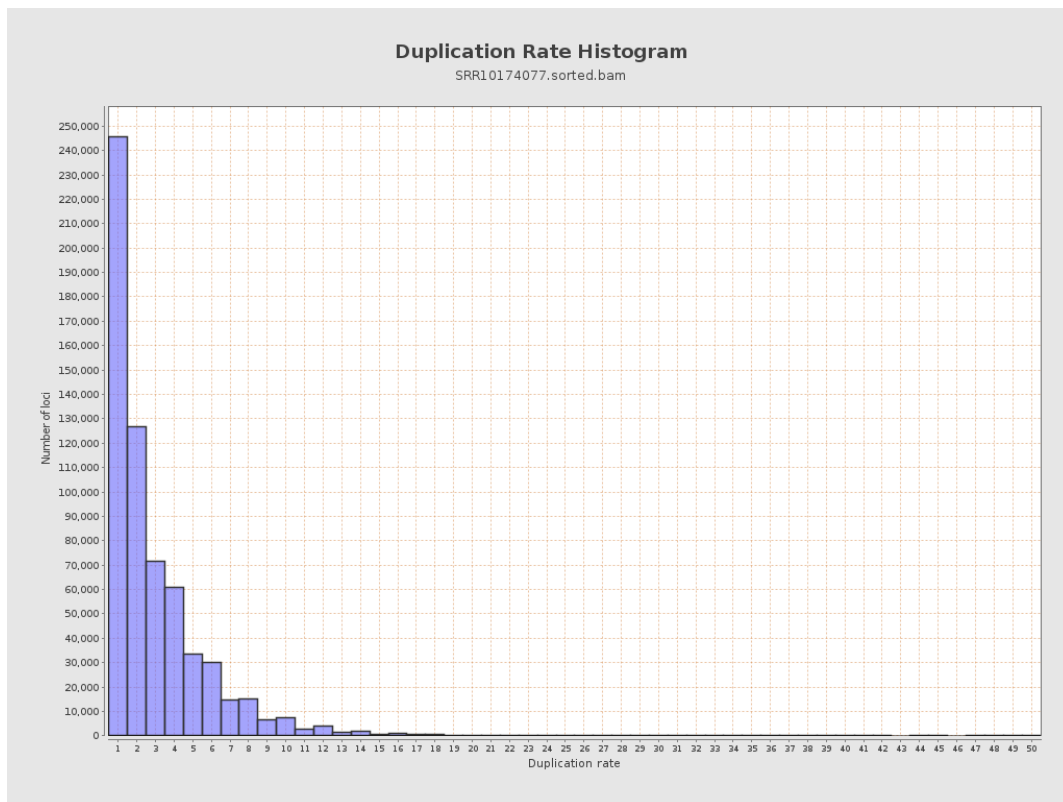
5. Results : Coverage Histogram (0-50X)



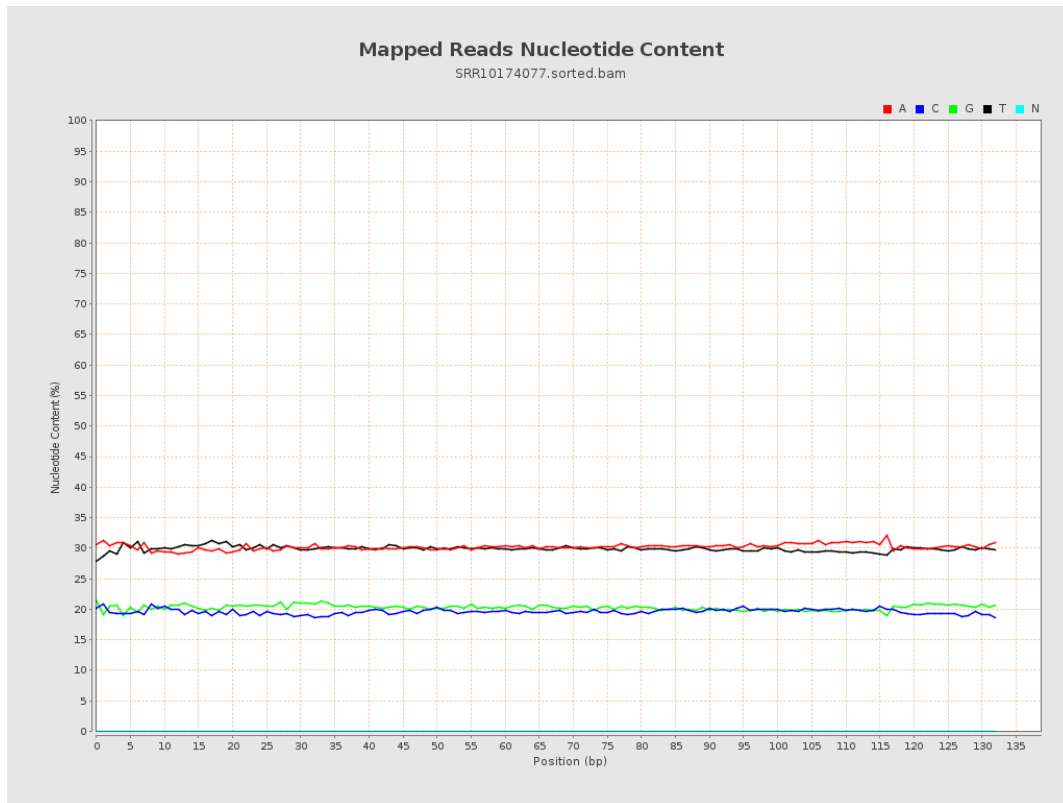
6. Results : Genome Fraction Coverage



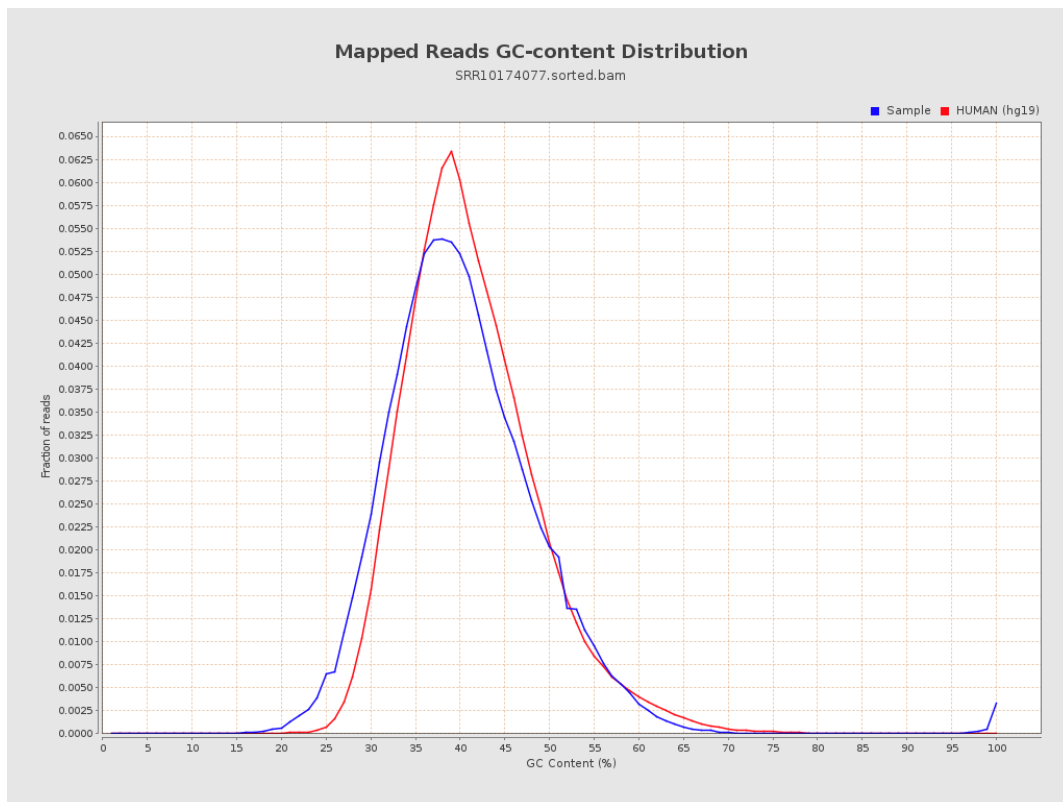
7. Results : Duplication Rate Histogram



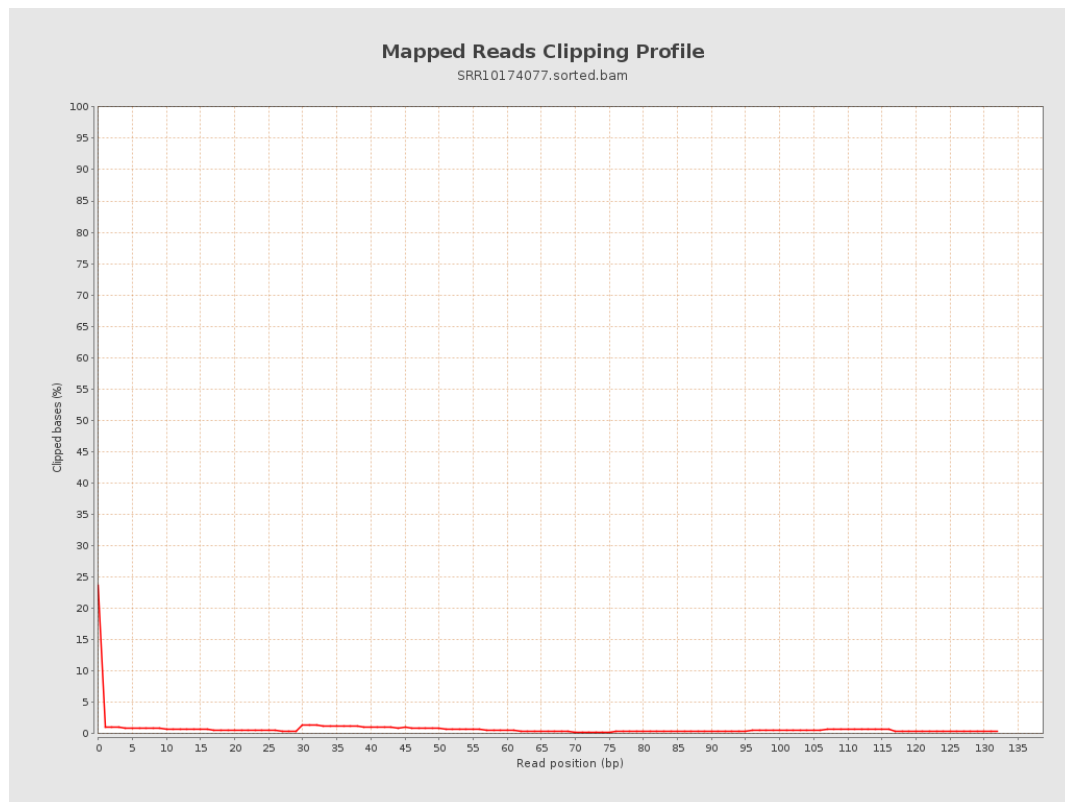
8. Results : Mapped Reads Nucleotide Content



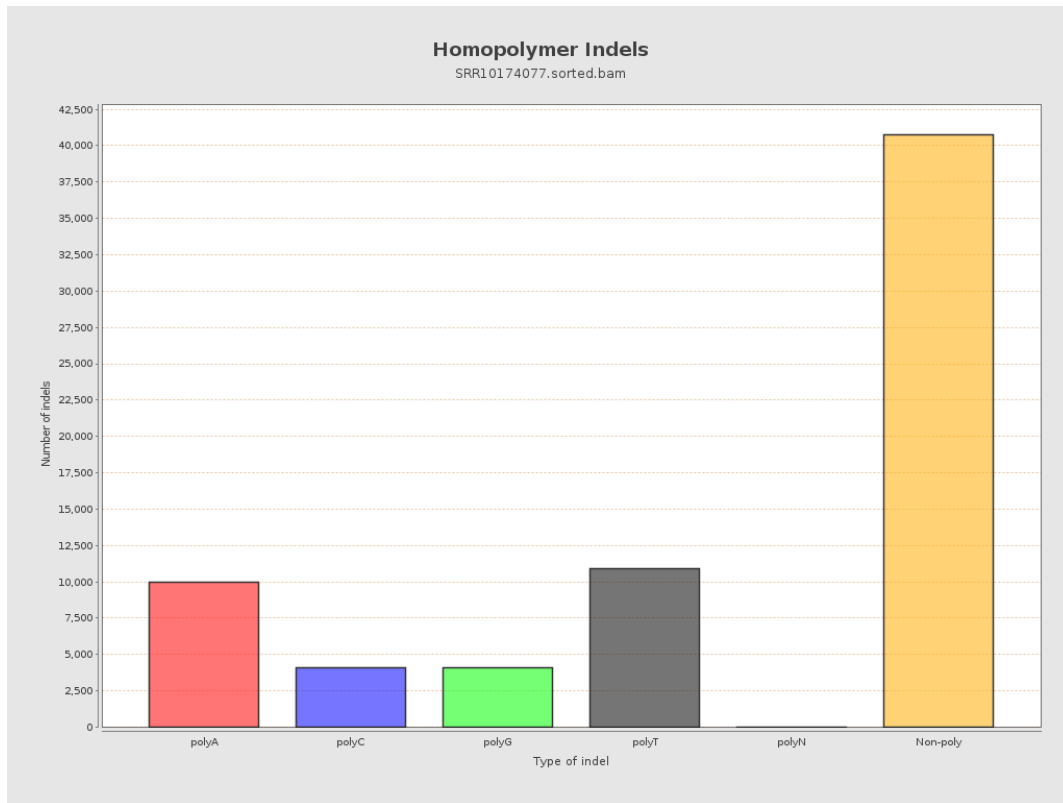
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



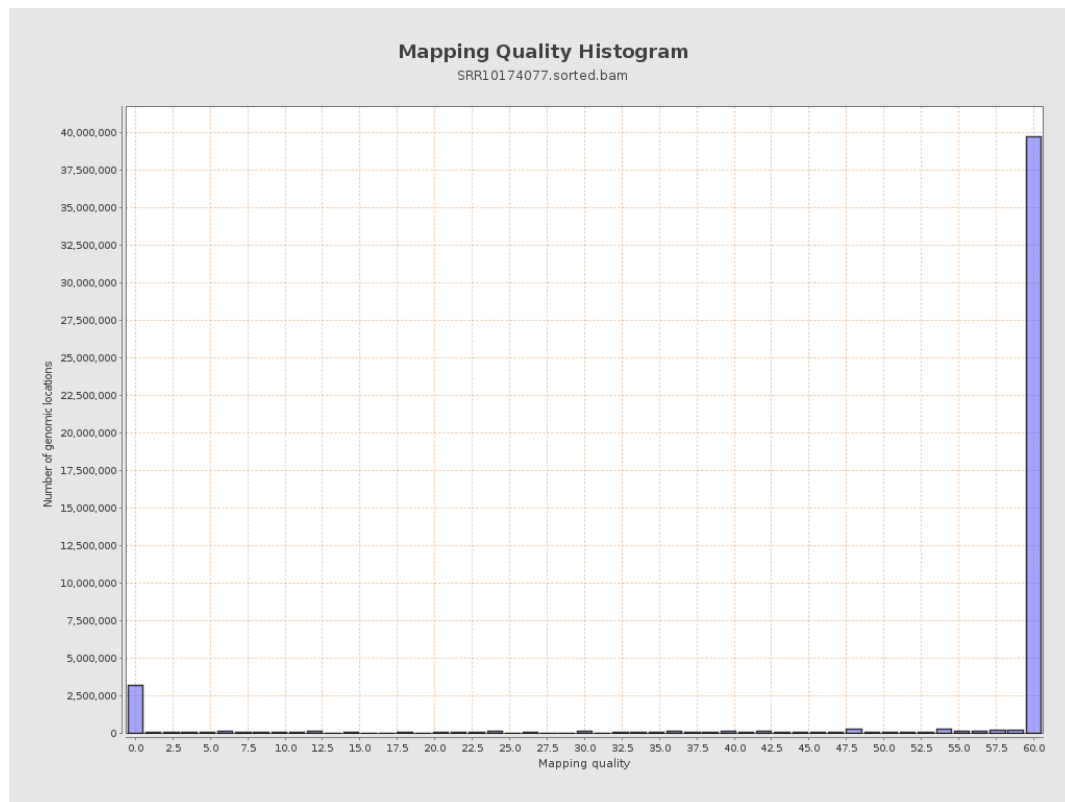
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

