

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 21:44:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472797.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_SRR3472797 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472797_1.fastq.gz SRR3472797_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 21:44:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472797.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	58,394,144
Mapped reads	58,022,155 / 99.36%
Unmapped reads	371,989 / 0.64%
Mapped paired reads	58,022,155 / 99.36%
Mapped reads, first in pair	29,150,727 / 49.92%
Mapped reads, second in pair	28,871,428 / 49.44%
Mapped reads, both in pair	57,720,860 / 98.85%
Mapped reads, singletons	301,295 / 0.52%
Secondary alignments	0
Supplementary alignments	70,605 / 0.12%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	23,458,333 / 40.17%
Duplication rate	38.52%
Clipped reads	3,188,337 / 5.46%

2.2. ACGT Content

Number/percentage of A's	1,624,546,347 / 28.31%
Number/percentage of C's	1,243,211,819 / 21.66%
Number/percentage of T's	1,648,067,520 / 28.72%
Number/percentage of G's	1,222,519,964 / 21.3%
Number/percentage of N's	591,687 / 0.01%

GC Percentage	42.96%
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2.3. Coverage

Mean	1.8541
Standard Deviation	12.6817

2.4. Mapping Quality

Mean Mapping Quality	53.65
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2.5. Insert size

Mean	20,844.61
Standard Deviation	1,426,869.54
P25/Median/P75	191 / 264 / 351

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	26,208,979
Insertions	272,405
Mapped reads with at least one insertion	0.46%
Deletions	322,146
Mapped reads with at least one deletion	0.55%
Homopolymer indels	46.14%

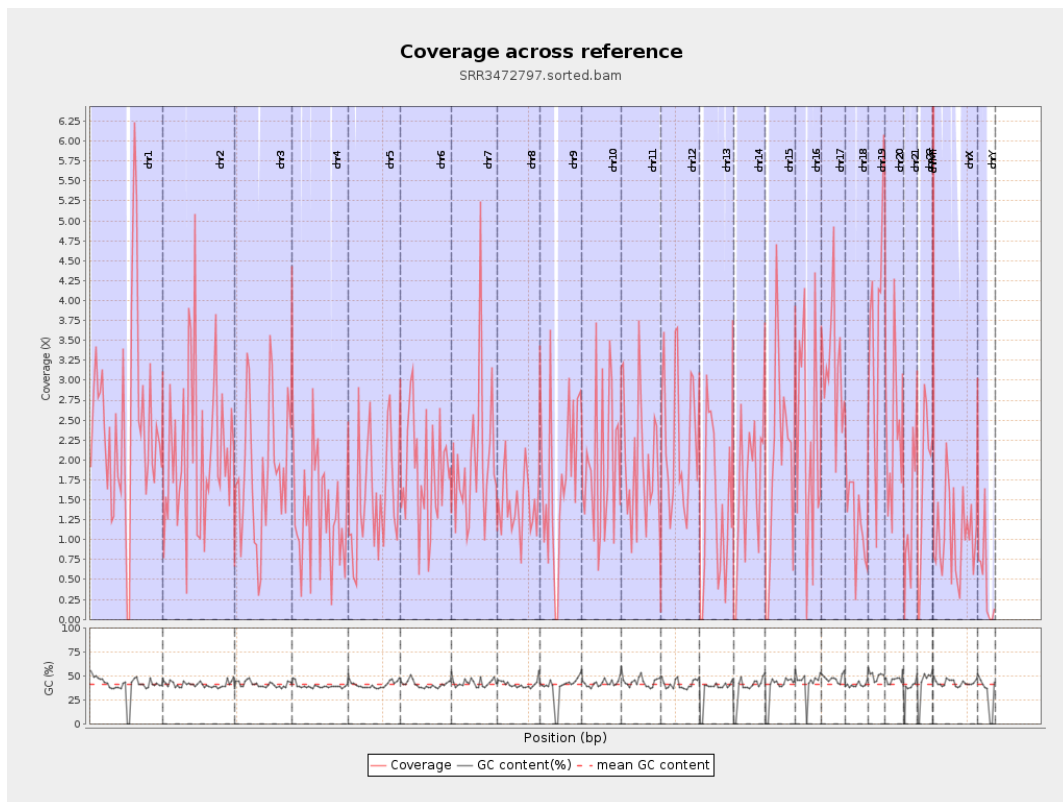
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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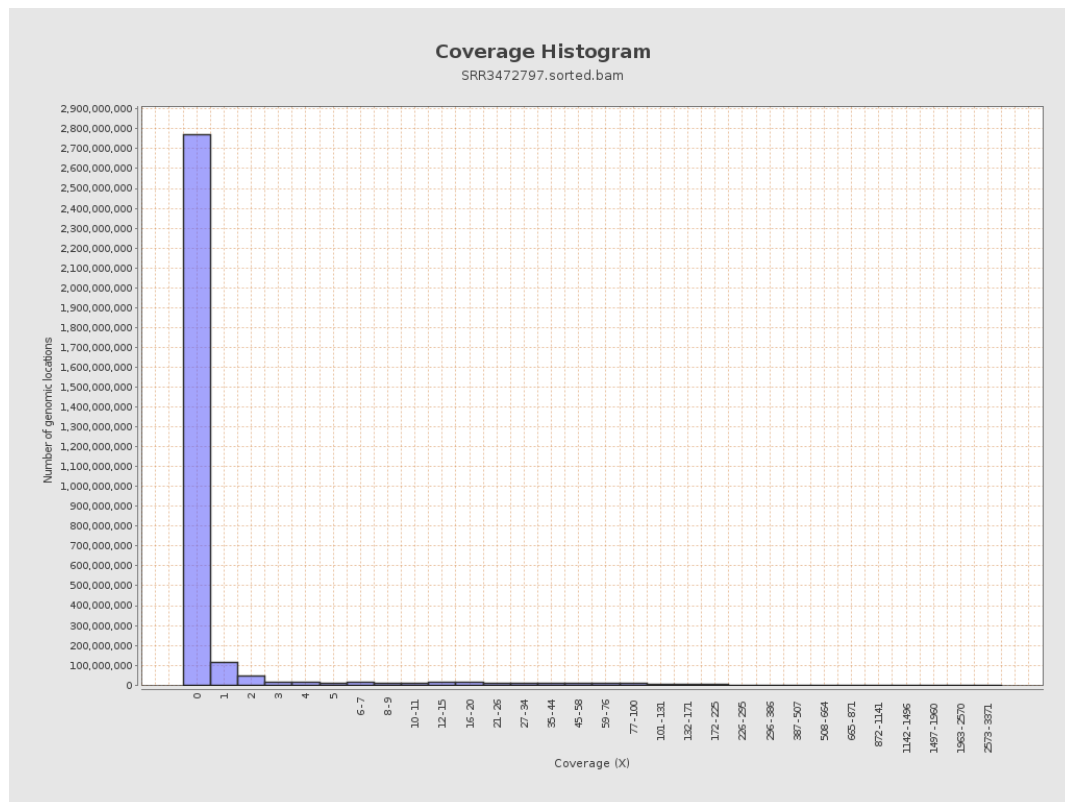
		bases	coverage	deviation
chr1	249250621	601198254	2.412	15.2216
chr2	243199373	515849654	2.1211	15.1265
chr3	198022430	364291060	1.8396	12.4775
chr4	191154276	252718500	1.3221	10.1727
chr5	180915260	284910699	1.5748	11.3637
chr6	171115067	312417499	1.8258	12.6211
chr7	159138663	315386262	1.9818	13.8936
chr8	146364022	211855255	1.4475	10.9185
chr9	141213431	245687958	1.7398	12.5379
chr10	135534747	262897614	1.9397	13.4262
chr11	135006516	263361322	1.9507	11.7558
chr12	133851895	305554438	2.2828	13.332
chr13	115169878	159624334	1.386	12.1444
chr14	107349540	173892143	1.6199	11.5255
chr15	102531392	197707398	1.9283	12.1544
chr16	90354753	203523004	2.2525	14.1139
chr17	81195210	259356681	3.1942	14.9692
chr18	78077248	99906311	1.2796	10.1529
chr19	59128983	217802699	3.6835	15.8196
chr20	63025520	142217756	2.2565	13.8911
chr21	48129895	66122109	1.3738	11.9599
chr22	51304566	88918937	1.7332	11.027
chrMT	16571	777705	46.9317	131.4766
chrX	155270560	165516215	1.066	8.4489

chrY	59373566	28202311	0.475	7.1172
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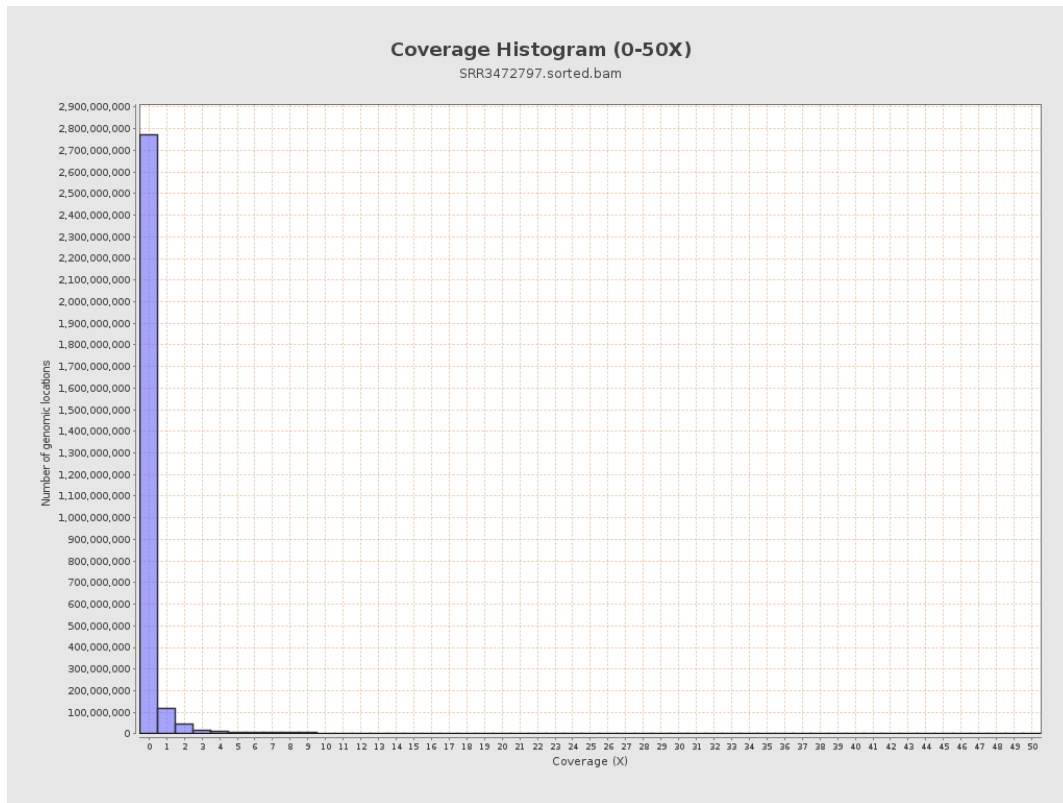
3. Results : Coverage across reference



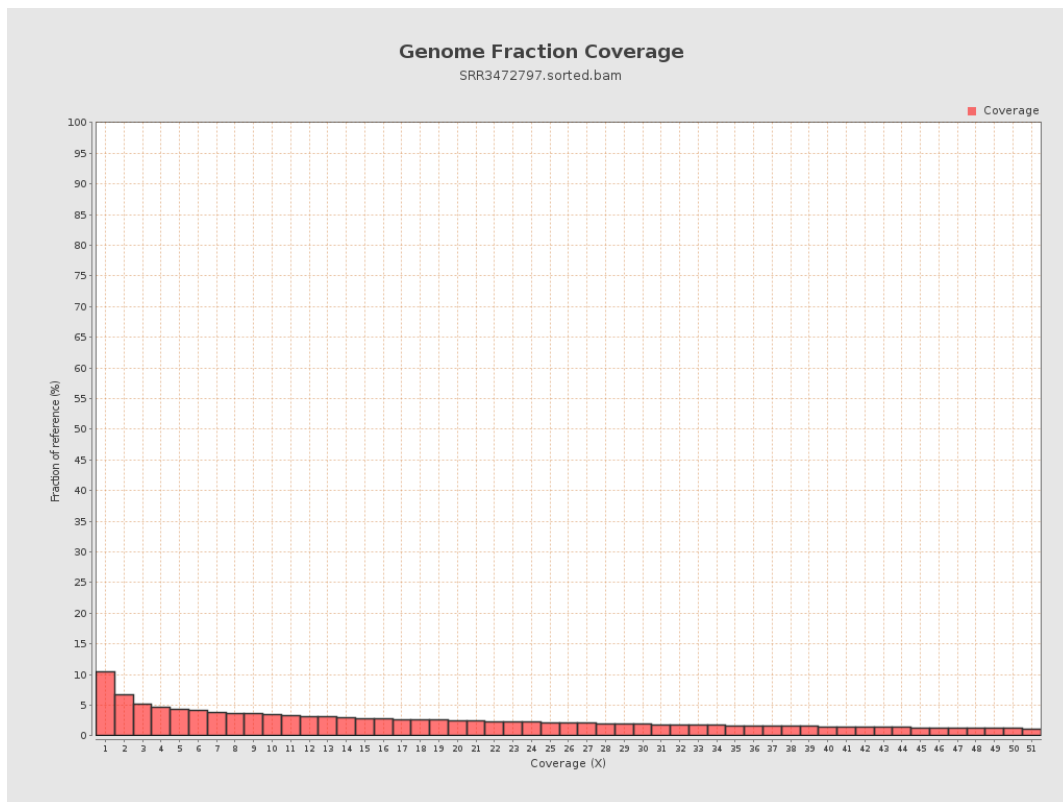
4. Results : Coverage Histogram



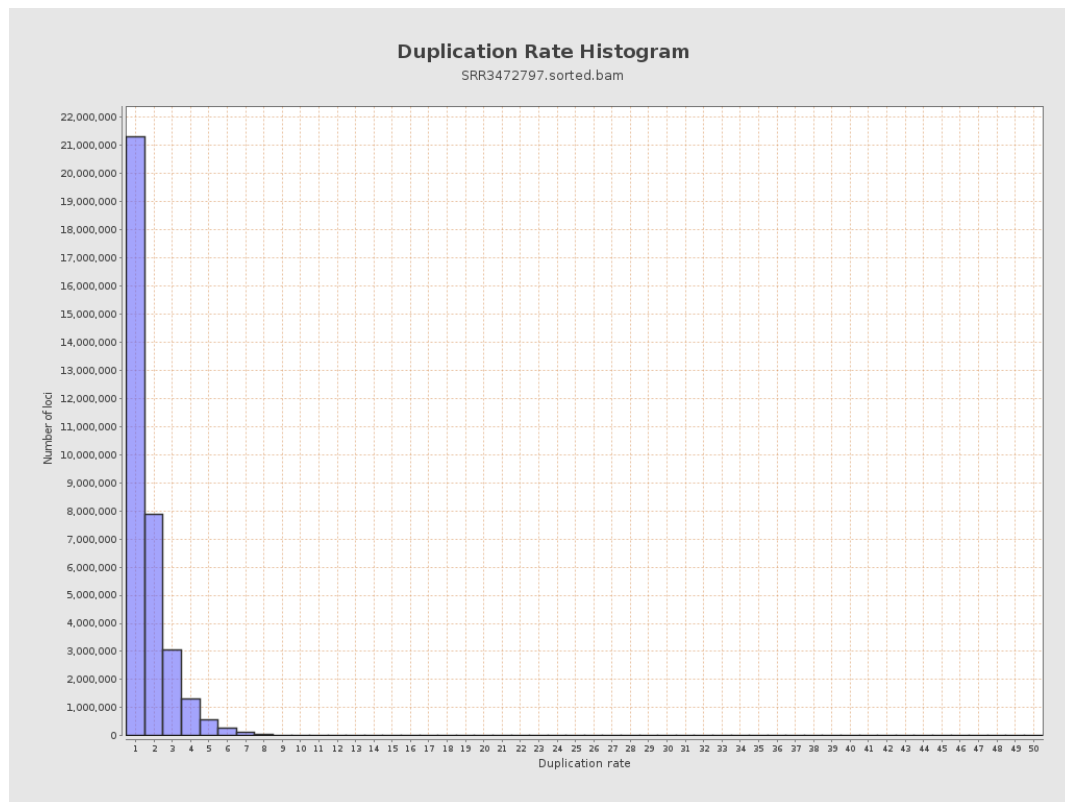
5. Results : Coverage Histogram (0-50X)



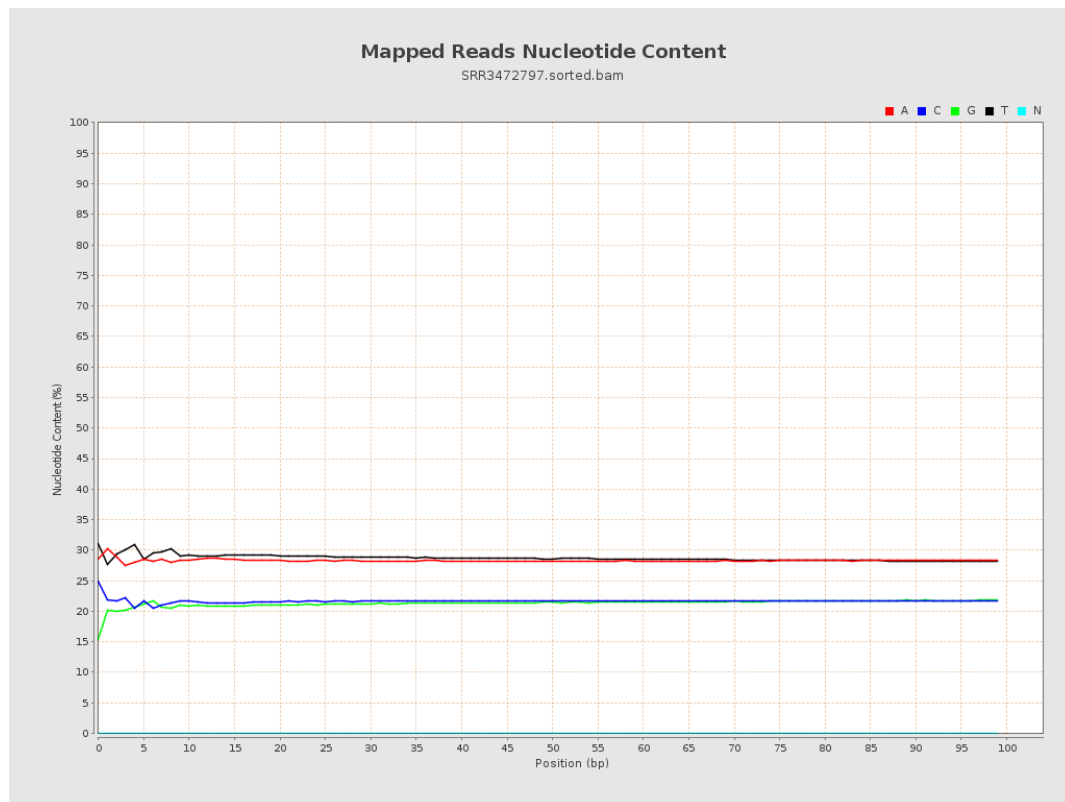
6. Results : Genome Fraction Coverage



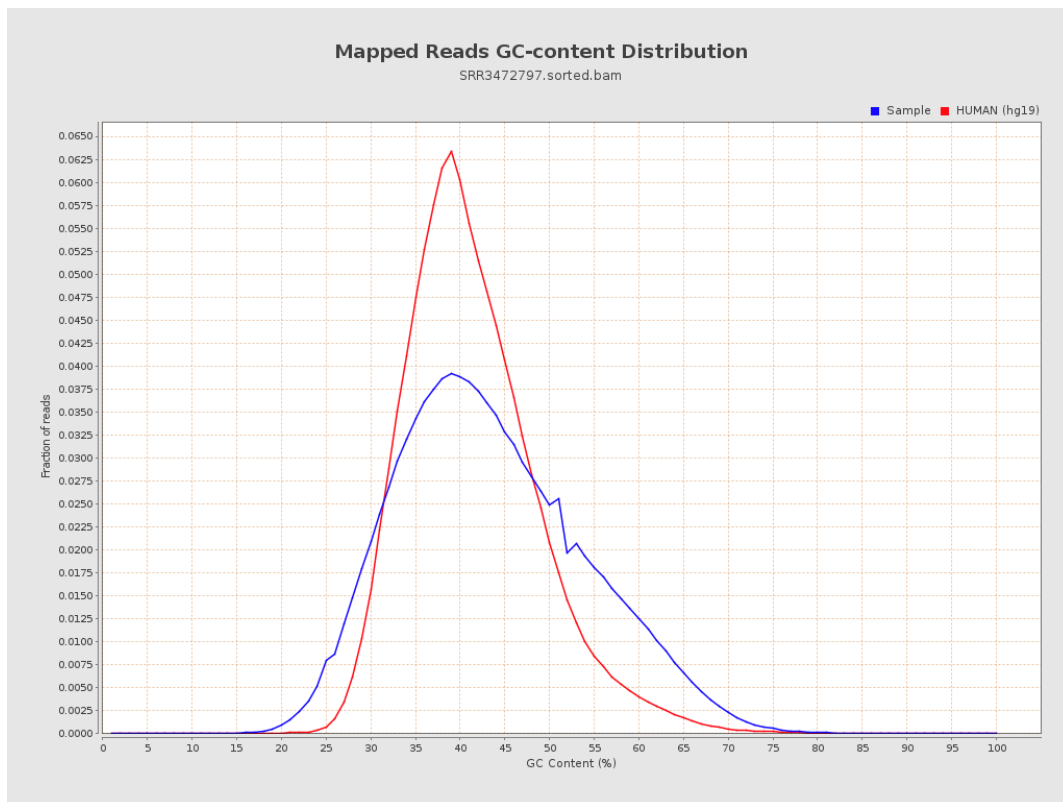
7. Results : Duplication Rate Histogram



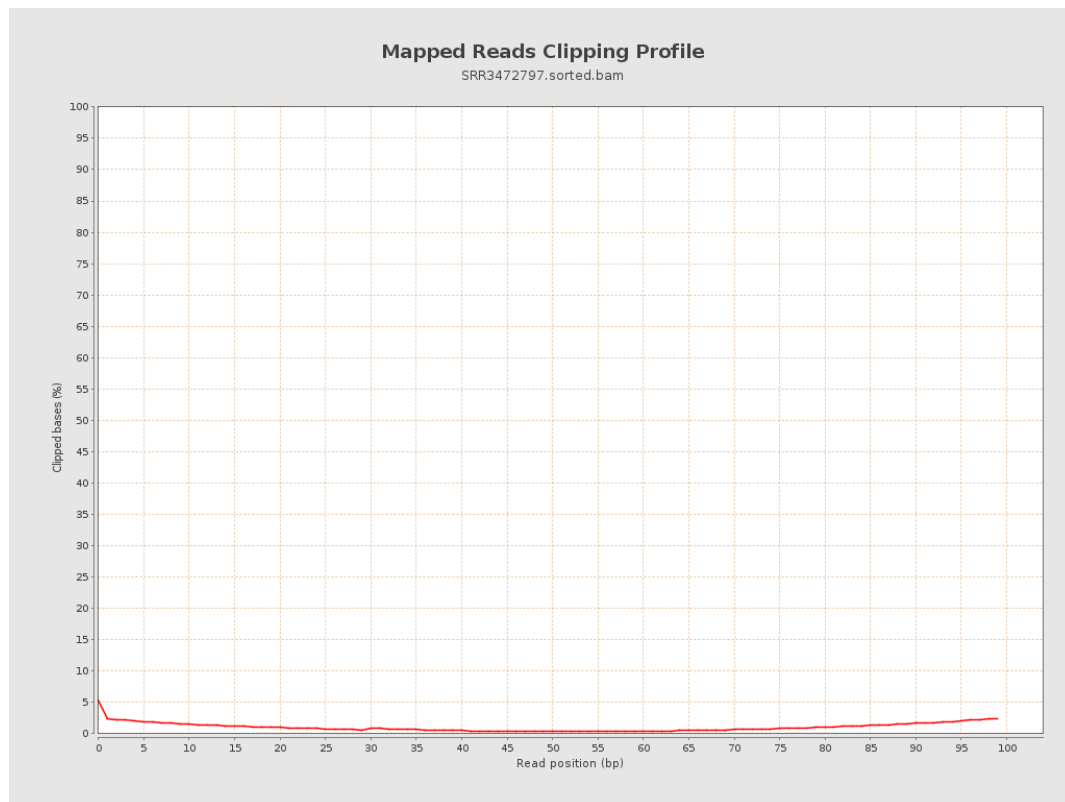
8. Results : Mapped Reads Nucleotide Content



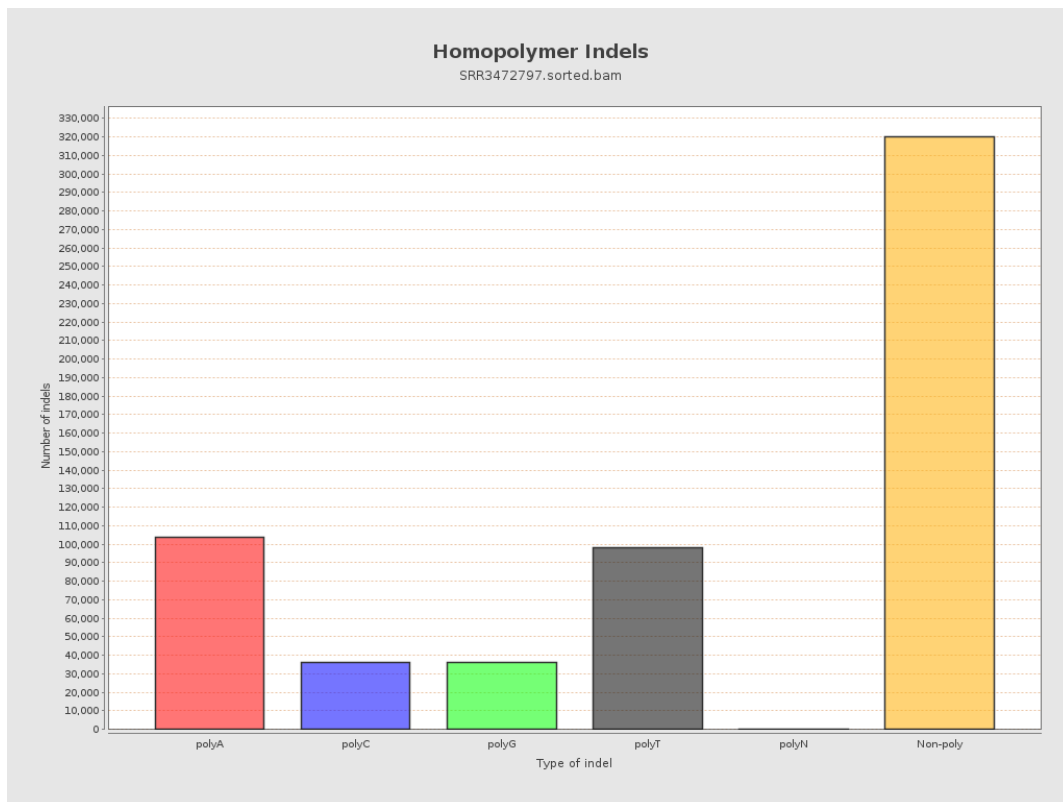
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



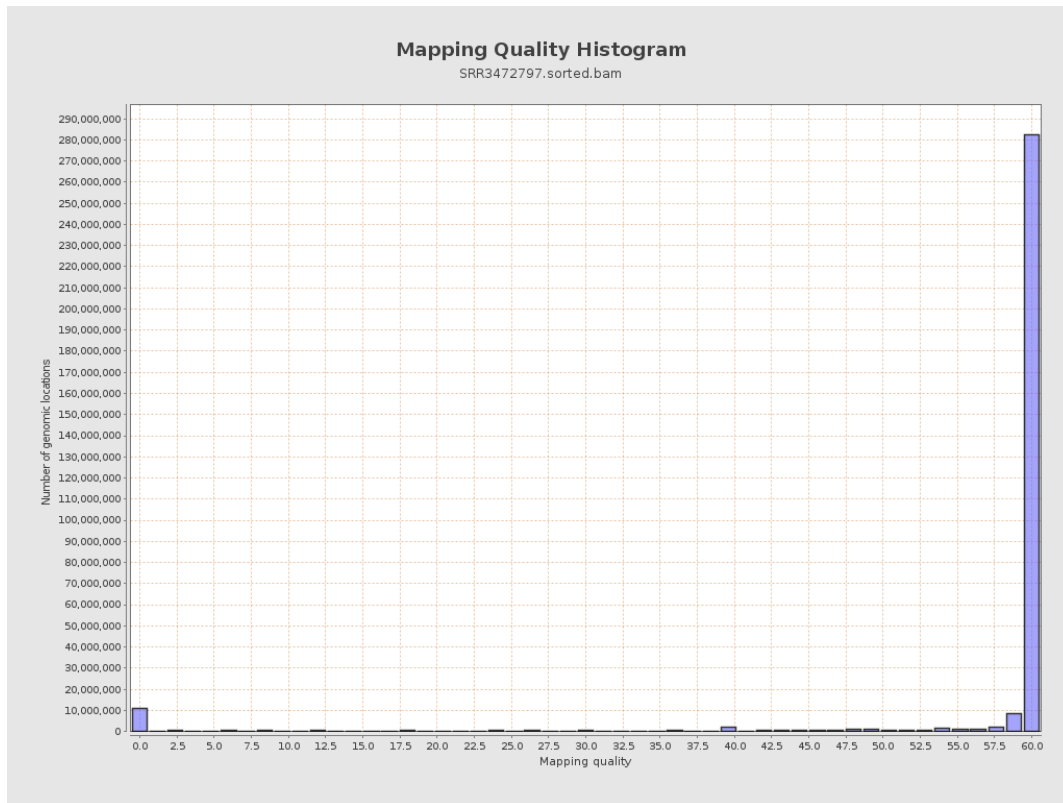
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

