Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/21 20:32:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504597.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_SRR504597 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504597_1.fastq.gz SRR504597_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 21 20:32:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504597.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	371,625,352
Mapped reads	355,400,145 / 95.63%
Unmapped reads	16,225,207 / 4.37%
Mapped paired reads	355,400,145 / 95.63%
Mapped reads, first in pair	177,956,024 / 47.89%
Mapped reads, second in pair	177,444,121 / 47.75%
Mapped reads, both in pair	352,595,840 / 94.88%
Mapped reads, singletons	2,804,305 / 0.75%
Secondary alignments	0
Supplementary alignments	1,037,034 / 0.28%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	78,842,762 / 21.22%
Duplication rate	18.21%
Clipped reads	55,489,789 / 14.93%

2.2. ACGT Content

Number/percentage of A's	9,702,218,681 / 28.42%
Number/percentage of C's	7,322,552,361 / 21.45%
Number/percentage of T's	9,604,634,821 / 28.13%
Number/percentage of G's	7,502,415,894 / 21.98%
Number/percentage of N's	8,574,031 / 0.03%

GC Percentage	43.42%

2.3. Coverage

Mean	11.0319
Standard Deviation	97.2833

2.4. Mapping Quality

Mean Mapping Quality	53.37

2.5. Insert size

Mean	34,565.13
Standard Deviation	1,768,037.39
P25/Median/P75	133 / 189 / 246

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	188,306,077
Insertions	3,453,615
Mapped reads with at least one insertion	0.94%
Deletions	4,247,783
Mapped reads with at least one deletion	1.16%
Homopolymer indels	40.41%

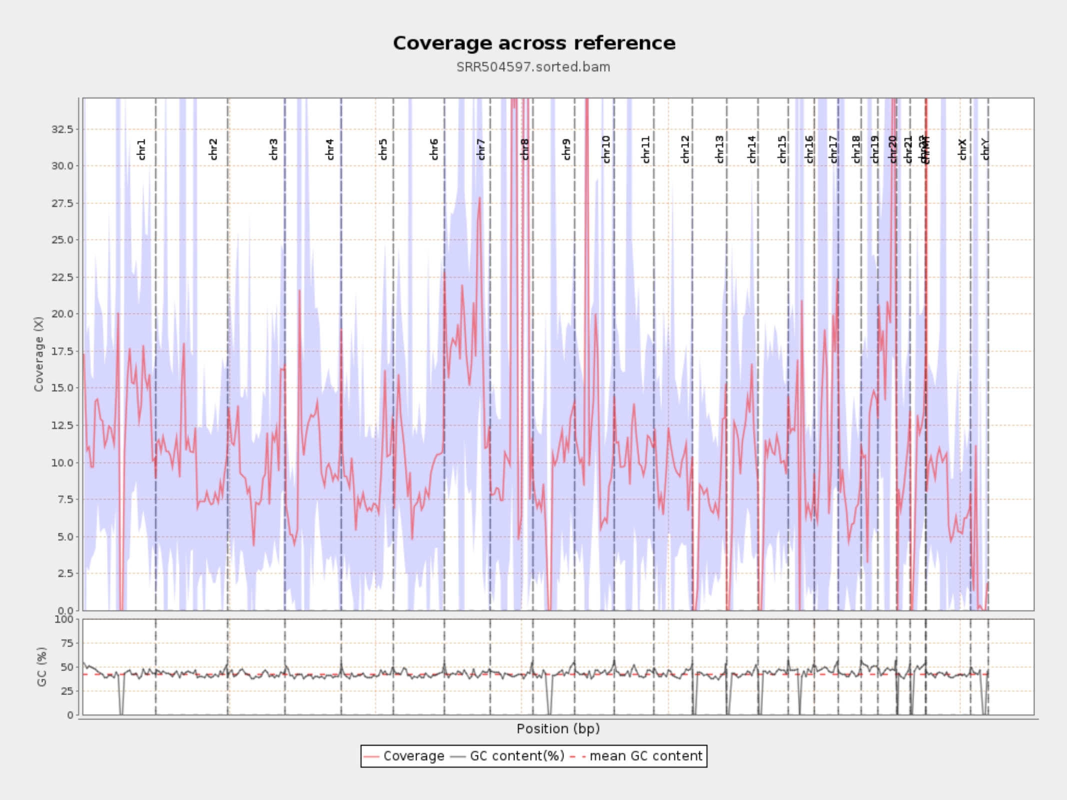
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

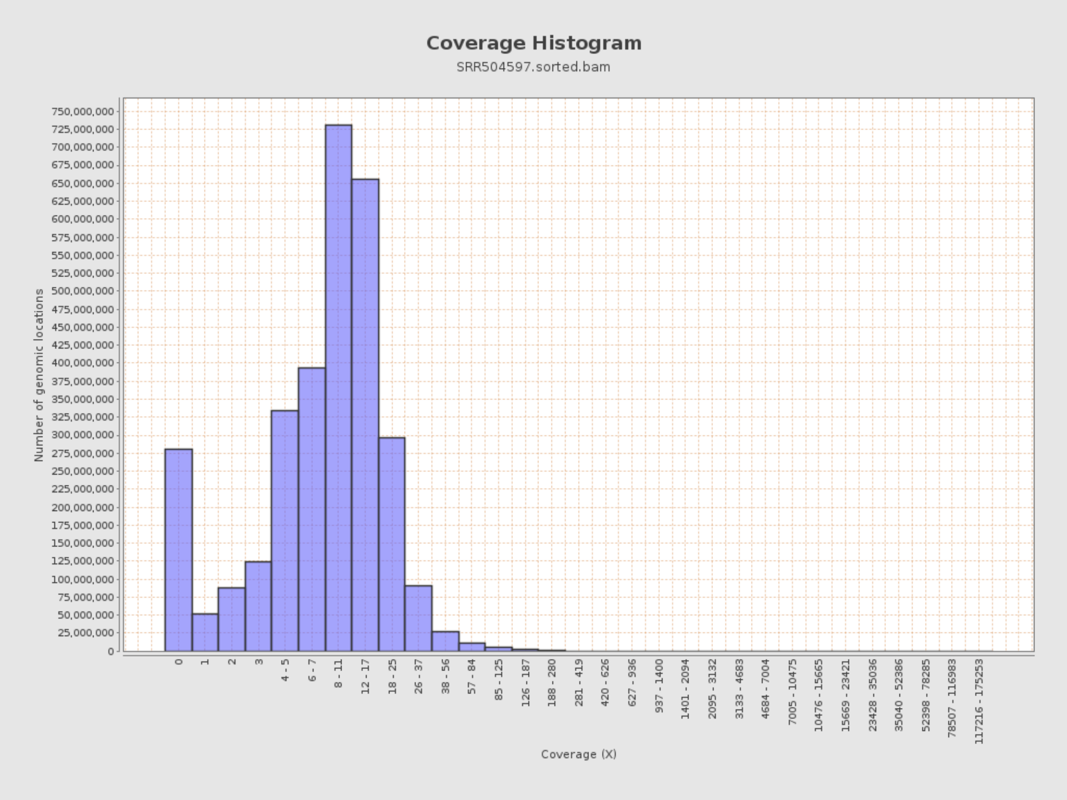
		bases	coverage	deviation
chr1	249250621	3176689562	12.745	176.2362
chr2	243199373	2411940633	9.9175	58.4043
chr3	198022430	2019954485	10.2006	16.7692
chr4	191154276	1936221389	10.1291	116.9363
chr5	180915260	1612187767	8.9113	10.4787
chr6	171115067	1600627718	9.3541	23.0732
chr7	159138663	2879949705	18.0971	139.5622
chr8	146364022	3002614859	20.5147	68.6342
chr9	141213431	1231210884	8.7188	61.914
chr10	135534747	1663057221	12.2703	264.1145
chr11	135006516	1466698735	10.8639	39.575
chr12	133851895	1277102784	9.5412	9.0081
chr13	115169878	828663299	7.1951	6.5961
chr14	107349540	1107773243	10.3193	9.7284
chr15	102531392	891281608	8.6928	7.4247
chr16	90354753	948387479	10.4963	74.7615
chr17	81195210	1058868537	13.041	45.8501
chr18	78077248	582430308	7.4597	96.3035
chr19	59128983	682804323	11.5477	91.4781
chr20	63025520	1436664907	22.795	29.6689
chr21	48129895	409611586	8.5105	40.9595
chr22	51304566	460535079	8.9765	9.6417
chrMT	16571	122353432	7,383.5877	1,565.2144
chrX	155270560	1212621911	7.8097	19.1052

chrY	59373566	131130854	2.2086	118.9892

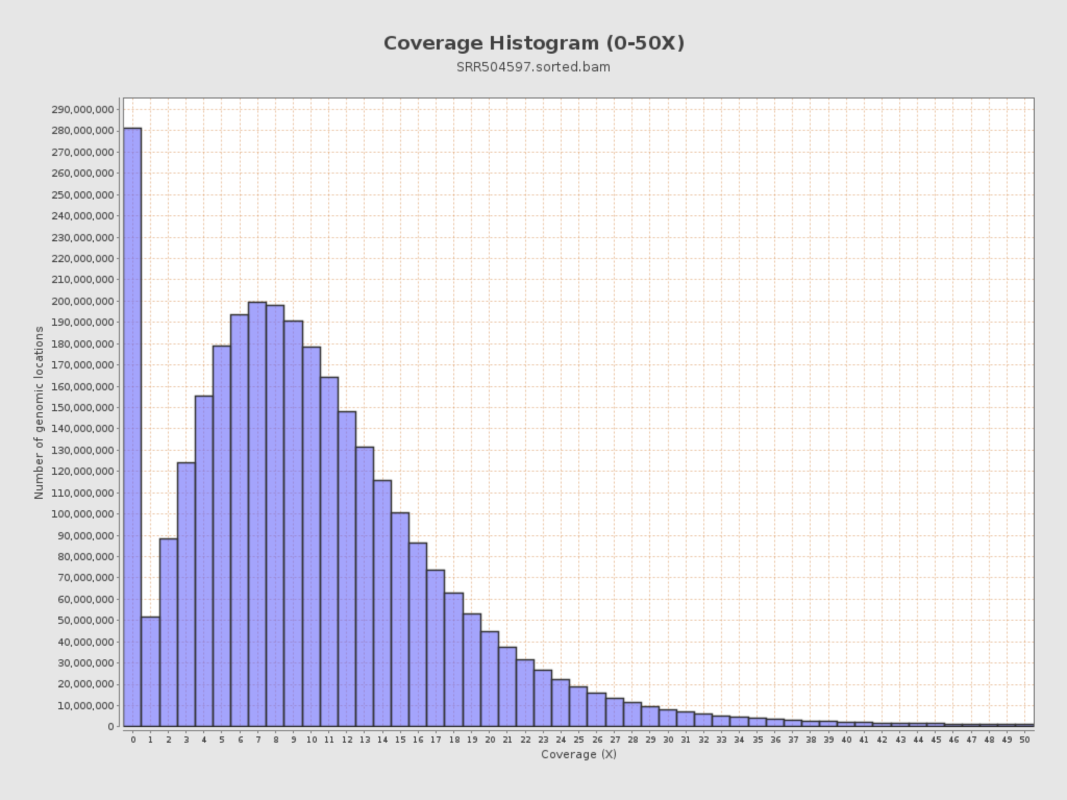
3. Results : Coverage across reference



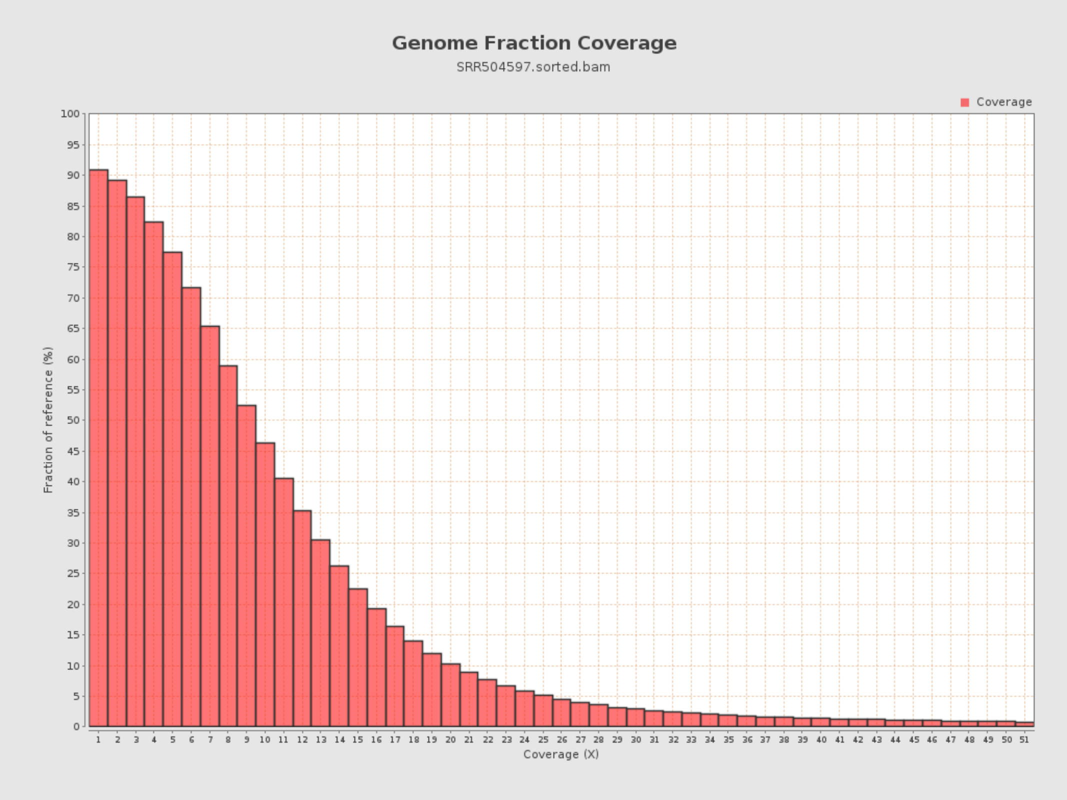
4. Results : Coverage Histogram



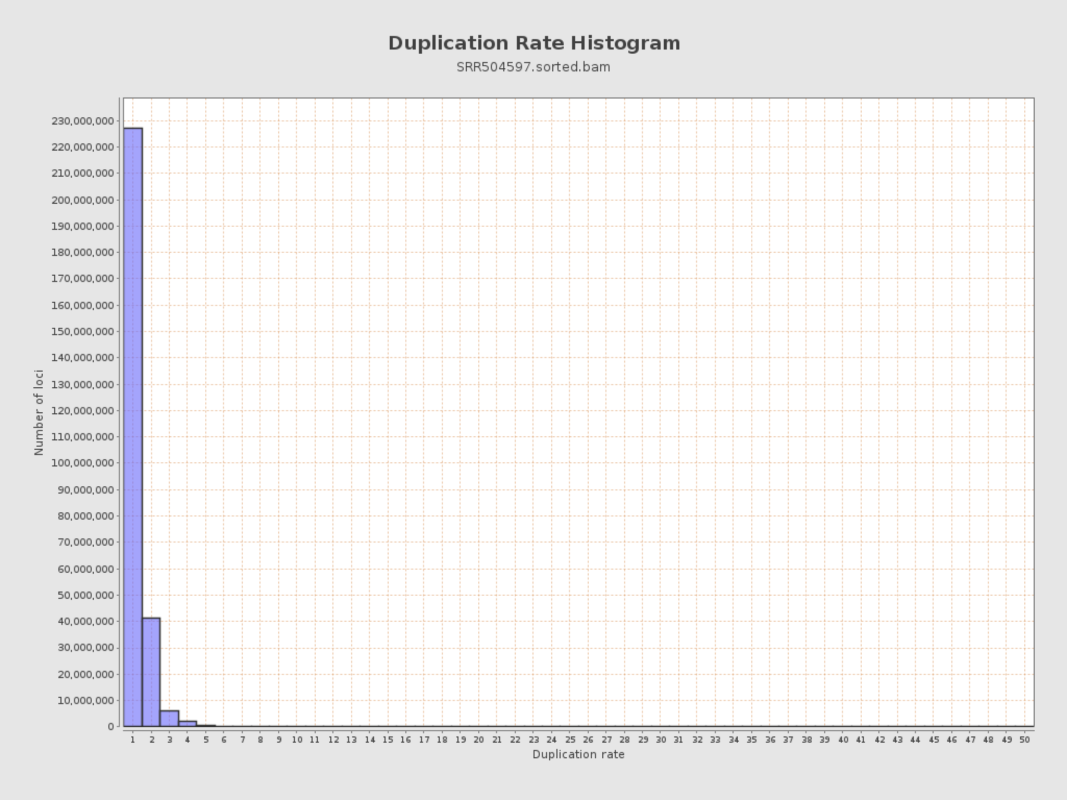
5. Results : Coverage Histogram (0-50X)



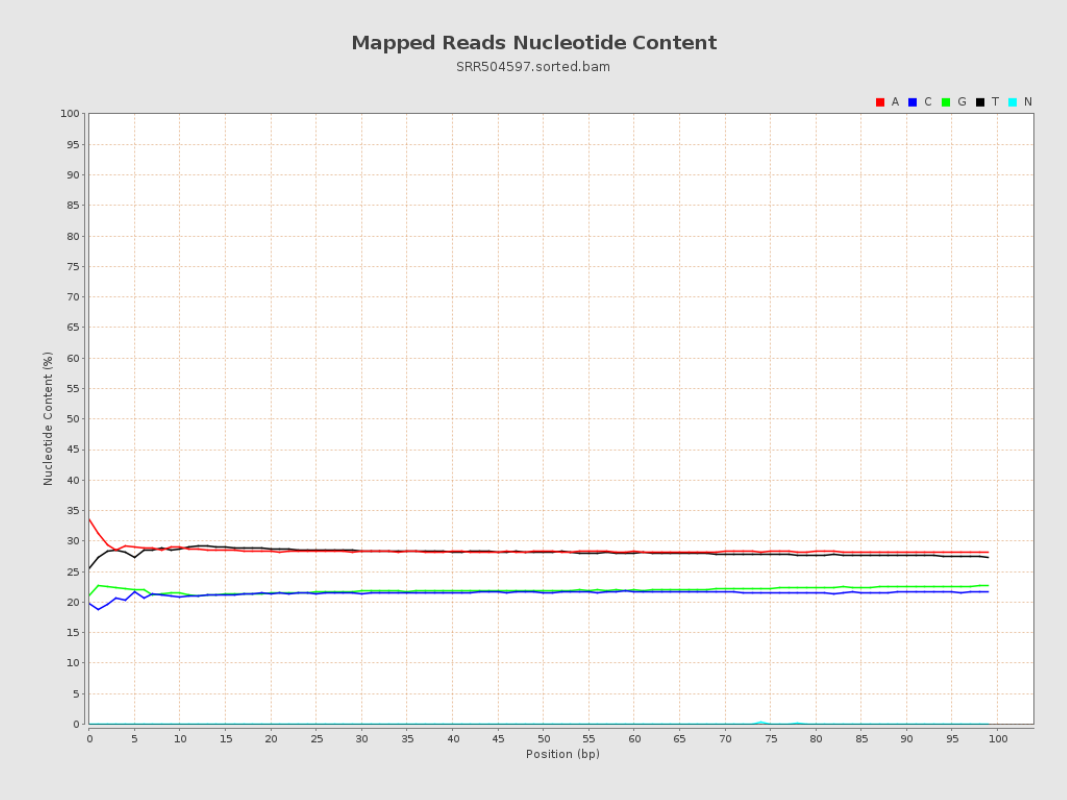
6. Results : Genome Fraction Coverage



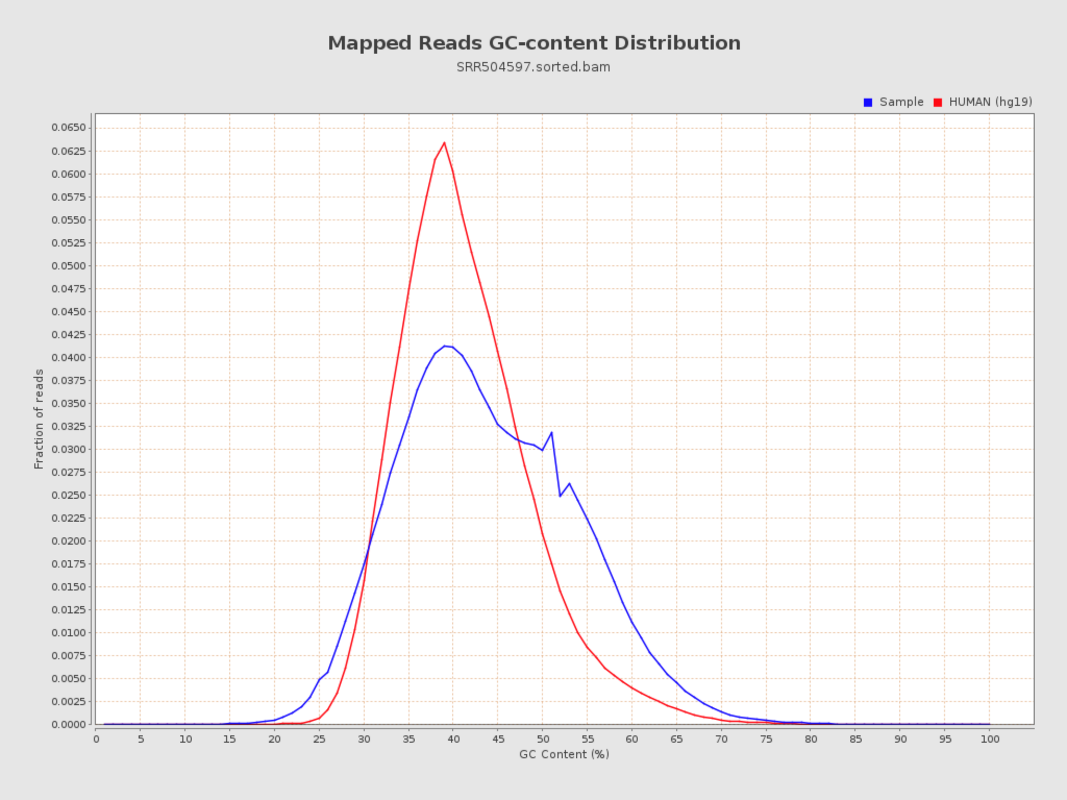
7. Results : Duplication Rate Histogram



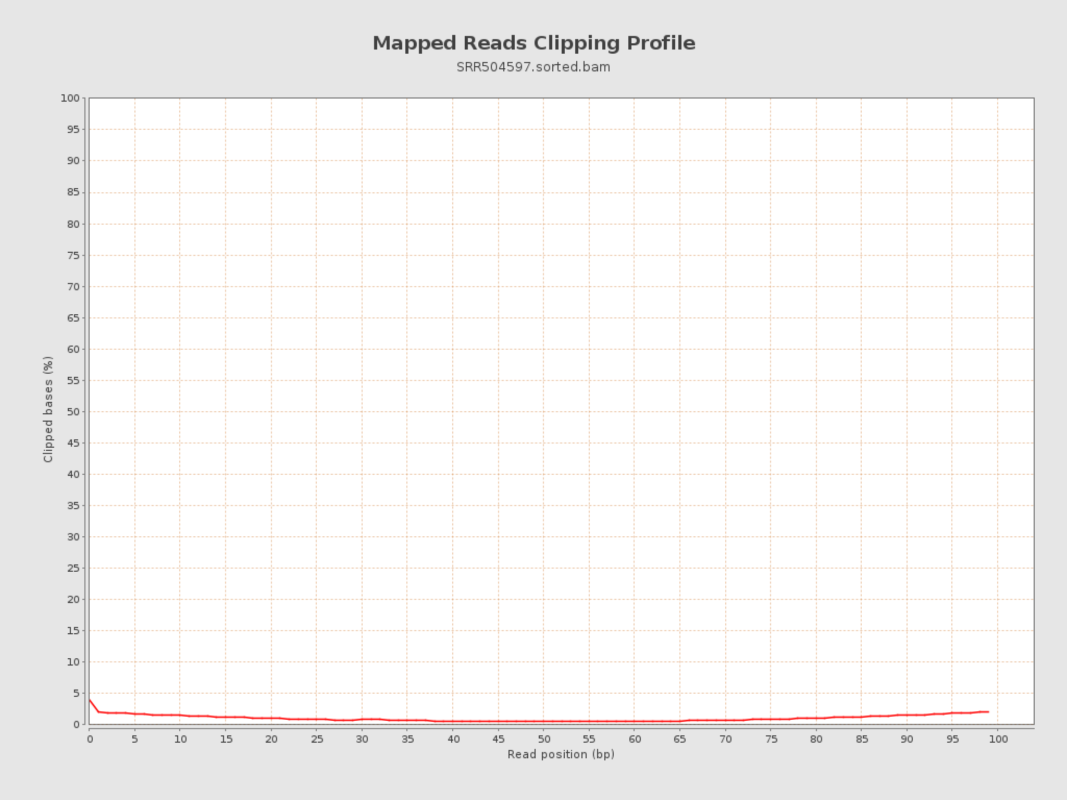
8. Results : Mapped Reads Nucleotide Content



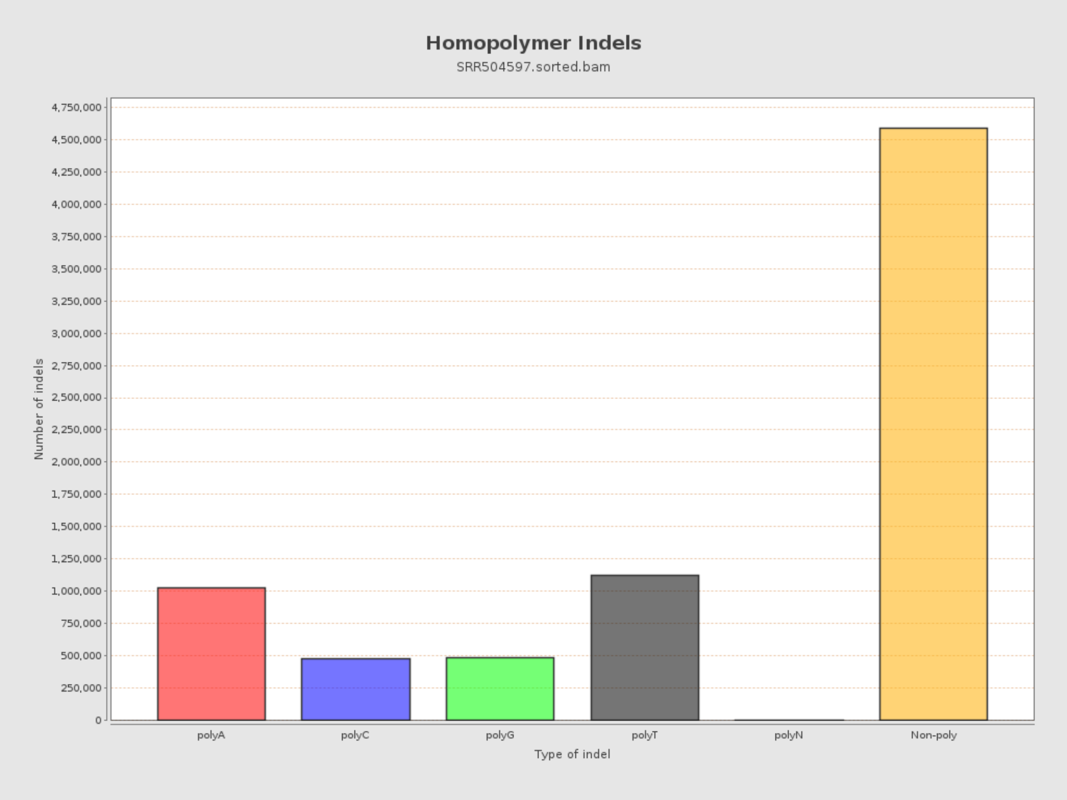
9. Results : Mapped Reads GC-content Distribution



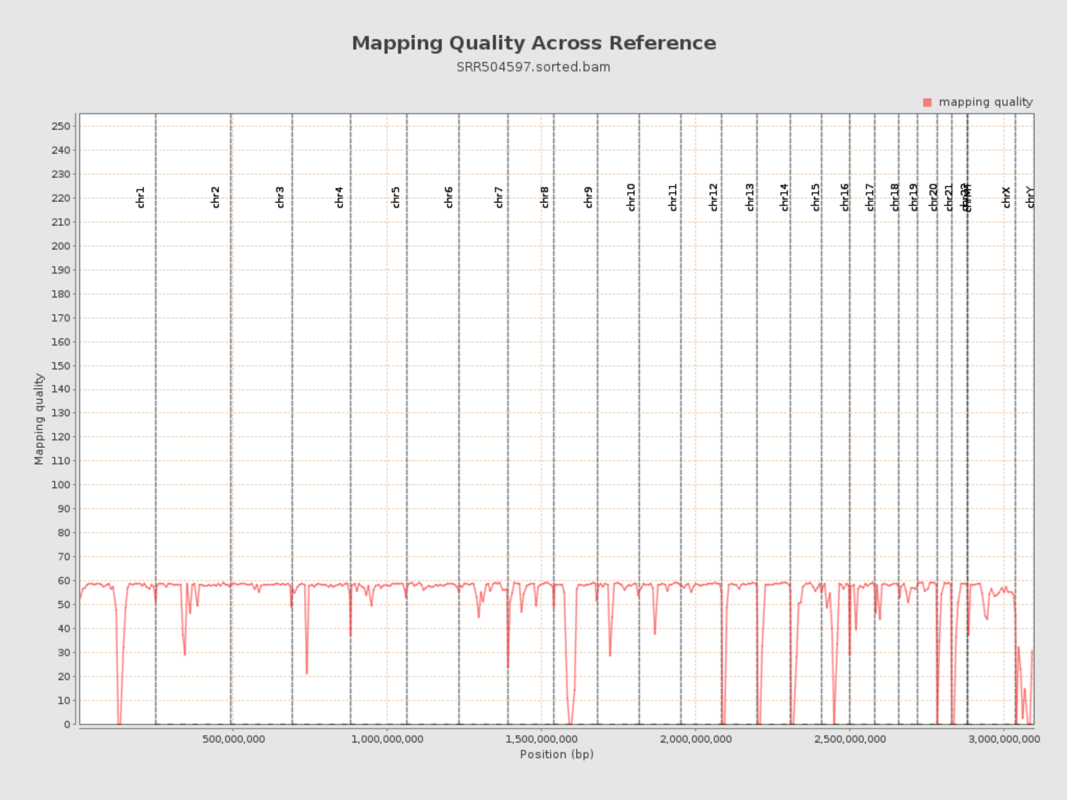
10. Results : Mapped Reads Clipping Profile



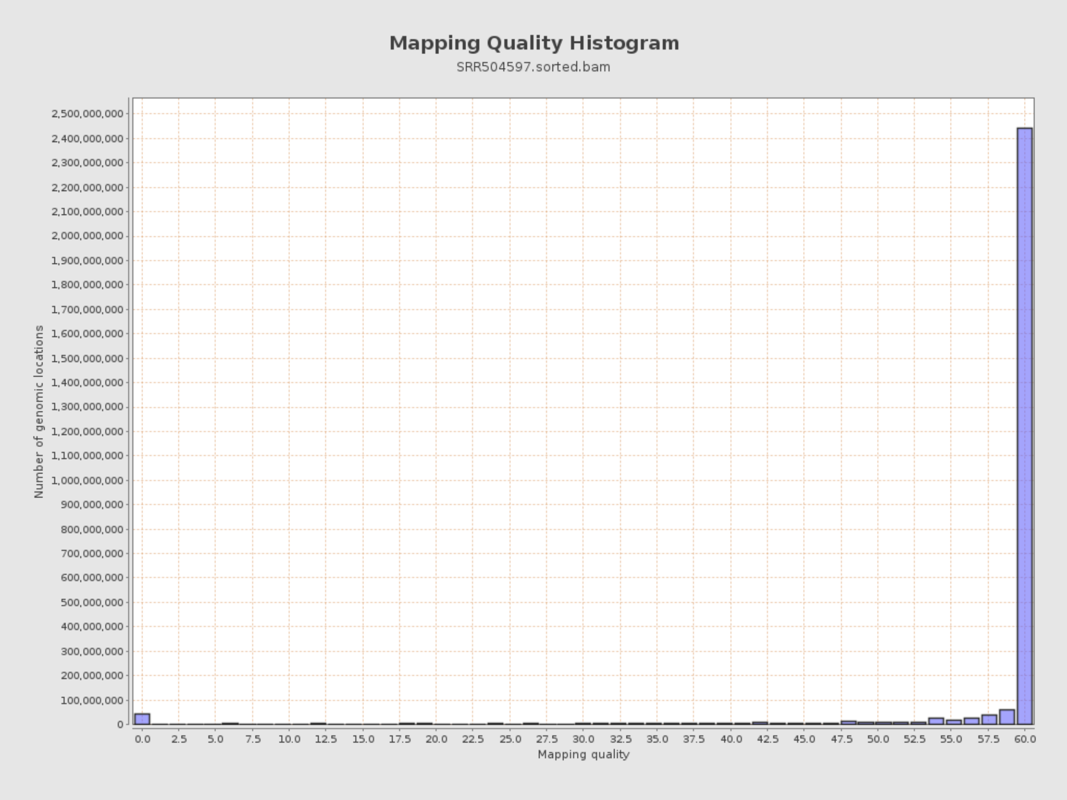
11. Results : Homopolymer Indels



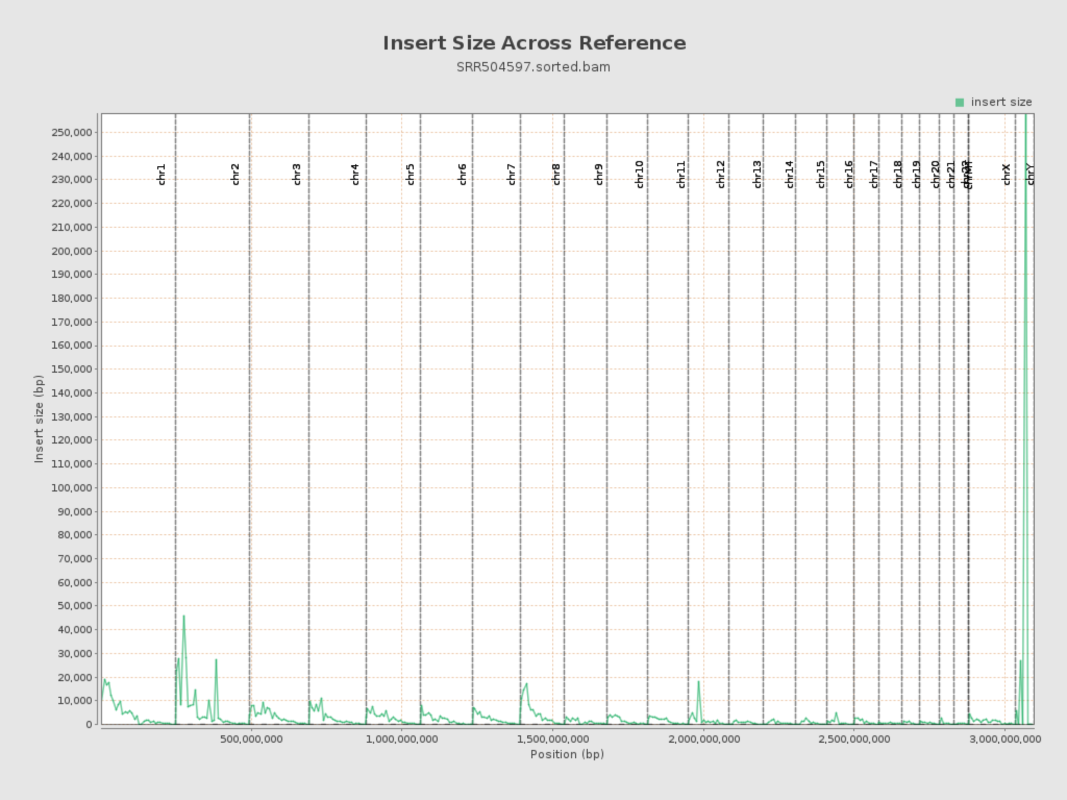
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram