Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 10:45:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124858.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_SRR3124858 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124858_1.fastq.gz SRR3124858_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 10:45:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124858.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	134,103,648
Mapped reads	131,381,175 / 97.97%
Unmapped reads	2,722,473 / 2.03%
Mapped paired reads	131,381,175 / 97.97%
Mapped reads, first in pair	65,718,108 / 49.01%
Mapped reads, second in pair	65,663,067 / 48.96%
Mapped reads, both in pair	130,795,226 / 97.53%
Mapped reads, singletons	585,949 / 0.44%
Secondary alignments	0
Supplementary alignments	21,730,575 / 16.2%
Read min/max/mean length	30 / 125 / 132.74
Duplicated reads (estimated)	61,138,443 / 45.59%
Duplication rate	35.92%
Clipped reads	116,383,356 / 86.79%

2.2. ACGT Content

Number/percentage of A's	4,055,054,788 / 28.77%
Number/percentage of C's	2,984,396,421 / 21.18%
Number/percentage of T's	3,975,231,846 / 28.21%
Number/percentage of G's	3,075,906,102 / 21.83%
Number/percentage of N's	2,030,557 / 0.01%

GC Percentage	43%

2.3. Coverage

Mean	4.5569
Standard Deviation	197.0583

2.4. Mapping Quality

Mean Mapping Quality	46.64

2.5. Insert size

Mean	715,353.19
Standard Deviation	8,206,147.64
P25/Median/P75	88 / 113 / 144

2.6. Mismatches and indels

General error rate	1.58%
Mismatches	209,865,081
Insertions	4,837,739
Mapped reads with at least one insertion	3.49%
Deletions	5,622,019
Mapped reads with at least one deletion	4.05%
Homopolymer indels	37.22%

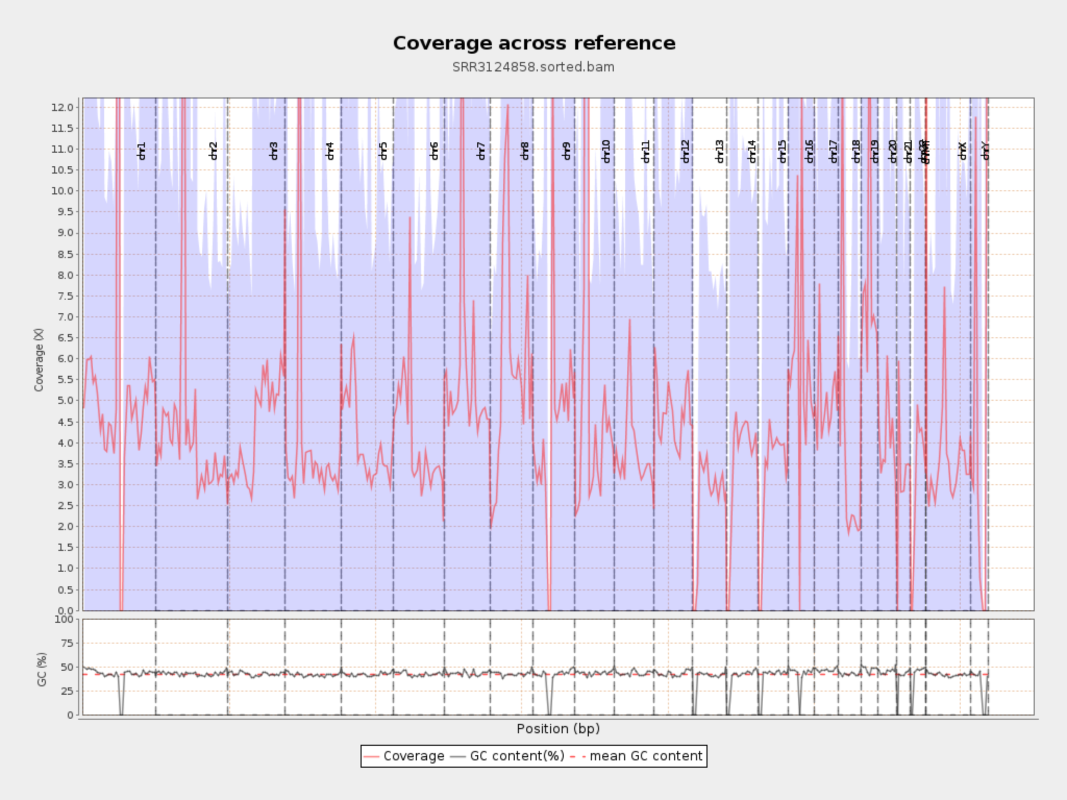
2.7. Chromosome stats

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

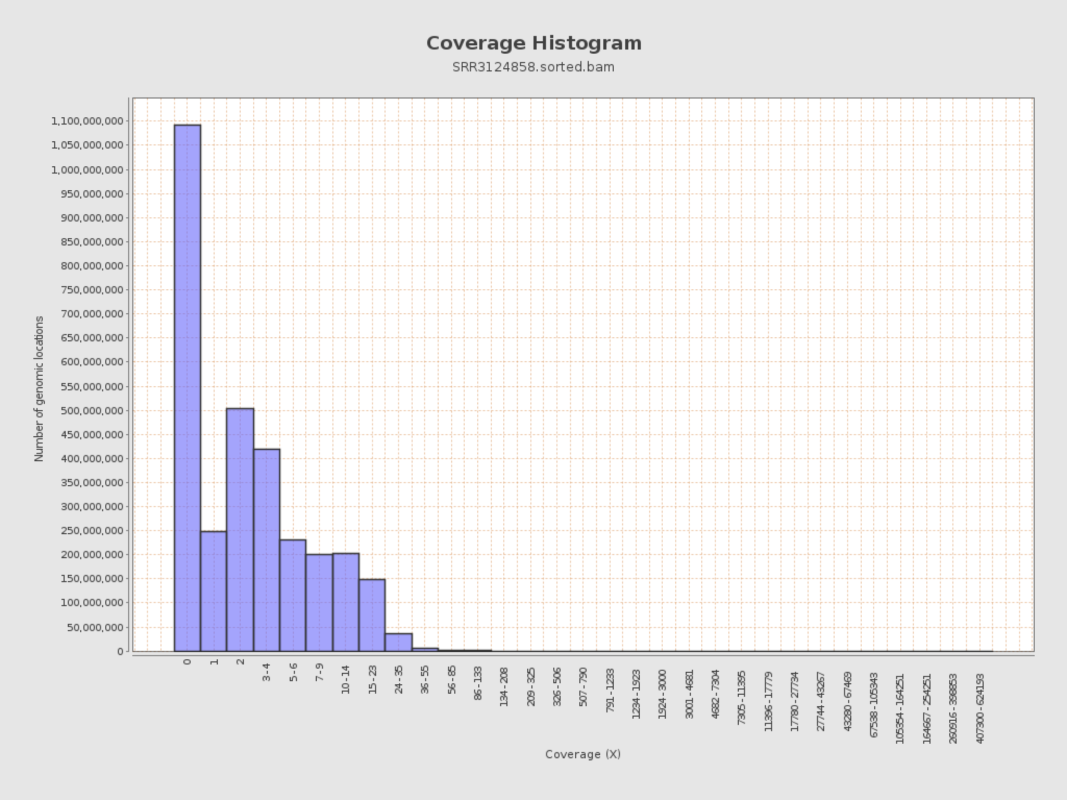
		bases	coverage	deviation
chr1	249250621	1378300974	5.5298	588.5141
chr2	243199373	1089659796	4.4805	93.0758
chr3	198022430	858930498	4.3375	30.0825
chr4	191154276	766983355	4.0124	95.545
chr5	180915260	737517113	4.0766	13.6789
chr6	171115067	703454698	4.111	52.8401
chr7	159138663	926721000	5.8234	149.2433
chr8	146364022	852049693	5.8214	66.8332
chr9	141213431	621054304	4.398	148.5353
chr10	135534747	853937421	6.3005	290.9595
chr11	135006516	515006856	3.8147	46.1085
chr12	133851895	636950884	4.7586	34.3692
chr13	115169878	302841856	2.6295	4.8045
chr14	107349540	381019704	3.5493	11.6622
chr15	102531392	324130780	3.1613	24.1248
chr16	90354753	535862828	5.9307	59.0943
chr17	81195210	407773365	5.0221	58.1939
chr18	78077248	299535780	3.8364	189.4302
chr19	59128983	475400677	8.0401	299.6066
chr20	63025520	255786970	4.0585	31.8952
chr21	48129895	160718948	3.3393	52.4337
chr22	51304566	154404756	3.0096	25.3768
chrMT	16571	32511395	1,961.9453	843.6234
chrX	155270560	553941688	3.5676	30.8106

chrY	59373566	282291871	4.7545	121.4766

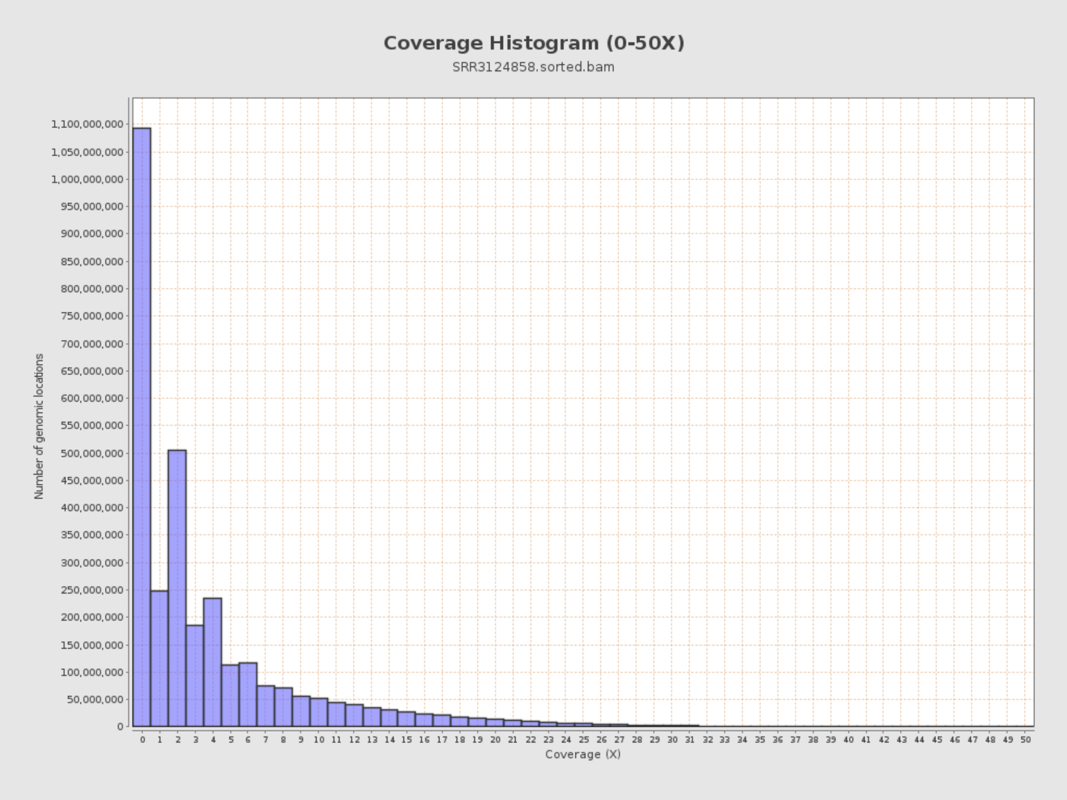
3. Results : Coverage across reference



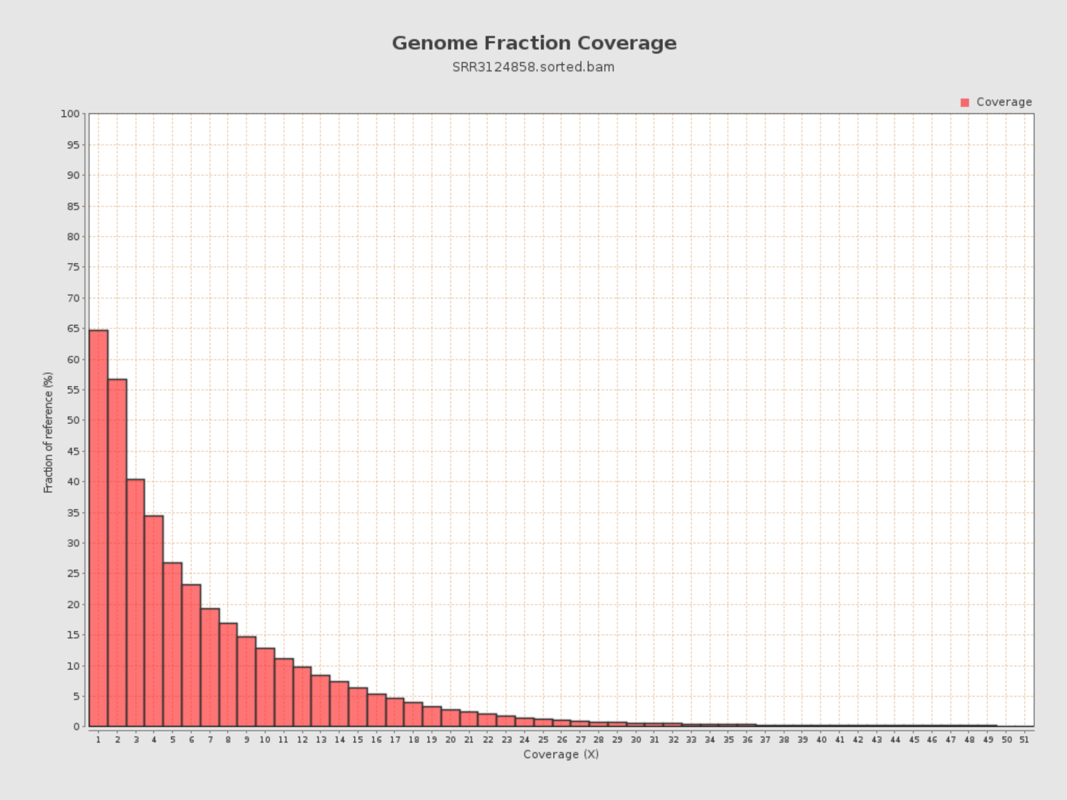
4. Results : Coverage Histogram



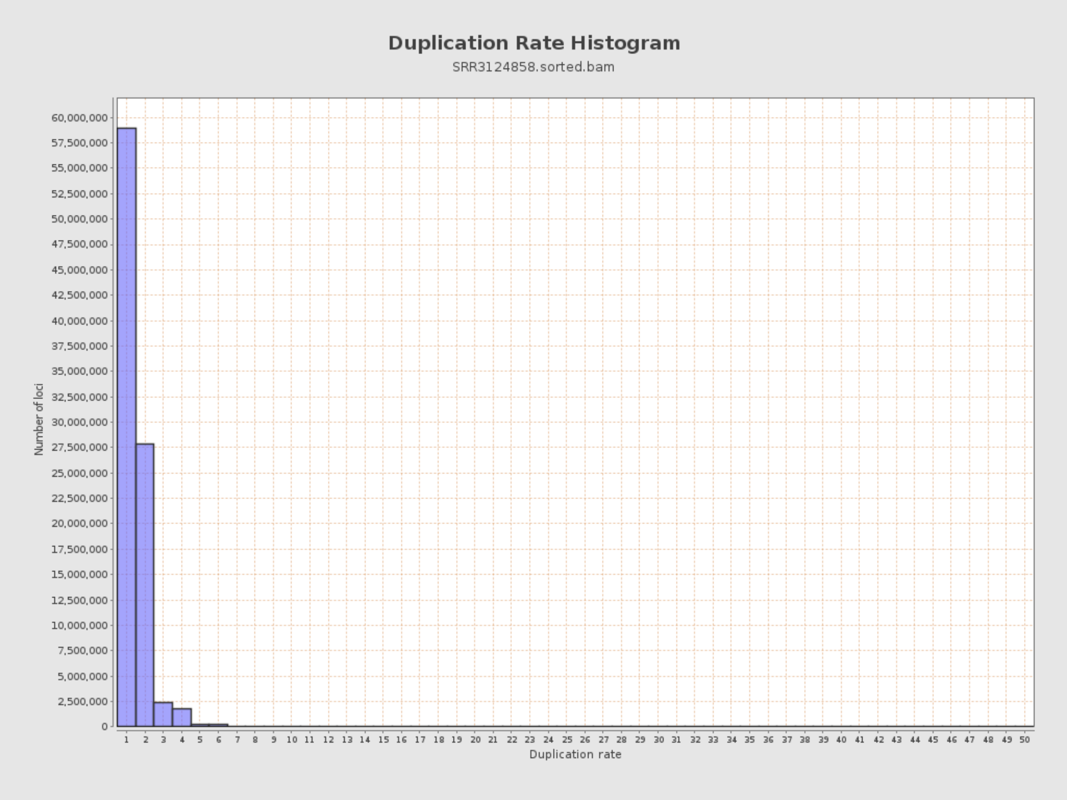
5. Results : Coverage Histogram (0-50X)



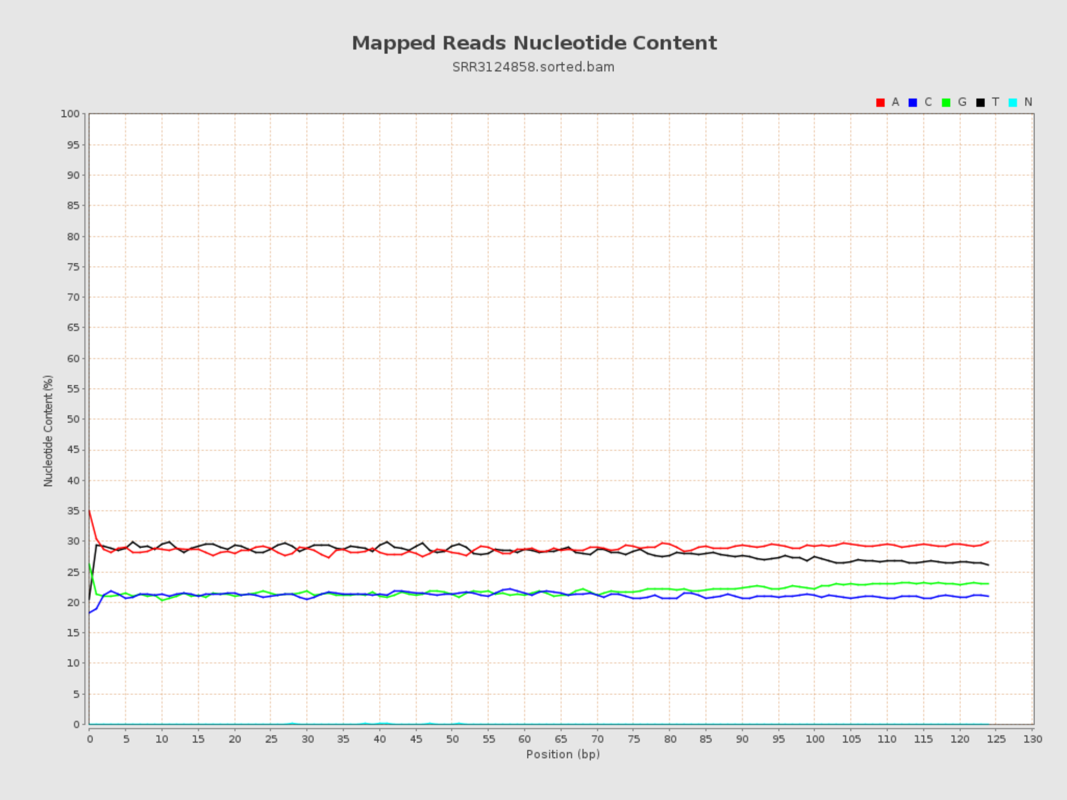
6. Results : Genome Fraction Coverage



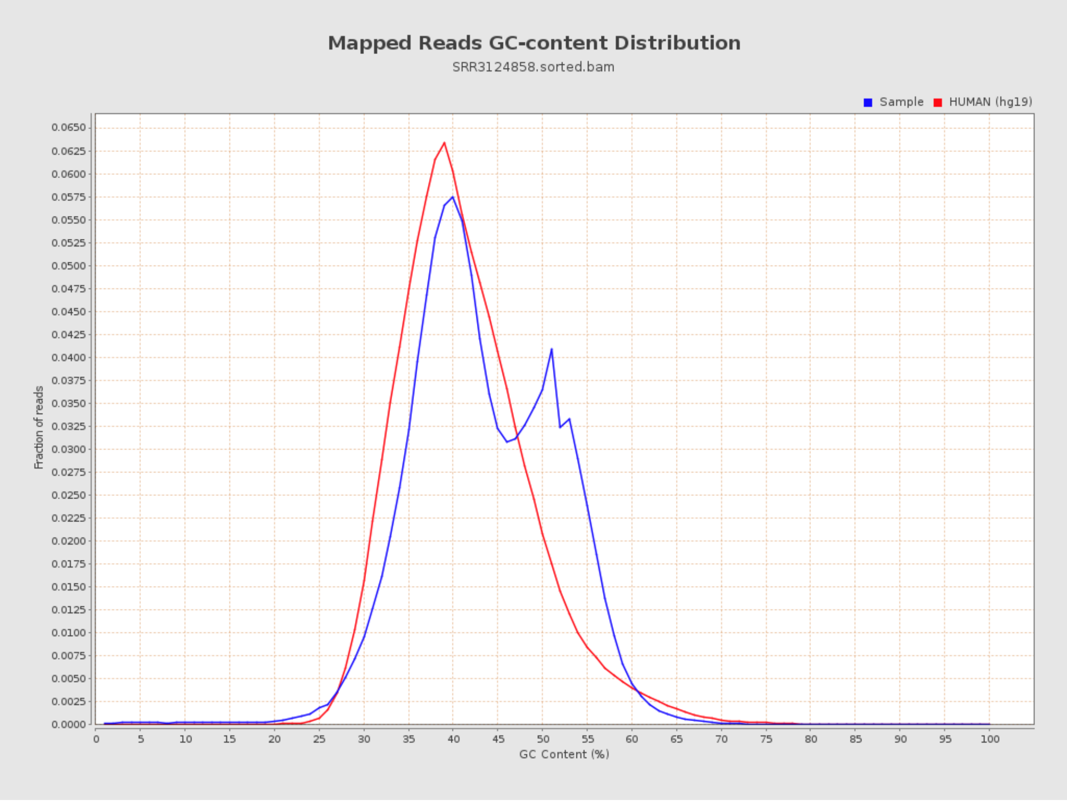
7. Results : Duplication Rate Histogram



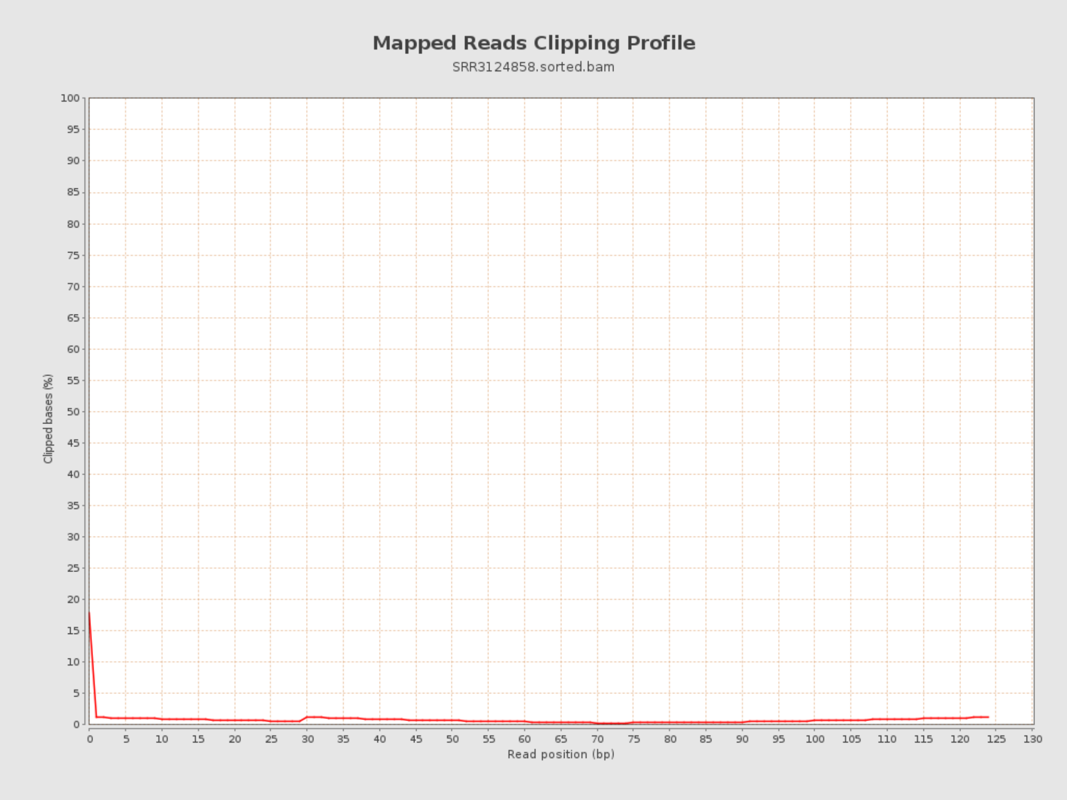
8. Results : Mapped Reads Nucleotide Content



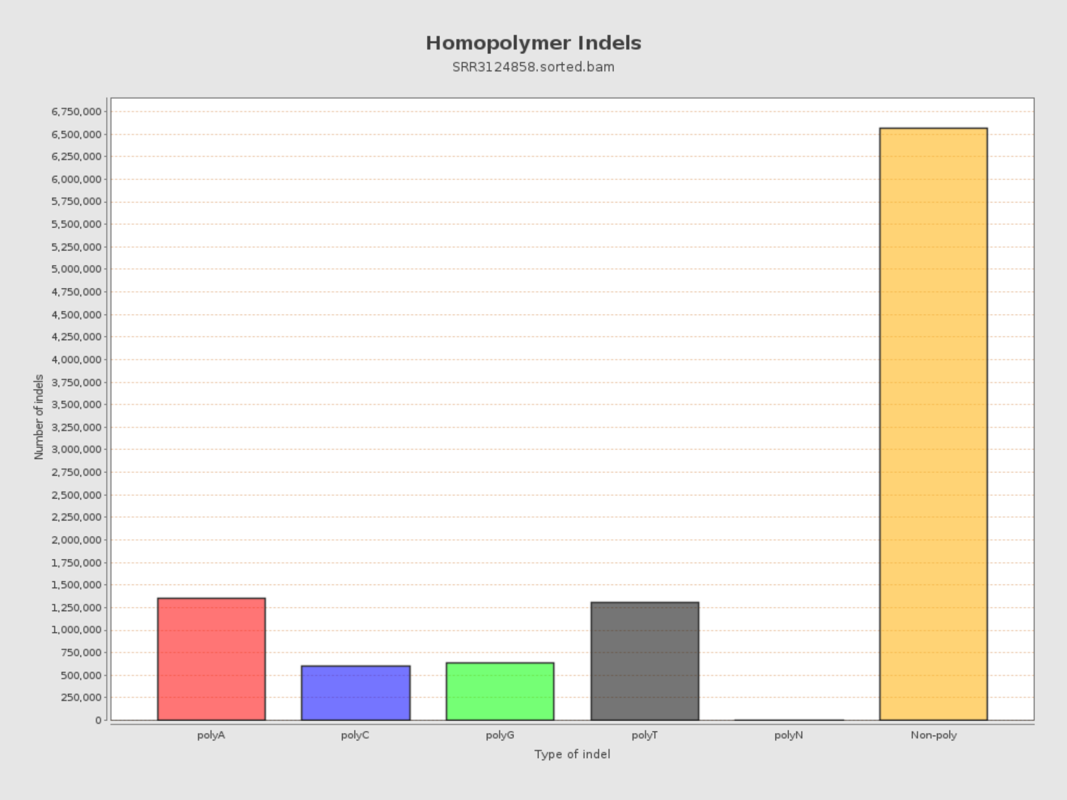
9. Results : Mapped Reads GC-content Distribution



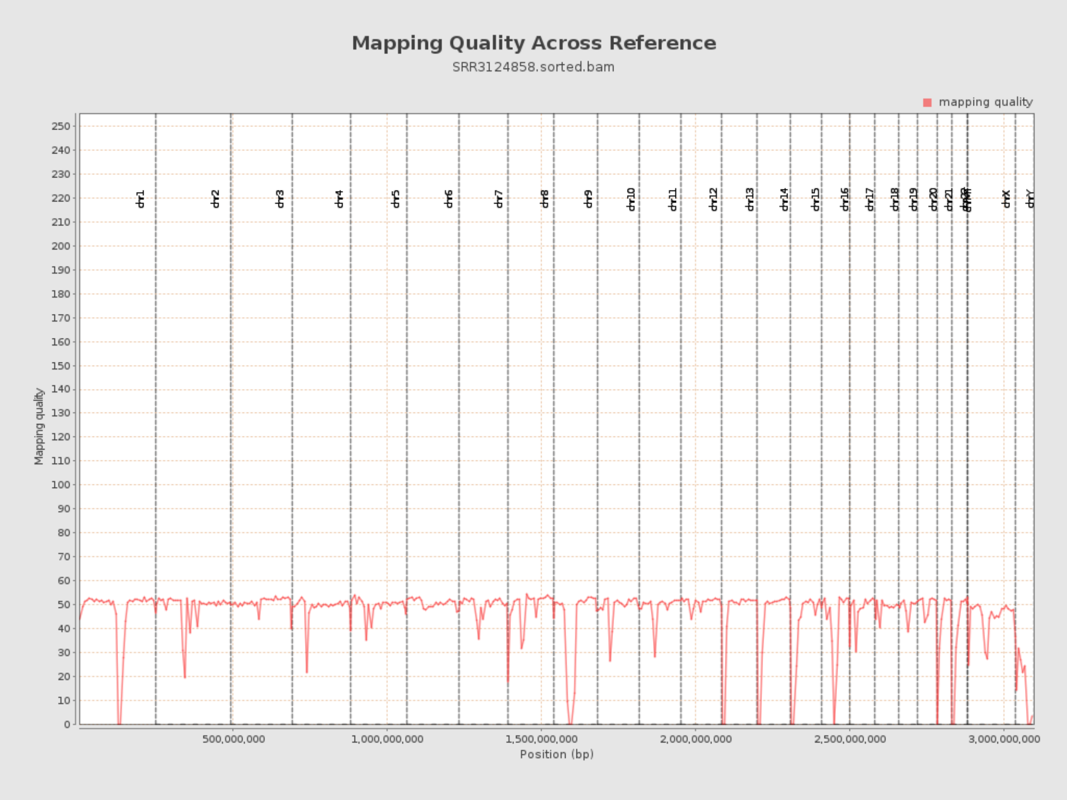
10. Results : Mapped Reads Clipping Profile



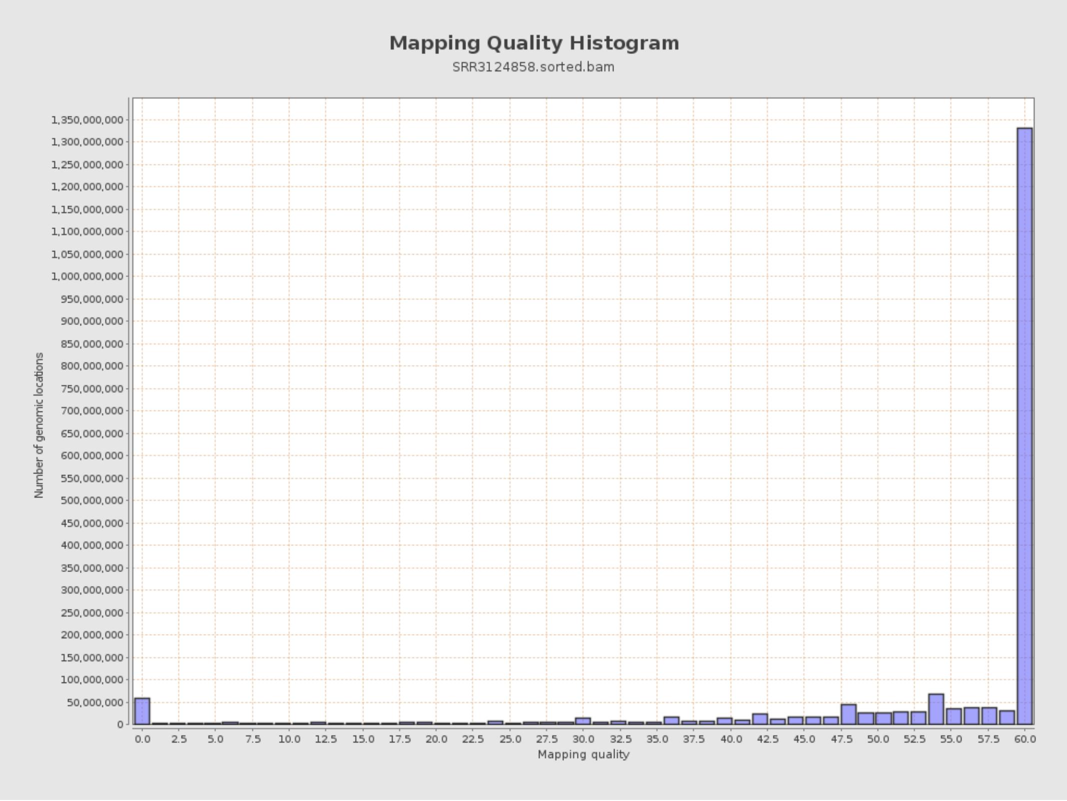
11. Results : Homopolymer Indels



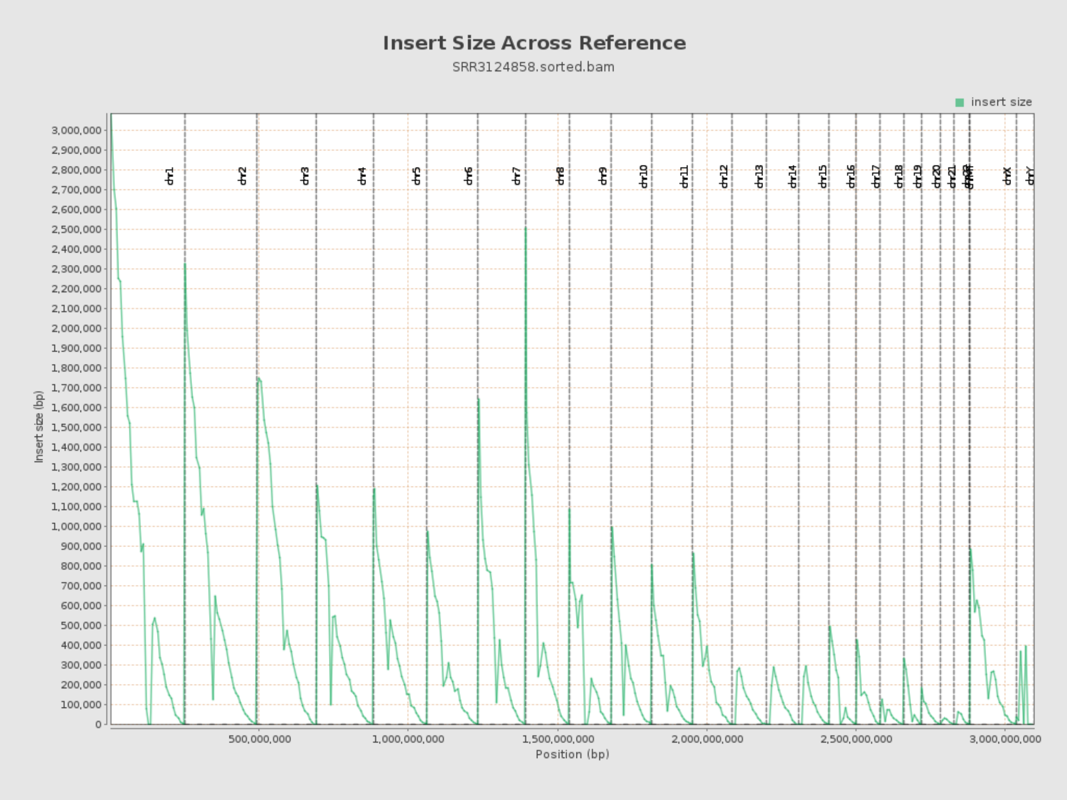
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram