Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 10:13:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124958.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_SRR3124958 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124958_1.fastq.gz SRR3124958_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 10:13:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124958.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,036,918
Mapped reads	5,897,505 / 97.69%
Unmapped reads	139,413 / 2.31%
Mapped paired reads	5,897,505 / 97.69%
Mapped reads, first in pair	2,957,178 / 48.98%
Mapped reads, second in pair	2,940,327 / 48.71%
Mapped reads, both in pair	5,859,570 / 97.06%
Mapped reads, singletons	37,935 / 0.63%
Secondary alignments	0
Supplementary alignments	60,854 / 1.01%
Read min/max/mean length	30 / 101 / 101.4
Duplicated reads (estimated)	887,282 / 14.7%
Duplication rate	9.82%
Clipped reads	3,273,477 / 54.22%

2.2. ACGT Content

Number/percentage of A's	142,580,507 / 28.46%
Number/percentage of C's	93,073,040 / 18.58%
Number/percentage of T's	150,524,135 / 30.05%
Number/percentage of G's	114,718,092 / 22.9%
Number/percentage of N's	5,235 / 0%

GC Percentage	41.48%

2.3. Coverage

Mean	0.1619
Standard Deviation	2.6133

2.4. Mapping Quality

Mean Mapping Quality	52.17

2.5. Insert size

Mean	96,848.93
Standard Deviation	2,935,443.74
P25/Median/P75	127 / 172 / 237

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	4,157,094
Insertions	90,924
Mapped reads with at least one insertion	1.48%
Deletions	174,342
Mapped reads with at least one deletion	2.88%
Homopolymer indels	44.24%

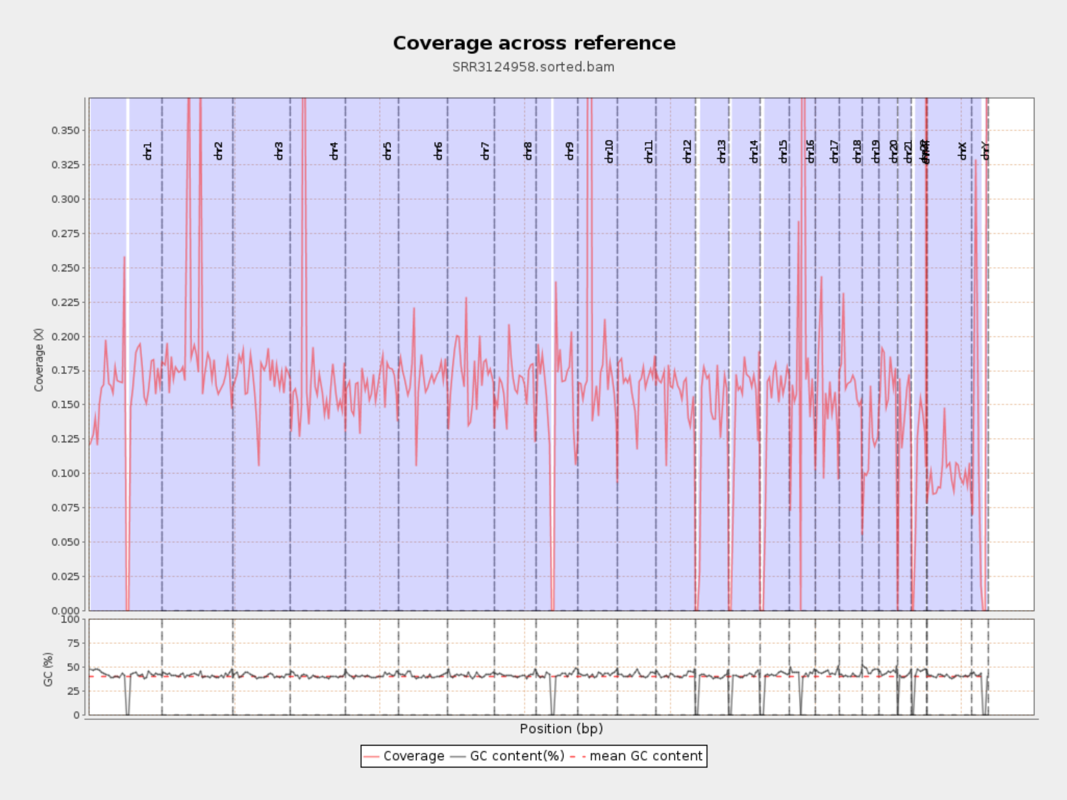
2.7. Chromosome stats

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

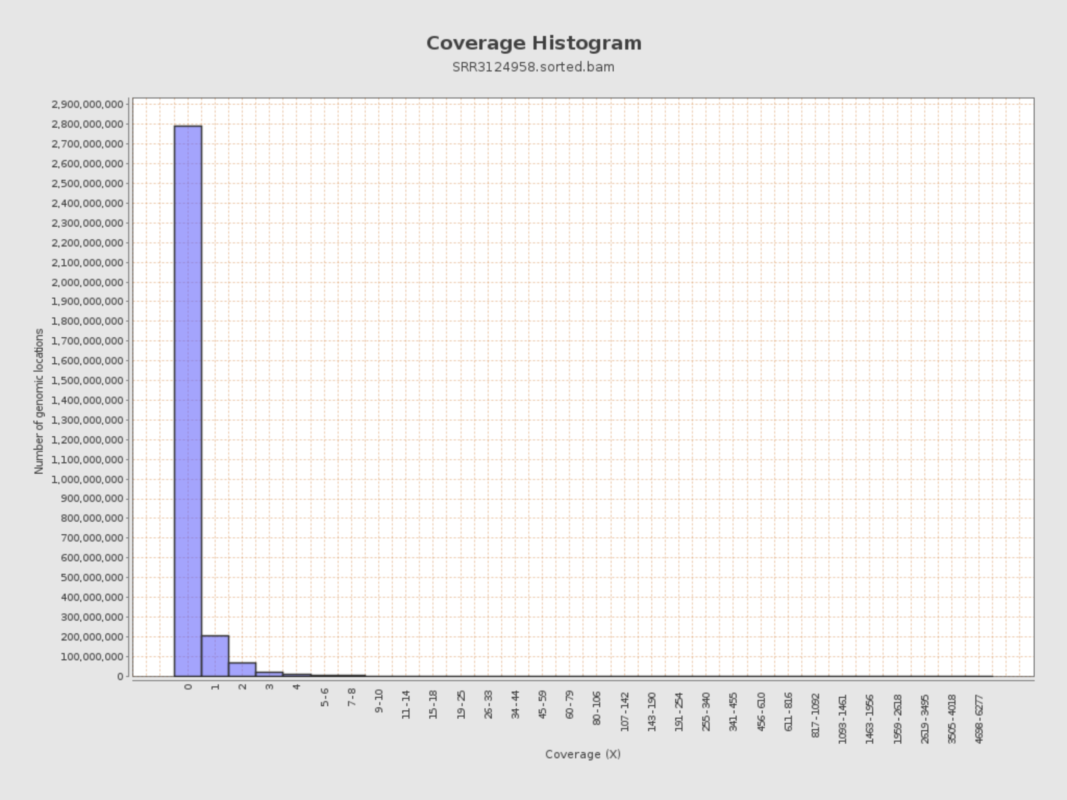
		bases	coverage	deviation
chr1	249250621	39026717	0.1566	1.6219
chr2	243199373	47259716	0.1943	3.3817
chr3	198022430	33560725	0.1695	0.6953
chr4	191154276	33126106	0.1733	2.2964
chr5	180915260	29501621	0.1631	0.6675
chr6	171115067	29147970	0.1703	0.9894
chr7	159138663	27607686	0.1735	1.4519
chr8	146364022	24105377	0.1647	0.7925
chr9	141213431	21446093	0.1519	2.2376
chr10	135534747	30460834	0.2247	9.0333
chr11	135006516	22330482	0.1654	1.1104
chr12	133851895	21247414	0.1587	0.5899
chr13	115169878	15095305	0.1311	0.5245
chr14	107349540	14668894	0.1366	0.7186
chr15	102531392	13928365	0.1358	0.558
chr16	90354753	18000680	0.1992	4.1229
chr17	81195210	12421682	0.153	1.6952
chr18	78077248	13358619	0.1711	2.439
chr19	59128983	6949328	0.1175	1.0137
chr20	63025520	10523088	0.167	0.9092
chr21	48129895	6454866	0.1341	1.1677
chr22	51304566	4911283	0.0957	0.5716
chrMT	16571	1583284	95.5455	53.1693
chrX	155270560	15337047	0.0988	0.7753

chrY	59373566	9192693	0.1548	4.3141

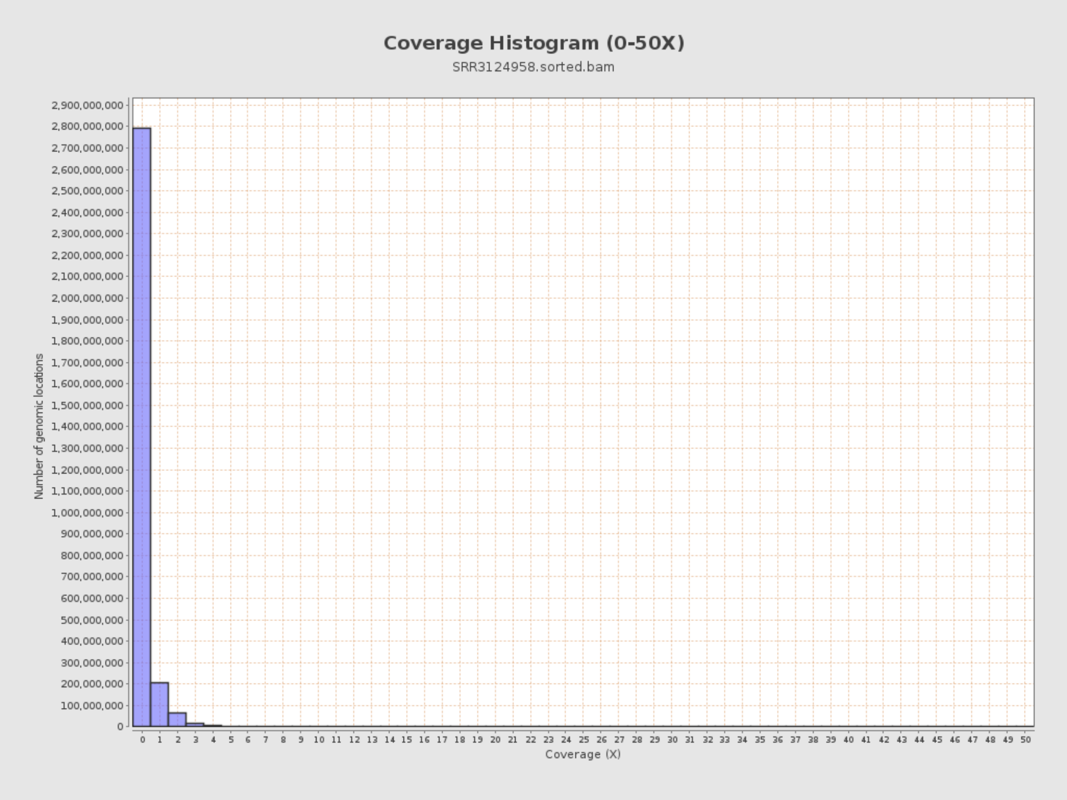
3. Results : Coverage across reference



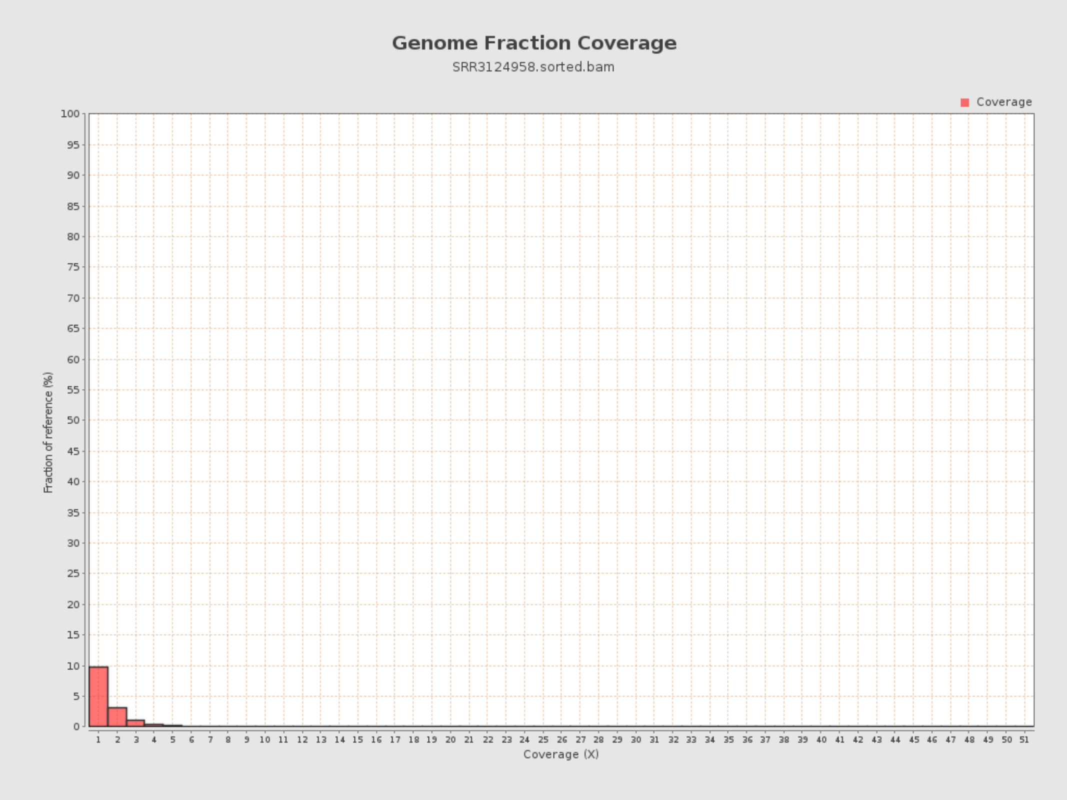
4. Results : Coverage Histogram



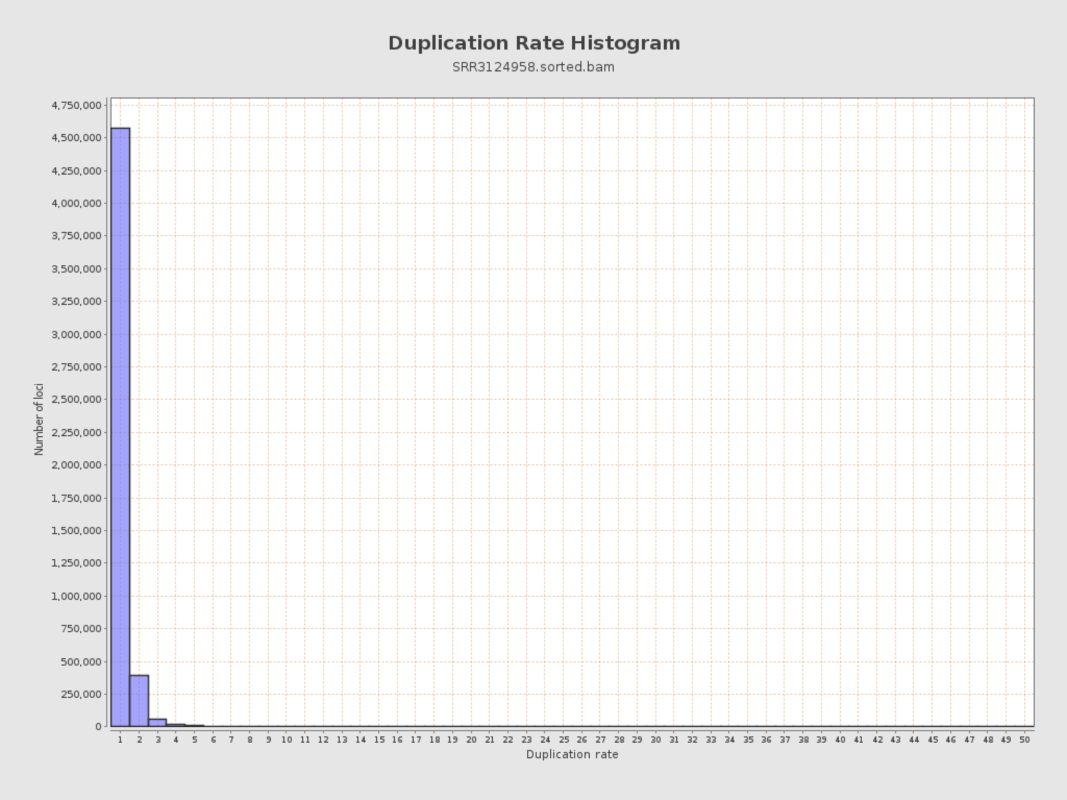
5. Results : Coverage Histogram (0-50X)



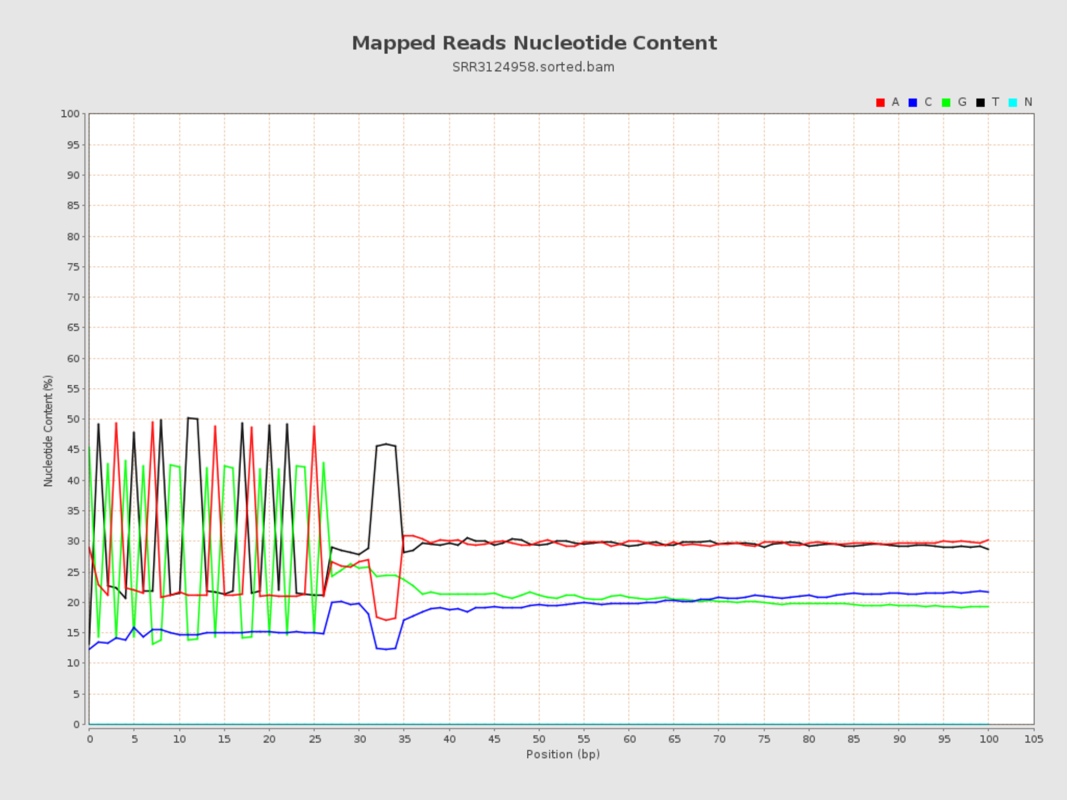
6. Results : Genome Fraction Coverage



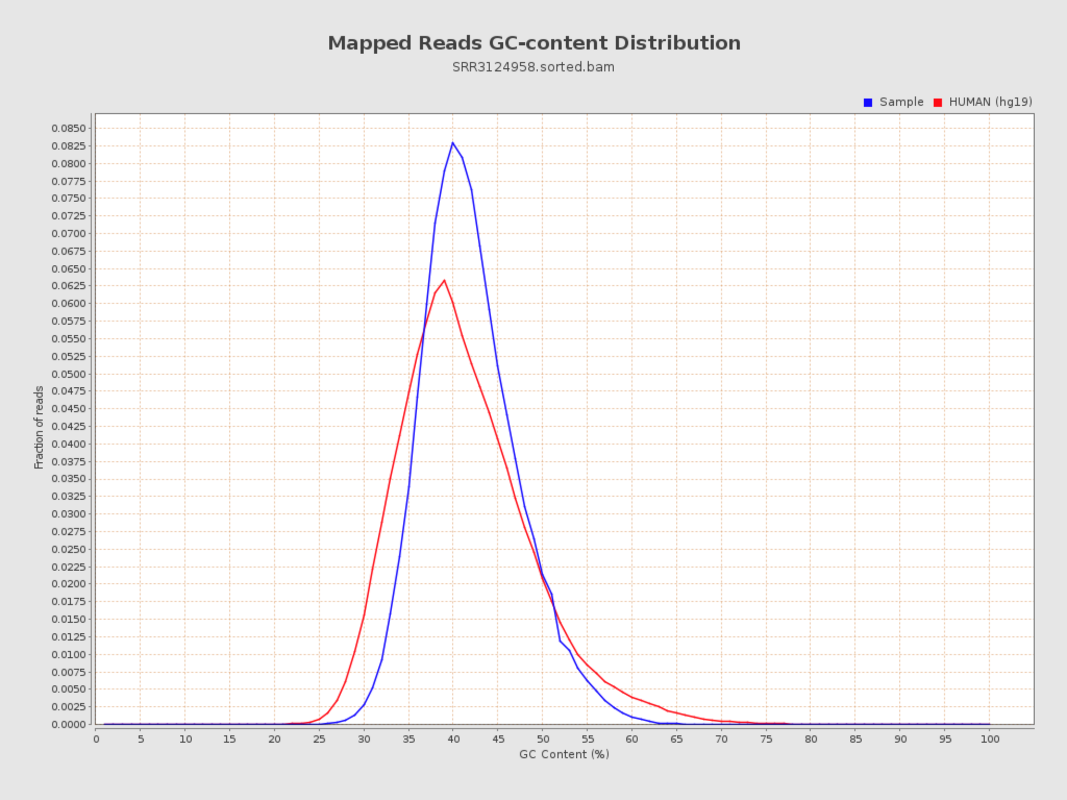
7. Results : Duplication Rate Histogram



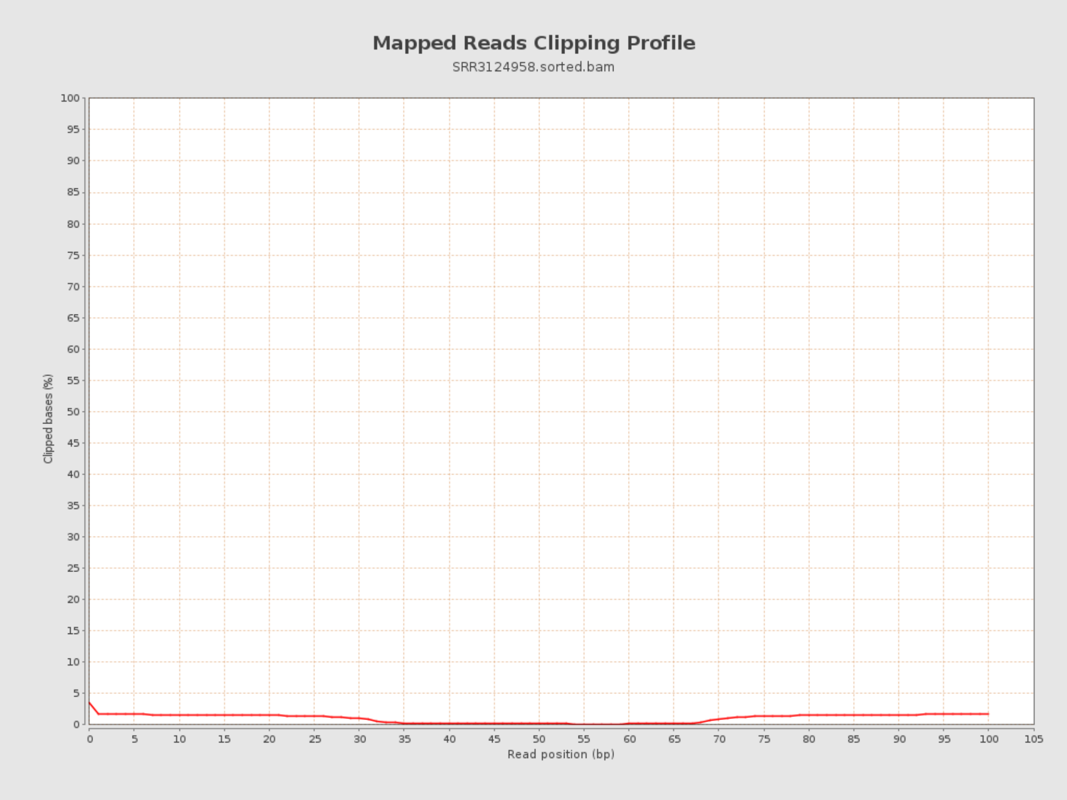
8. Results : Mapped Reads Nucleotide Content



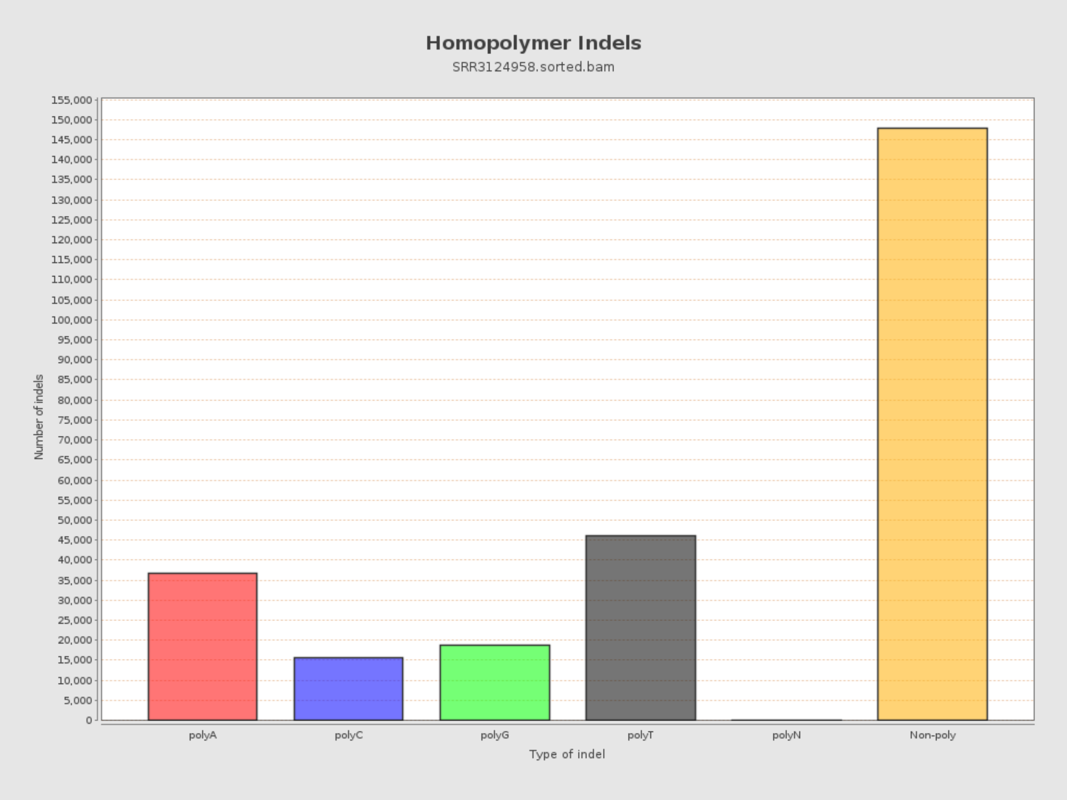
9. Results : Mapped Reads GC-content Distribution



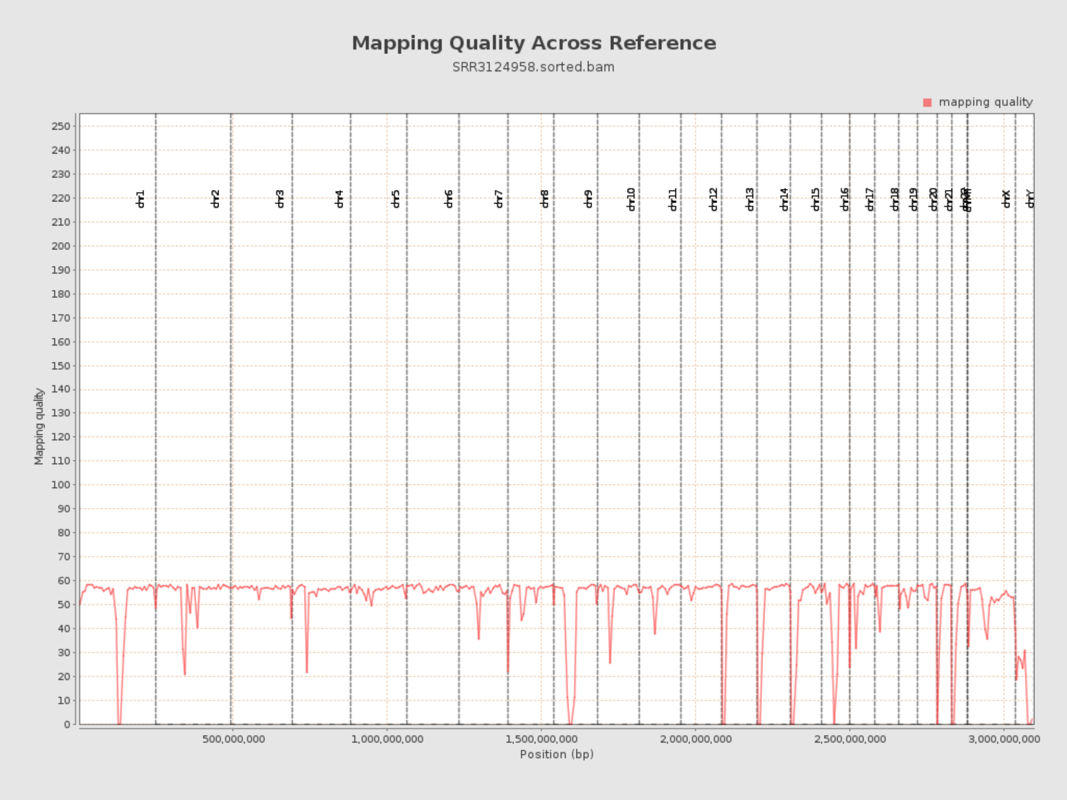
10. Results : Mapped Reads Clipping Profile



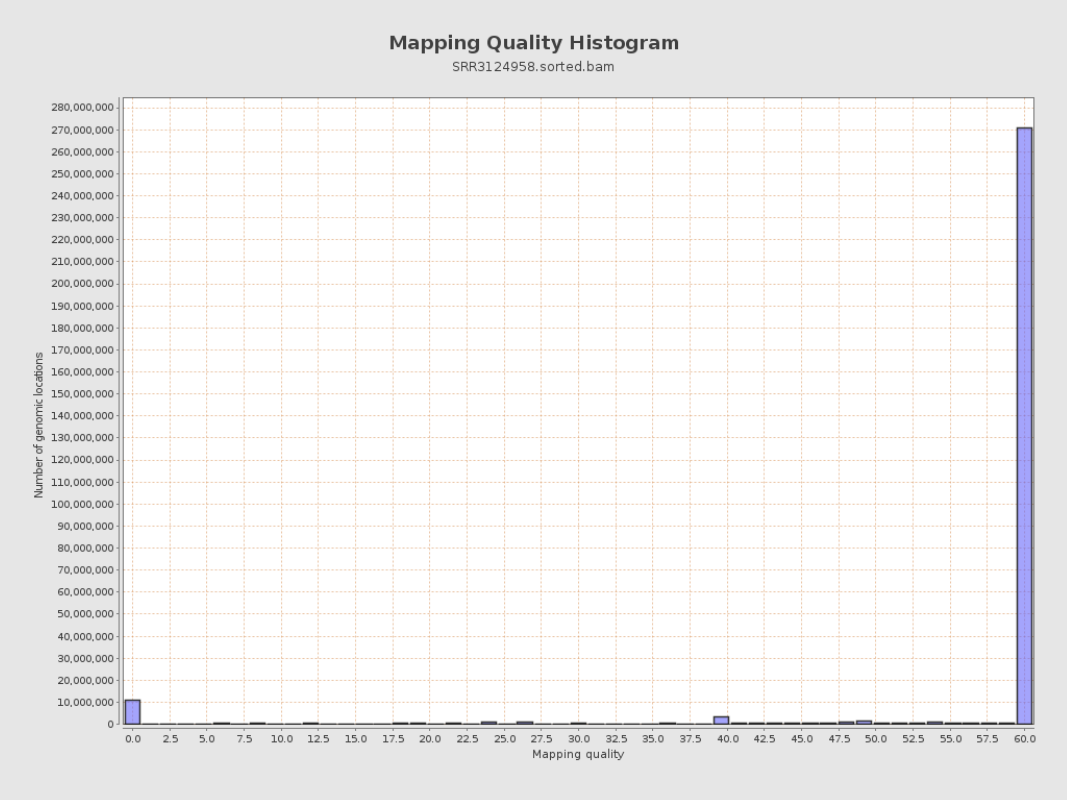
11. Results : Homopolymer Indels



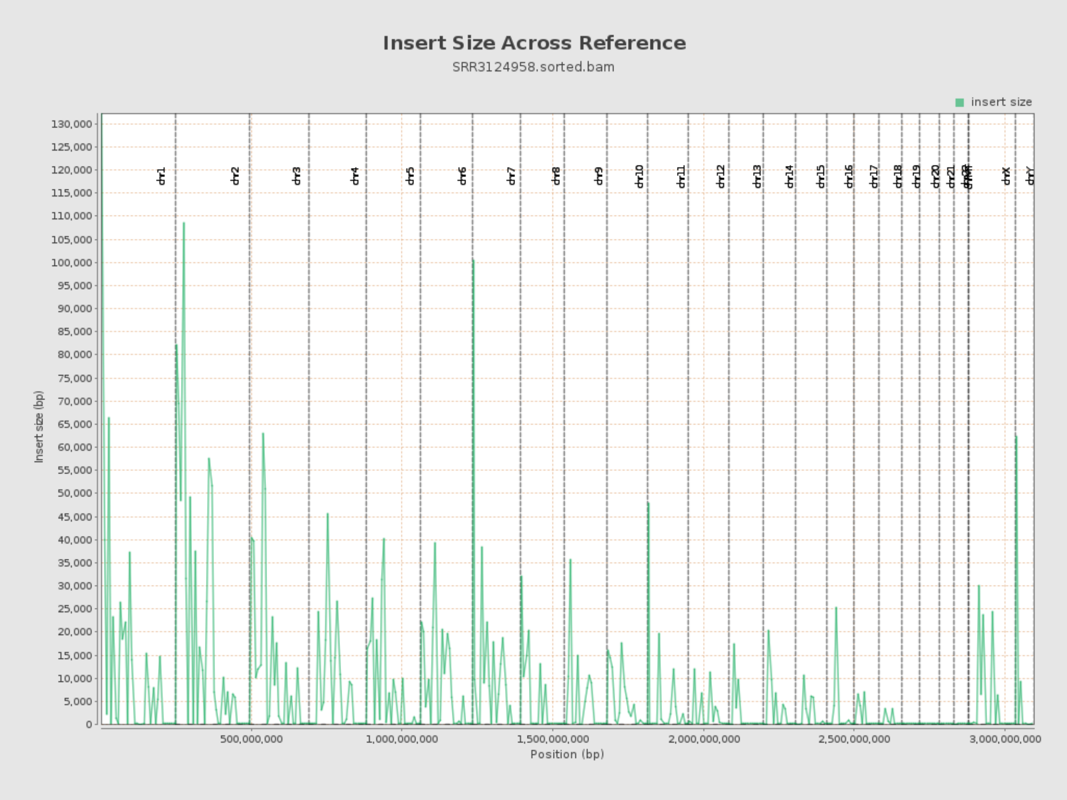
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram