Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 02:36:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124898.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_SRR3124898 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124898_1.fastq.gz SRR3124898_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 02:36:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124898.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,258,960
Mapped reads	6,180,016 / 98.74%
Unmapped reads	78,944 / 1.26%
Mapped paired reads	6,180,016 / 98.74%
Mapped reads, first in pair	3,091,643 / 49.4%
Mapped reads, second in pair	3,088,373 / 49.34%
Mapped reads, both in pair	6,154,668 / 98.33%
Mapped reads, singletons	25,348 / 0.4%
Secondary alignments	0
Supplementary alignments	32,741 / 0.52%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	427,739 / 6.83%
Duplication rate	3.05%
Clipped reads	3,762,923 / 60.12%

2.2. ACGT Content

Number/percentage of A's	161,387,246 / 28.59%
Number/percentage of C's	110,560,617 / 19.59%
Number/percentage of T's	169,680,431 / 30.06%
Number/percentage of G's	122,864,625 / 21.77%
Number/percentage of N's	9,807 / 0%

GC Percentage	41.35%

2.3. Coverage

Mean	0.1825
Standard Deviation	2.6256

2.4. Mapping Quality

Mean Mapping Quality	52.83

2.5. Insert size

Mean	62,206.07
Standard Deviation	2,346,386.28
P25/Median/P75	138 / 171 / 217

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	4,390,329
Insertions	95,821
Mapped reads with at least one insertion	1.51%
Deletions	176,029
Mapped reads with at least one deletion	2.79%
Homopolymer indels	45.47%

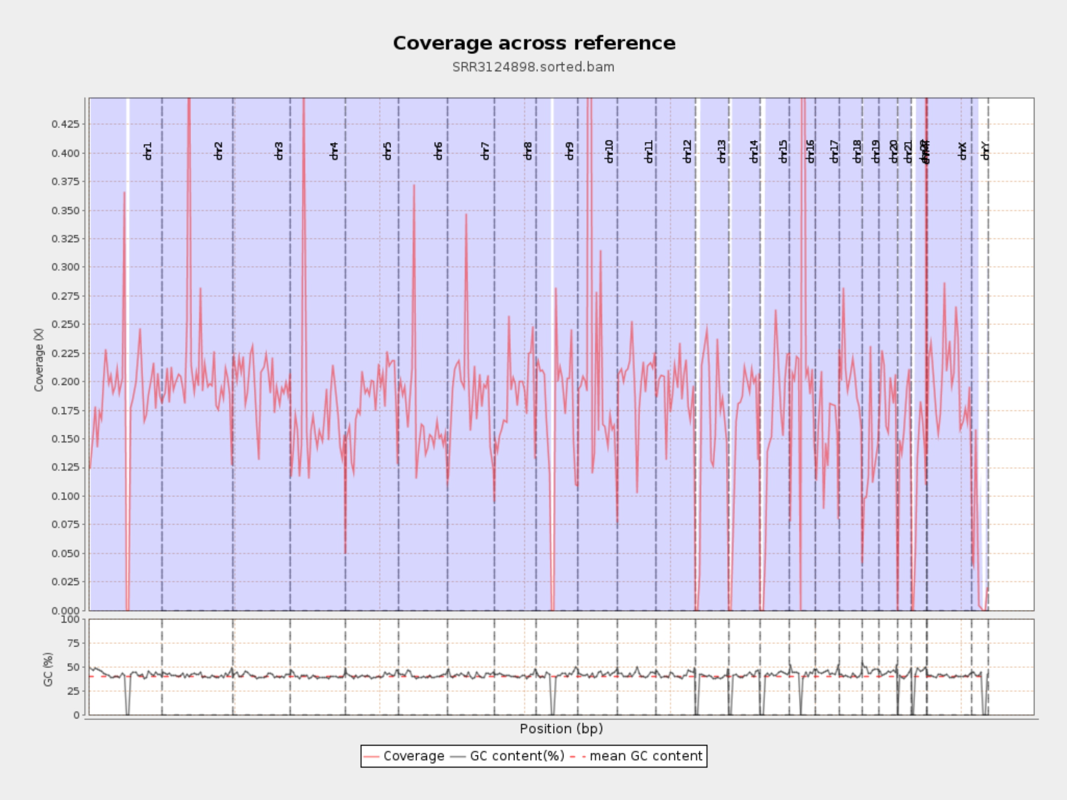
2.7. Chromosome stats

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

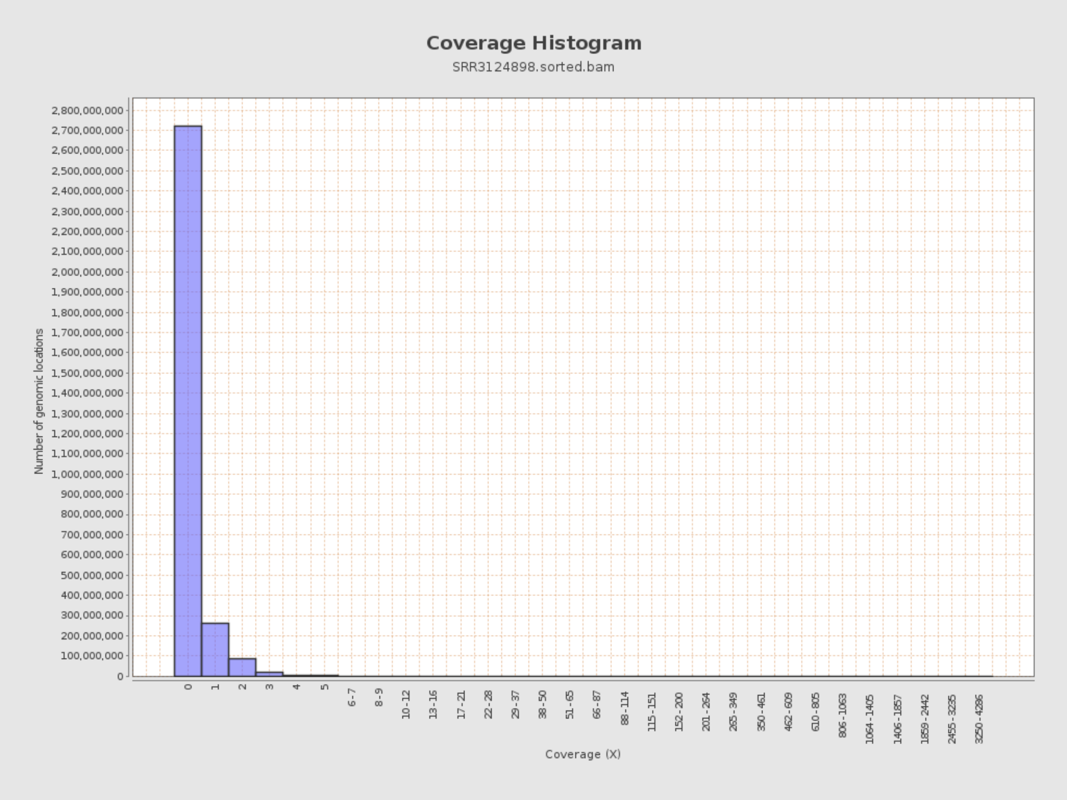
		bases	coverage	deviation
chr1	249250621	45814132	0.1838	3.1303
chr2	243199373	51626853	0.2123	2.4005
chr3	198022430	39486935	0.1994	0.7414
chr4	191154276	32469993	0.1699	1.9622
chr5	180915260	33464075	0.185	0.5759
chr6	171115067	29155694	0.1704	1.9461
chr7	159138663	30842807	0.1938	2.6488
chr8	146364022	27454835	0.1876	0.8657
chr9	141213431	24381216	0.1727	2.957
chr10	135534747	32396115	0.239	8.3626
chr11	135006516	27057201	0.2004	1.632
chr12	133851895	25747959	0.1924	0.577
chr13	115169878	17600781	0.1528	0.5024
chr14	107349540	16727283	0.1558	0.6179
chr15	102531392	15471528	0.1509	0.5038
chr16	90354753	21611696	0.2392	4.5495
chr17	81195210	12213485	0.1504	1.41
chr18	78077248	16168222	0.2071	3.1611
chr19	59128983	7635751	0.1291	1.6594
chr20	63025520	11752207	0.1865	0.7138
chr21	48129895	7110708	0.1477	0.886
chr22	51304566	5438508	0.106	0.4581
chrMT	16571	74424	4.4912	3.5266
chrX	155270560	31149205	0.2006	1.0547

chrY	59373566	1961387	0.033	2.1432

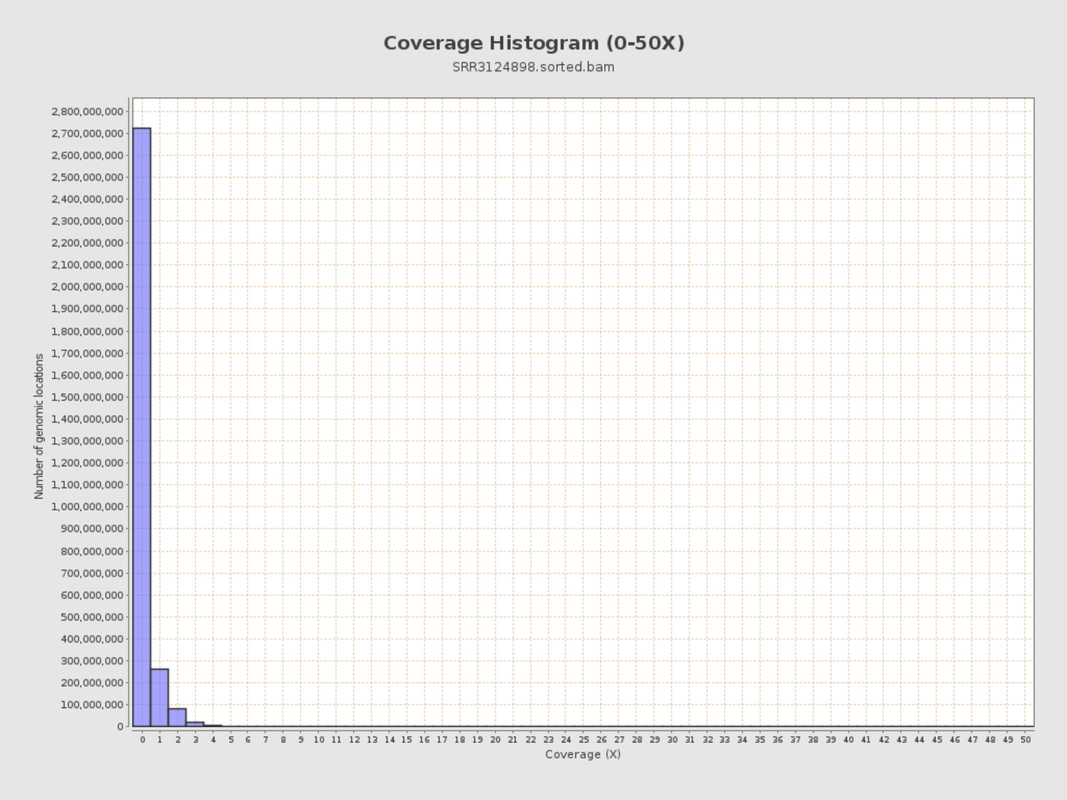
3. Results : Coverage across reference



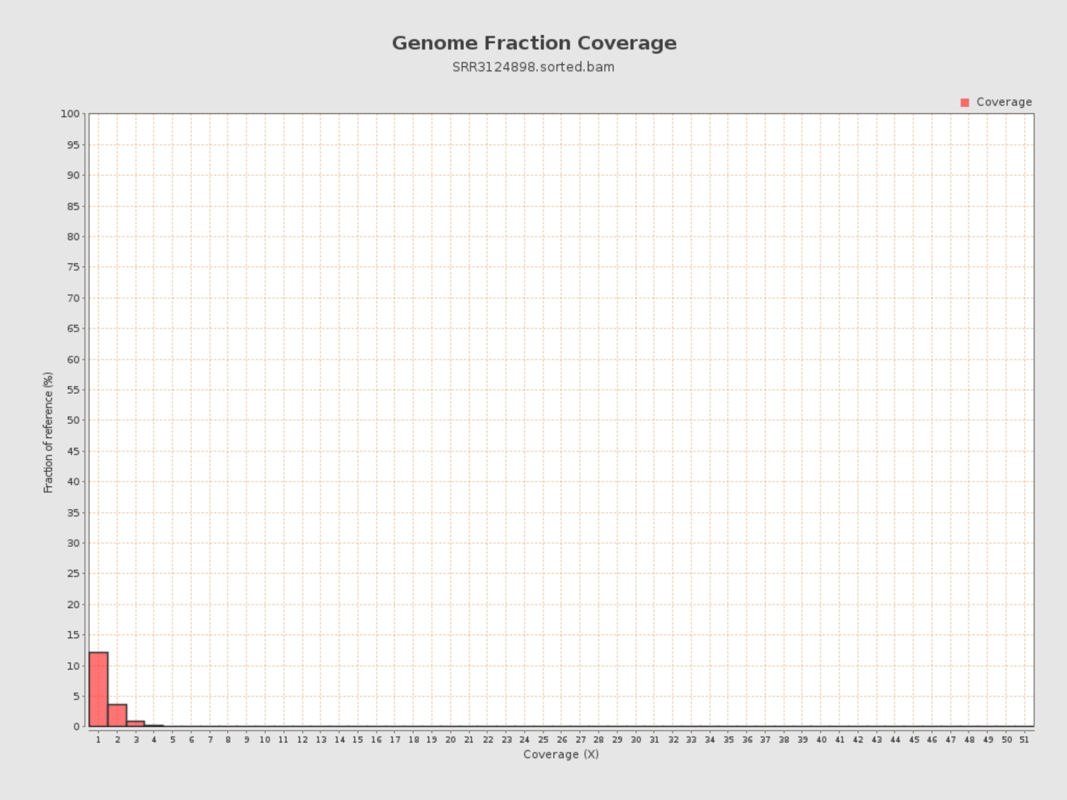
4. Results : Coverage Histogram



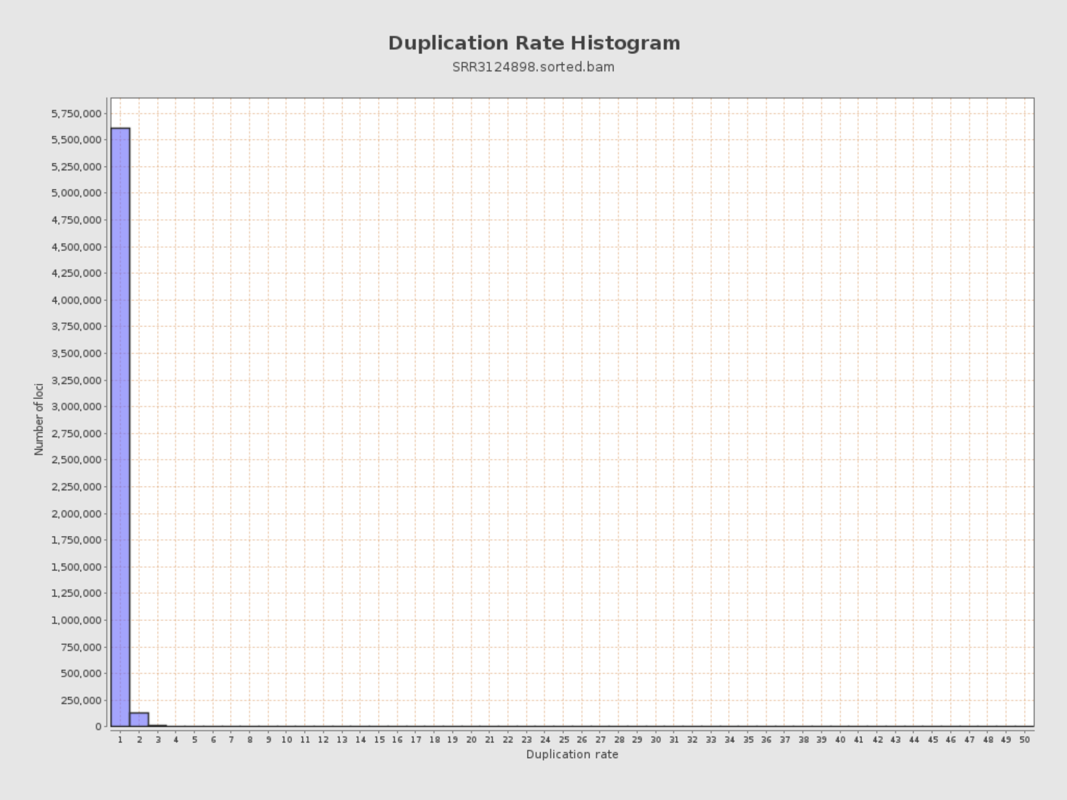
5. Results : Coverage Histogram (0-50X)



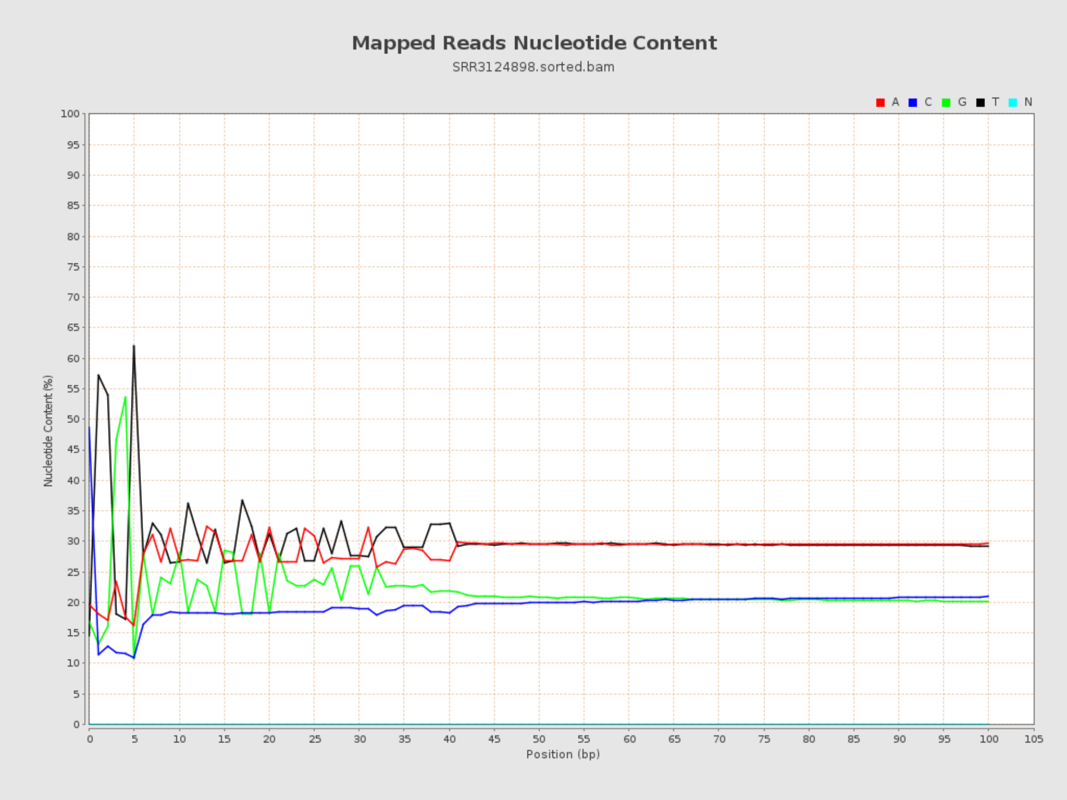
6. Results : Genome Fraction Coverage



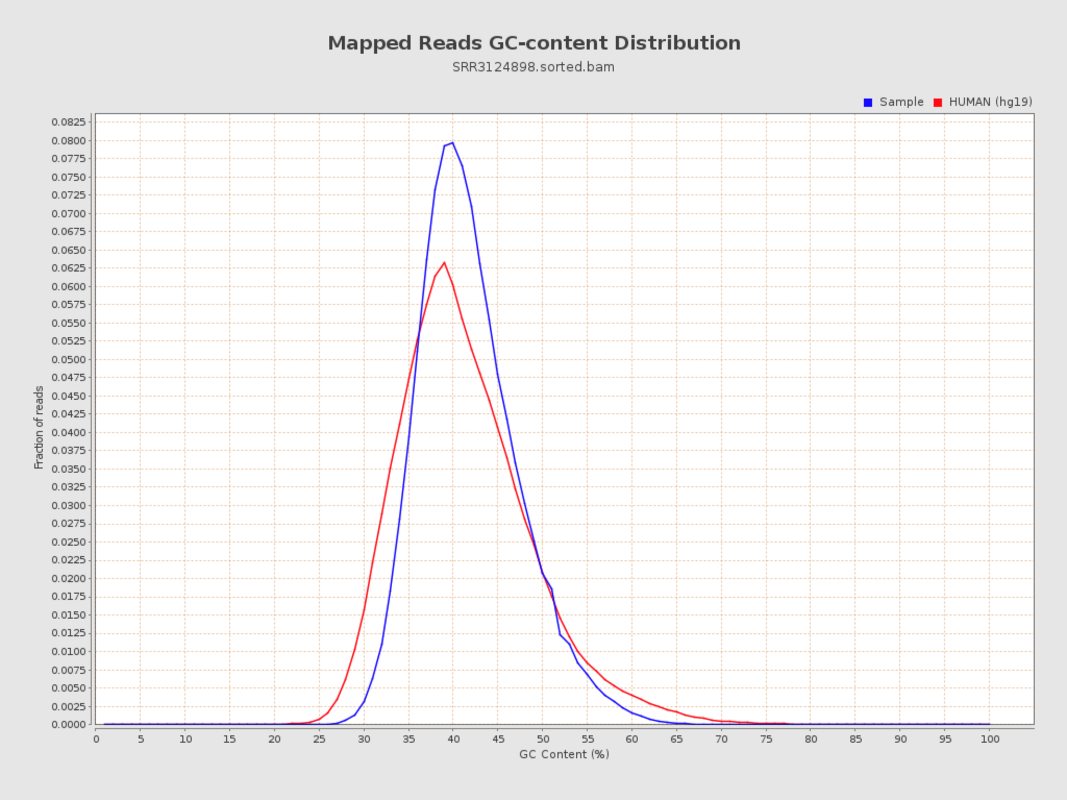
7. Results : Duplication Rate Histogram



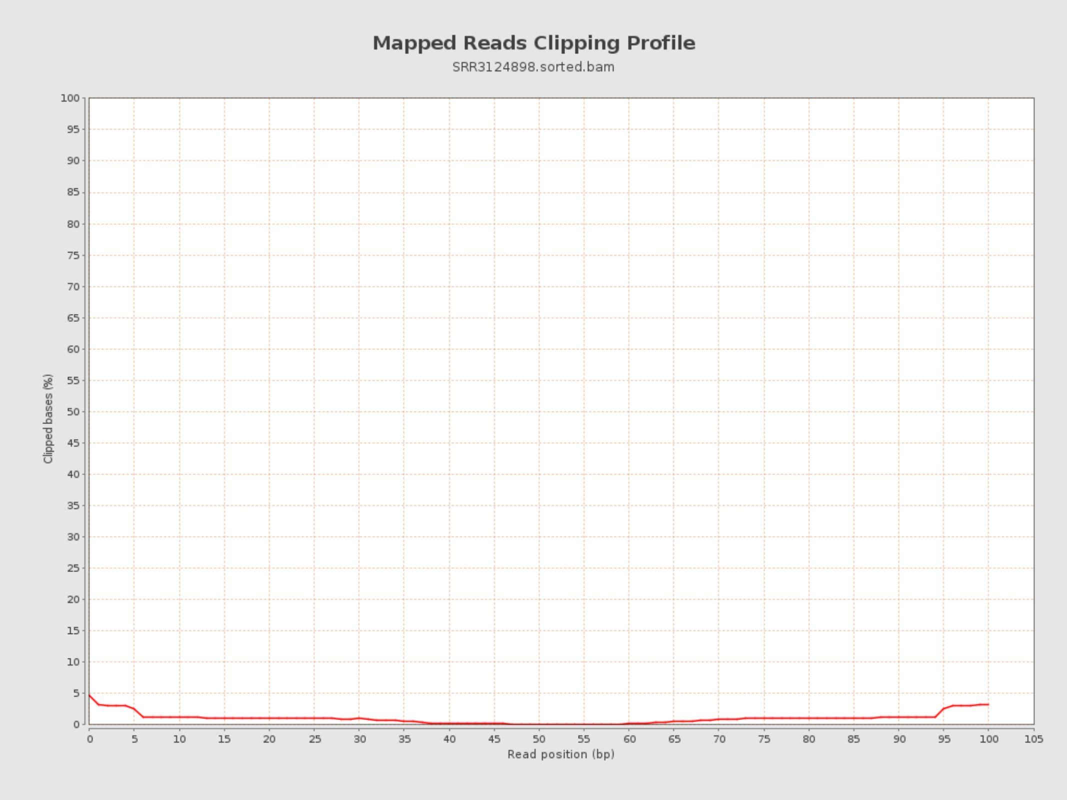
8. Results : Mapped Reads Nucleotide Content



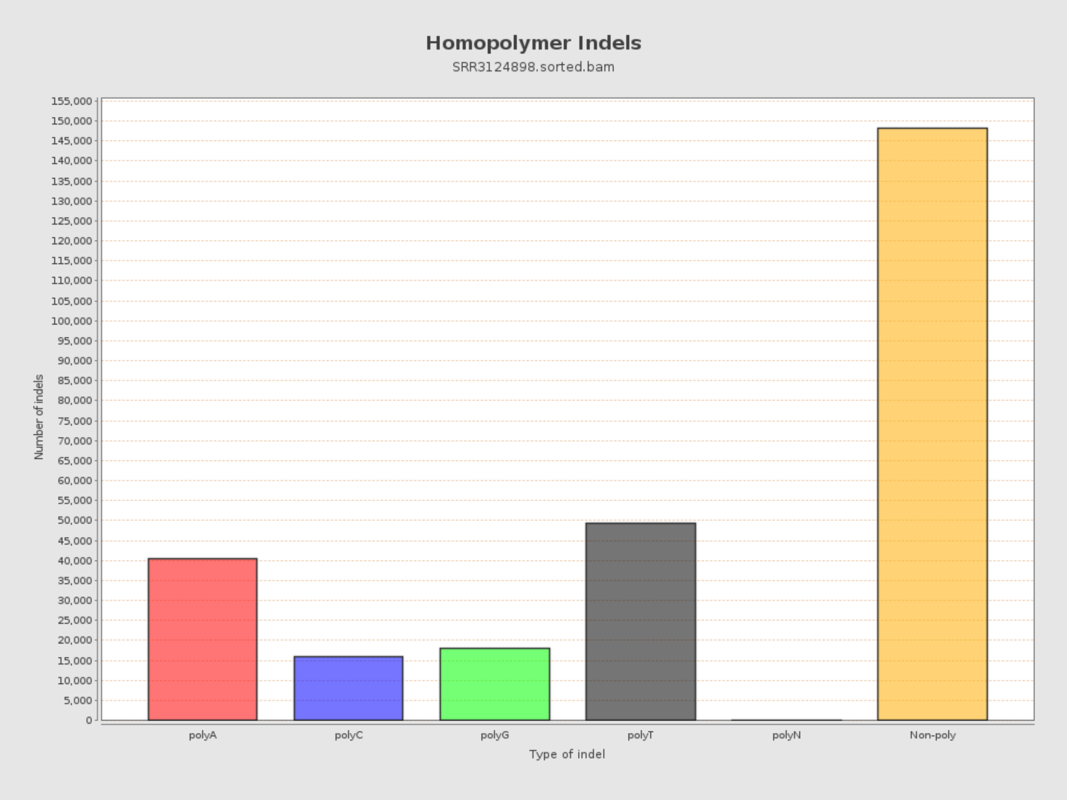
9. Results : Mapped Reads GC-content Distribution



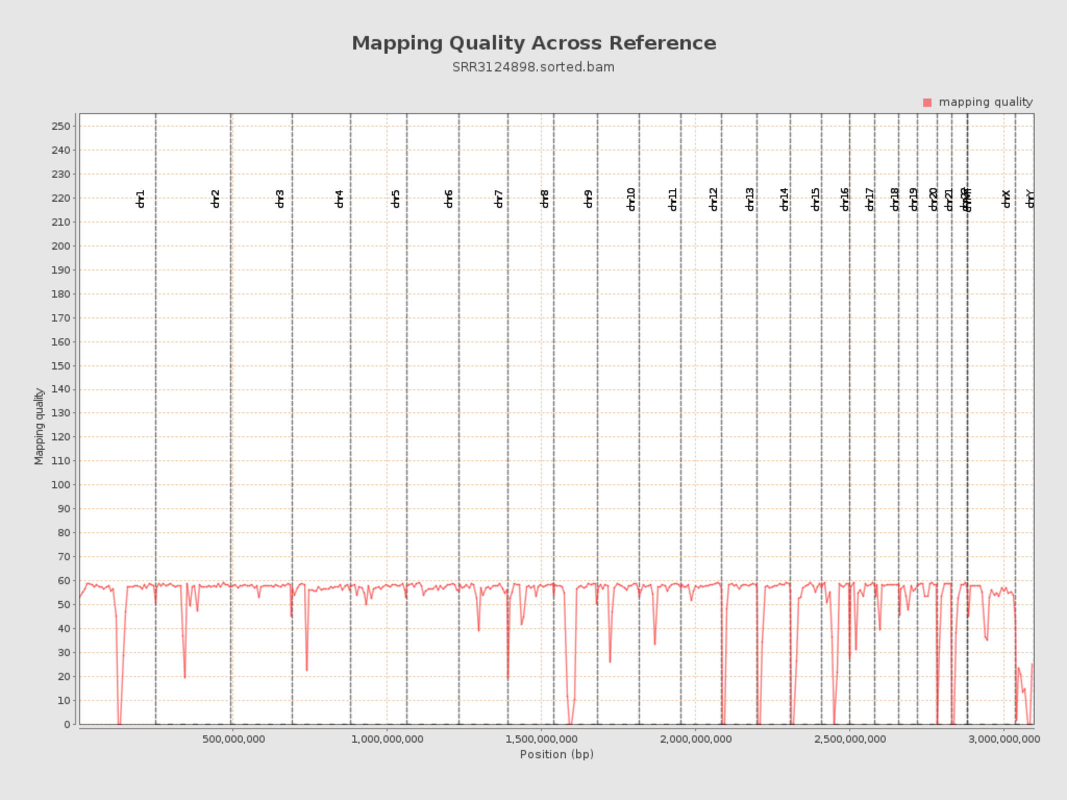
10. Results : Mapped Reads Clipping Profile



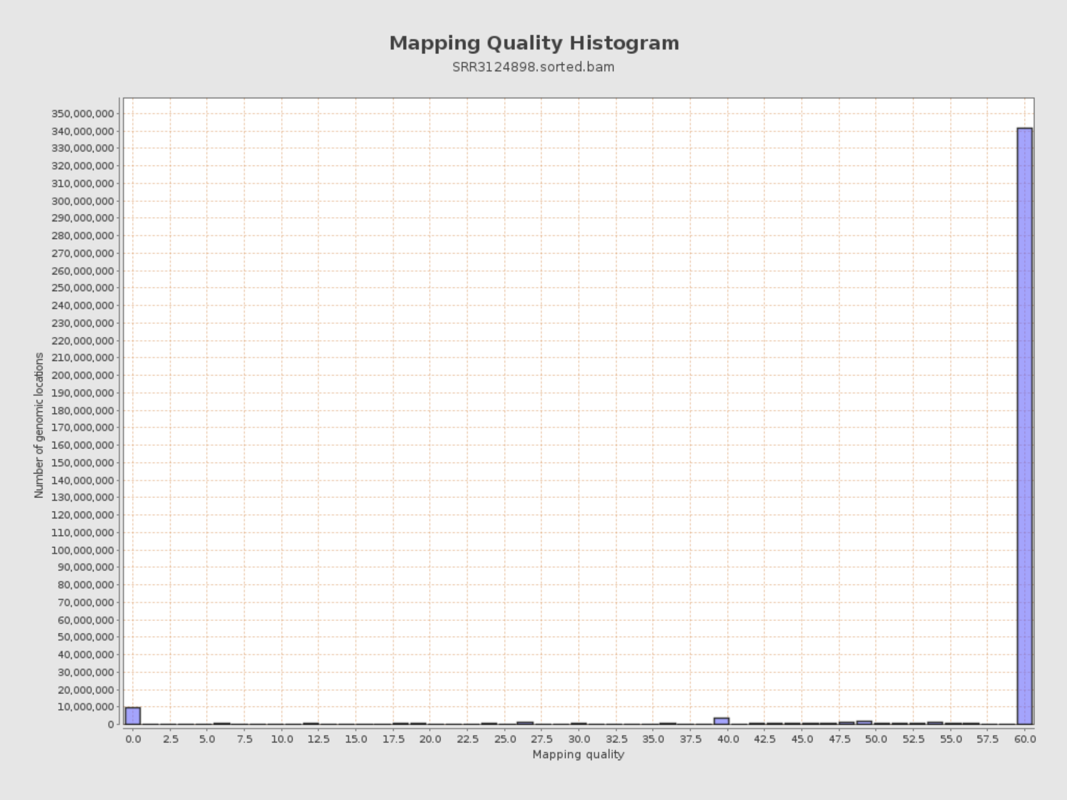
11. Results : Homopolymer Indels



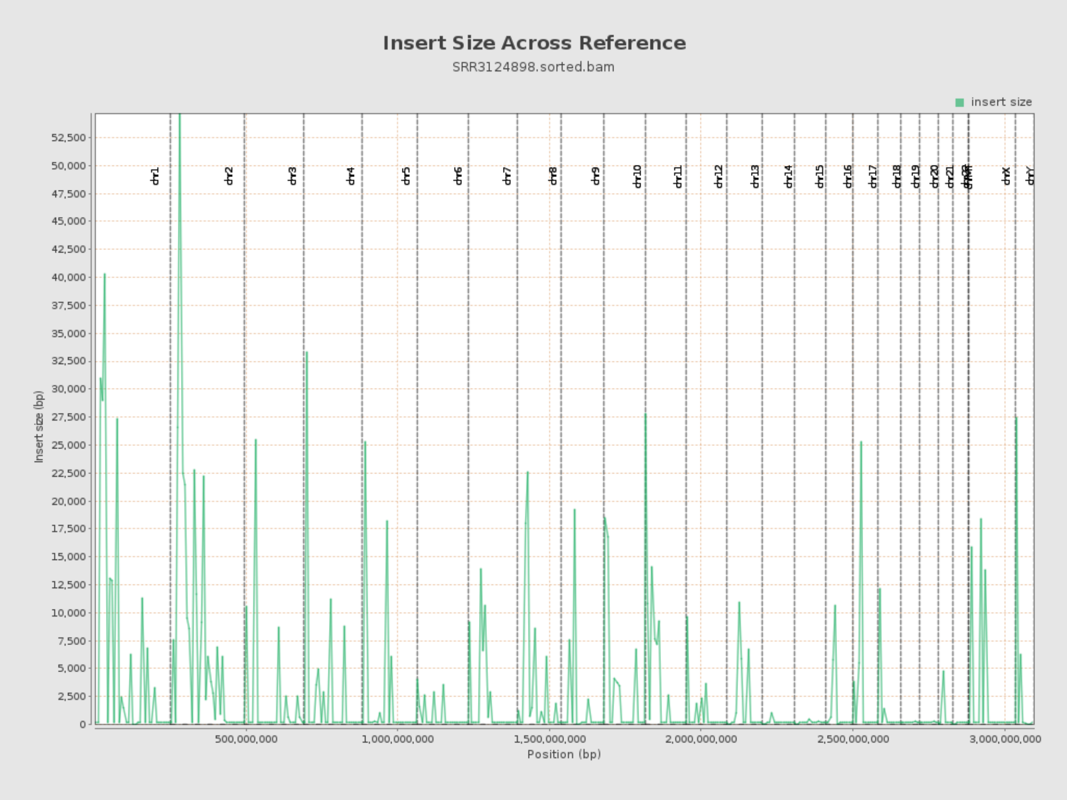
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram