Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 02:43:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124899.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_SRR3124899 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124899_1.fastq.gz SRR3124899_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 02:43:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124899.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,586,056
Mapped reads	4,545,113 / 99.11%
Unmapped reads	40,943 / 0.89%
Mapped paired reads	4,545,113 / 99.11%
Mapped reads, first in pair	2,274,866 / 49.6%
Mapped reads, second in pair	2,270,247 / 49.5%
Mapped reads, both in pair	4,530,686 / 98.79%
Mapped reads, singletons	14,427 / 0.31%
Secondary alignments	0
Supplementary alignments	22,067 / 0.48%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	309,428 / 6.75%
Duplication rate	4.76%
Clipped reads	1,883,638 / 41.07%

2.2. ACGT Content

Number/percentage of A's	115,793,407 / 28.49%
Number/percentage of C's	77,254,671 / 19.01%
Number/percentage of T's	120,847,246 / 29.73%
Number/percentage of G's	92,538,089 / 22.77%
Number/percentage of N's	6,060 / 0%

GC Percentage	41.78%

2.3. Coverage

Mean	0.1314
Standard Deviation	1.128

2.4. Mapping Quality

Mean Mapping Quality	53.18

2.5. Insert size

Mean	44,010
Standard Deviation	1,958,684.82
P25/Median/P75	148 / 193 / 263

2.6. Mismatches and indels

General error rate	0.74%
Mismatches	2,915,840
Insertions	50,749
Mapped reads with at least one insertion	1.09%
Deletions	129,161
Mapped reads with at least one deletion	2.79%
Homopolymer indels	47.79%

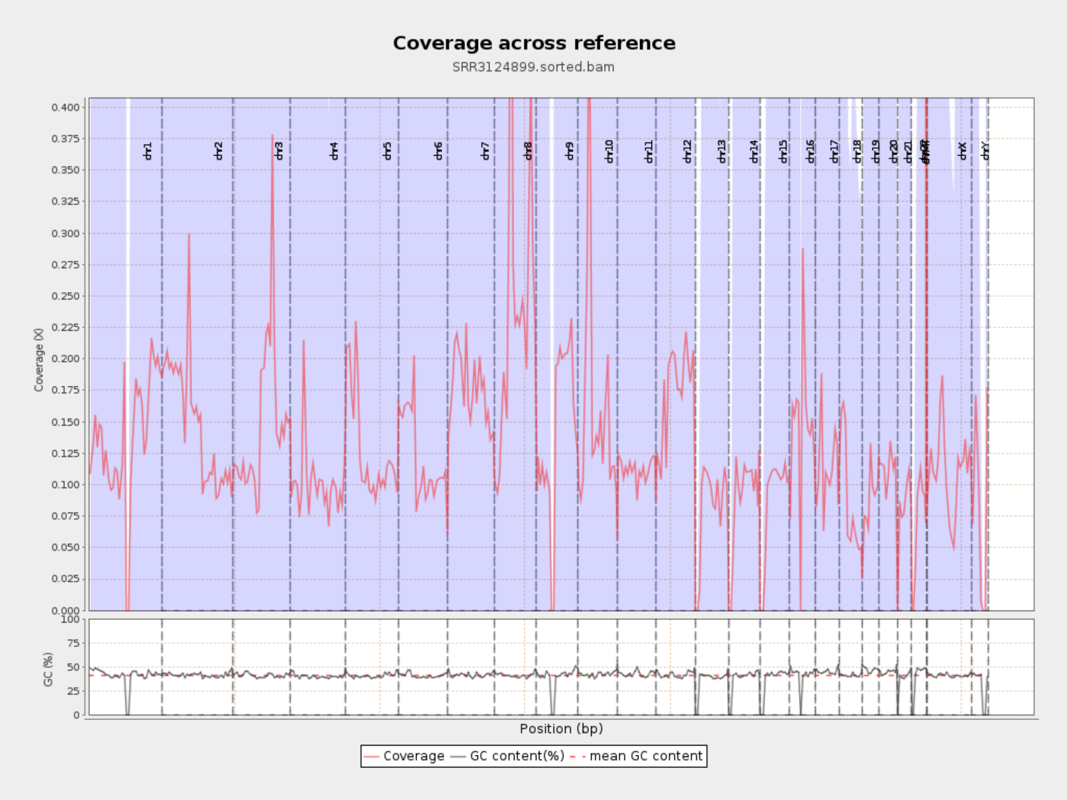
2.7. Chromosome stats

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

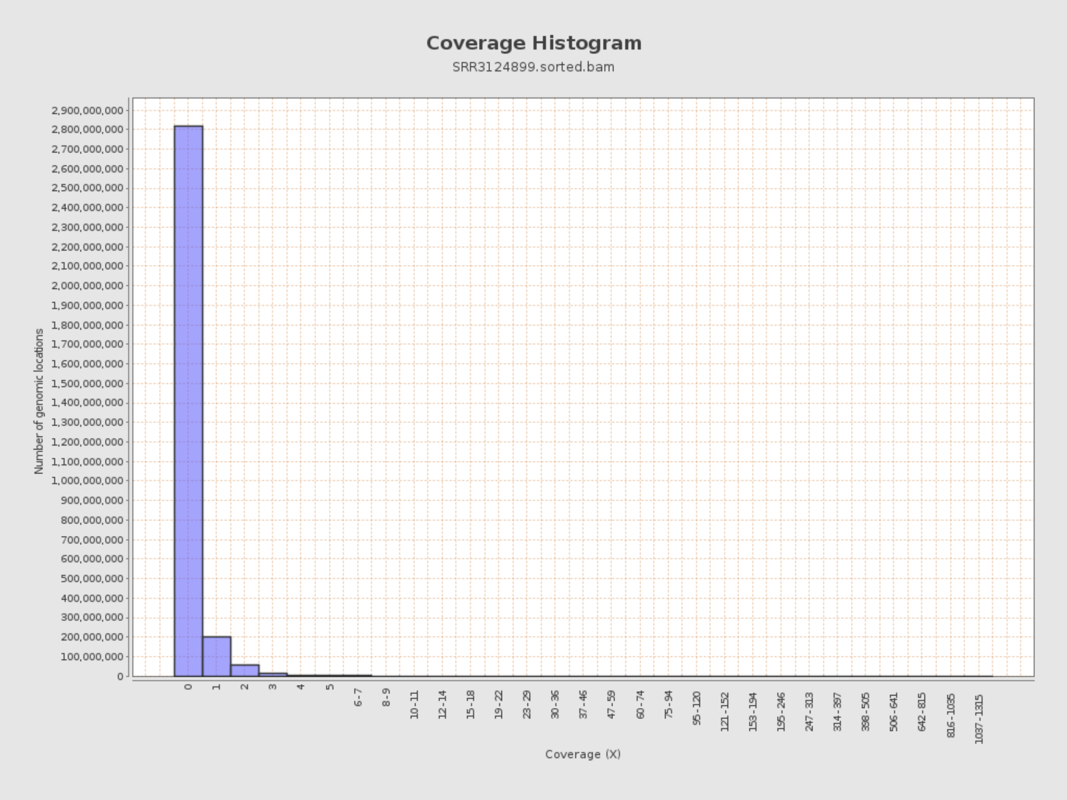
		bases	coverage	deviation
chr1	249250621	33935867	0.1362	1.3924
chr2	243199373	36477364	0.15	1.1628
chr3	198022430	29524282	0.1491	0.52
chr4	191154276	19094019	0.0999	0.8828
chr5	180915260	23134647	0.1279	0.4759
chr6	171115067	20872018	0.122	0.7523
chr7	159138663	28208360	0.1773	1.639
chr8	146364022	36414961	0.2488	0.8966
chr9	141213431	20364679	0.1442	1.4852
chr10	135534747	21623828	0.1595	2.6962
chr11	135006516	14997278	0.1111	0.7396
chr12	133851895	23367447	0.1746	0.5618
chr13	115169878	9313750	0.0809	0.3638
chr14	107349540	9298860	0.0866	0.4182
chr15	102531392	8949938	0.0873	0.3844
chr16	90354753	13240512	0.1465	1.2868
chr17	81195210	9132452	0.1125	1.6102
chr18	78077248	7078466	0.0907	1.4607
chr19	59128983	5247750	0.0888	1.0707
chr20	63025520	7012119	0.1113	0.4925
chr21	48129895	3922189	0.0815	0.4807
chr22	51304566	3403341	0.0663	0.3501
chrMT	16571	165198	9.9691	6.9926
chrX	155270560	17258968	0.1112	0.6284

chrY	59373566	4614354	0.0777	1.1882

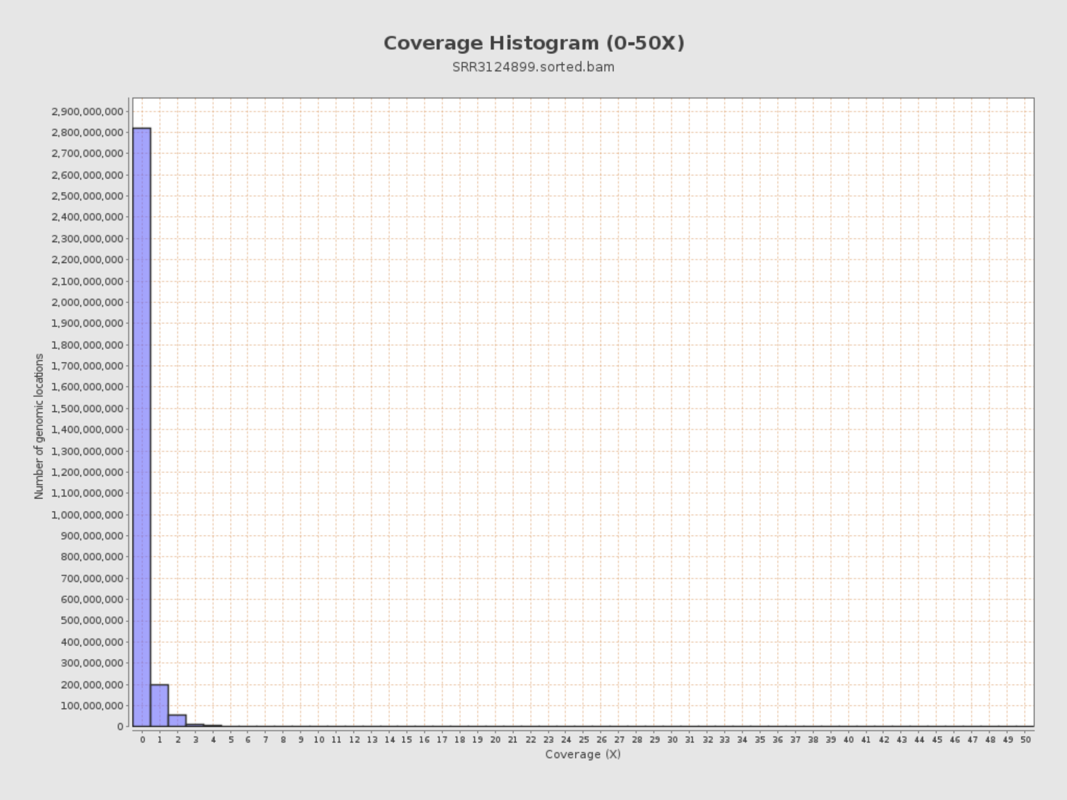
3. Results : Coverage across reference



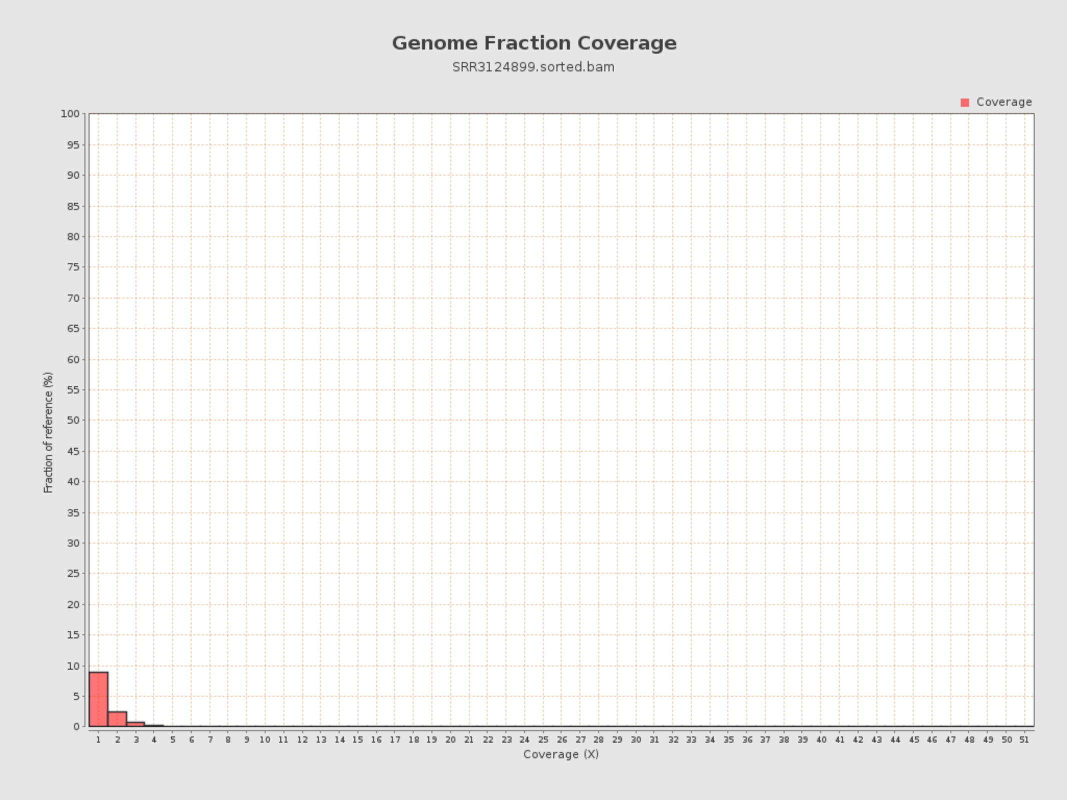
4. Results : Coverage Histogram



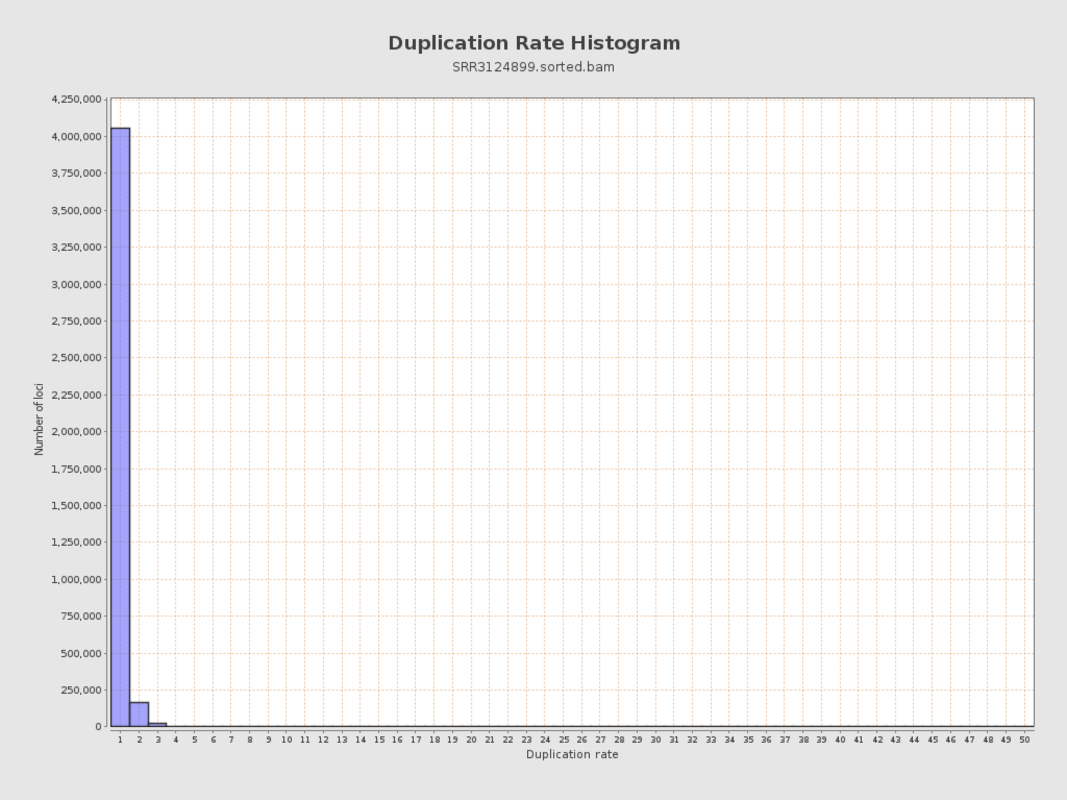
5. Results : Coverage Histogram (0-50X)



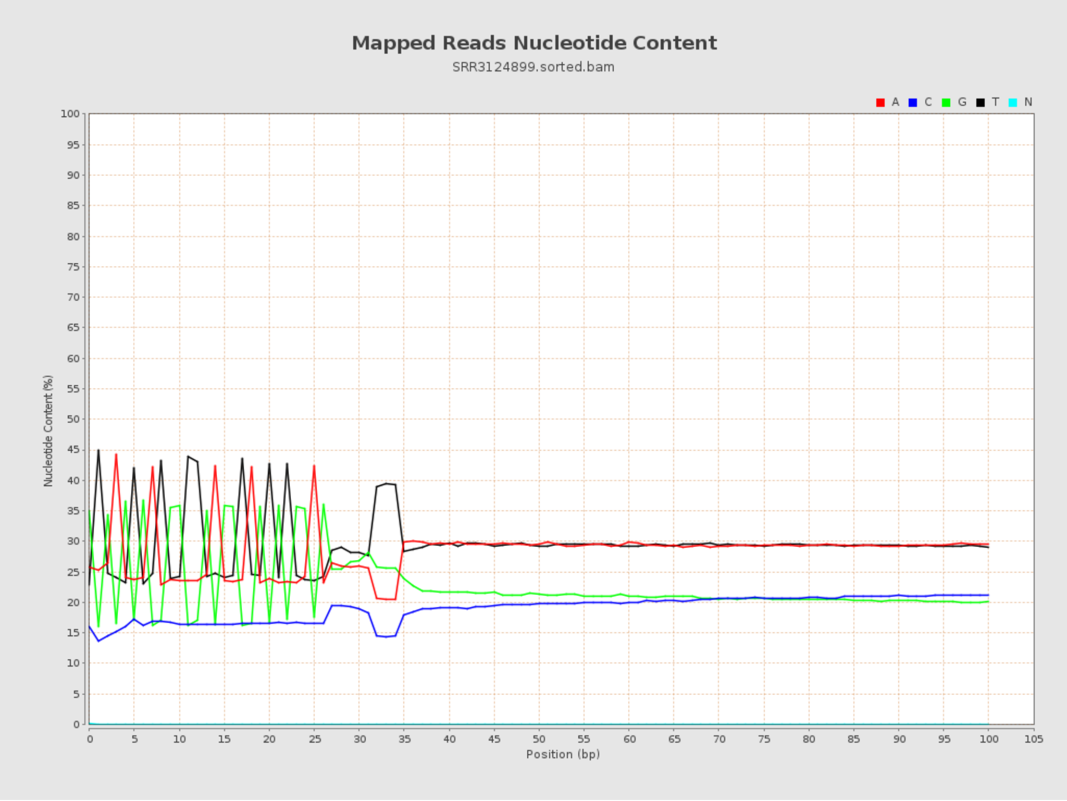
6. Results : Genome Fraction Coverage



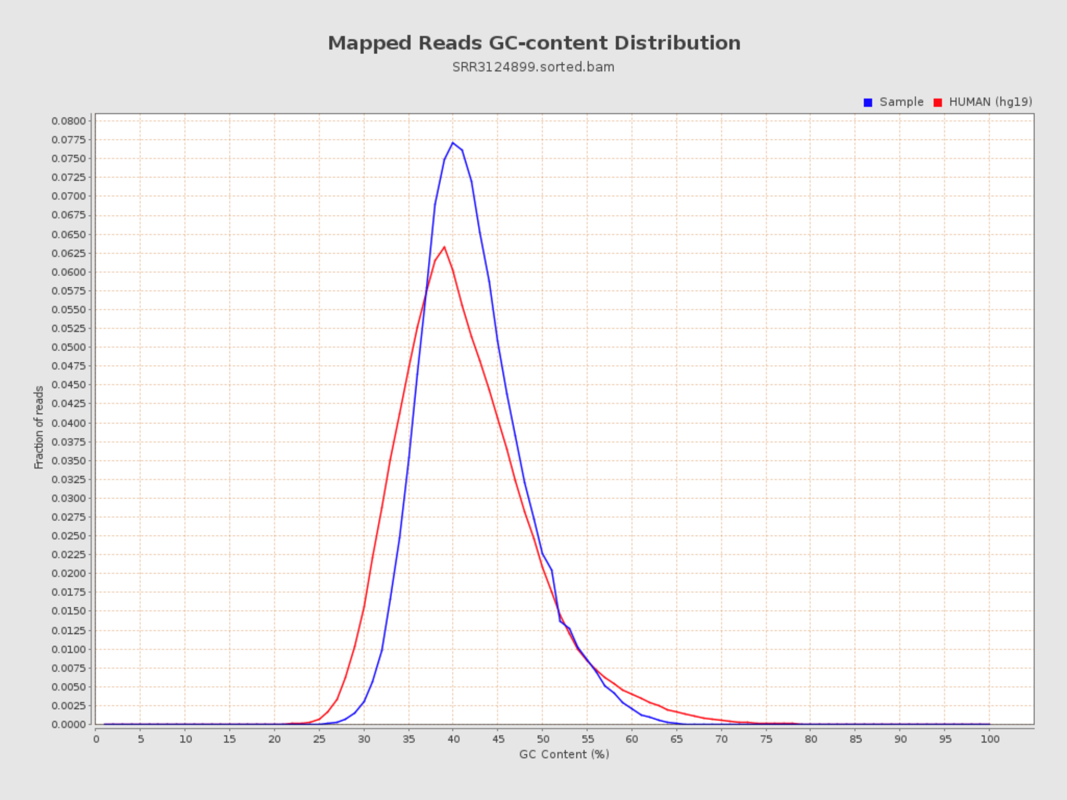
7. Results : Duplication Rate Histogram



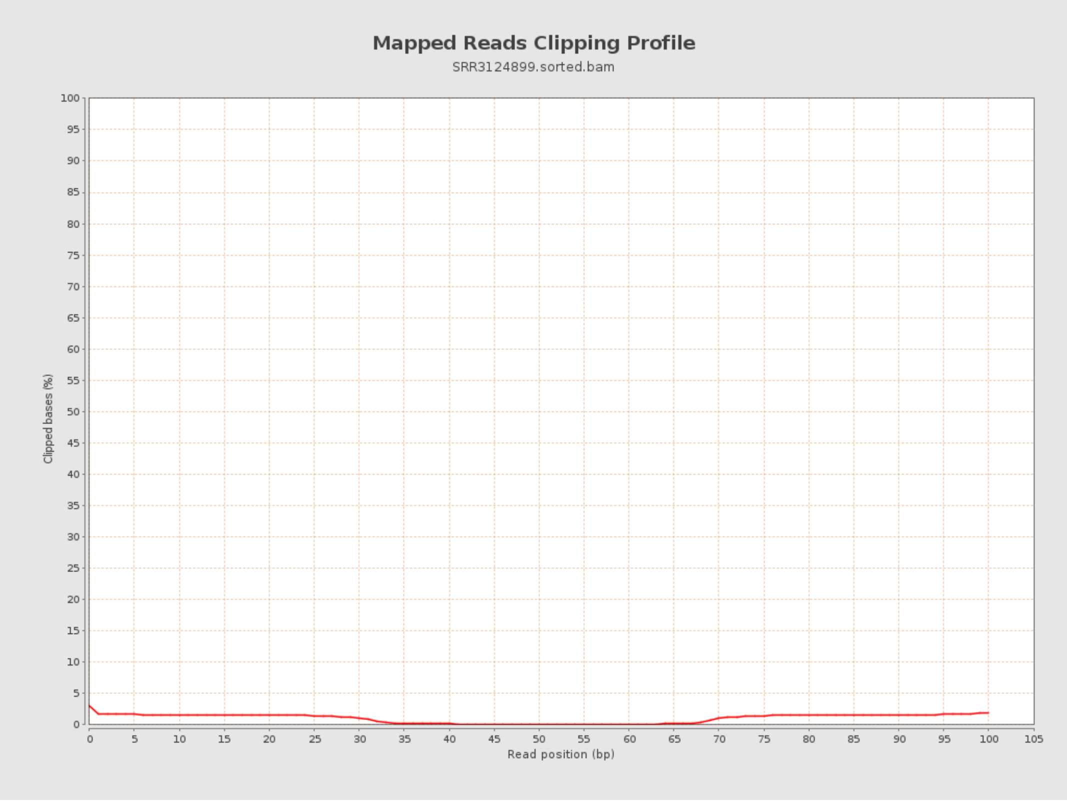
8. Results : Mapped Reads Nucleotide Content



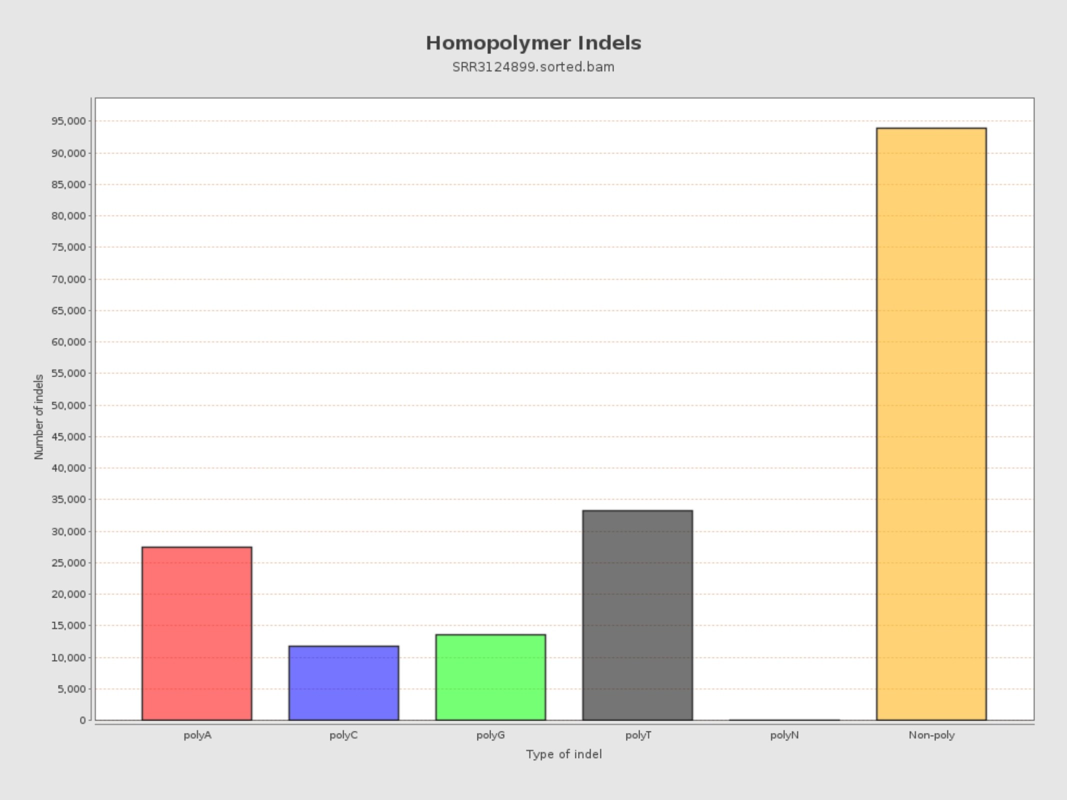
9. Results : Mapped Reads GC-content Distribution



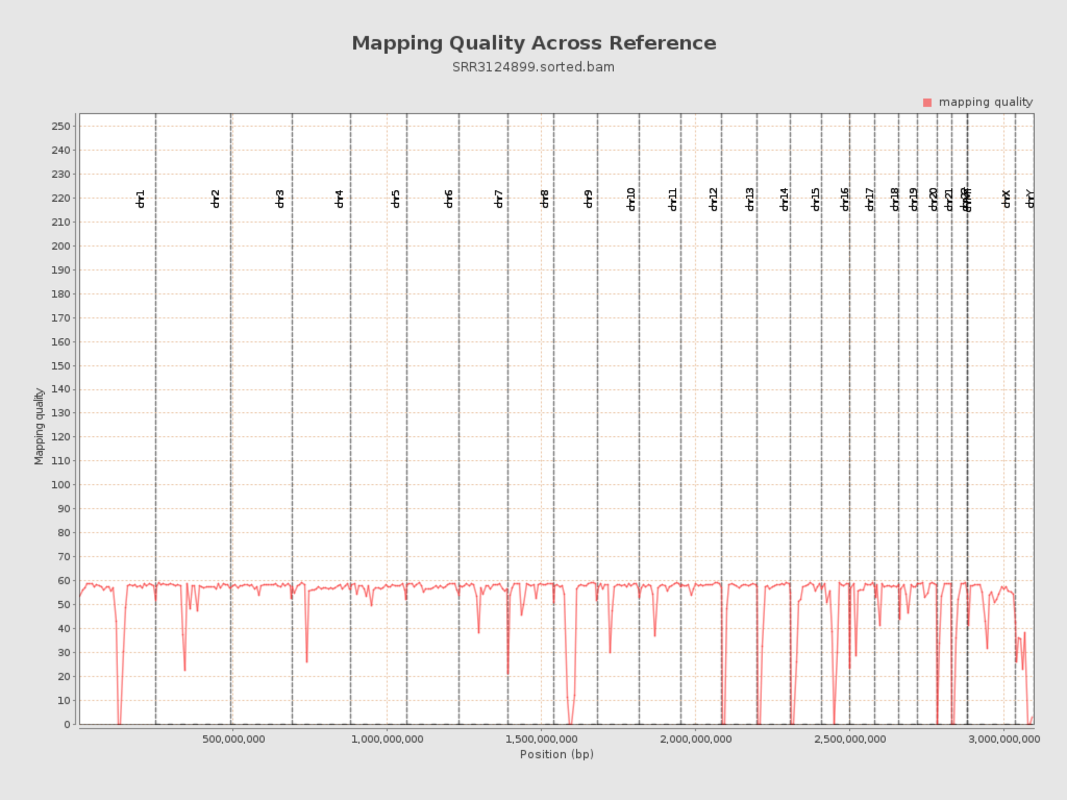
10. Results : Mapped Reads Clipping Profile



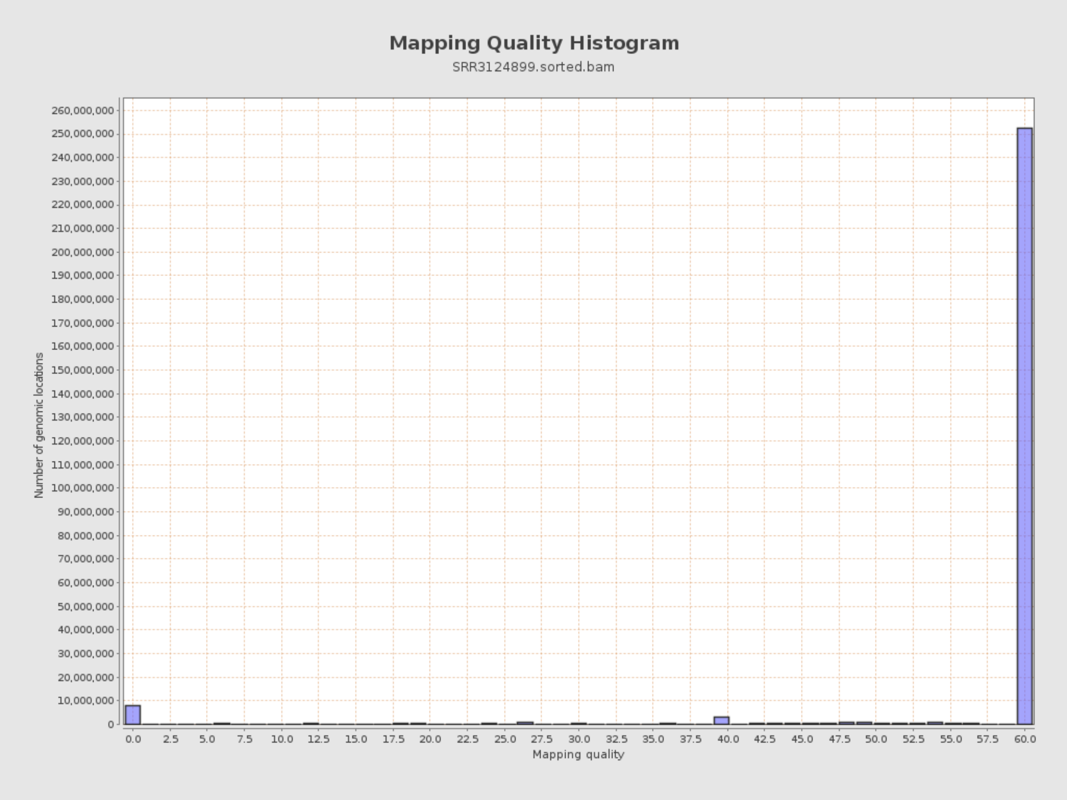
11. Results : Homopolymer Indels



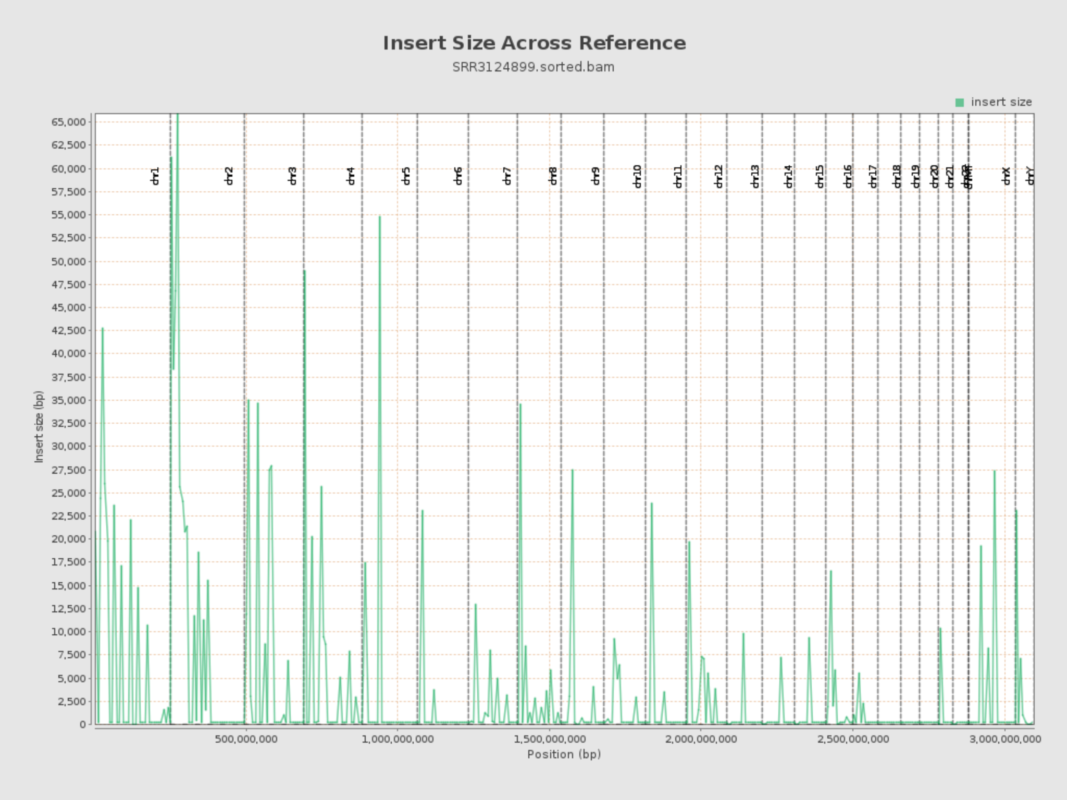
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram