Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 02:28:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124897.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_SRR3124897 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124897_1.fastq.gz SRR3124897_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 02:28:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124897.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,159,858
Mapped reads	2,141,086 / 99.13%
Unmapped reads	18,772 / 0.87%
Mapped paired reads	2,141,086 / 99.13%
Mapped reads, first in pair	1,072,046 / 49.64%
Mapped reads, second in pair	1,069,040 / 49.5%
Mapped reads, both in pair	2,132,358 / 98.73%
Mapped reads, singletons	8,728 / 0.4%
Secondary alignments	0
Supplementary alignments	630,581 / 29.2%
Read min/max/mean length	30 / 151 / 166.43
Duplicated reads (estimated)	738,181 / 34.18%
Duplication rate	23.55%
Clipped reads	2,455,107 / 113.67%

2.2. ACGT Content

Number/percentage of A's	83,520,986 / 28.92%
Number/percentage of C's	60,522,124 / 20.96%
Number/percentage of T's	83,472,584 / 28.9%
Number/percentage of G's	61,255,523 / 21.21%
Number/percentage of N's	23,863 / 0.01%

GC Percentage	42.17%

2.3. Coverage

Mean	0.0934
Standard Deviation	4.1715

2.4. Mapping Quality

Mean Mapping Quality	47.37

2.5. Insert size

Mean	1,366,629.15
Standard Deviation	11,027,432.06
P25/Median/P75	109 / 143 / 185

2.6. Mismatches and indels

General error rate	1.78%
Mismatches	4,860,985
Insertions	93,530
Mapped reads with at least one insertion	4.08%
Deletions	170,740
Mapped reads with at least one deletion	7.58%
Homopolymer indels	43.74%

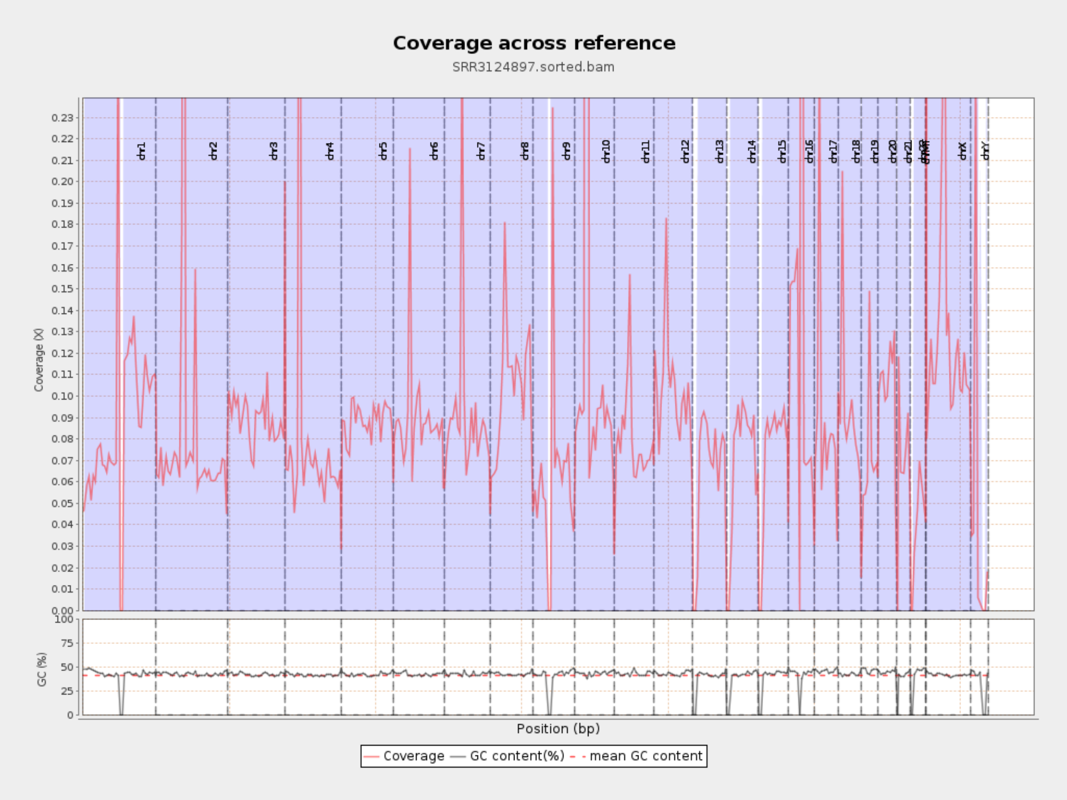
2.7. Chromosome stats

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

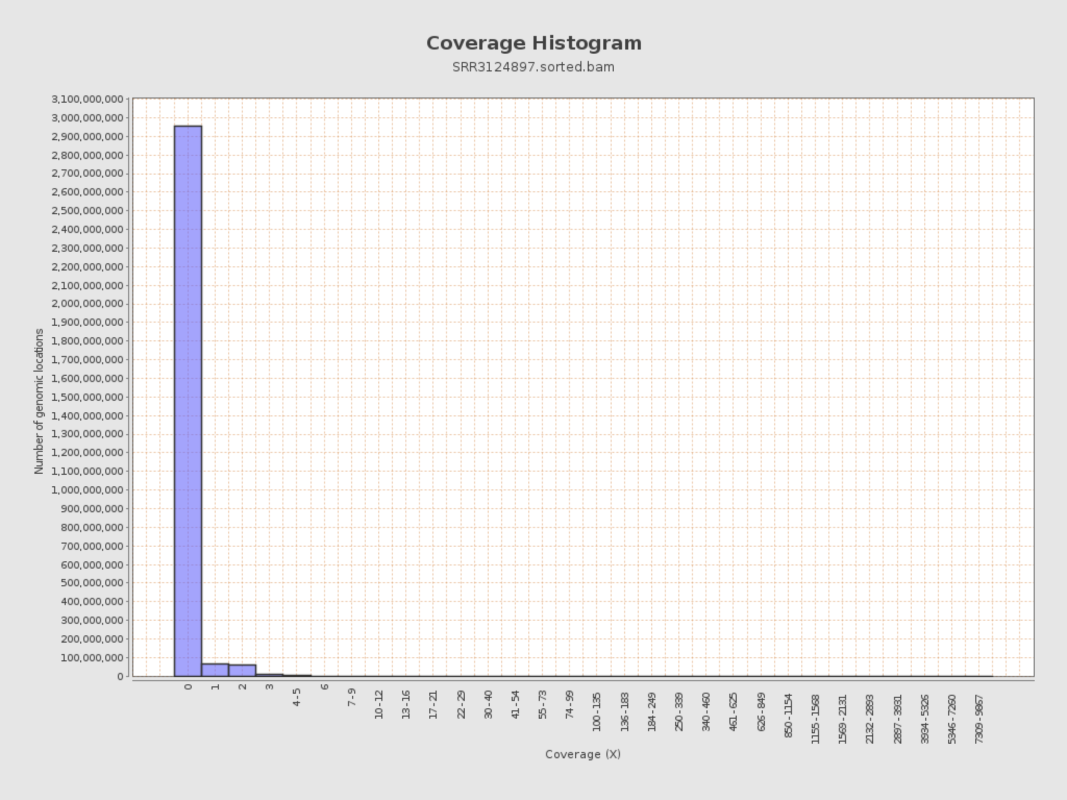
		bases	coverage	deviation
chr1	249250621	22055683	0.0885	2.6046
chr2	243199373	21130266	0.0869	2.747
chr3	198022430	17793554	0.0899	1.33
chr4	191154276	15731780	0.0823	2.0739
chr5	180915260	15981883	0.0883	0.4688
chr6	171115067	15482710	0.0905	1.4677
chr7	159138663	14665186	0.0922	2.6787
chr8	146364022	15264773	0.1043	0.8568
chr9	141213431	8941042	0.0633	2.9826
chr10	135534747	26491348	0.1955	17.3534
chr11	135006516	10794441	0.08	1.1444
chr12	133851895	13860763	0.1036	0.4988
chr13	115169878	7437944	0.0646	0.3731
chr14	107349540	7575298	0.0706	0.4595
chr15	102531392	7219518	0.0704	0.3924
chr16	90354753	14257558	0.1578	4.7521
chr17	81195210	7513840	0.0925	3.3213
chr18	78077248	7460300	0.0956	2.6901
chr19	59128983	4193168	0.0709	1.4782
chr20	63025520	6866308	0.1089	0.8074
chr21	48129895	3453295	0.0717	1.3282
chr22	51304566	2057915	0.0401	0.3503
chrMT	16571	90744	5.4761	4.6064
chrX	155270560	20061139	0.1292	1.0714

chrY	59373566	2763472	0.0465	4.5563

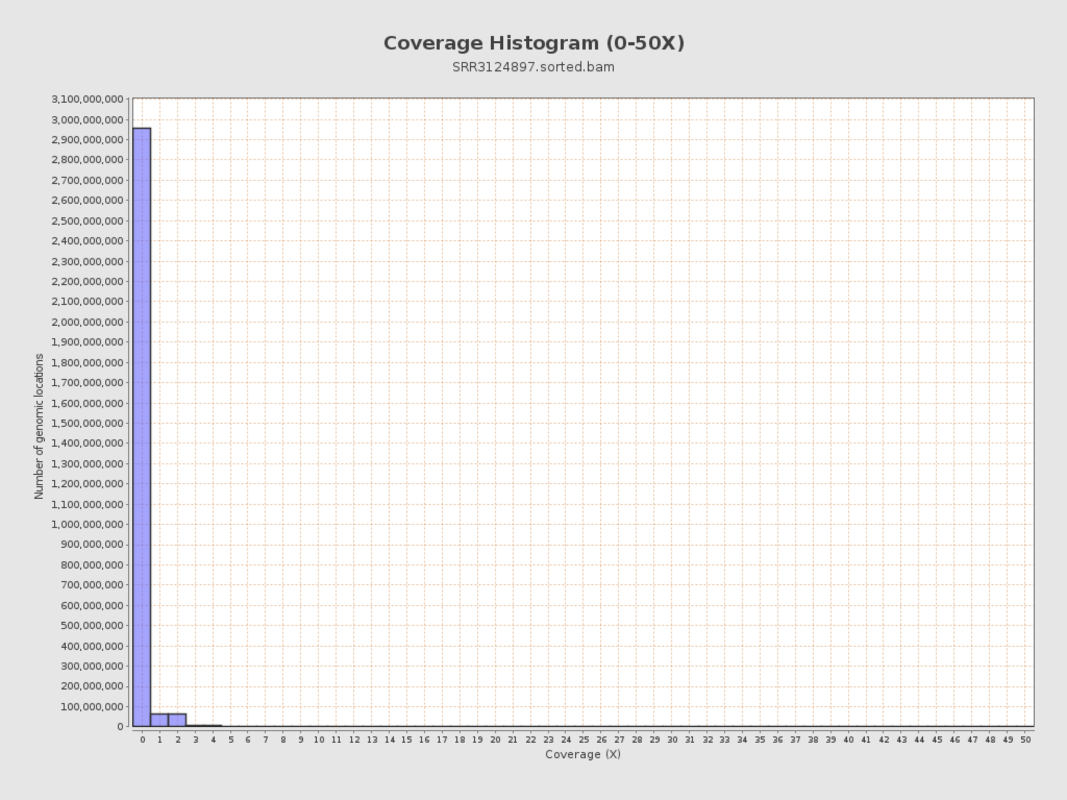
3. Results : Coverage across reference



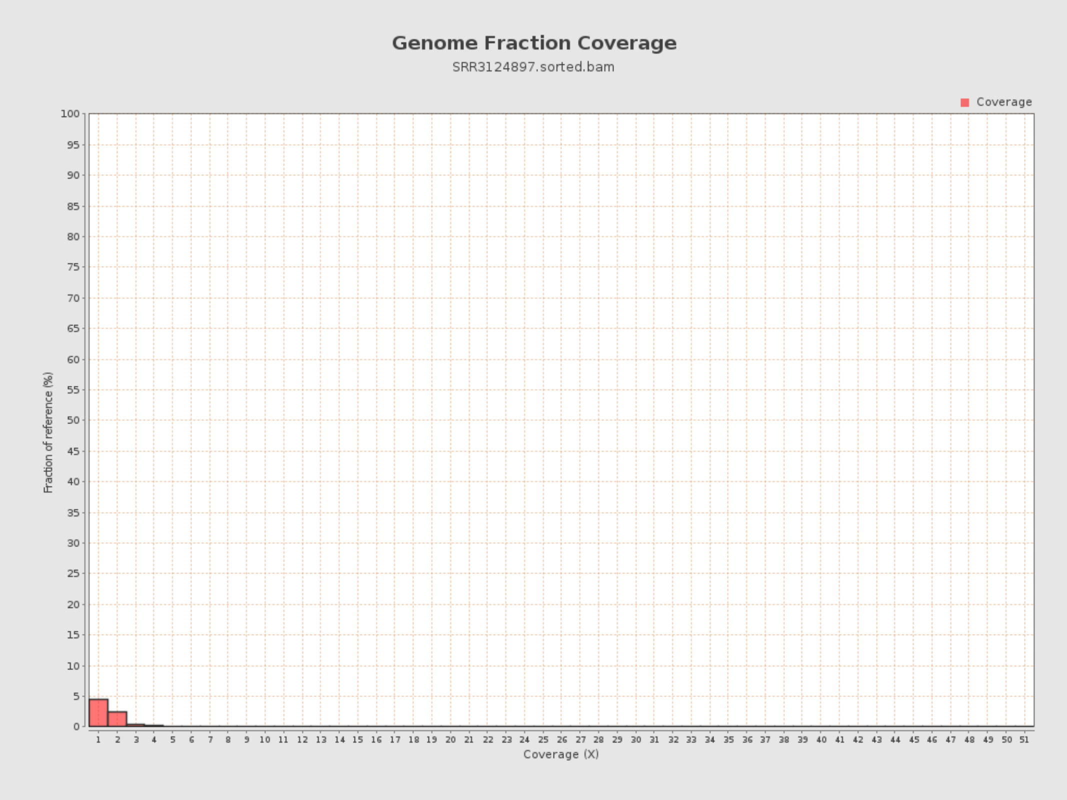
4. Results : Coverage Histogram



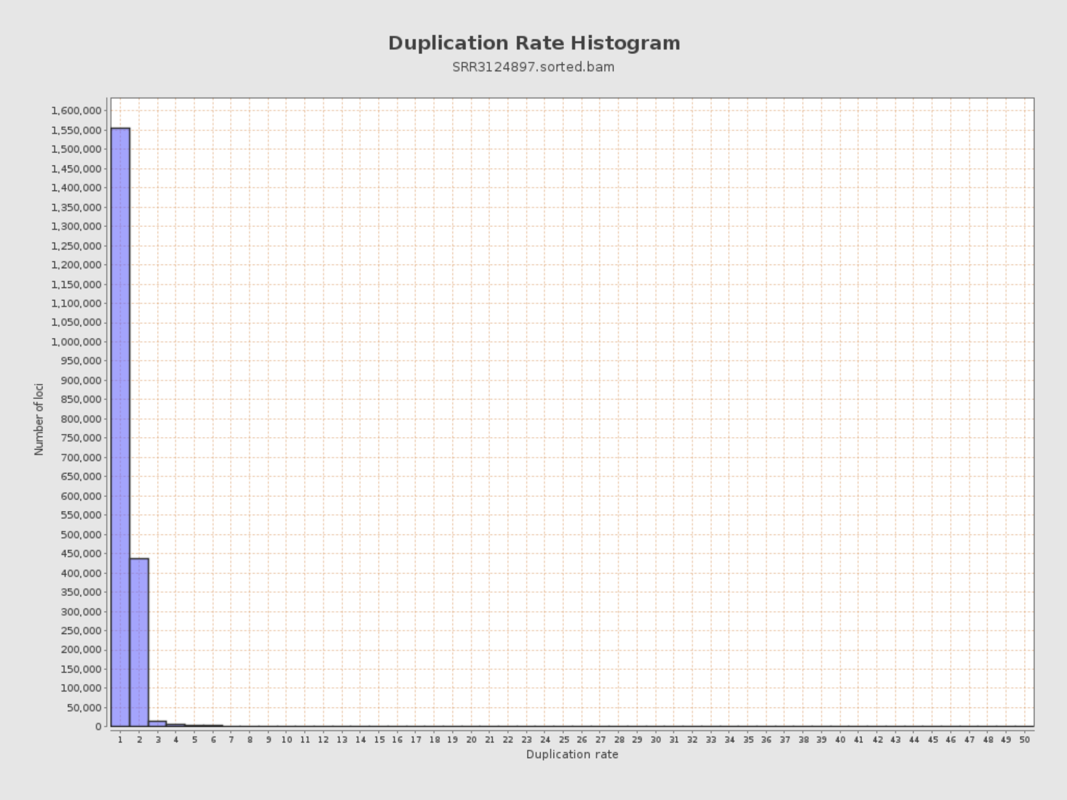
5. Results : Coverage Histogram (0-50X)



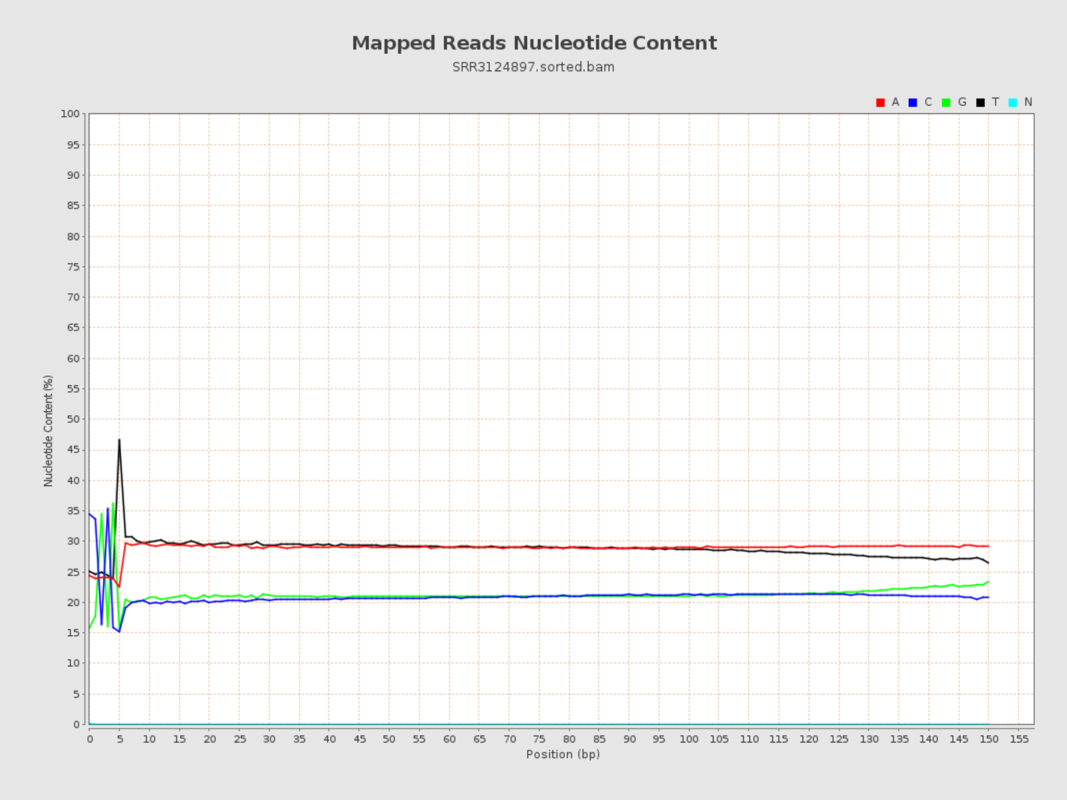
6. Results : Genome Fraction Coverage



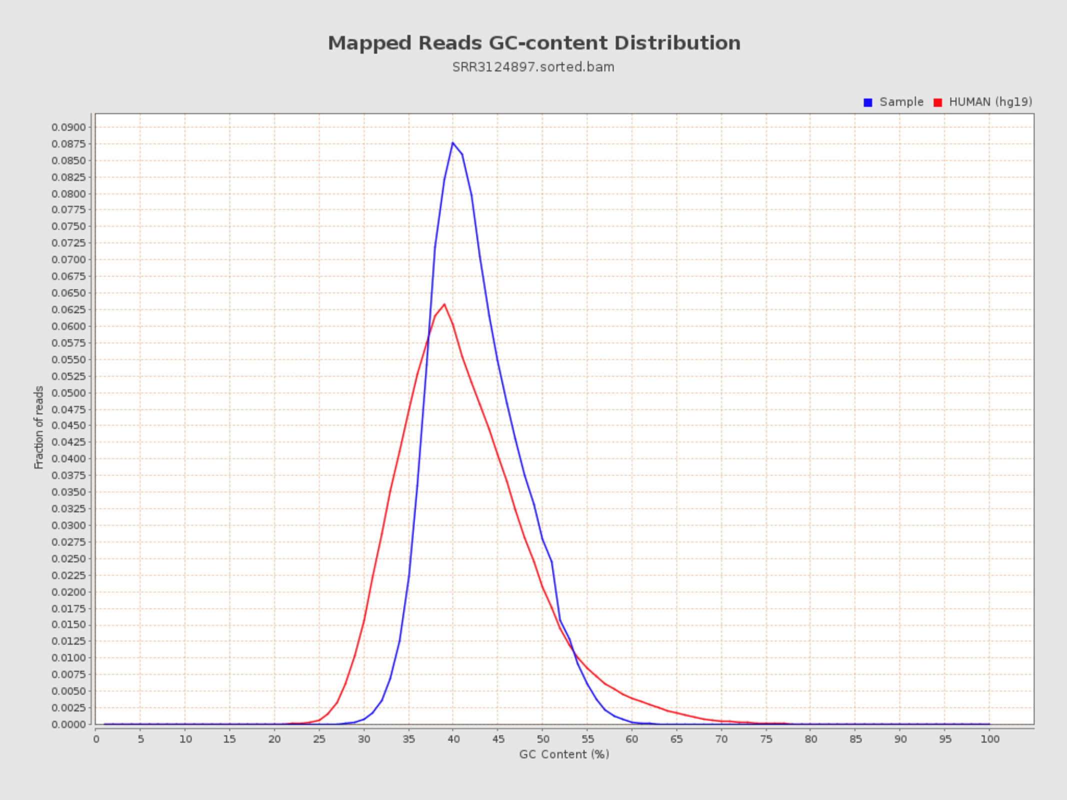
7. Results : Duplication Rate Histogram



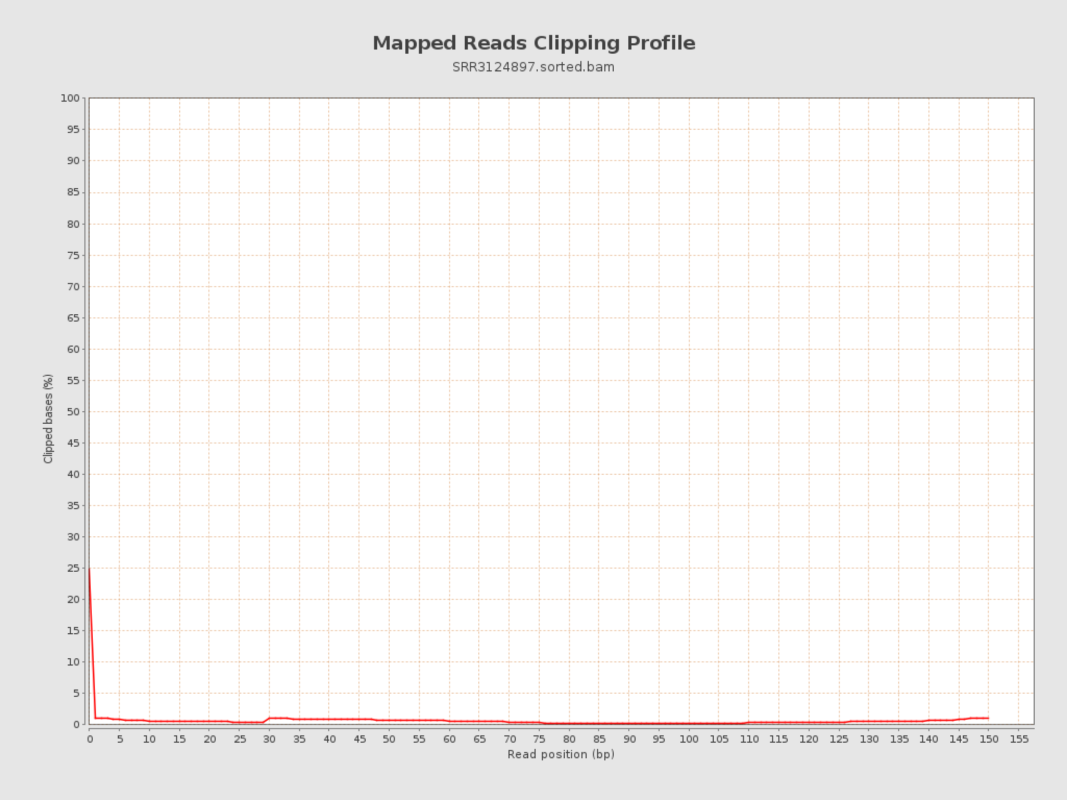
8. Results : Mapped Reads Nucleotide Content



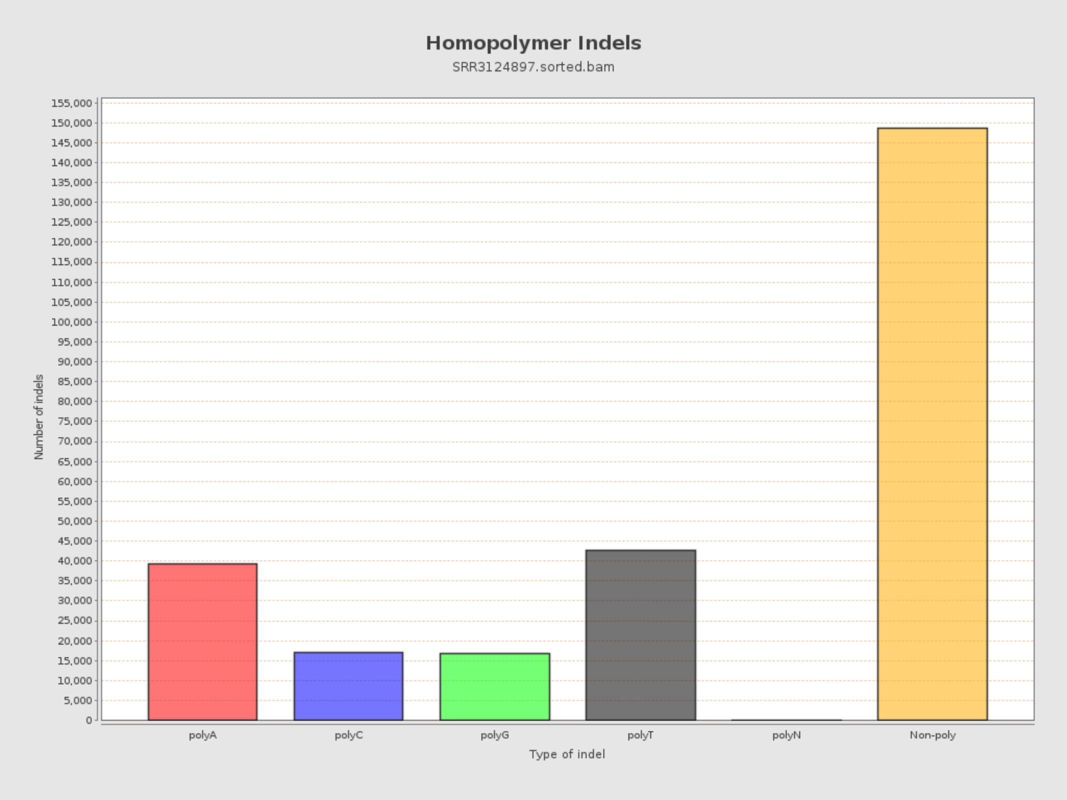
9. Results : Mapped Reads GC-content Distribution



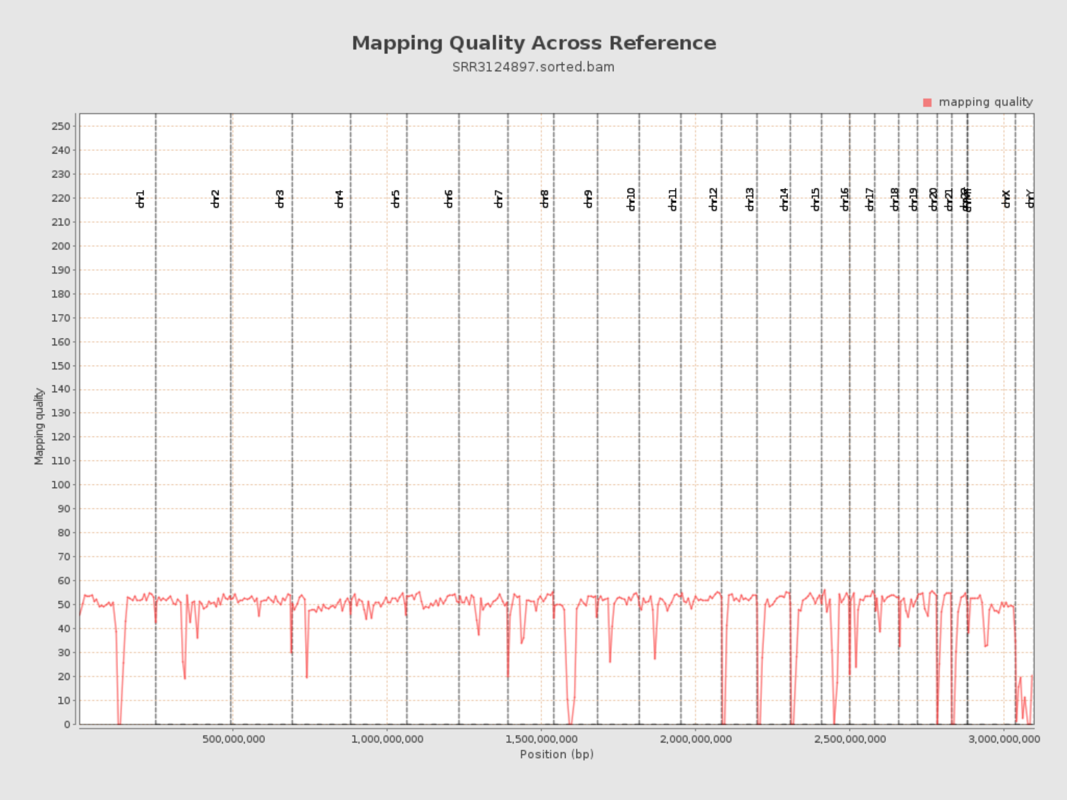
10. Results : Mapped Reads Clipping Profile



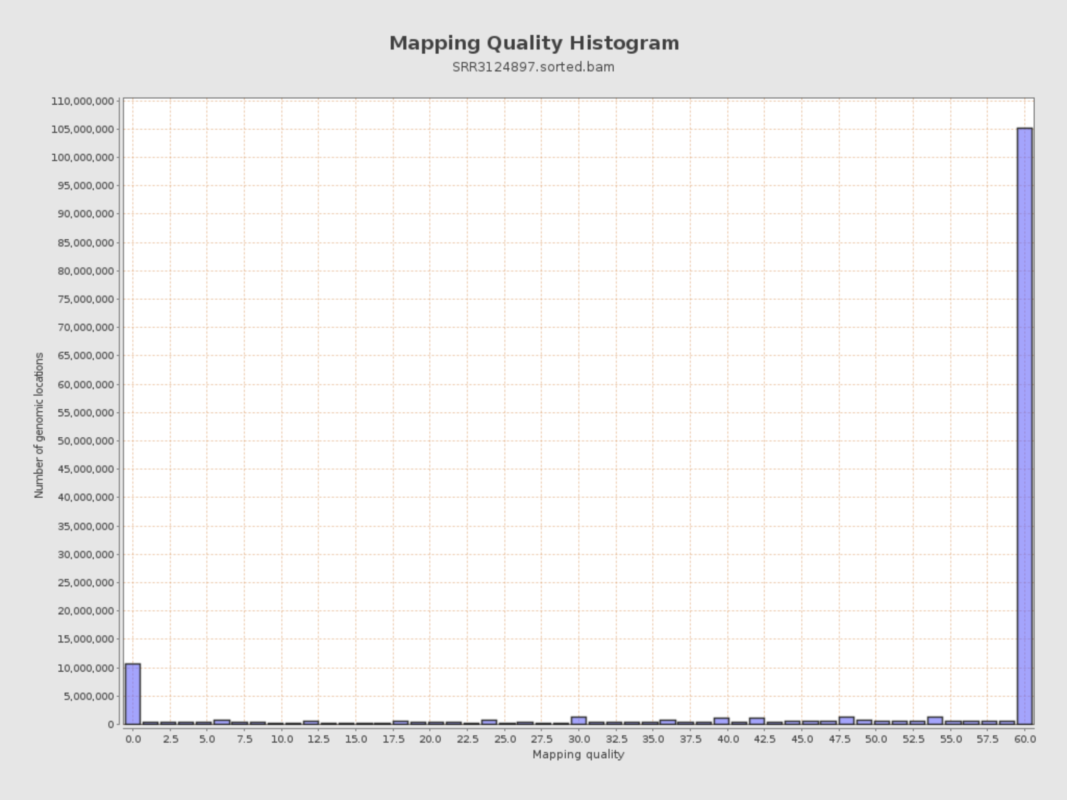
11. Results : Homopolymer Indels



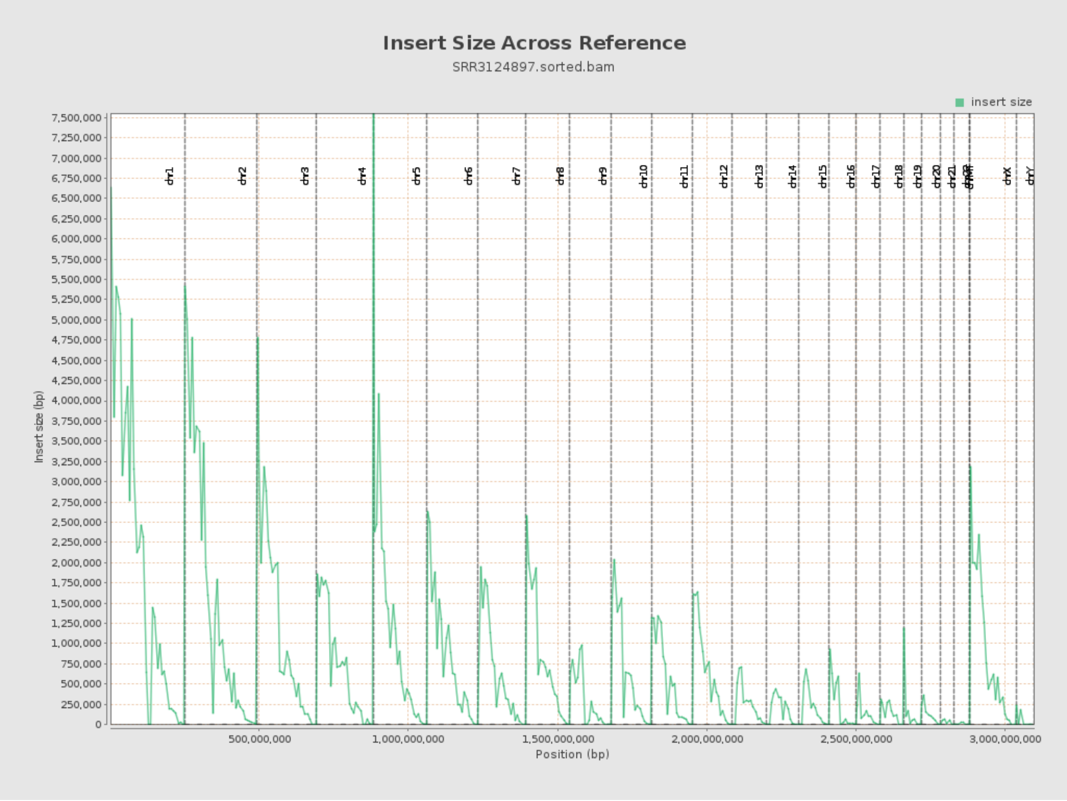
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram