Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 09:20:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124951.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_SRR3124951 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124951_1.fastq.gz SRR3124951_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 09:20:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124951.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,557,026
Mapped reads	2,535,822 / 99.17%
Unmapped reads	21,204 / 0.83%
Mapped paired reads	2,535,822 / 99.17%
Mapped reads, first in pair	1,268,810 / 49.62%
Mapped reads, second in pair	1,267,012 / 49.55%
Mapped reads, both in pair	2,530,308 / 98.96%
Mapped reads, singletons	5,514 / 0.22%
Secondary alignments	0
Supplementary alignments	33,790 / 1.32%
Read min/max/mean length	30 / 151 / 151.63
Duplicated reads (estimated)	408,820 / 15.99%
Duplication rate	14.85%
Clipped reads	1,872,010 / 73.21%

2.2. ACGT Content

Number/percentage of A's	100,281,416 / 29.45%
Number/percentage of C's	67,841,941 / 19.92%
Number/percentage of T's	99,909,149 / 29.34%
Number/percentage of G's	72,427,809 / 21.27%
Number/percentage of N's	29,689 / 0.01%

GC Percentage	41.2%

2.3. Coverage

Mean	0.1101
Standard Deviation	1.4918

2.4. Mapping Quality

Mean Mapping Quality	53.59

2.5. Insert size

Mean	69,020.82
Standard Deviation	2,505,811.15
P25/Median/P75	137 / 170 / 217

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	3,454,262
Insertions	71,062
Mapped reads with at least one insertion	2.63%
Deletions	126,275
Mapped reads with at least one deletion	4.76%
Homopolymer indels	45.13%

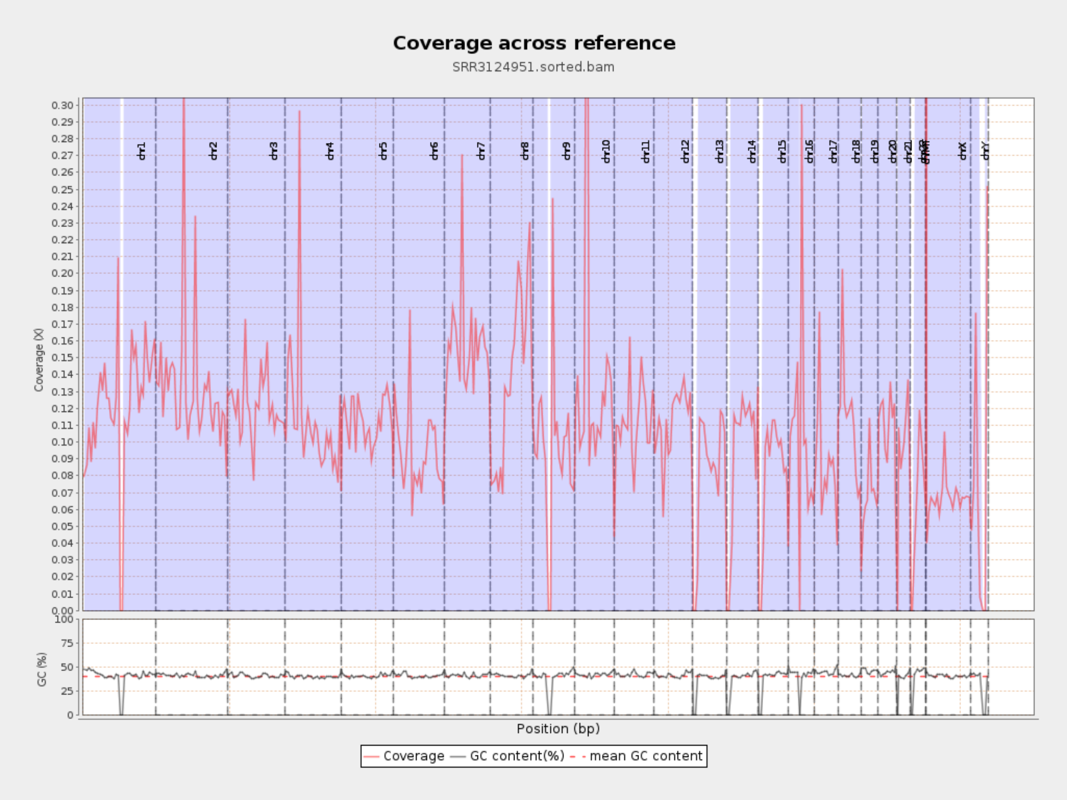
2.7. Chromosome stats

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

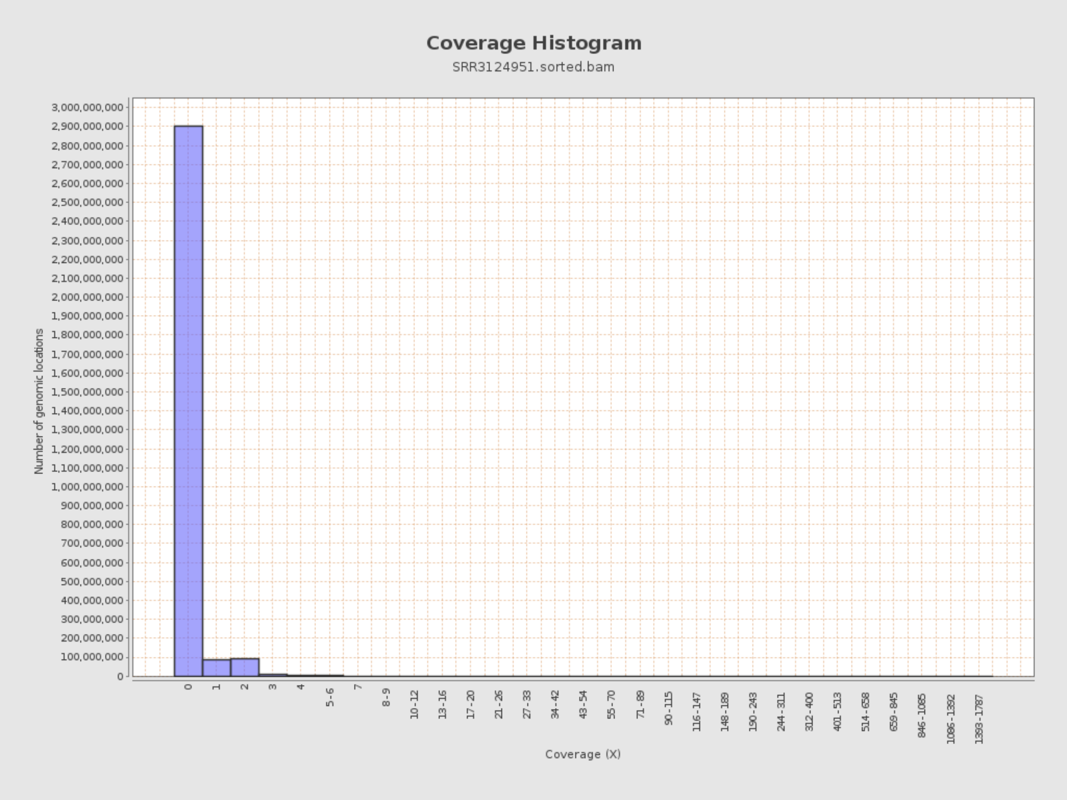
		bases	coverage	deviation
chr1	249250621	30279738	0.1215	1.6594
chr2	243199373	32687537	0.1344	1.6837
chr3	198022430	24118115	0.1218	0.5019
chr4	191154276	22000042	0.1151	1.1369
chr5	180915260	20331354	0.1124	0.4788
chr6	171115067	16256371	0.095	0.9141
chr7	159138663	25051978	0.1574	2.4712
chr8	146364022	20182170	0.1379	0.6197
chr9	141213431	13552732	0.096	2.6443
chr10	135534747	18707877	0.138	3.3825
chr11	135006516	15240437	0.1129	1.1998
chr12	133851895	14986948	0.112	0.4681
chr13	115169878	9413452	0.0817	0.3946
chr14	107349540	10033870	0.0935	0.4601
chr15	102531392	8166705	0.0797	0.3903
chr16	90354753	9316012	0.1031	1.602
chr17	81195210	7260176	0.0894	1.4302
chr18	78077248	8985524	0.1151	2.2775
chr19	59128983	4071682	0.0689	0.8979
chr20	63025520	7068634	0.1122	0.5723
chr21	48129895	4579887	0.0952	0.6711
chr22	51304566	3304298	0.0644	0.3696
chrMT	16571	60557	3.6544	3.4134
chrX	155270560	10406893	0.067	0.5221

chrY	59373566	4688091	0.079	2.0155

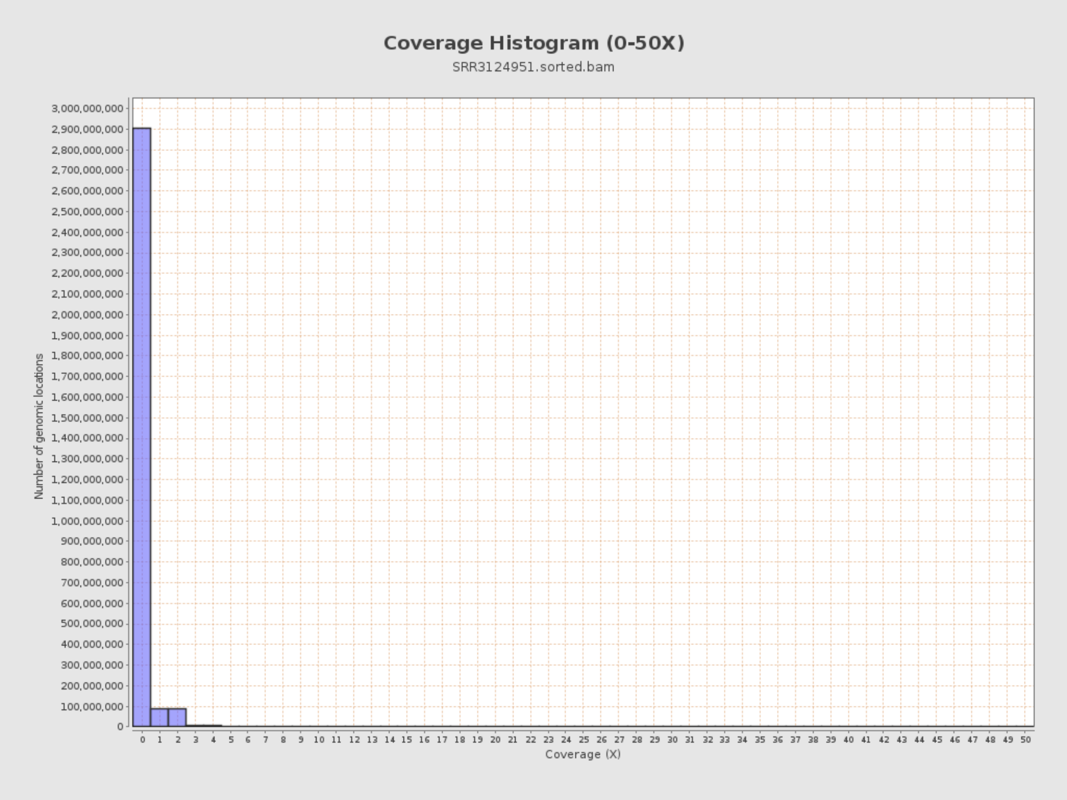
3. Results : Coverage across reference



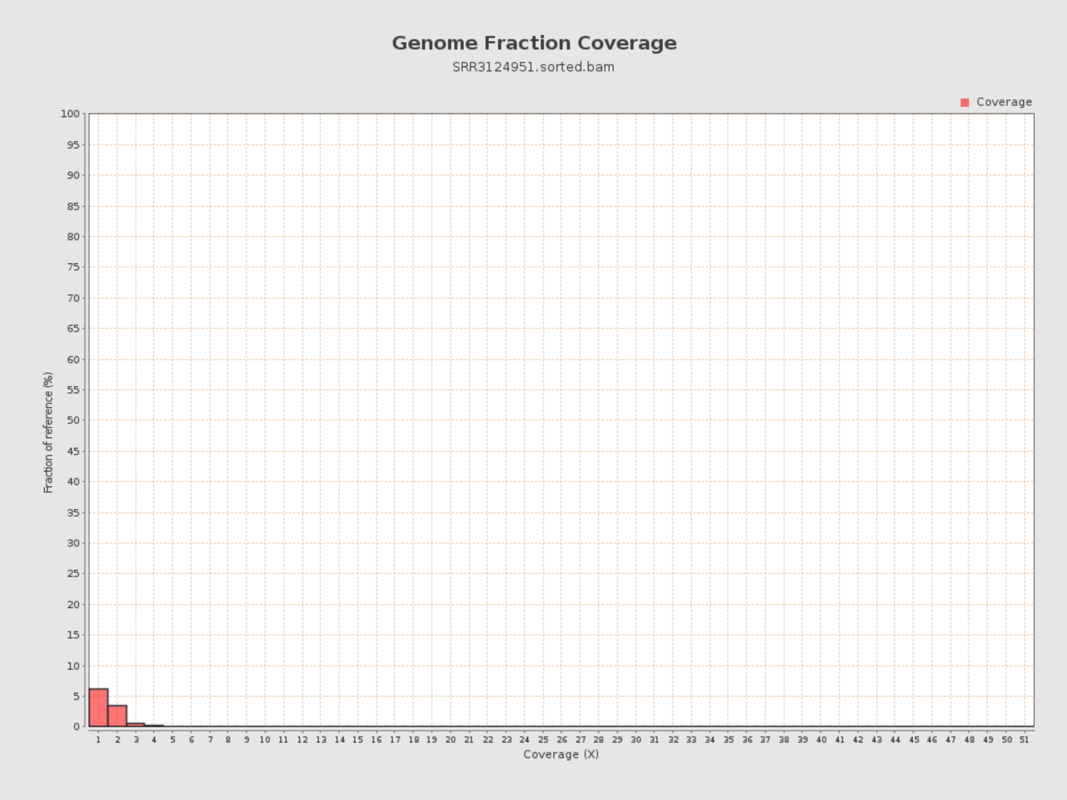
4. Results : Coverage Histogram



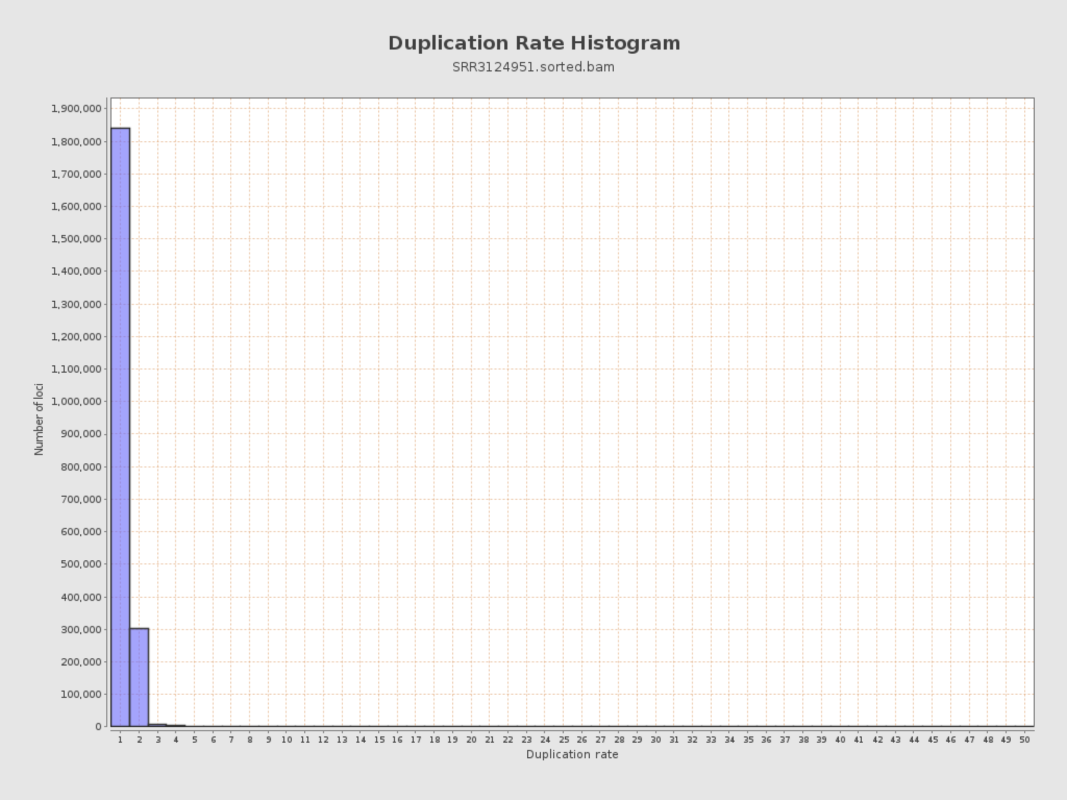
5. Results : Coverage Histogram (0-50X)



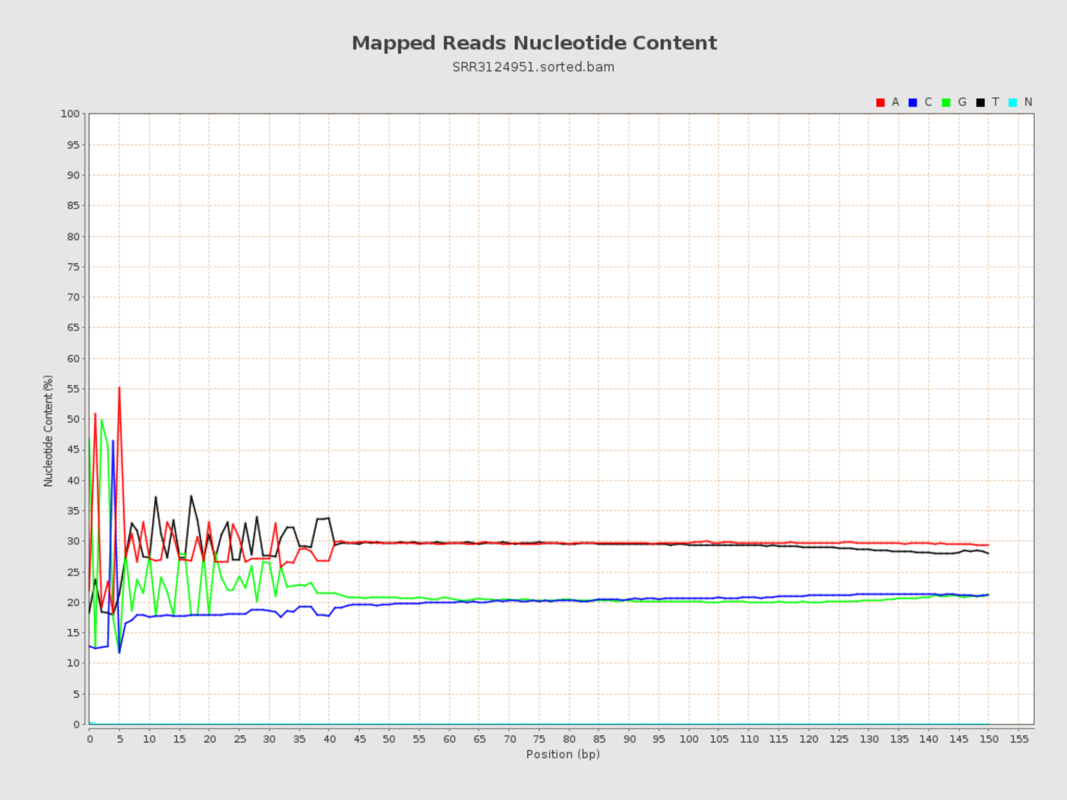
6. Results : Genome Fraction Coverage



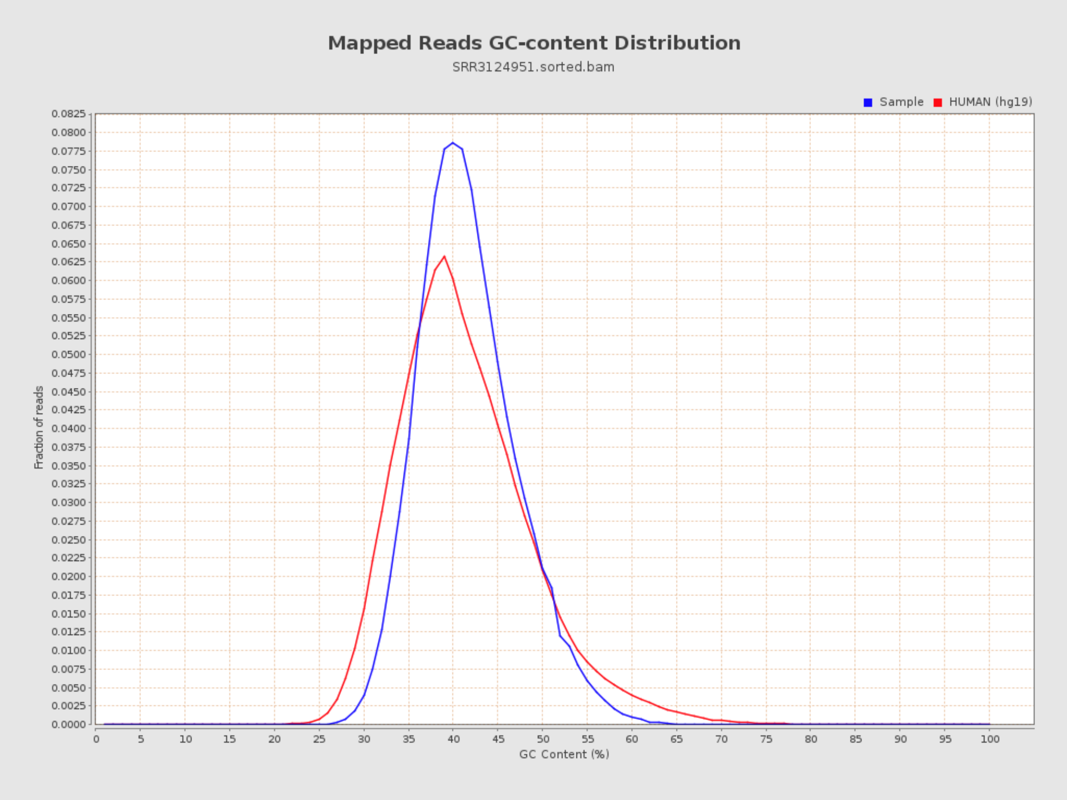
7. Results : Duplication Rate Histogram



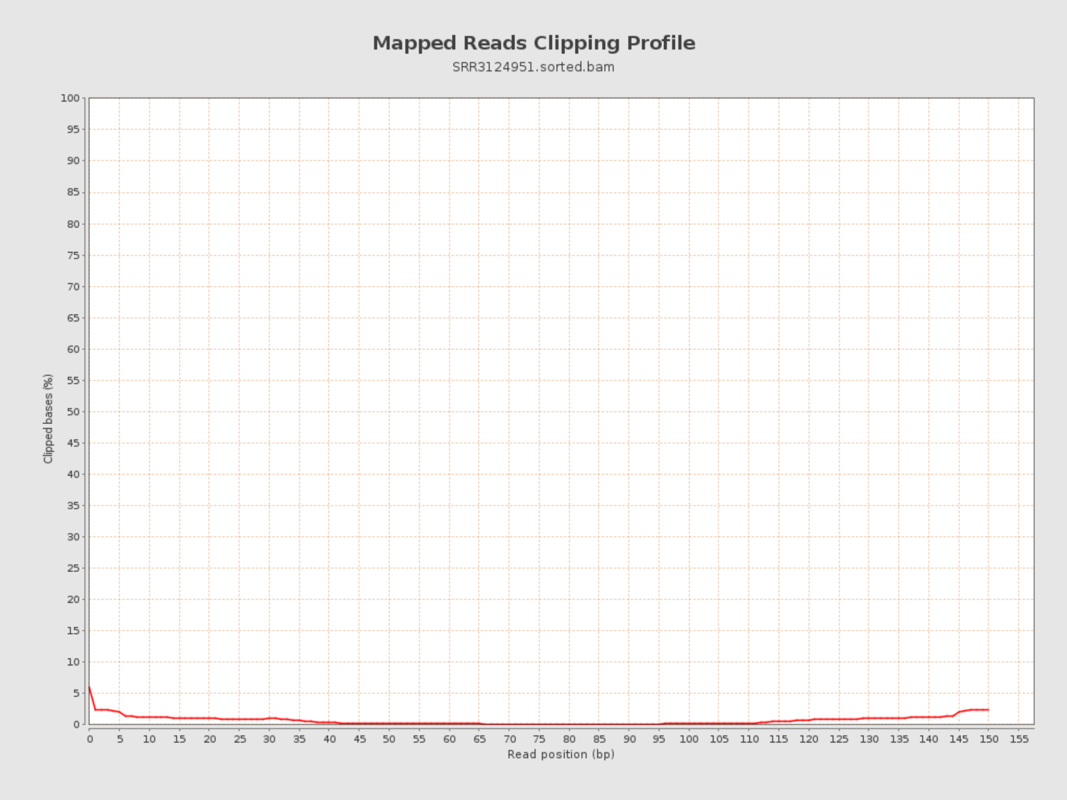
8. Results : Mapped Reads Nucleotide Content



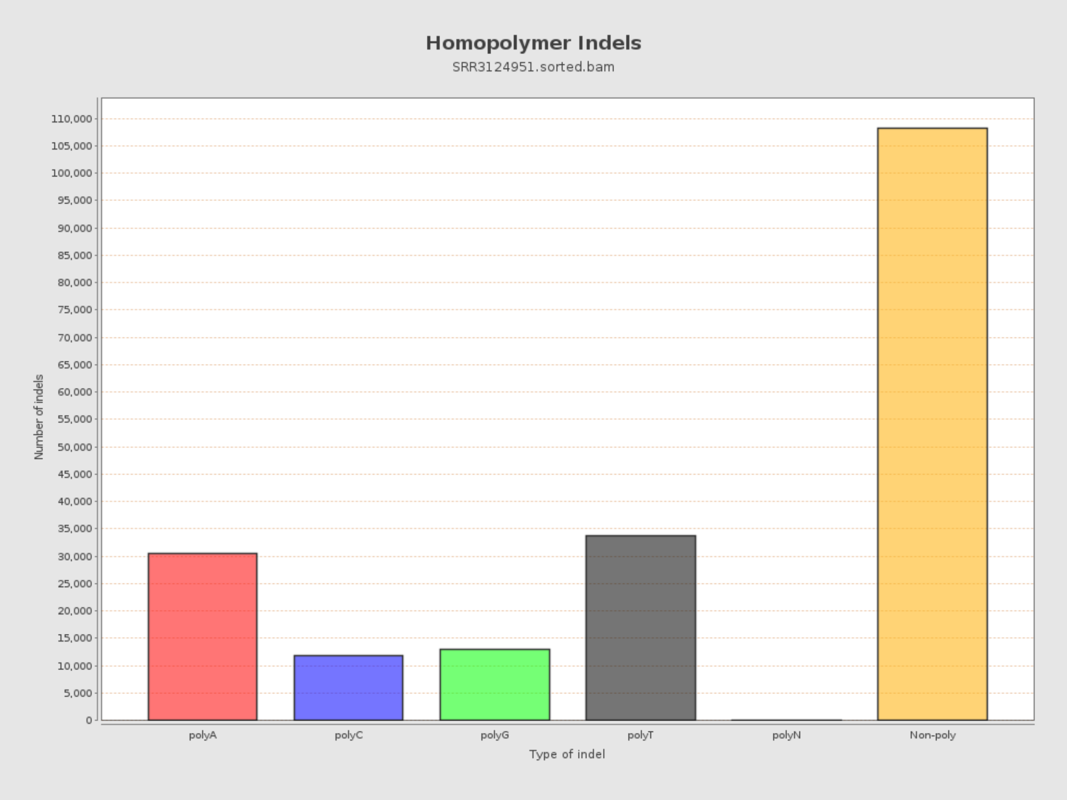
9. Results : Mapped Reads GC-content Distribution



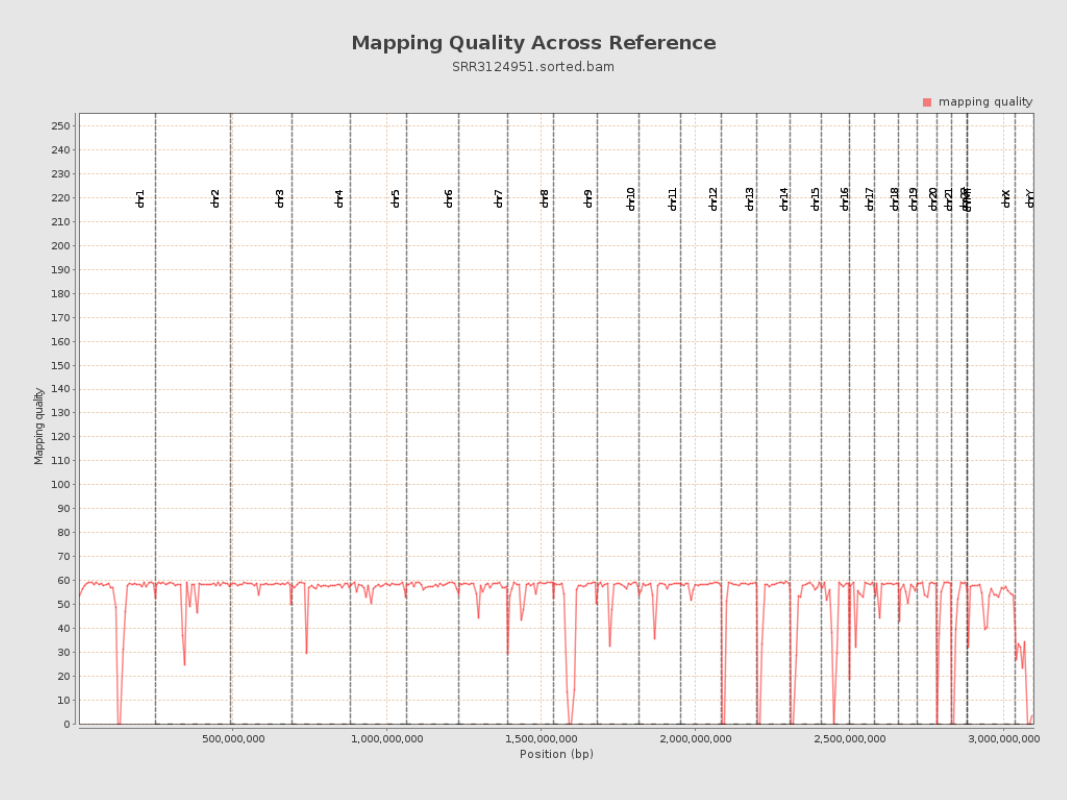
10. Results : Mapped Reads Clipping Profile



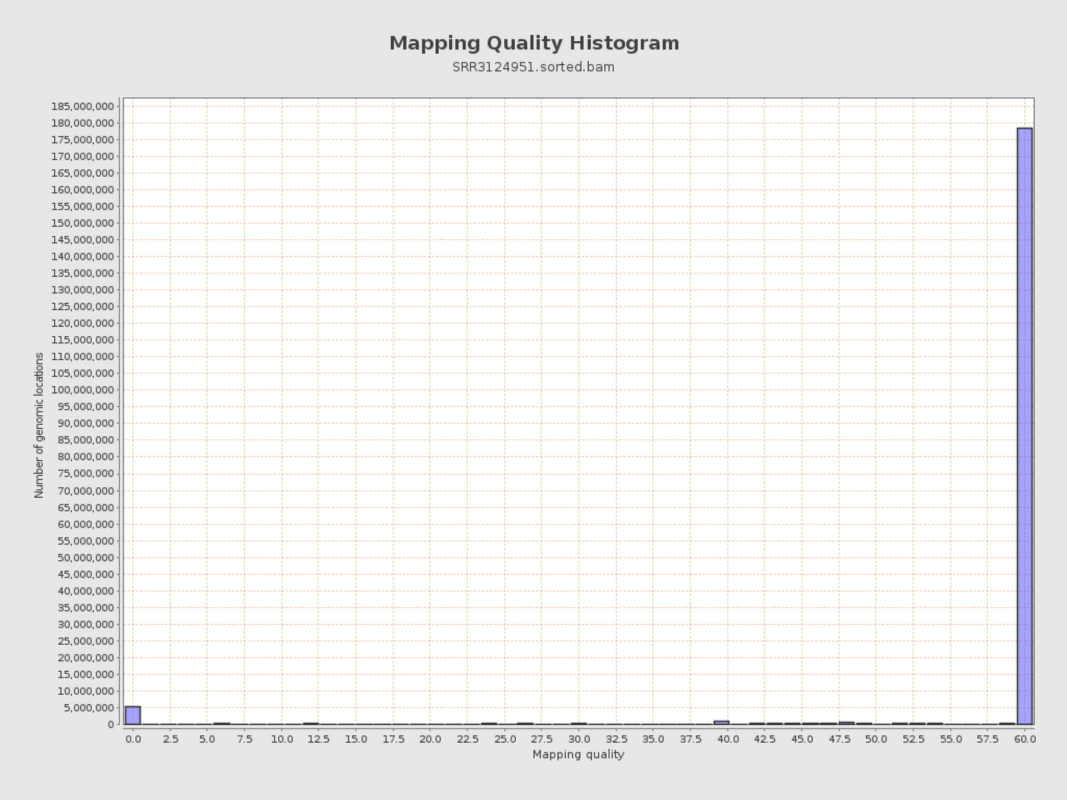
11. Results : Homopolymer Indels



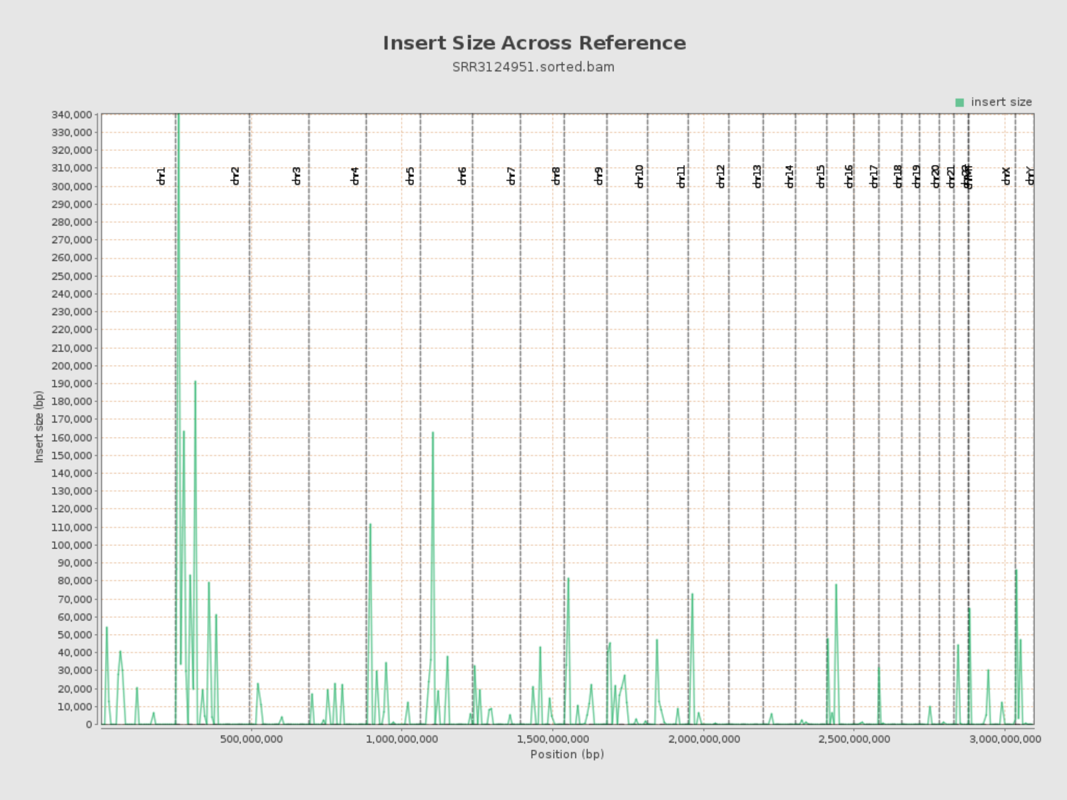
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram