Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 13:16:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124983.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_SRR3124983 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124983_1.fastq.gz SRR3124983_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 13:16:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124983.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,689,630
Mapped reads	4,542,630 / 96.87%
Unmapped reads	147,000 / 3.13%
Mapped paired reads	4,542,630 / 96.87%
Mapped reads, first in pair	2,301,435 / 49.07%
Mapped reads, second in pair	2,241,195 / 47.79%
Mapped reads, both in pair	4,466,320 / 95.24%
Mapped reads, singletons	76,310 / 1.63%
Secondary alignments	0
Supplementary alignments	10,893 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	231,680 / 4.94%
Duplication rate	3.65%
Clipped reads	2,342,136 / 49.94%

2.2. ACGT Content

Number/percentage of A's	76,642,657 / 27.54%
Number/percentage of C's	49,699,174 / 17.86%
Number/percentage of T's	82,679,075 / 29.71%
Number/percentage of G's	69,234,064 / 24.88%
Number/percentage of N's	2 / 0%

GC Percentage	42.74%

2.3. Coverage

Mean	0.0899
Standard Deviation	0.6722

2.4. Mapping Quality

Mean Mapping Quality	51.79

2.5. Insert size

Mean	68,806.96
Standard Deviation	2,552,095.67
P25/Median/P75	123 / 164 / 225

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	1,722,732
Insertions	29,280
Mapped reads with at least one insertion	0.64%
Deletions	66,760
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.39%

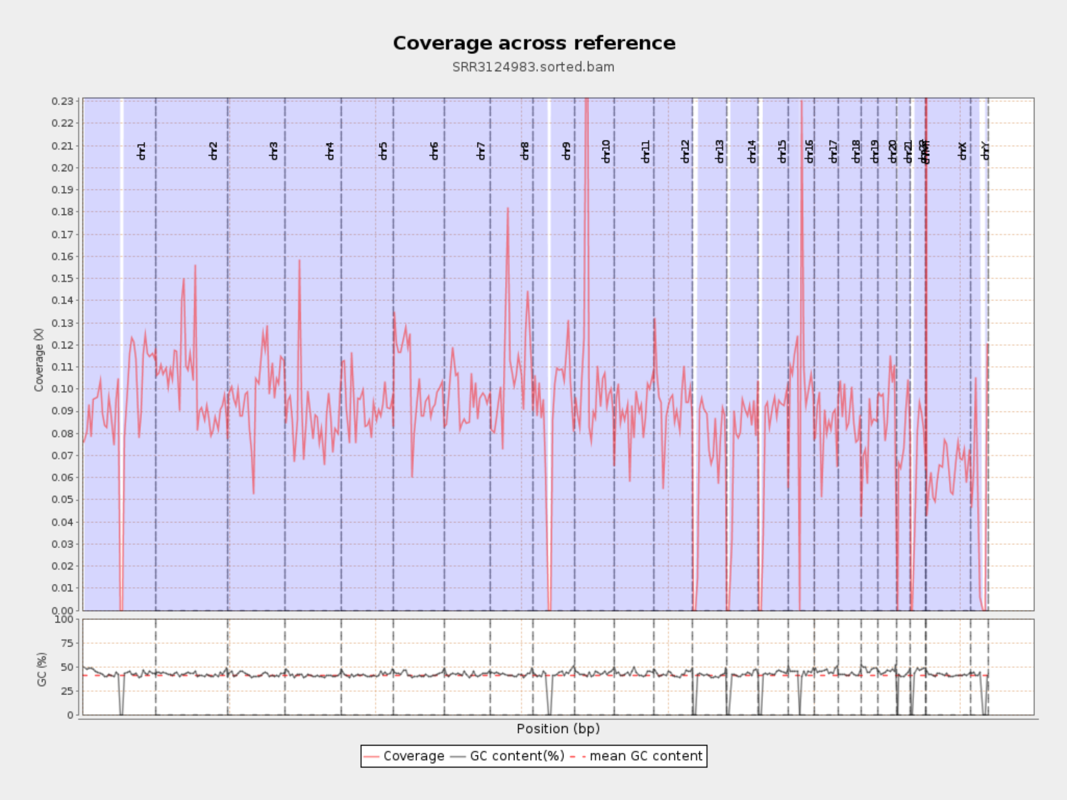
2.7. Chromosome stats

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

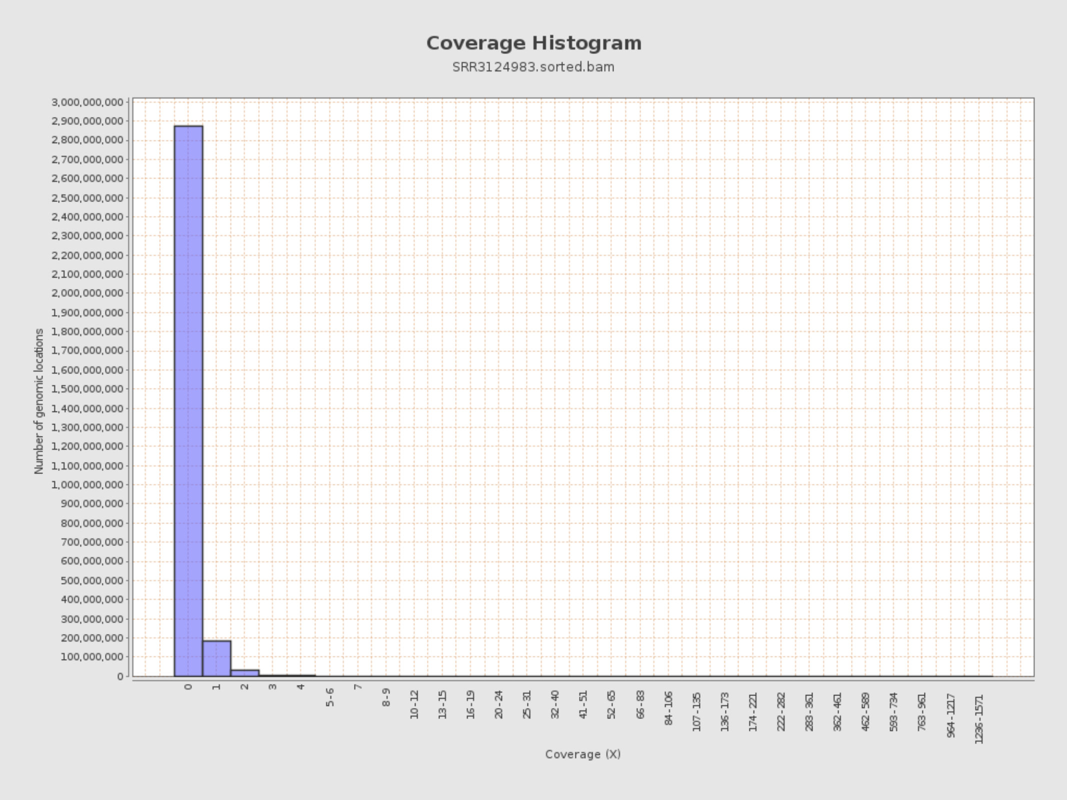
		bases	coverage	deviation
chr1	249250621	23074357	0.0926	0.5017
chr2	243199373	25058948	0.103	0.8759
chr3	198022430	19728672	0.0996	0.383
chr4	191154276	16744879	0.0876	0.5365
chr5	180915260	16789804	0.0928	0.3823
chr6	171115067	17520441	0.1024	0.4439
chr7	159138663	15155005	0.0952	0.4817
chr8	146364022	15905189	0.1087	0.424
chr9	141213431	12524366	0.0887	0.5323
chr10	135534747	14642128	0.108	1.9871
chr11	135006516	12148479	0.09	0.4041
chr12	133851895	12656430	0.0946	0.3685
chr13	115169878	7818444	0.0679	0.305
chr14	107349540	7717015	0.0719	0.3508
chr15	102531392	7704760	0.0751	0.3356
chr16	90354753	9529354	0.1055	1.1548
chr17	81195210	6729849	0.0829	0.5159
chr18	78077248	6961465	0.0892	0.6642
chr19	59128983	4596220	0.0777	0.4838
chr20	63025520	6058534	0.0961	0.4567
chr21	48129895	3484310	0.0724	0.4053
chr22	51304566	3035555	0.0592	0.3271
chrMT	16571	44722	2.6988	2.5256
chrX	155270560	9803638	0.0631	0.3548

chrY	59373566	2930201	0.0494	0.9524

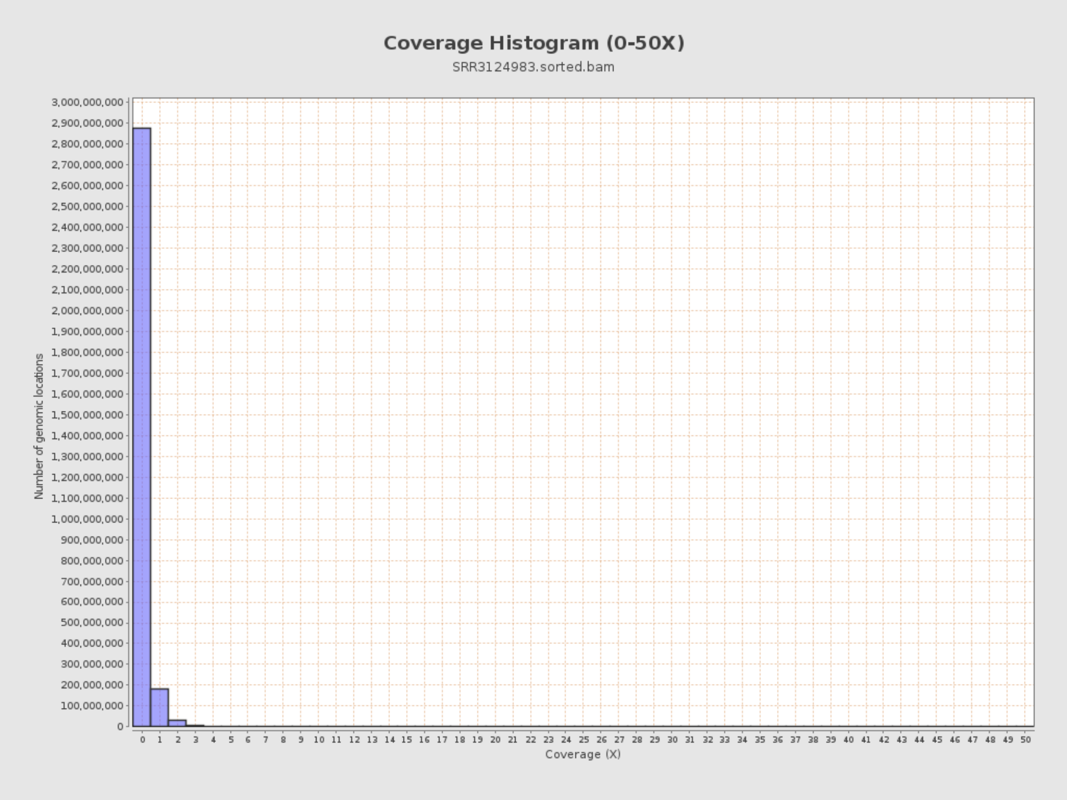
3. Results : Coverage across reference



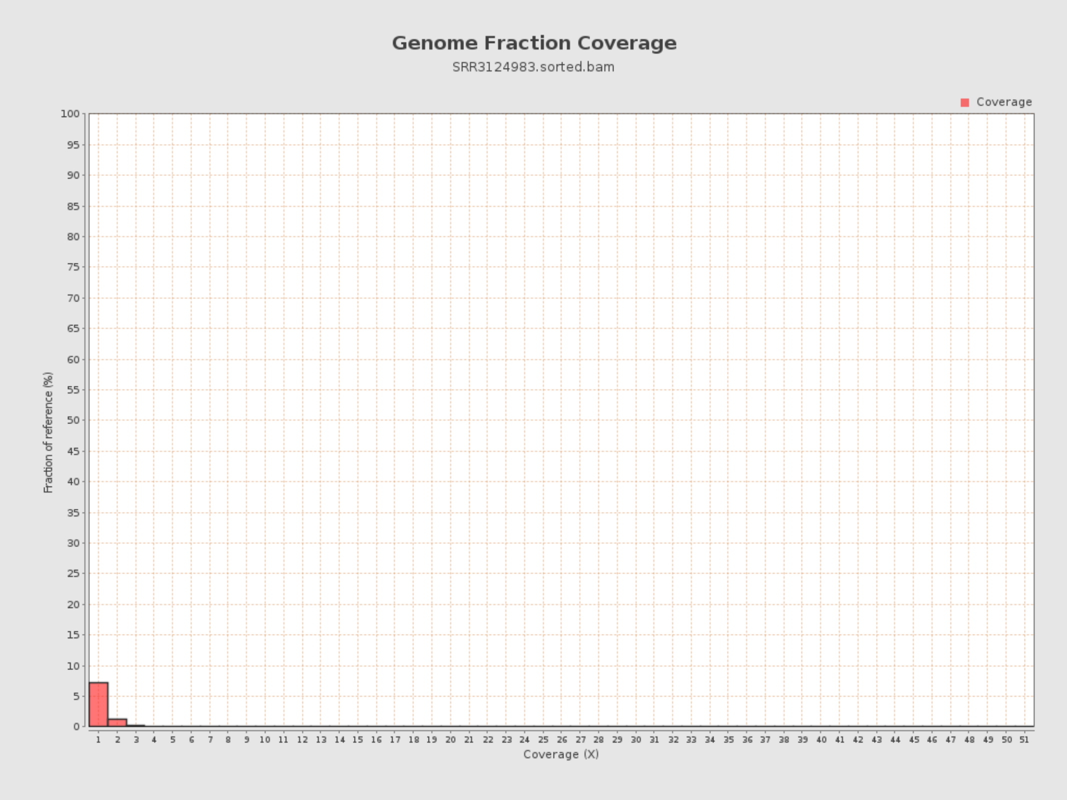
4. Results : Coverage Histogram



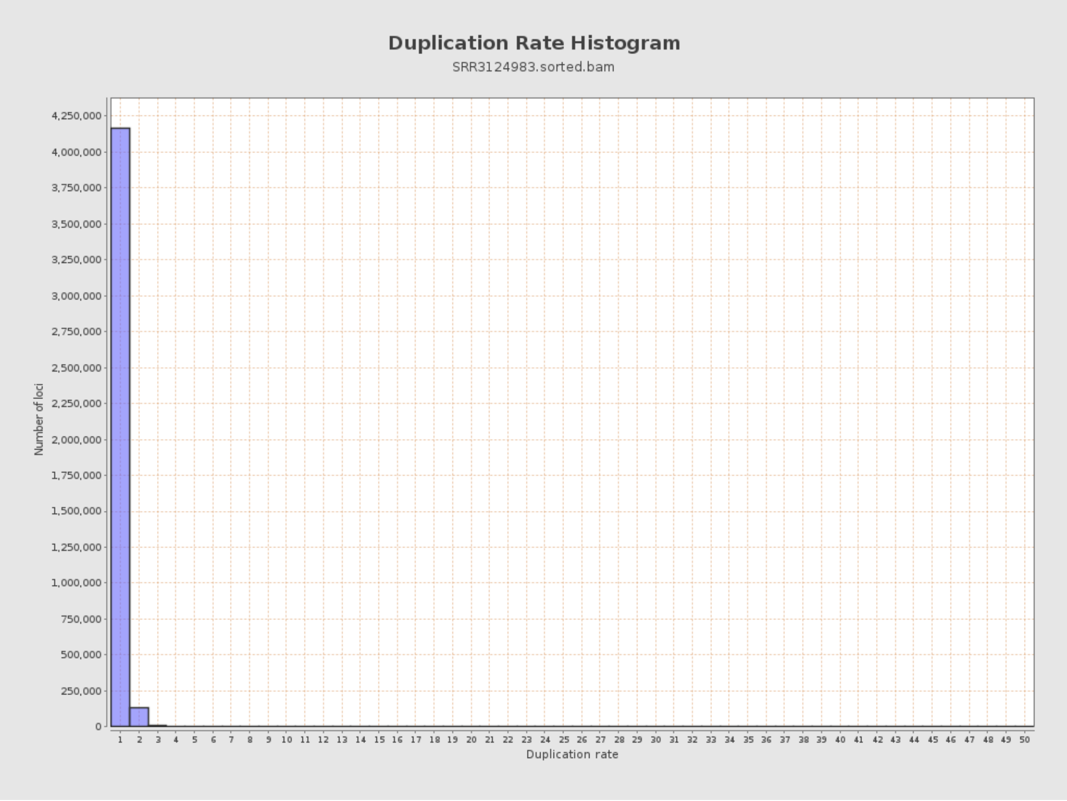
5. Results : Coverage Histogram (0-50X)



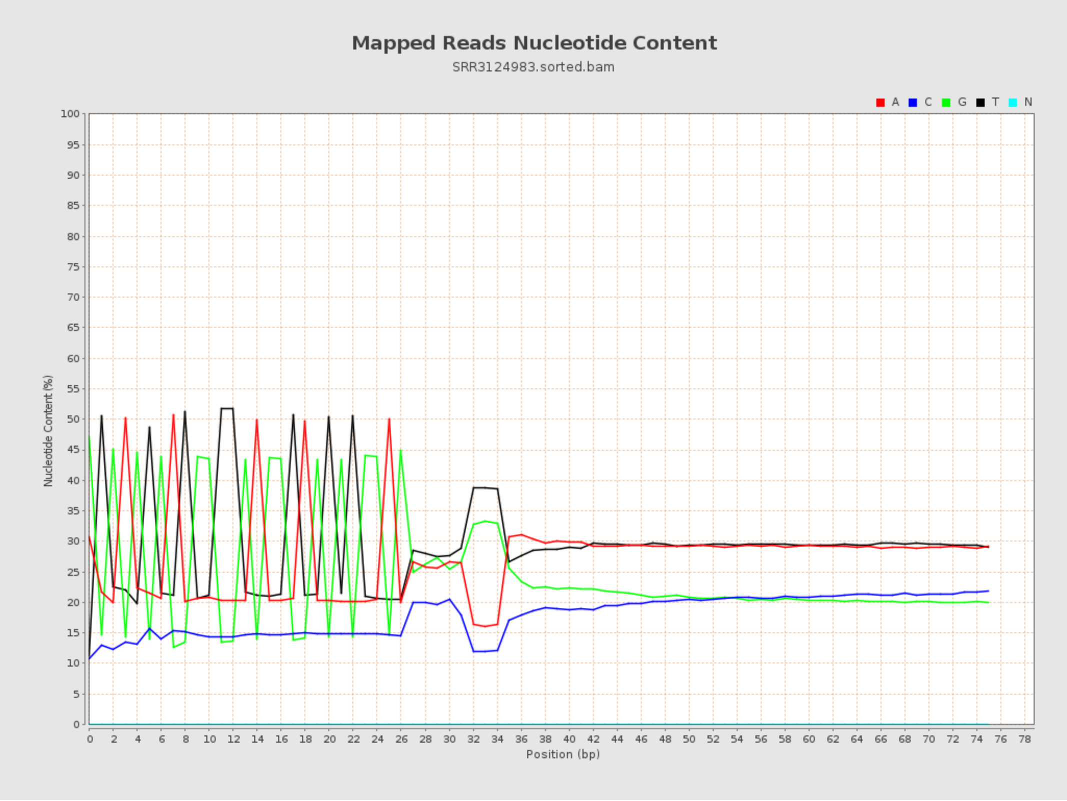
6. Results : Genome Fraction Coverage



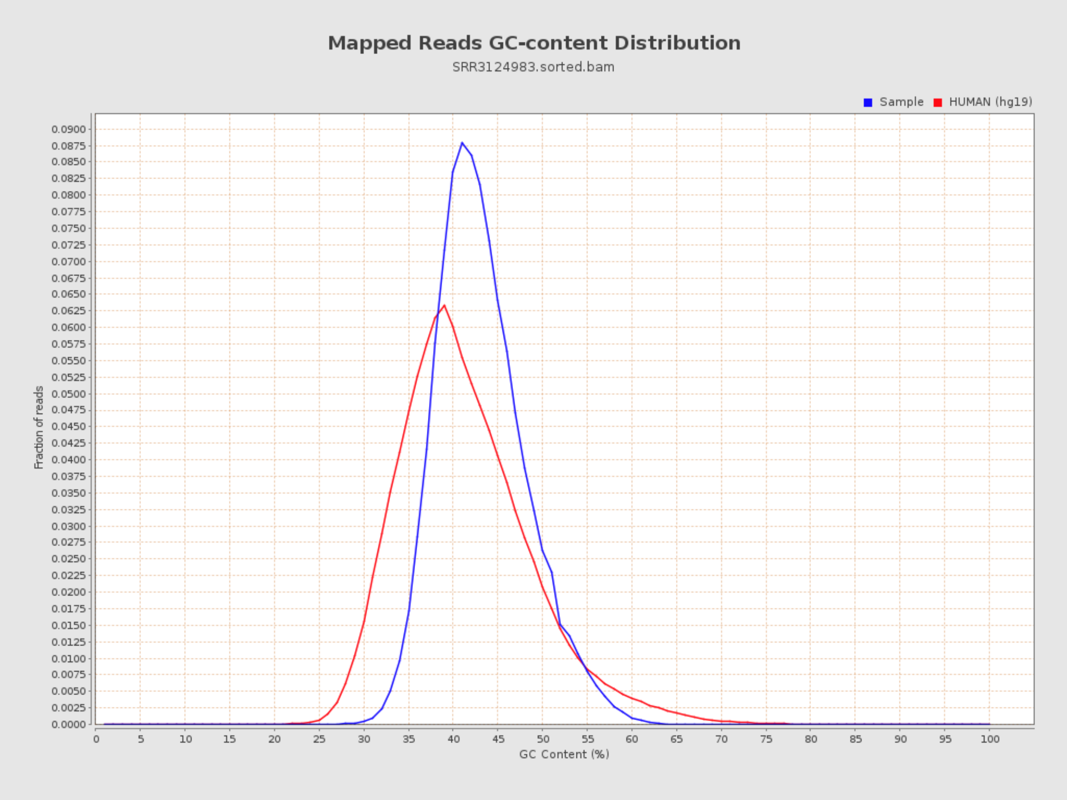
7. Results : Duplication Rate Histogram



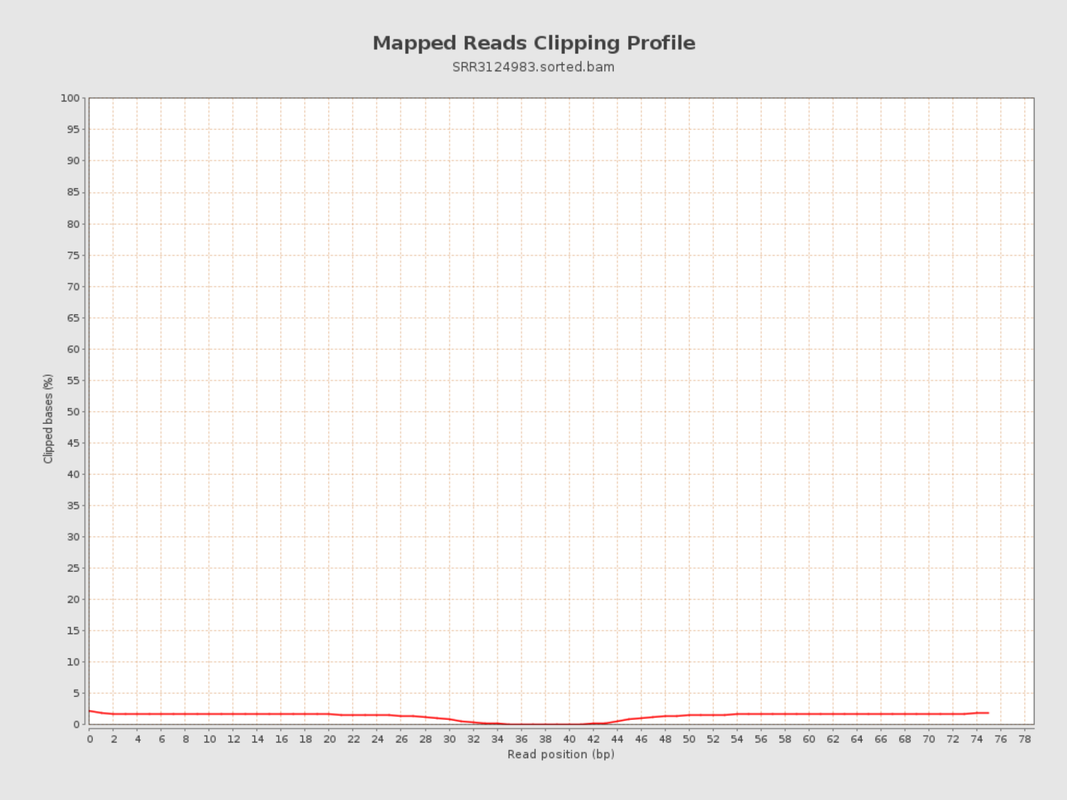
8. Results : Mapped Reads Nucleotide Content



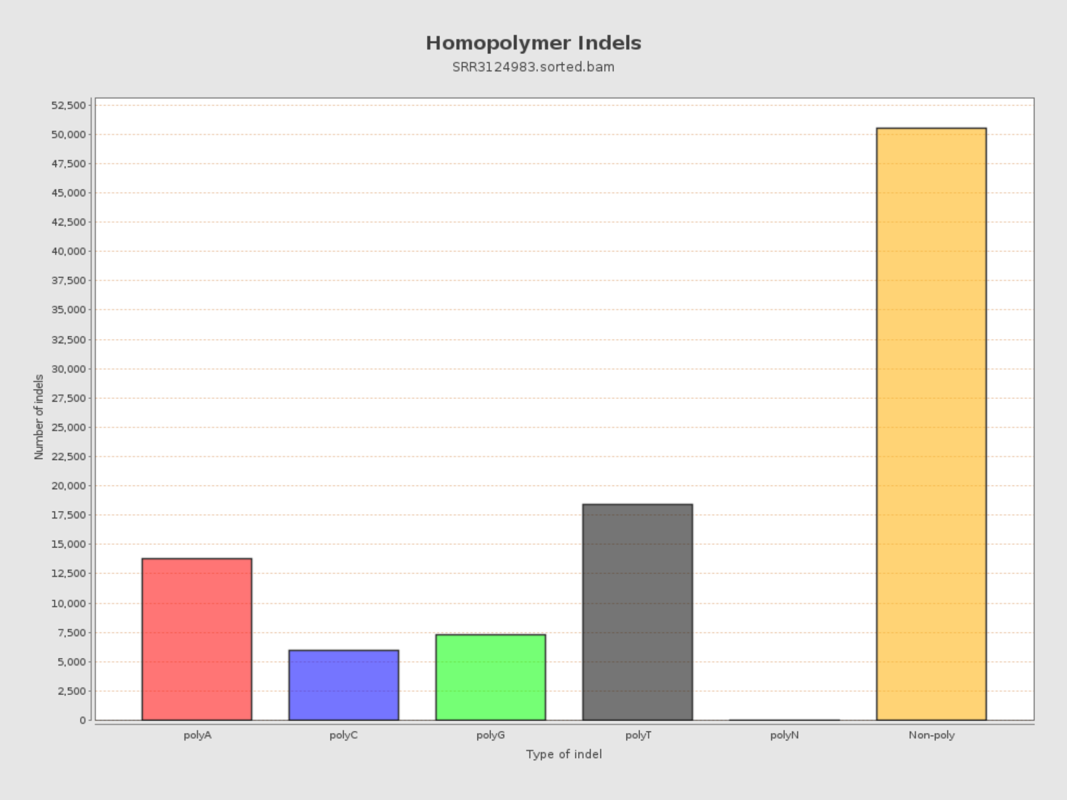
9. Results : Mapped Reads GC-content Distribution



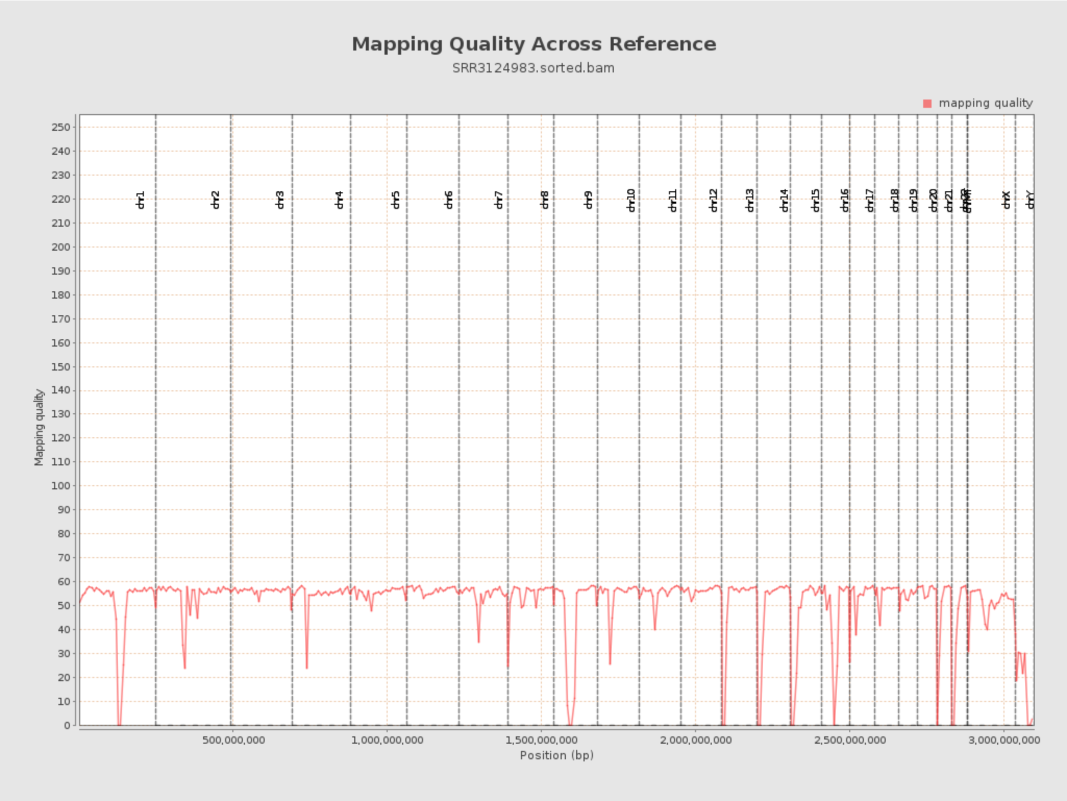
10. Results : Mapped Reads Clipping Profile



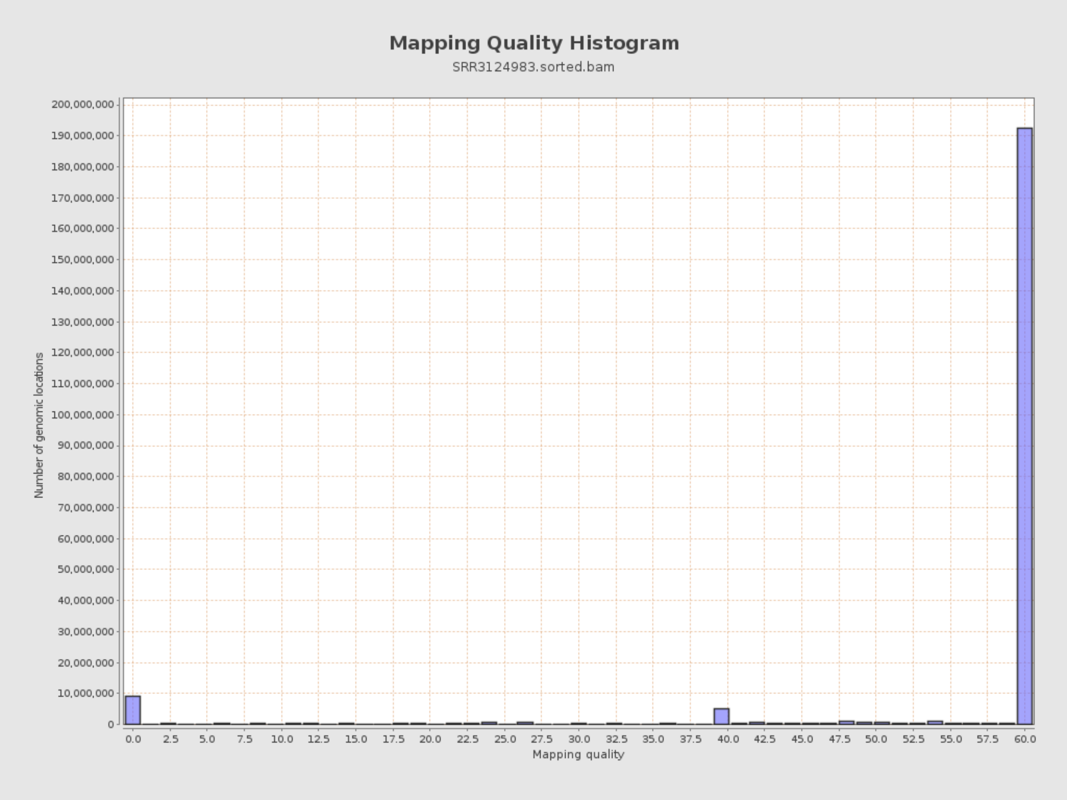
11. Results : Homopolymer Indels



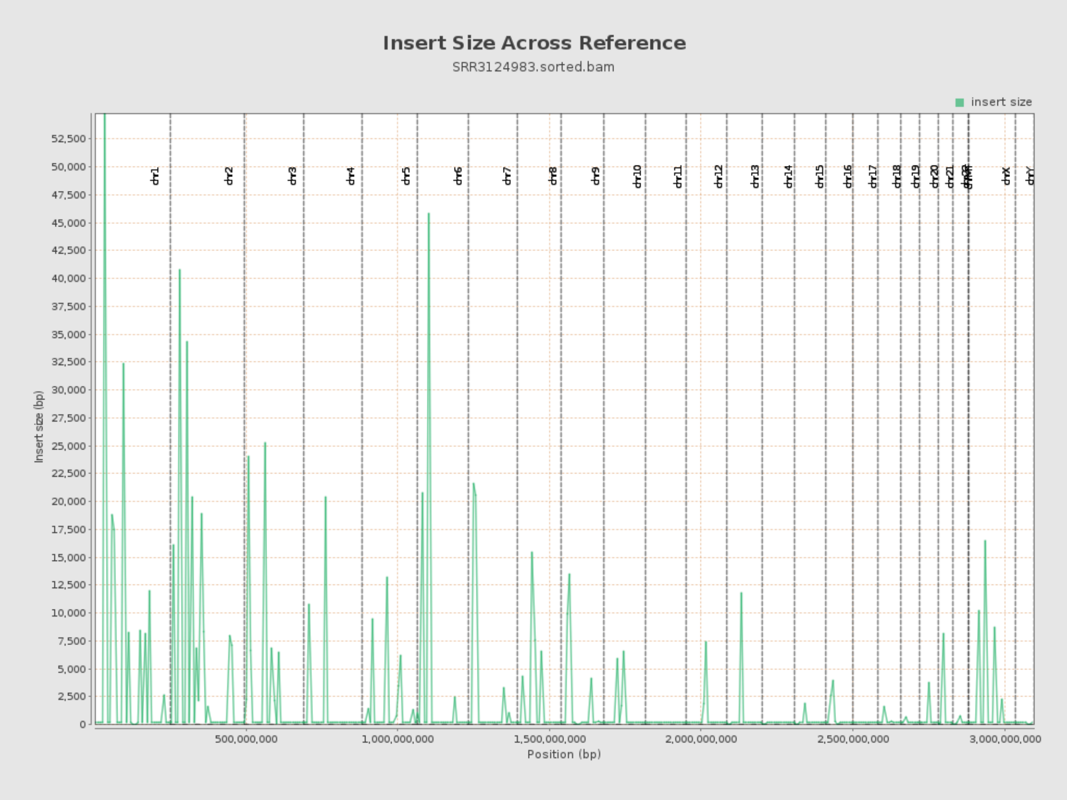
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram