Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 08:58:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124948.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_SRR3124948 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124948_1.fastq.gz SRR3124948_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 08:58:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124948.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,903,298
Mapped reads	4,356,824 / 88.85%
Unmapped reads	546,474 / 11.15%
Mapped paired reads	4,356,824 / 88.85%
Mapped reads, first in pair	2,228,270 / 45.44%
Mapped reads, second in pair	2,128,554 / 43.41%
Mapped reads, both in pair	4,158,436 / 84.81%
Mapped reads, singletons	198,388 / 4.05%
Secondary alignments	0
Supplementary alignments	16,858 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	251,674 / 5.13%
Duplication rate	3.07%
Clipped reads	1,484,129 / 30.27%

2.2. ACGT Content

Number/percentage of A's	82,416,801 / 28.55%
Number/percentage of C's	54,279,166 / 18.8%
Number/percentage of T's	85,953,780 / 29.77%
Number/percentage of G's	66,030,681 / 22.87%
Number/percentage of N's	2,282 / 0%

GC Percentage	41.68%

2.3. Coverage

Mean	0.0933
Standard Deviation	1.8437

2.4. Mapping Quality

Mean Mapping Quality	51.22

2.5. Insert size

Mean	92,971.71
Standard Deviation	2,856,307.1
P25/Median/P75	145 / 186 / 248

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	1,769,855
Insertions	32,774
Mapped reads with at least one insertion	0.74%
Deletions	80,720
Mapped reads with at least one deletion	1.83%
Homopolymer indels	47.77%

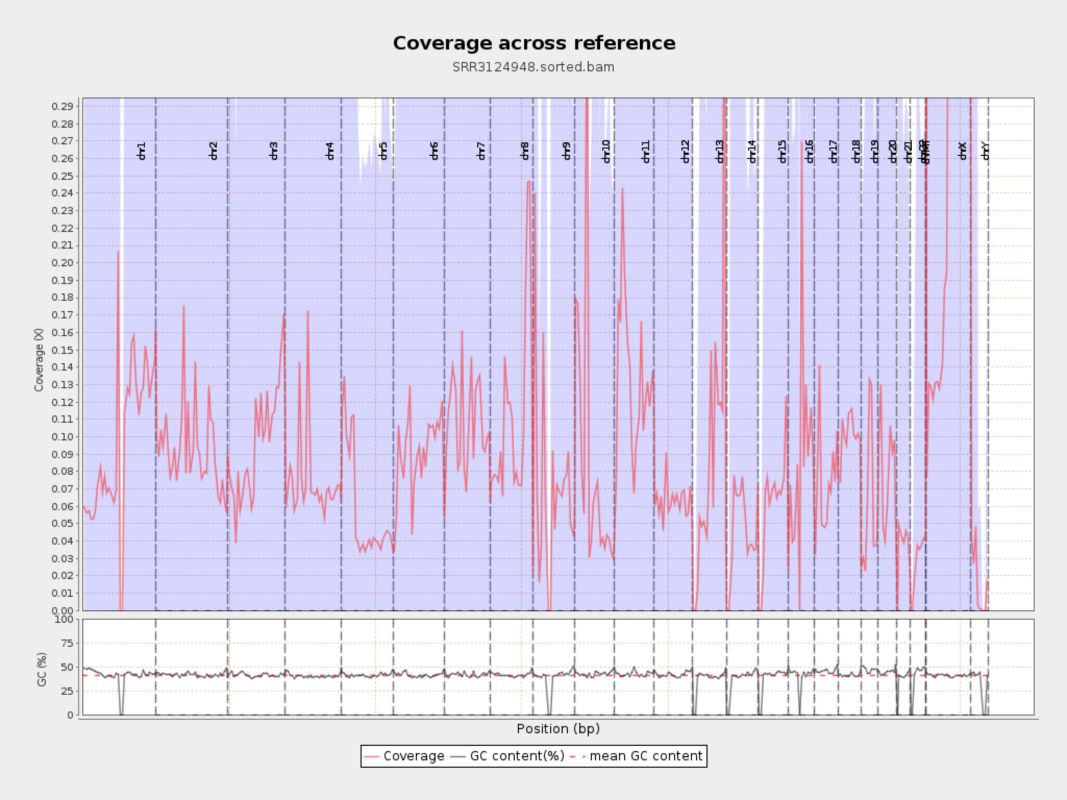
2.7. Chromosome stats

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

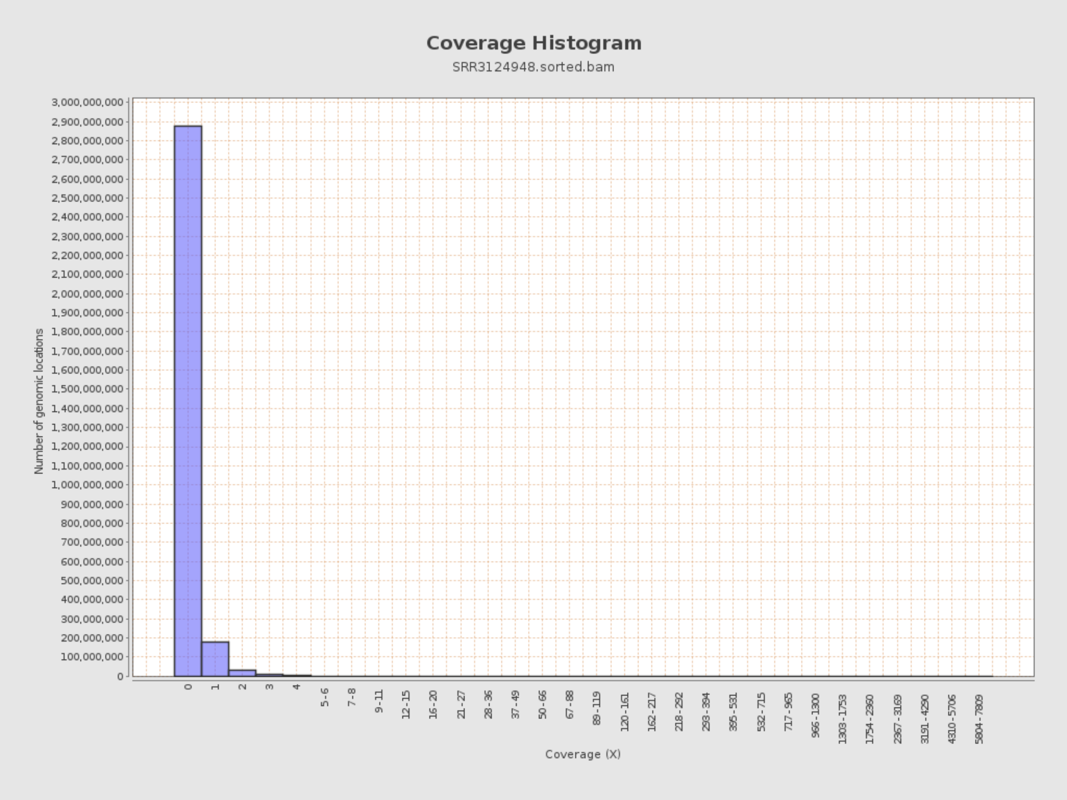
		bases	coverage	deviation
chr1	249250621	23875167	0.0958	1.1053
chr2	243199373	22760192	0.0936	2.2358
chr3	198022430	18978888	0.0958	0.3973
chr4	191154276	14318120	0.0749	4.9991
chr5	180915260	10443500	0.0577	0.8165
chr6	171115067	15690325	0.0917	0.6159
chr7	159138663	17317770	0.1088	1.0889
chr8	146364022	16656766	0.1138	0.4831
chr9	141213431	9862254	0.0698	2.3107
chr10	135534747	11733502	0.0866	2.5848
chr11	135006516	17965900	0.1331	3.3912
chr12	133851895	8433852	0.063	0.3016
chr13	115169878	11890438	0.1032	0.4697
chr14	107349540	4824021	0.0449	0.5523
chr15	102531392	6261192	0.0611	0.2938
chr16	90354753	7969330	0.0882	1.2598
chr17	81195210	5882480	0.0724	0.7298
chr18	78077248	7794175	0.0998	1.3046
chr19	59128983	3691241	0.0624	0.7104
chr20	63025520	5159698	0.0819	0.3822
chr21	48129895	1814651	0.0377	0.3099
chr22	51304566	1390806	0.0271	0.2082
chrMT	16571	62576	3.7762	2.9751
chrX	155270560	43066729	0.2774	0.7675

chrY	59373566	966478	0.0163	0.7188

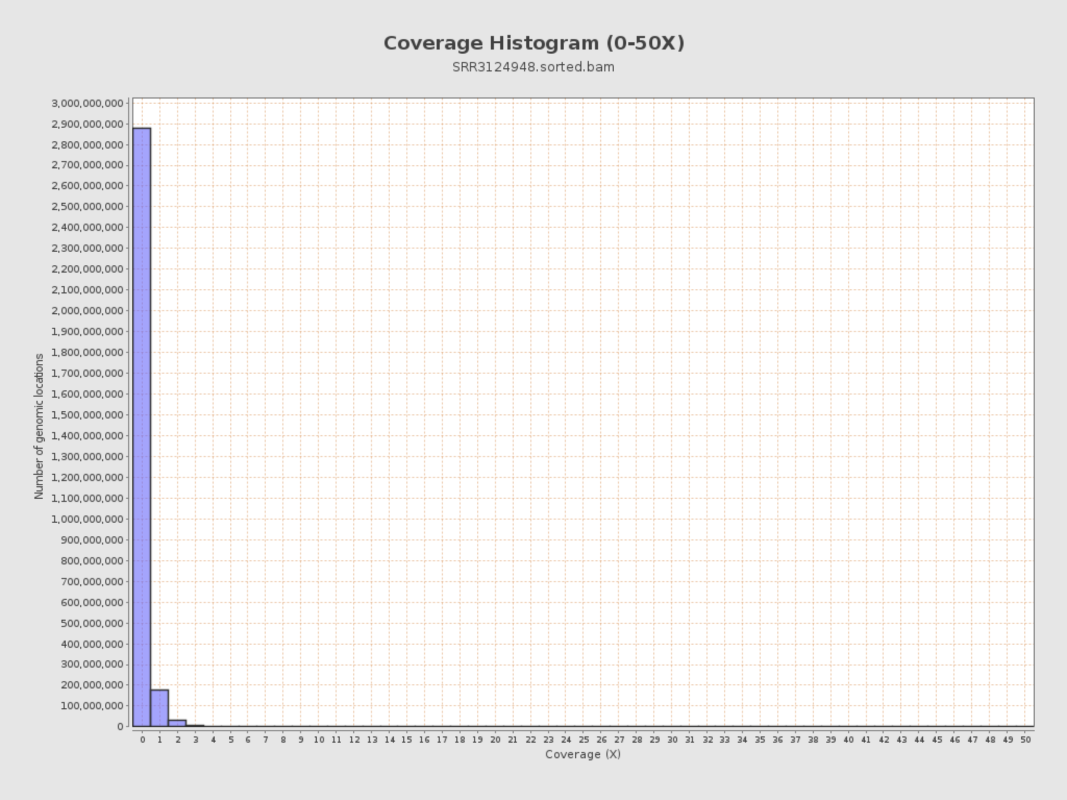
3. Results : Coverage across reference



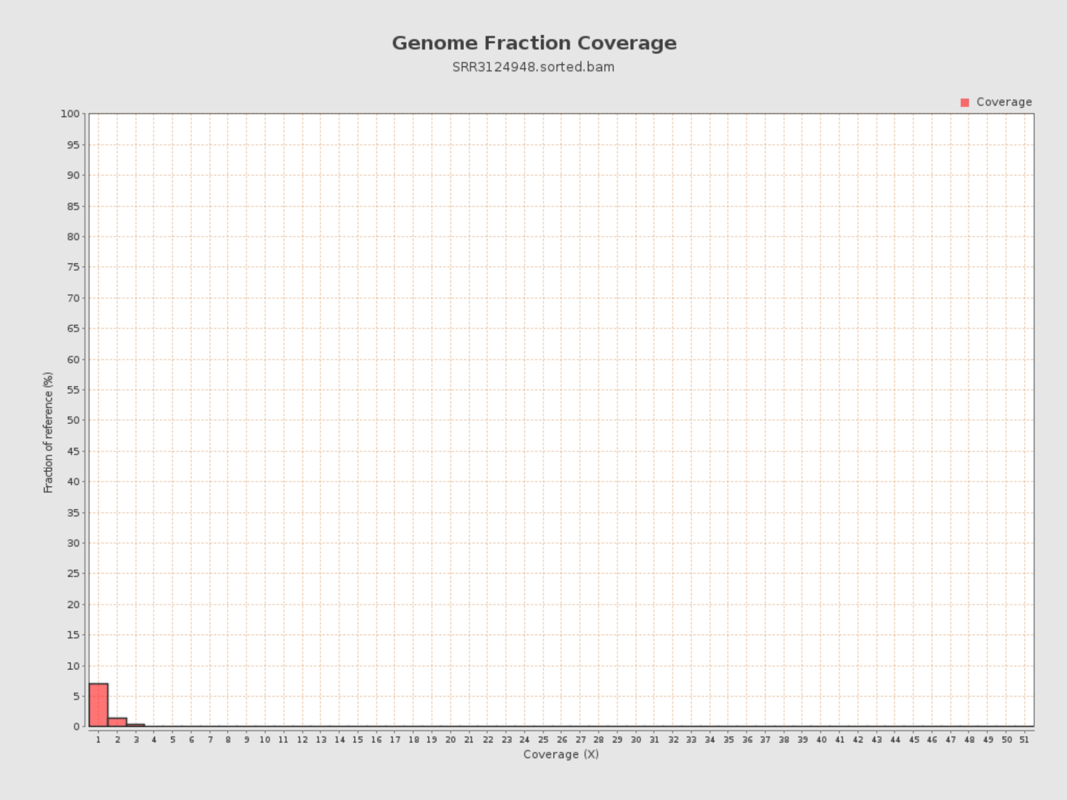
4. Results : Coverage Histogram



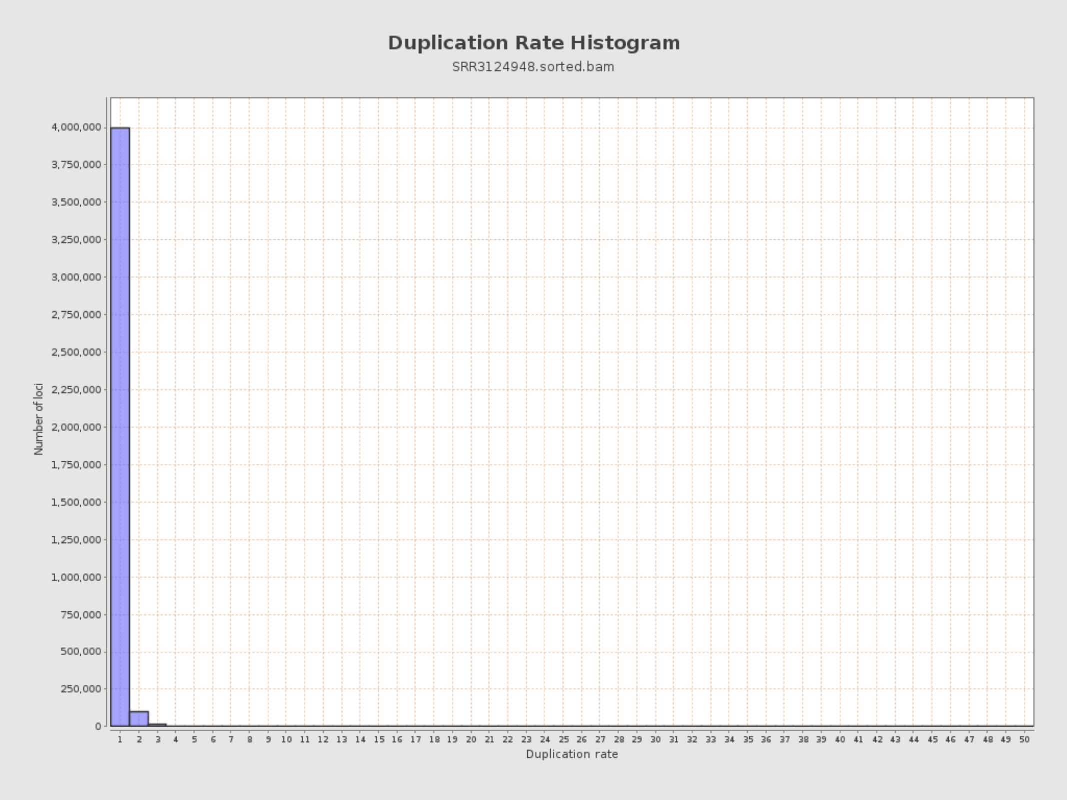
5. Results : Coverage Histogram (0-50X)



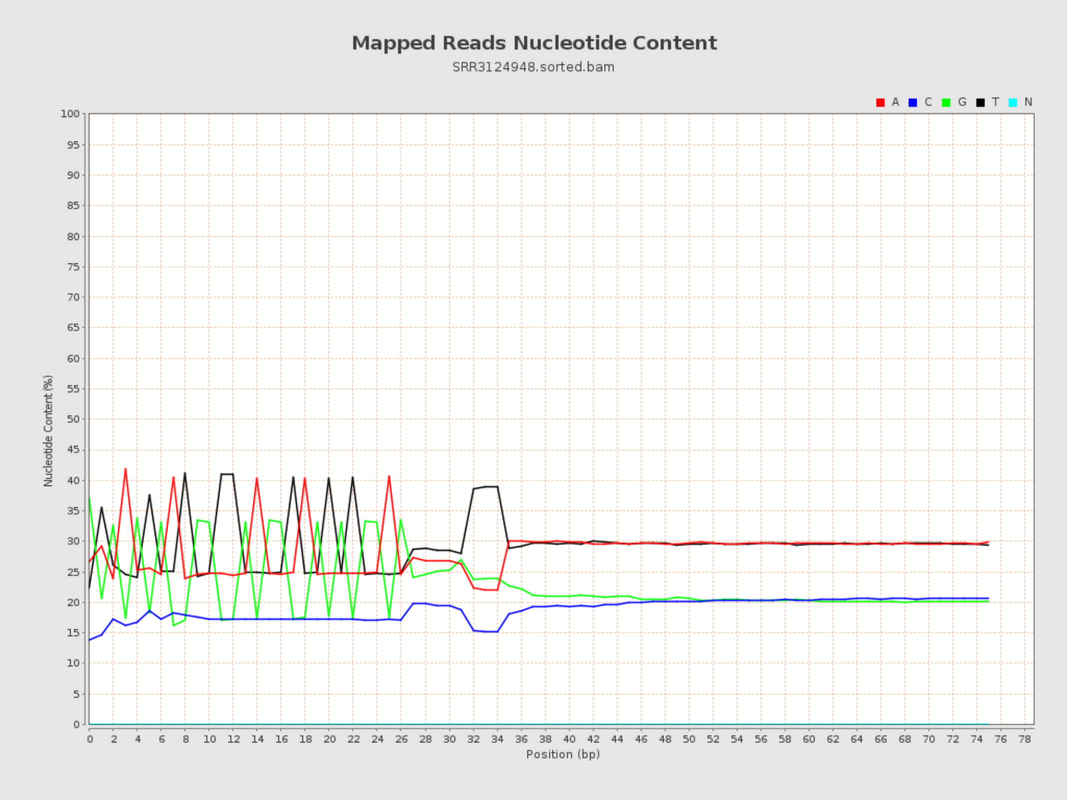
6. Results : Genome Fraction Coverage



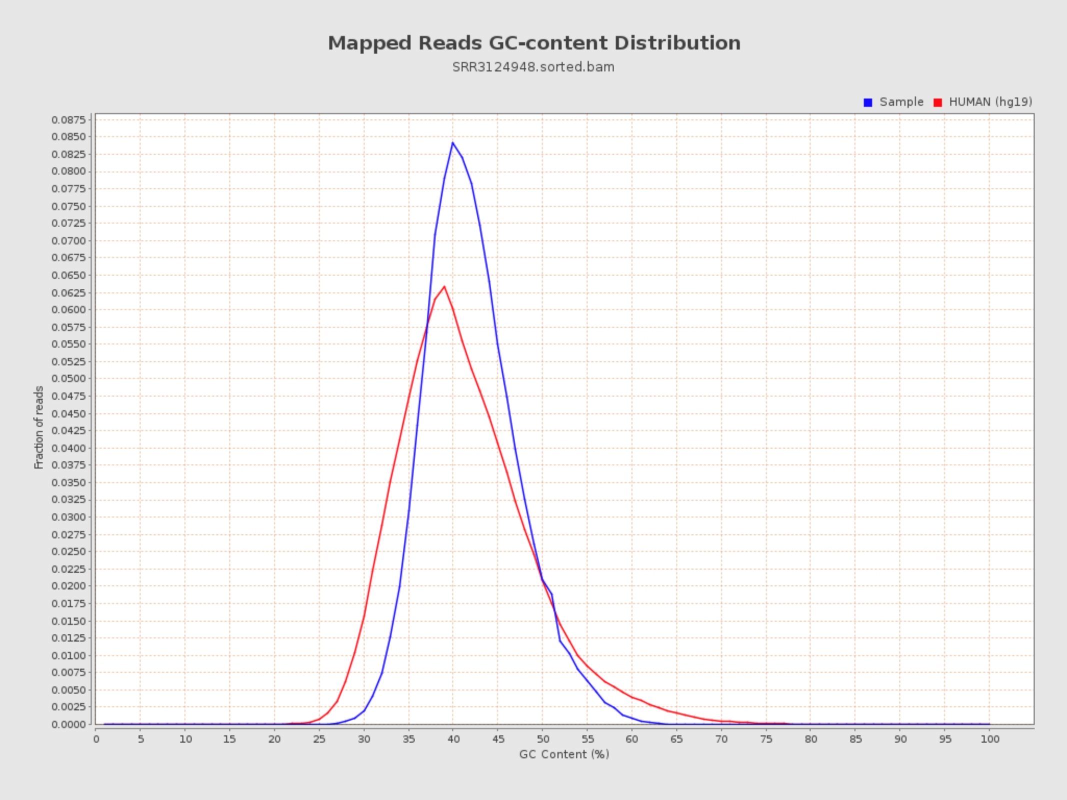
7. Results : Duplication Rate Histogram



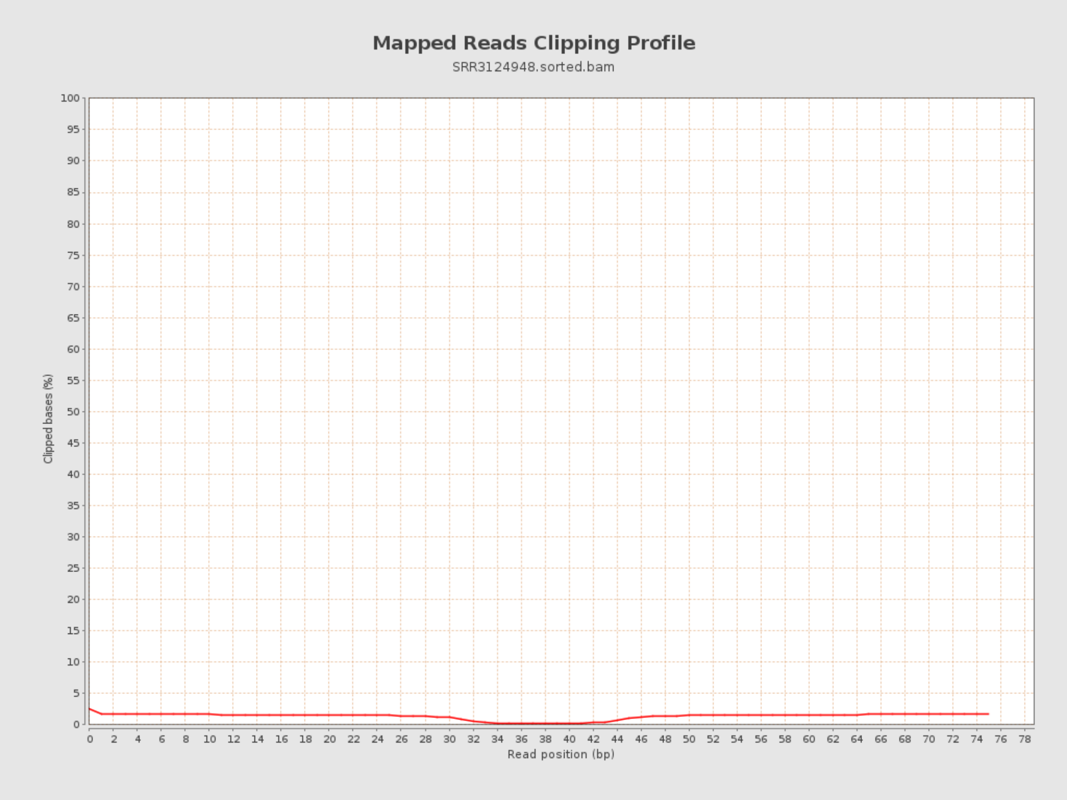
8. Results : Mapped Reads Nucleotide Content



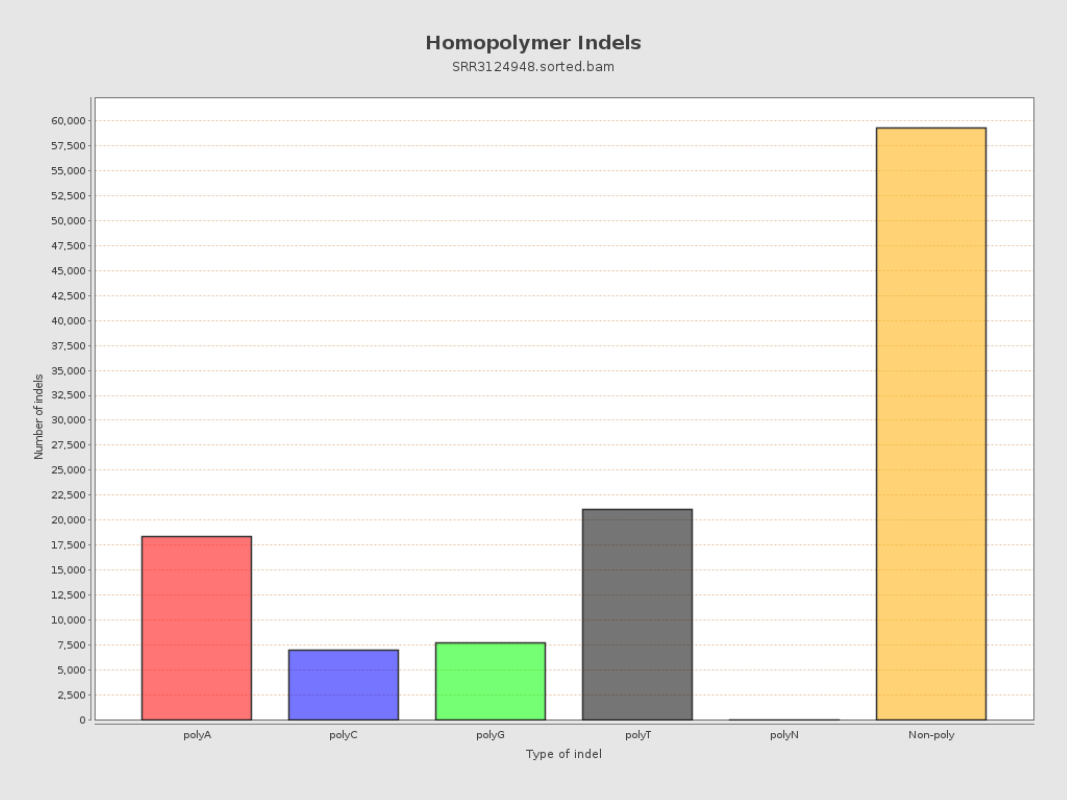
9. Results : Mapped Reads GC-content Distribution



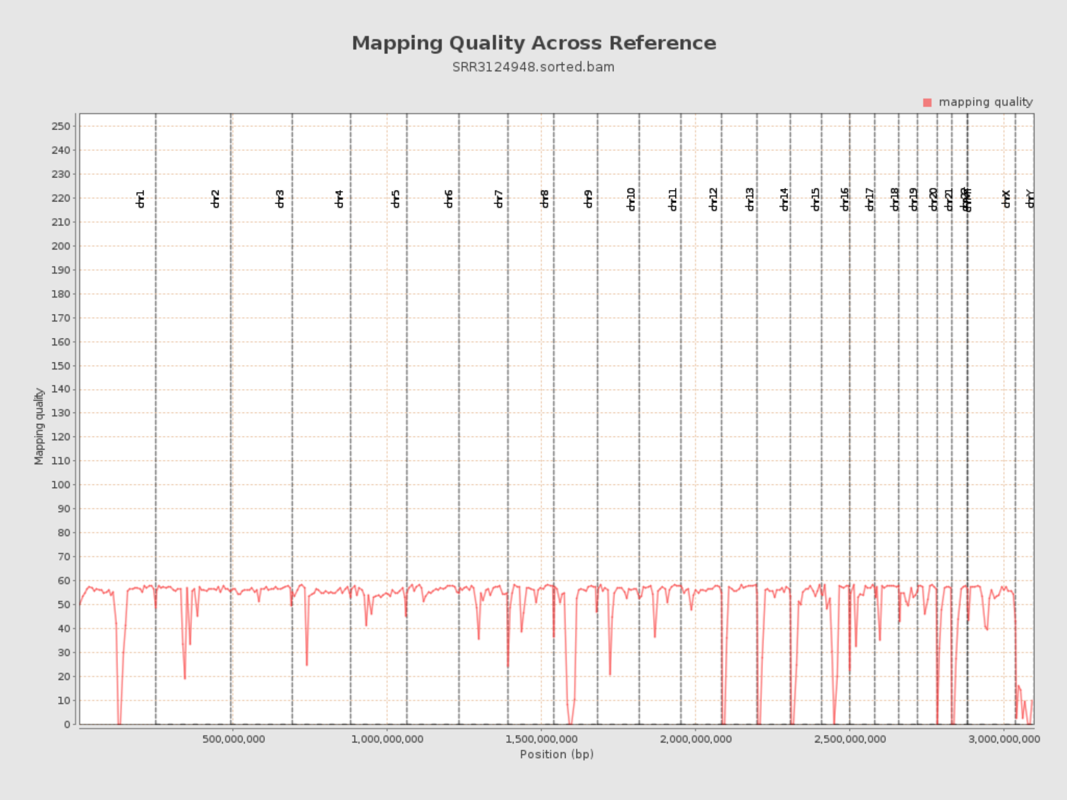
10. Results : Mapped Reads Clipping Profile



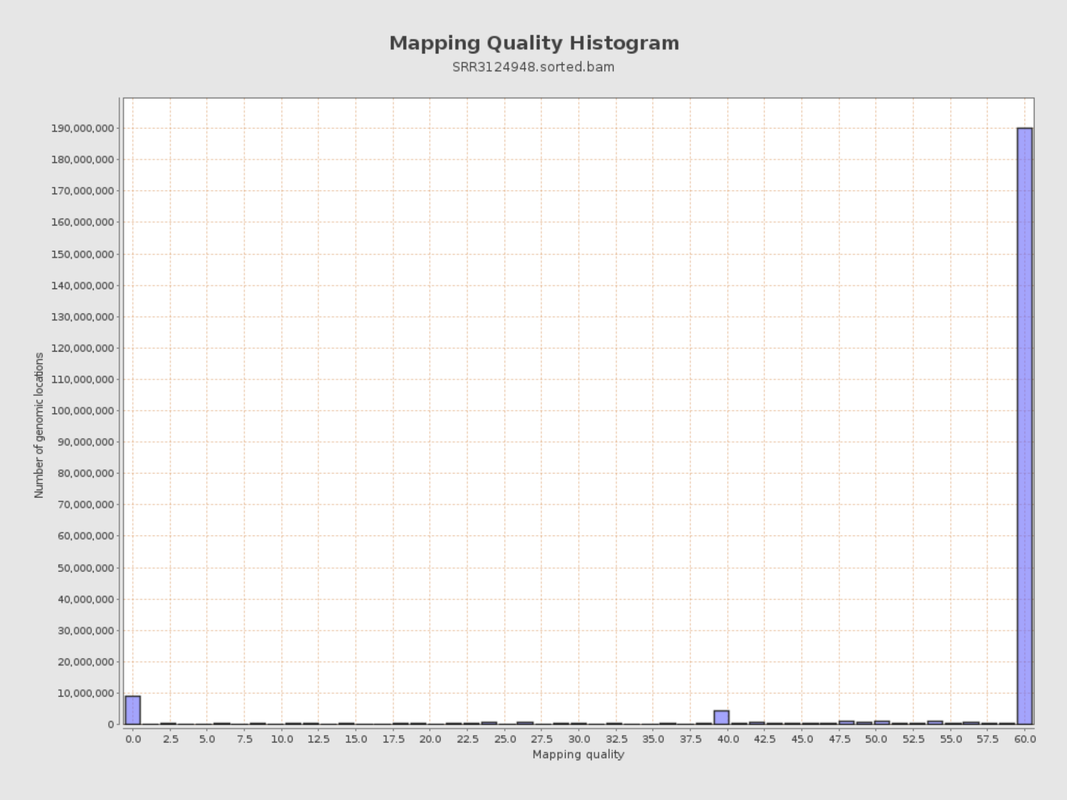
11. Results : Homopolymer Indels



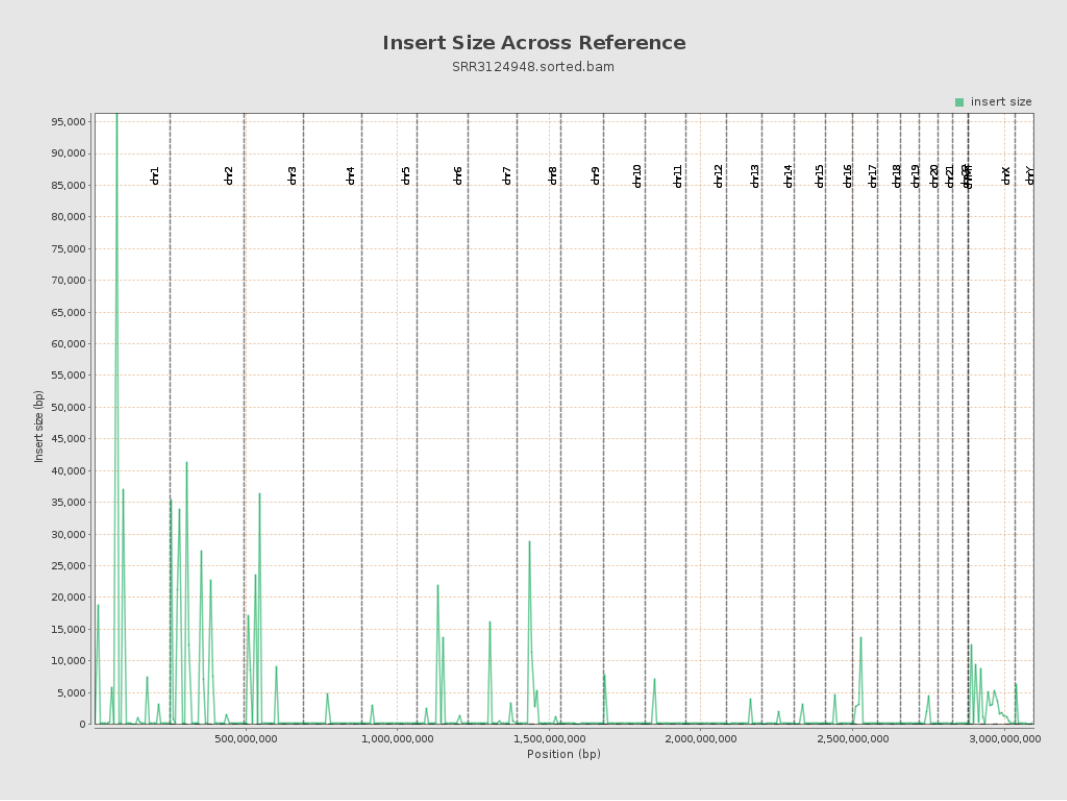
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram