Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 23:10:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124868.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_SRR3124868 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124868_1.fastq.gz SRR3124868_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 23:10:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124868.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,327,684
Mapped reads	2,306,037 / 99.07%
Unmapped reads	21,647 / 0.93%
Mapped paired reads	2,306,037 / 99.07%
Mapped reads, first in pair	1,154,543 / 49.6%
Mapped reads, second in pair	1,151,494 / 49.47%
Mapped reads, both in pair	2,296,834 / 98.67%
Mapped reads, singletons	9,203 / 0.4%
Secondary alignments	0
Supplementary alignments	687,673 / 29.54%
Read min/max/mean length	30 / 151 / 166.6
Duplicated reads (estimated)	855,819 / 36.77%
Duplication rate	25.01%
Clipped reads	2,666,497 / 114.56%

2.2. ACGT Content

Number/percentage of A's	91,139,651 / 29.52%
Number/percentage of C's	63,204,457 / 20.47%
Number/percentage of T's	90,188,642 / 29.21%
Number/percentage of G's	64,177,475 / 20.79%
Number/percentage of N's	24,907 / 0.01%

GC Percentage	41.26%

2.3. Coverage

Mean	0.0999
Standard Deviation	4.824

2.4. Mapping Quality

Mean Mapping Quality	46.96

2.5. Insert size

Mean	1,386,891.15
Standard Deviation	11,115,138.2
P25/Median/P75	107 / 140 / 181

2.6. Mismatches and indels

General error rate	1.88%
Mismatches	5,456,554
Insertions	118,843
Mapped reads with at least one insertion	4.79%
Deletions	199,860
Mapped reads with at least one deletion	8.19%
Homopolymer indels	42.84%

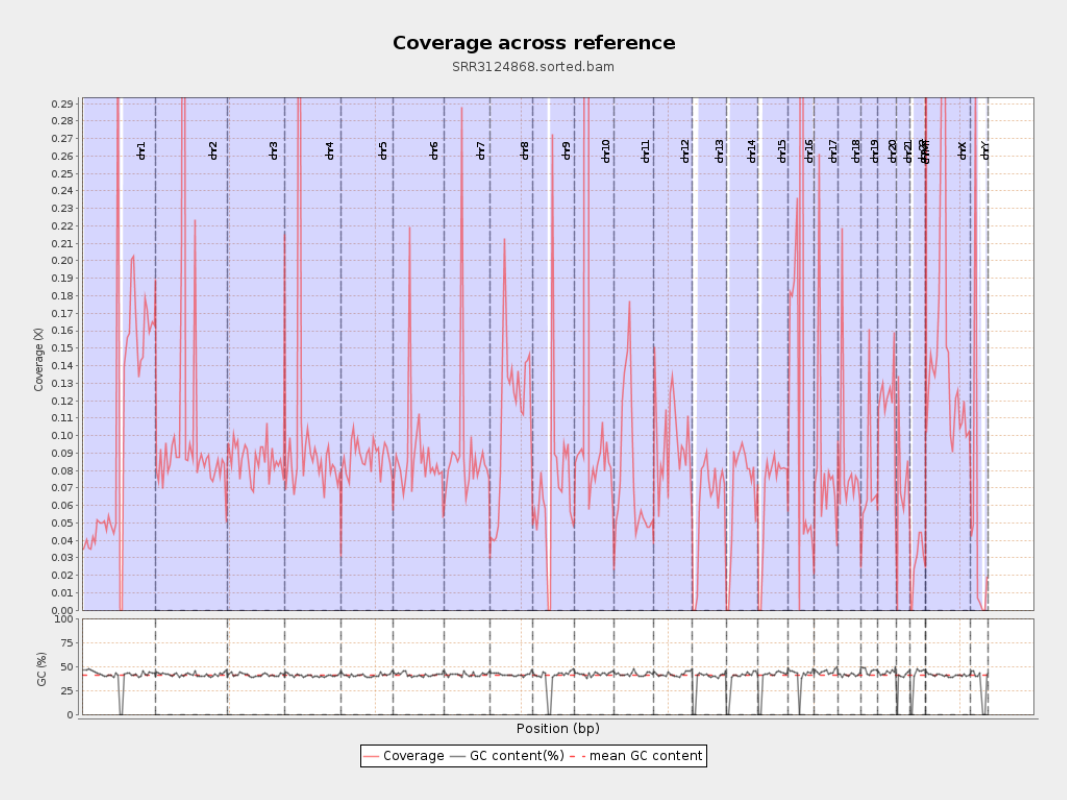
2.7. Chromosome stats

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

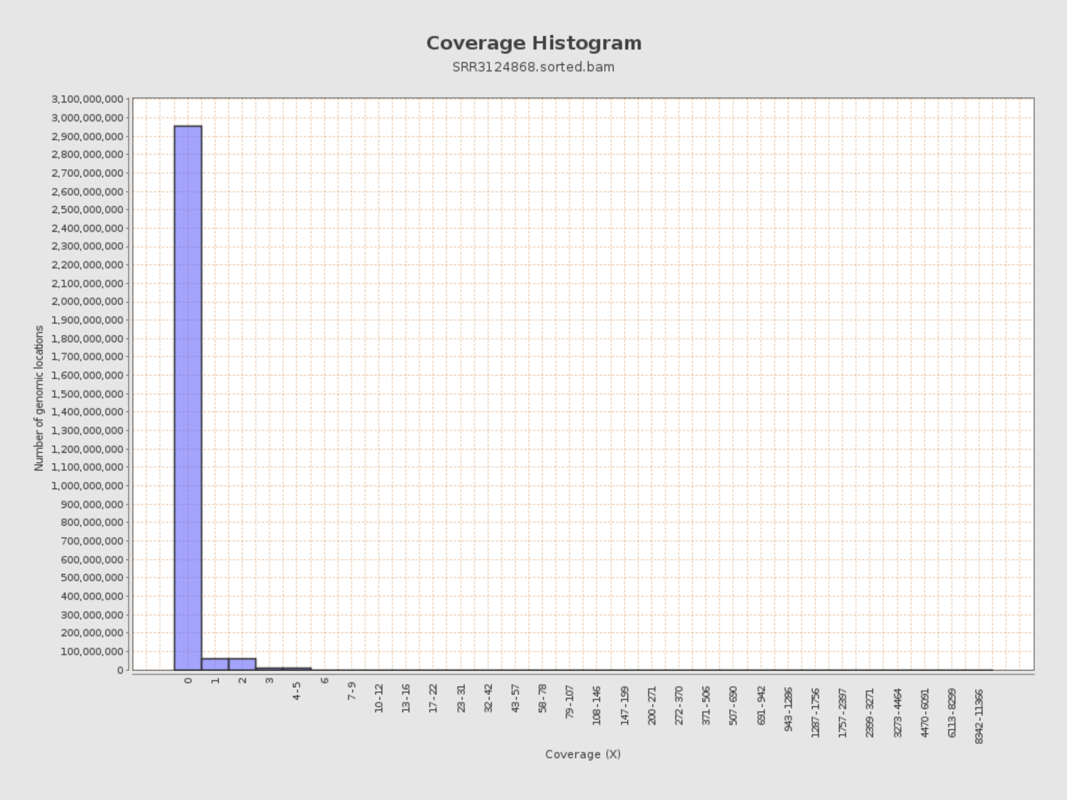
		bases	coverage	deviation
chr1	249250621	25943789	0.1041	3.1227
chr2	243199373	26851743	0.1104	3.4969
chr3	198022430	17336397	0.0875	1.5464
chr4	191154276	19988547	0.1046	2.7959
chr5	180915260	15808099	0.0874	0.5008
chr6	171115067	15236093	0.089	1.4979
chr7	159138663	14575815	0.0916	2.6986
chr8	146364022	16421456	0.1122	1.0457
chr9	141213431	10435469	0.0739	3.4184
chr10	135534747	27922791	0.206	19.9022
chr11	135006516	10534786	0.078	1.1924
chr12	133851895	13025860	0.0973	0.5169
chr13	115169878	7003862	0.0608	0.3768
chr14	107349540	7391486	0.0689	0.5017
chr15	102531392	6781604	0.0661	0.3904
chr16	90354753	16405765	0.1816	6.1323
chr17	81195210	7113935	0.0876	3.2248
chr18	78077248	6725013	0.0861	3.0039
chr19	59128983	4288309	0.0725	1.8705
chr20	63025520	7755589	0.1231	1.0715
chr21	48129895	3462049	0.0719	1.5715
chr22	51304566	1414601	0.0276	0.367
chrMT	16571	61896	3.7352	3.7363
chrX	155270560	23479577	0.1512	1.431

chrY	59373566	3191723	0.0538	5.2284

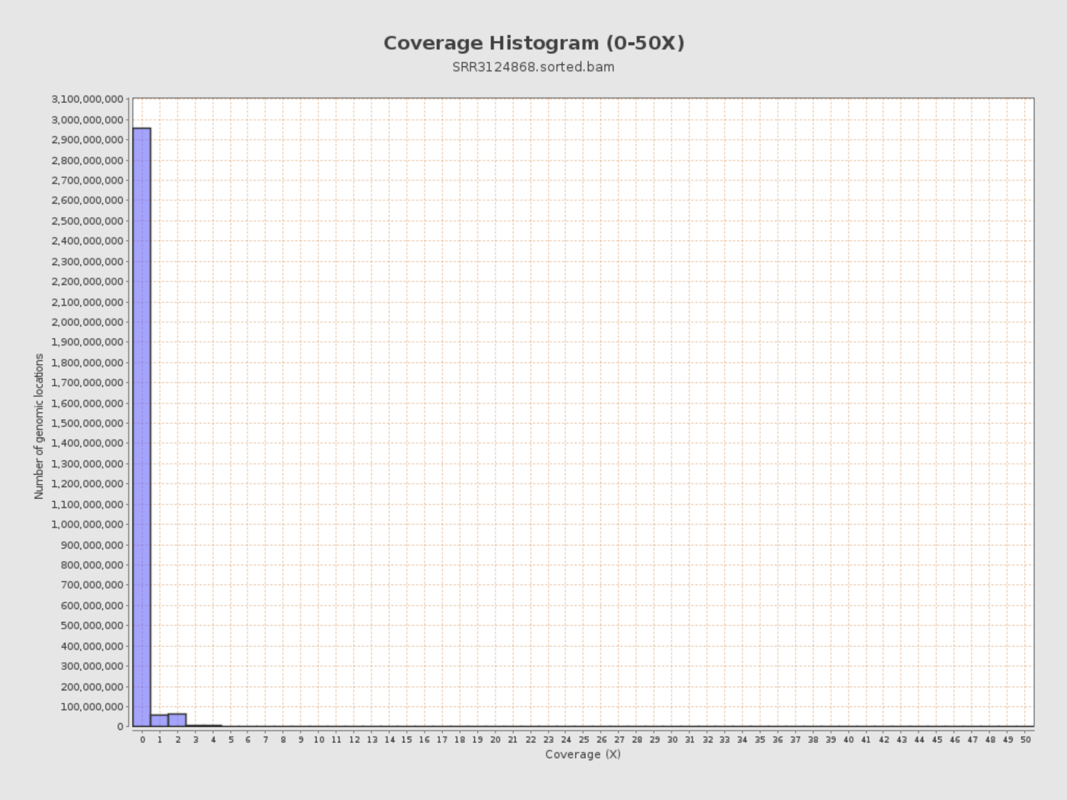
3. Results : Coverage across reference



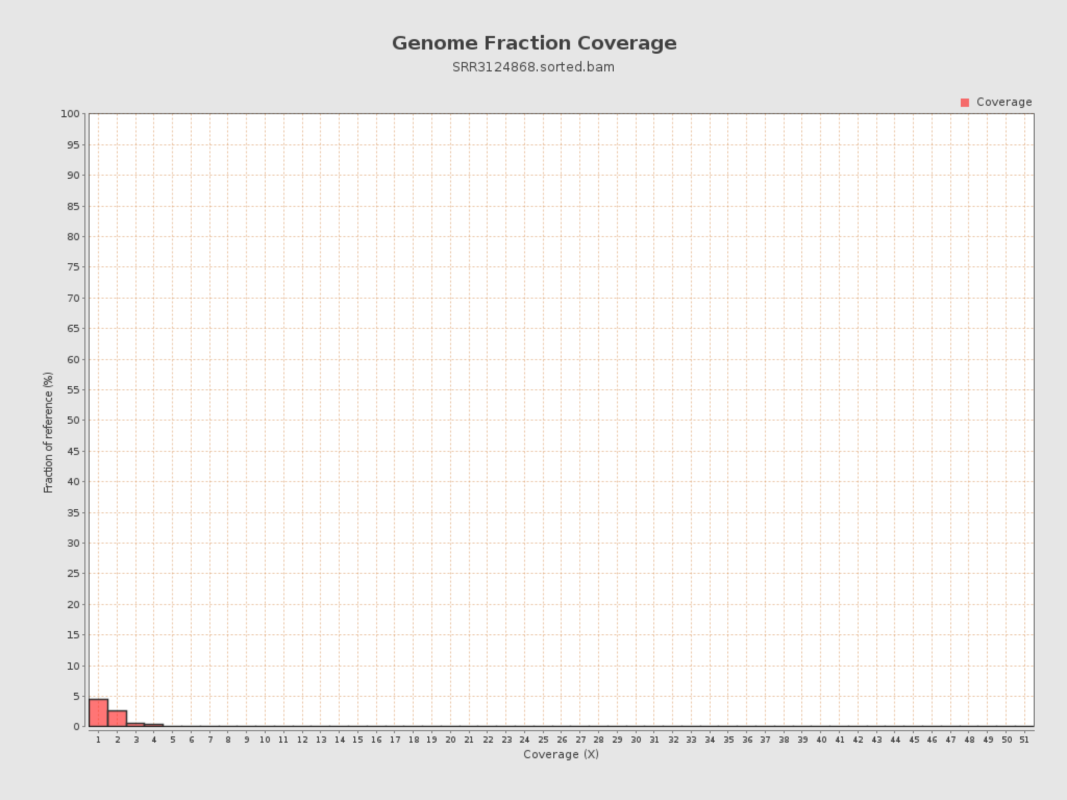
4. Results : Coverage Histogram



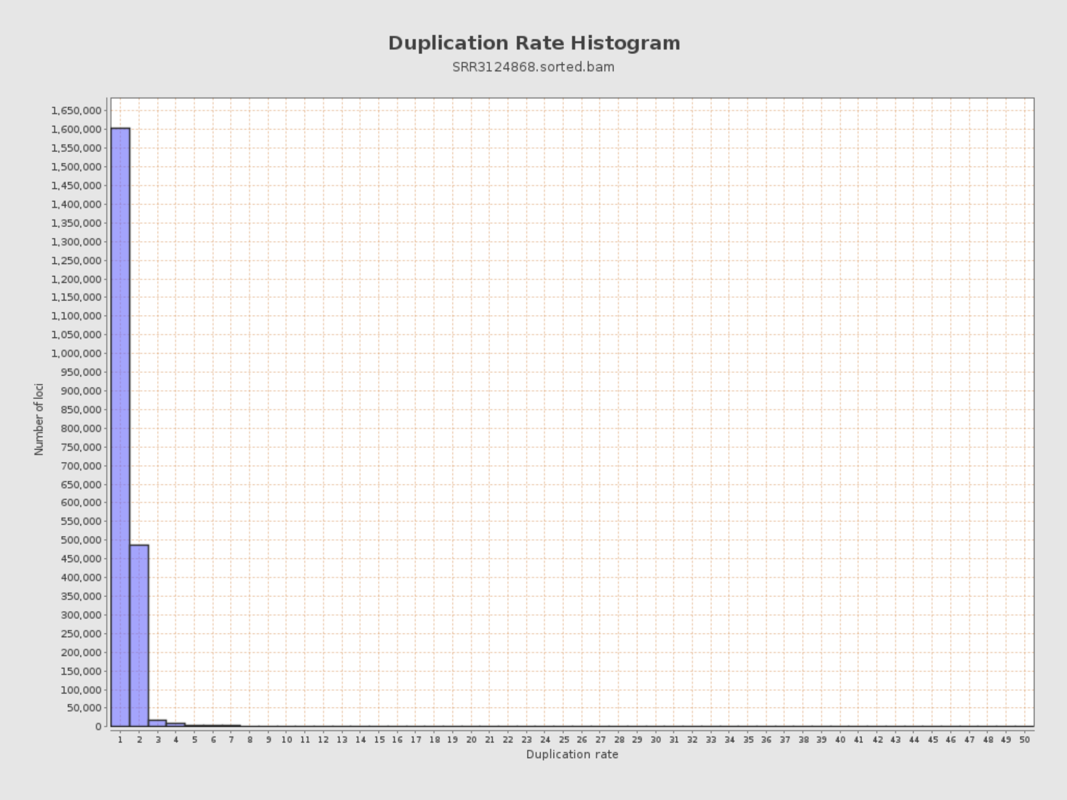
5. Results : Coverage Histogram (0-50X)



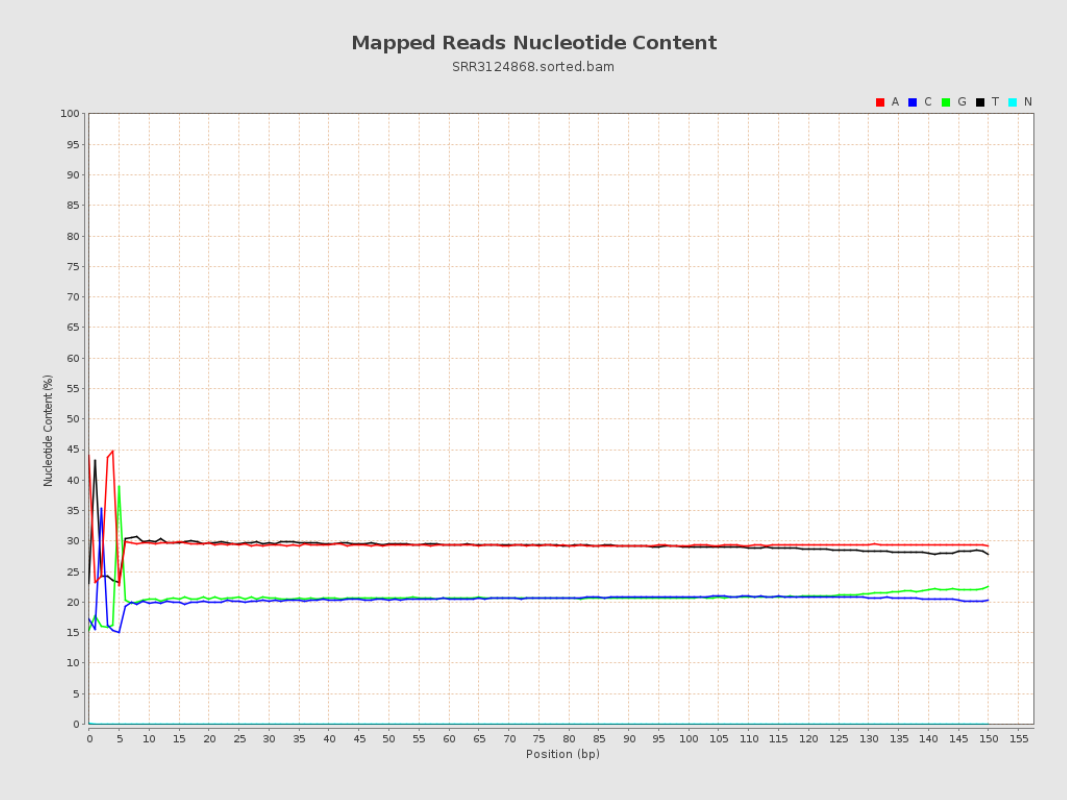
6. Results : Genome Fraction Coverage



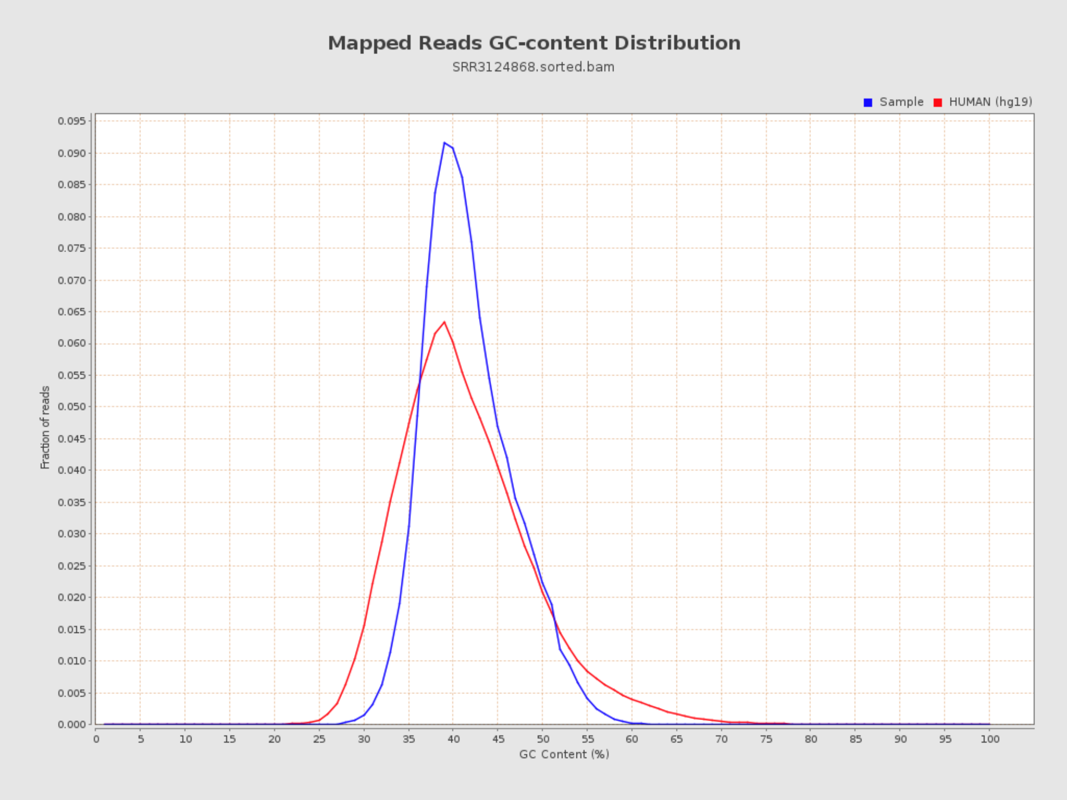
7. Results : Duplication Rate Histogram



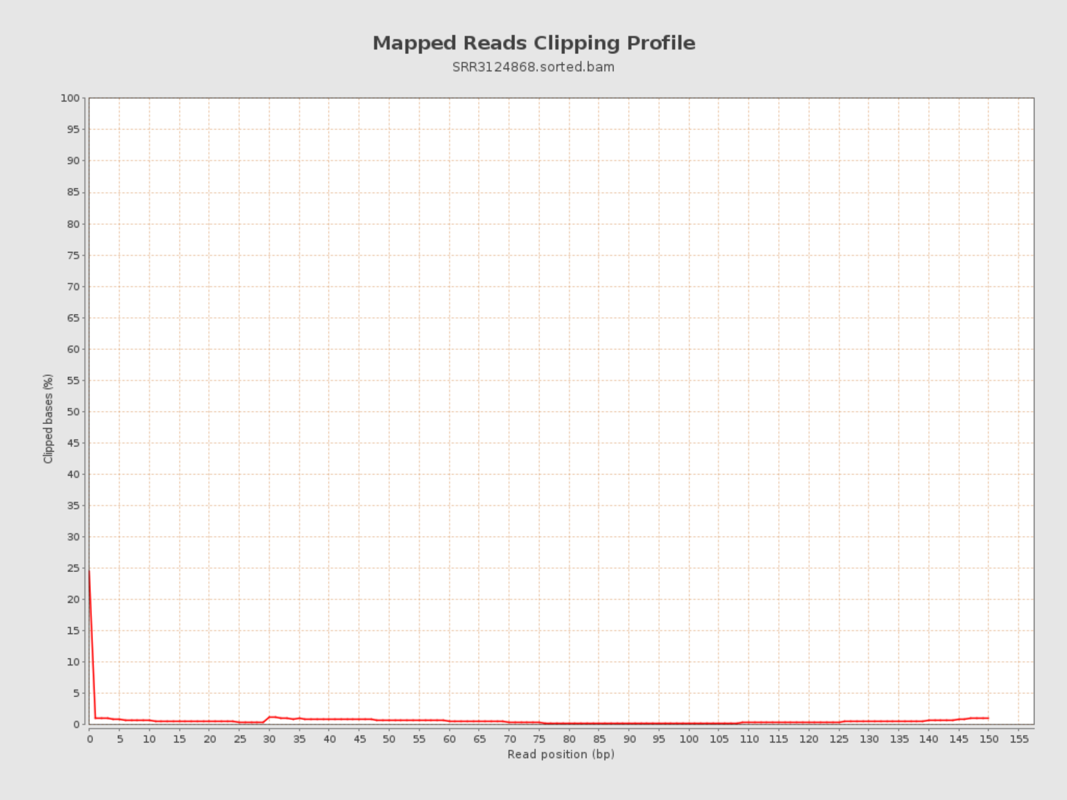
8. Results : Mapped Reads Nucleotide Content



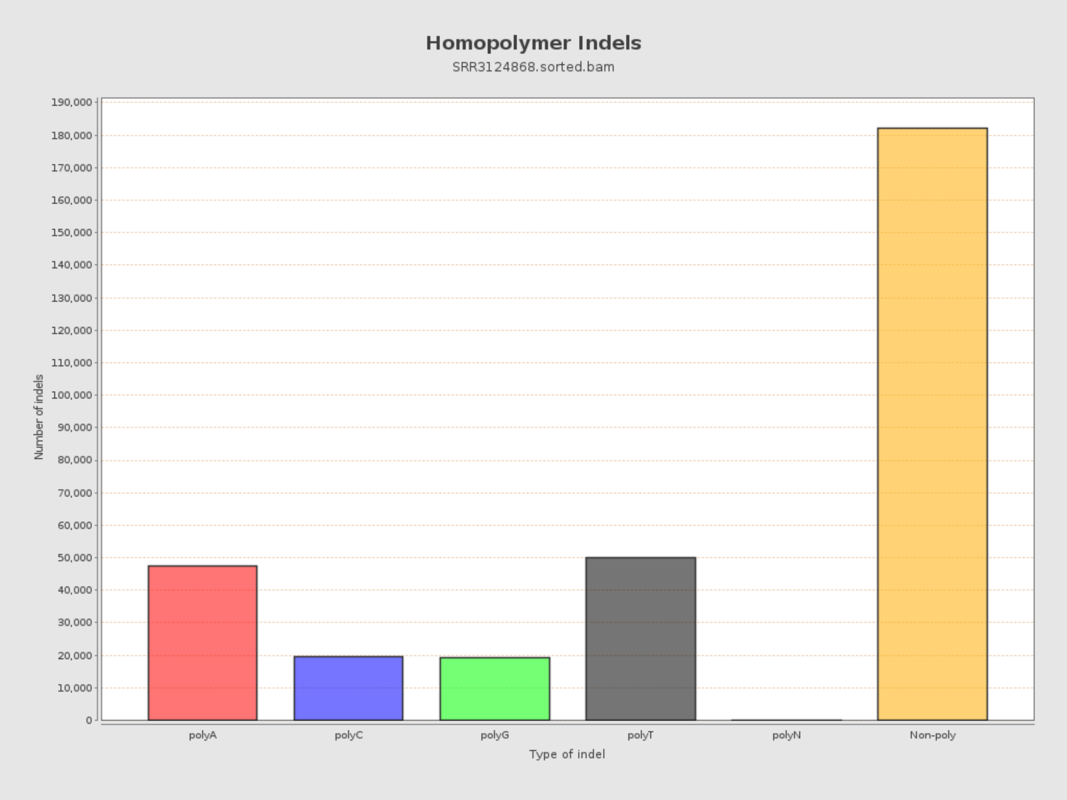
9. Results : Mapped Reads GC-content Distribution



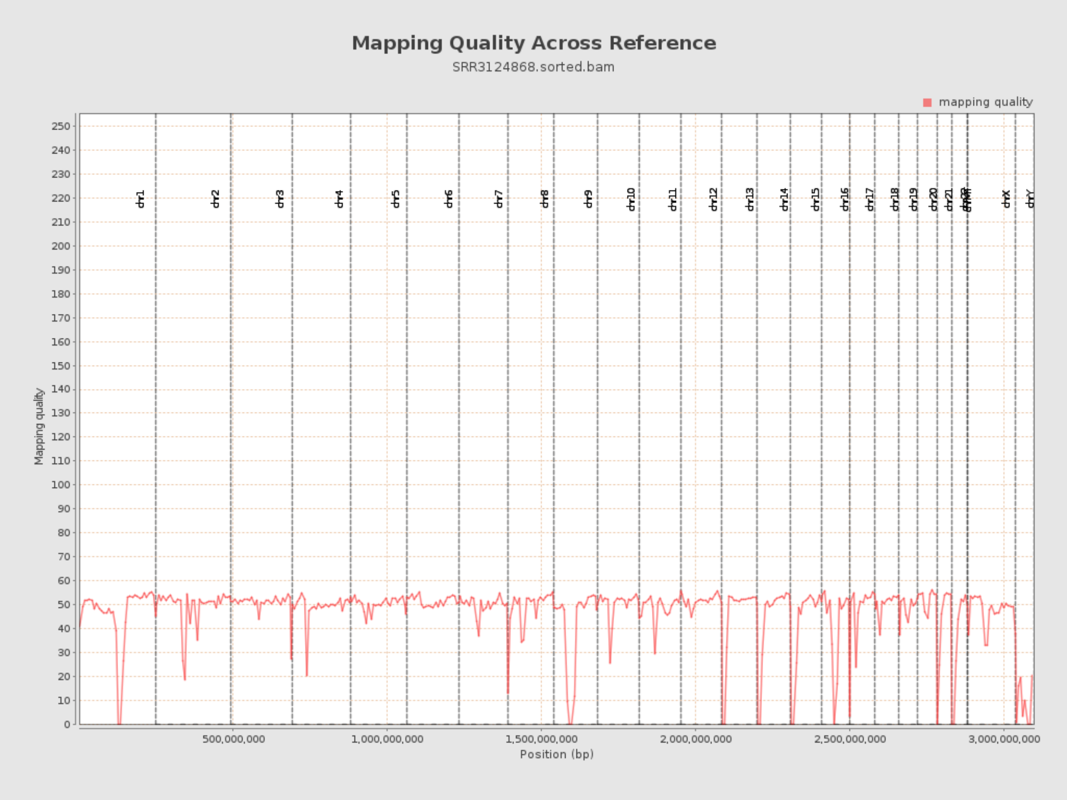
10. Results : Mapped Reads Clipping Profile



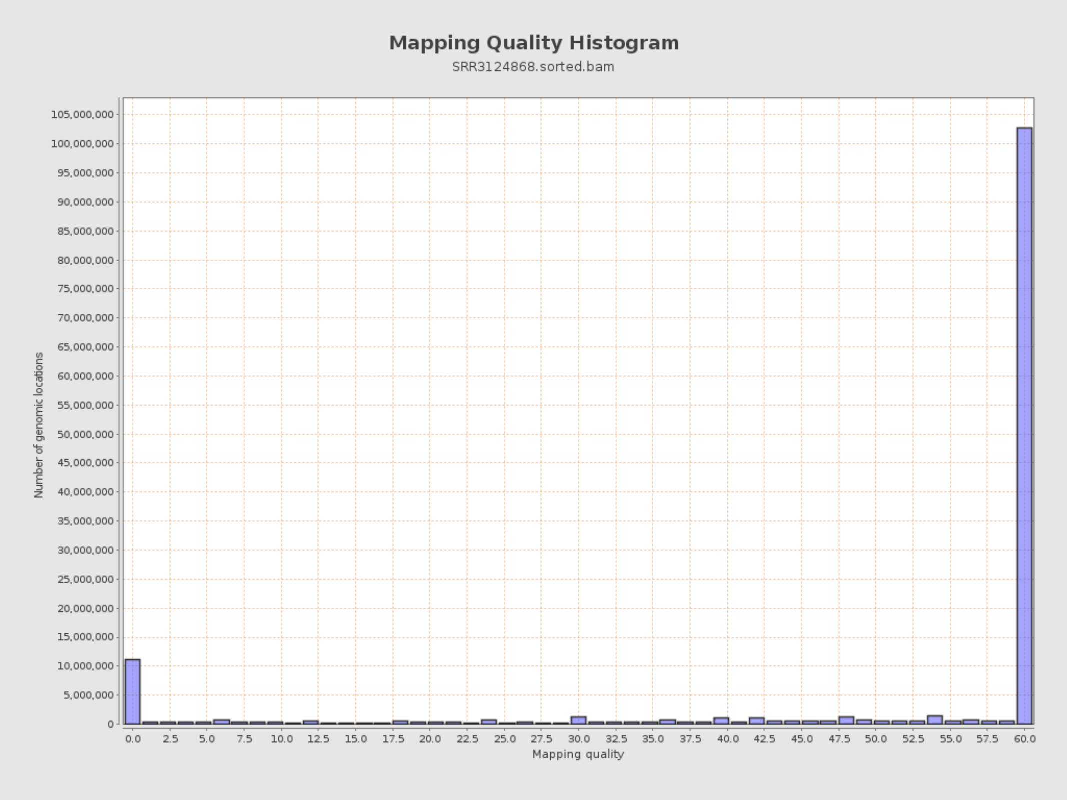
11. Results : Homopolymer Indels



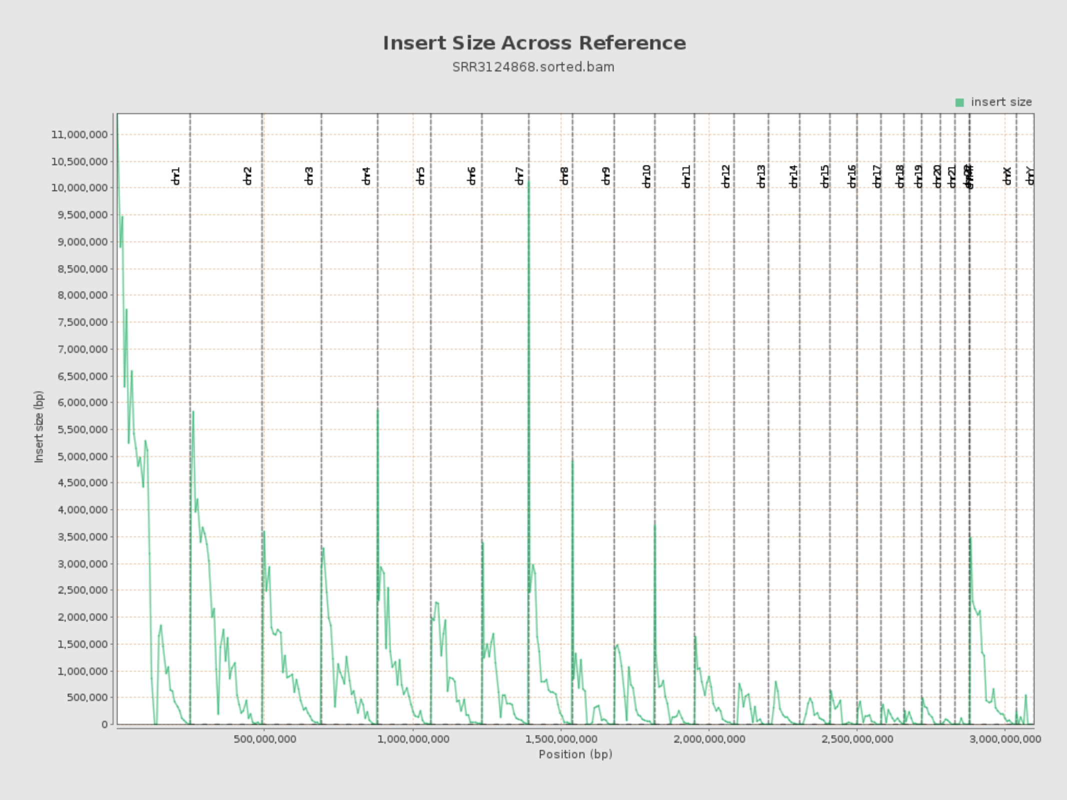
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram