Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 14:53:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124859.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_SRR3124859 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124859_1.fastq.gz SRR3124859_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 14:53:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124859.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	130,711,296
Mapped reads	128,339,290 / 98.19%
Unmapped reads	2,372,006 / 1.81%
Mapped paired reads	128,339,290 / 98.19%
Mapped reads, first in pair	64,243,533 / 49.15%
Mapped reads, second in pair	64,095,757 / 49.04%
Mapped reads, both in pair	127,768,872 / 97.75%
Mapped reads, singletons	570,418 / 0.44%
Secondary alignments	0
Supplementary alignments	24,219,952 / 18.53%
Read min/max/mean length	30 / 125 / 133.82
Duplicated reads (estimated)	63,000,551 / 48.2%
Duplication rate	39.22%
Clipped reads	120,477,330 / 92.17%

2.2. ACGT Content

Number/percentage of A's	3,886,428,748 / 28.43%
Number/percentage of C's	2,950,488,976 / 21.58%
Number/percentage of T's	3,807,351,878 / 27.85%
Number/percentage of G's	3,024,935,672 / 22.13%
Number/percentage of N's	1,909,549 / 0.01%

GC Percentage	43.71%

2.3. Coverage

Mean	4.4206
Standard Deviation	168.0159

2.4. Mapping Quality

Mean Mapping Quality	46.55

2.5. Insert size

Mean	781,230.58
Standard Deviation	8,556,573.51
P25/Median/P75	85 / 110 / 139

2.6. Mismatches and indels

General error rate	1.56%
Mismatches	200,356,931
Insertions	4,837,774
Mapped reads with at least one insertion	3.56%
Deletions	5,379,960
Mapped reads with at least one deletion	3.97%
Homopolymer indels	36.87%

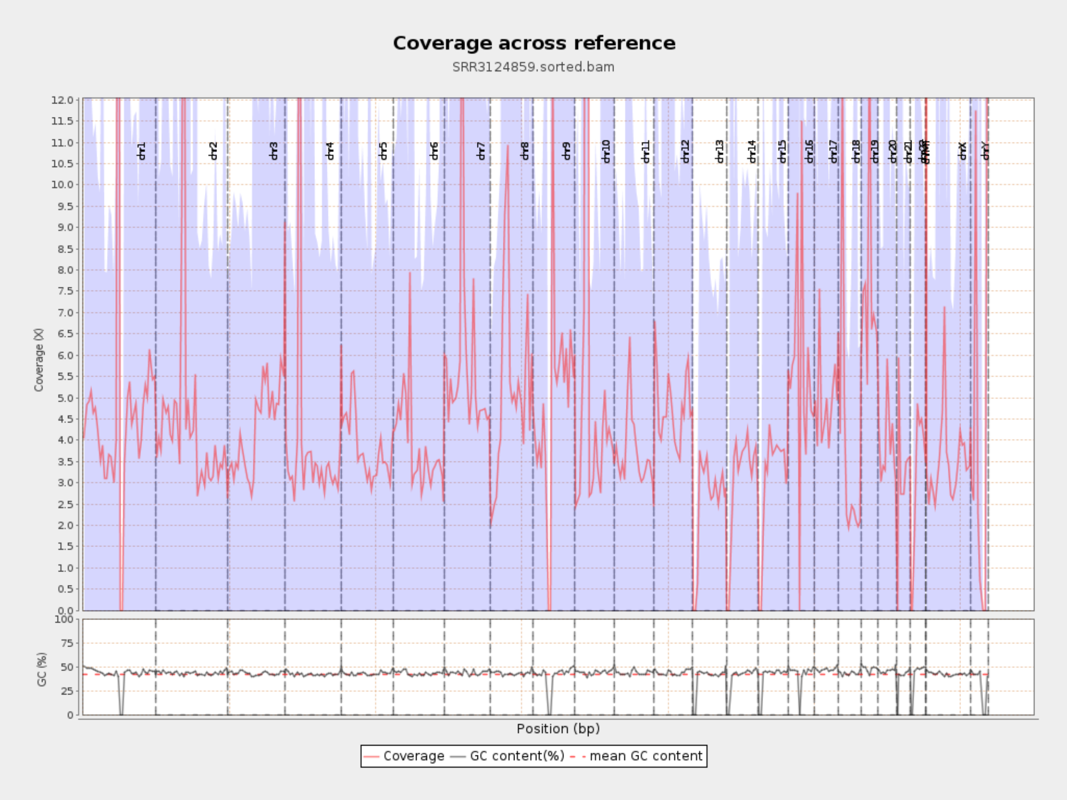
2.7. Chromosome stats

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

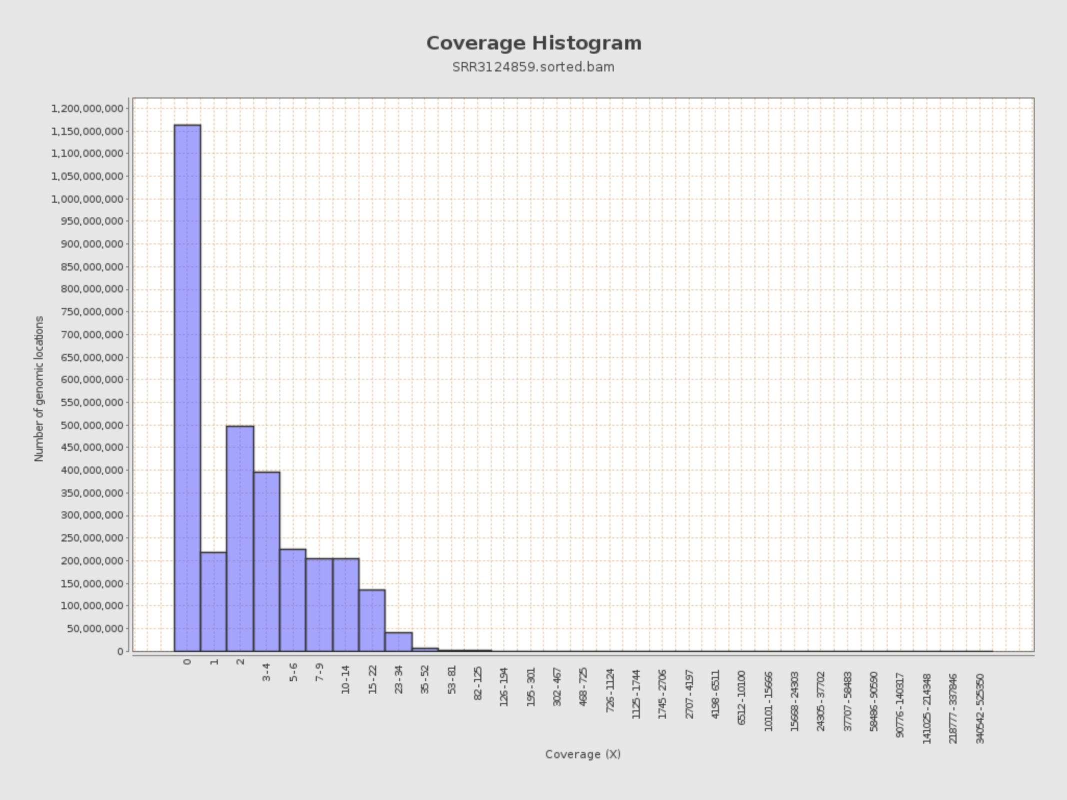
		bases	coverage	deviation
chr1	249250621	1221808439	4.9019	485.4123
chr2	243199373	1108266742	4.557	89.5016
chr3	198022430	846629805	4.2754	26.6314
chr4	191154276	773697569	4.0475	112.0168
chr5	180915260	698502043	3.8609	12.3016
chr6	171115067	667903520	3.9032	42.6934
chr7	159138663	938799694	5.8993	139.5669
chr8	146364022	771762932	5.2729	46.4068
chr9	141213431	692725886	4.9055	137.3144
chr10	135534747	811391555	5.9866	259.811
chr11	135006516	507381676	3.7582	42.6803
chr12	133851895	644017021	4.8114	23.8419
chr13	115169878	294808842	2.5598	4.7194
chr14	107349540	332063801	3.0933	11.3034
chr15	102531392	308065289	3.0046	19.3828
chr16	90354753	509508935	5.639	54.9164
chr17	81195210	400191877	4.9288	54.6889
chr18	78077248	303558525	3.8879	177.9472
chr19	59128983	451437633	7.6348	250.8399
chr20	63025520	244005245	3.8715	35.2854
chr21	48129895	160627354	3.3374	60.6072
chr22	51304566	157261626	3.0653	21.2539
chrMT	16571	33704660	2,033.9545	998.3441
chrX	155270560	547007413	3.5229	27.863

chrY	59373566	259693565	4.3739	132.0393

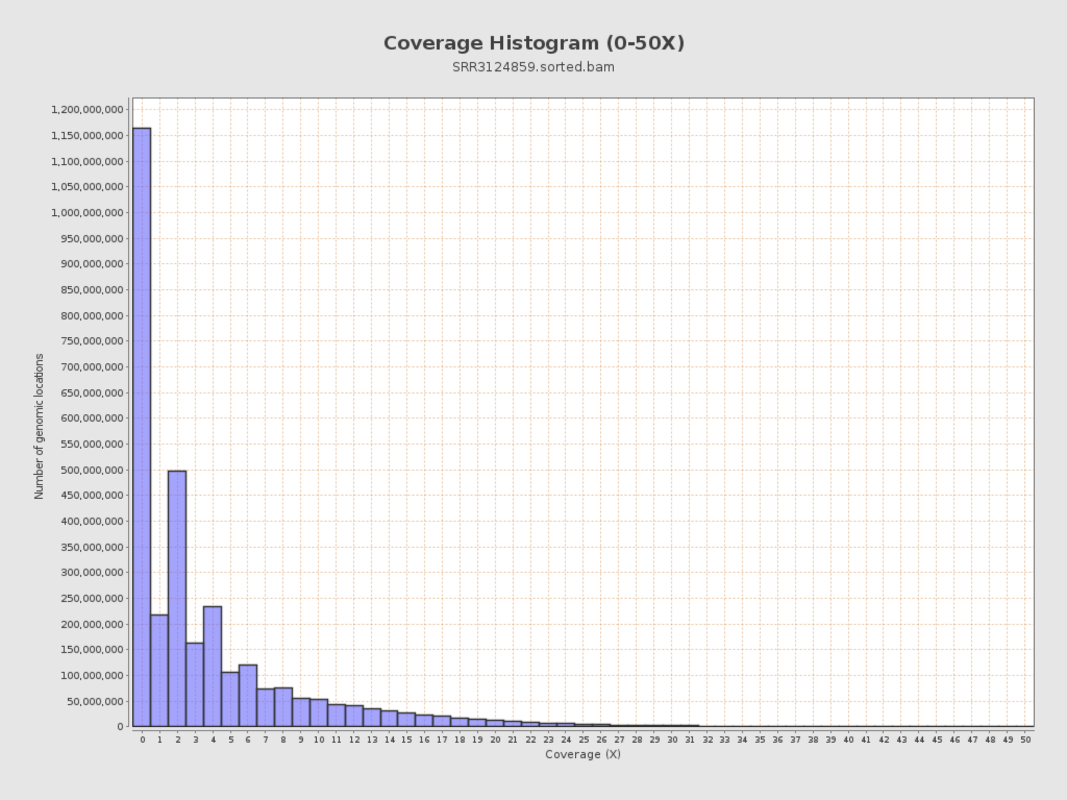
3. Results : Coverage across reference



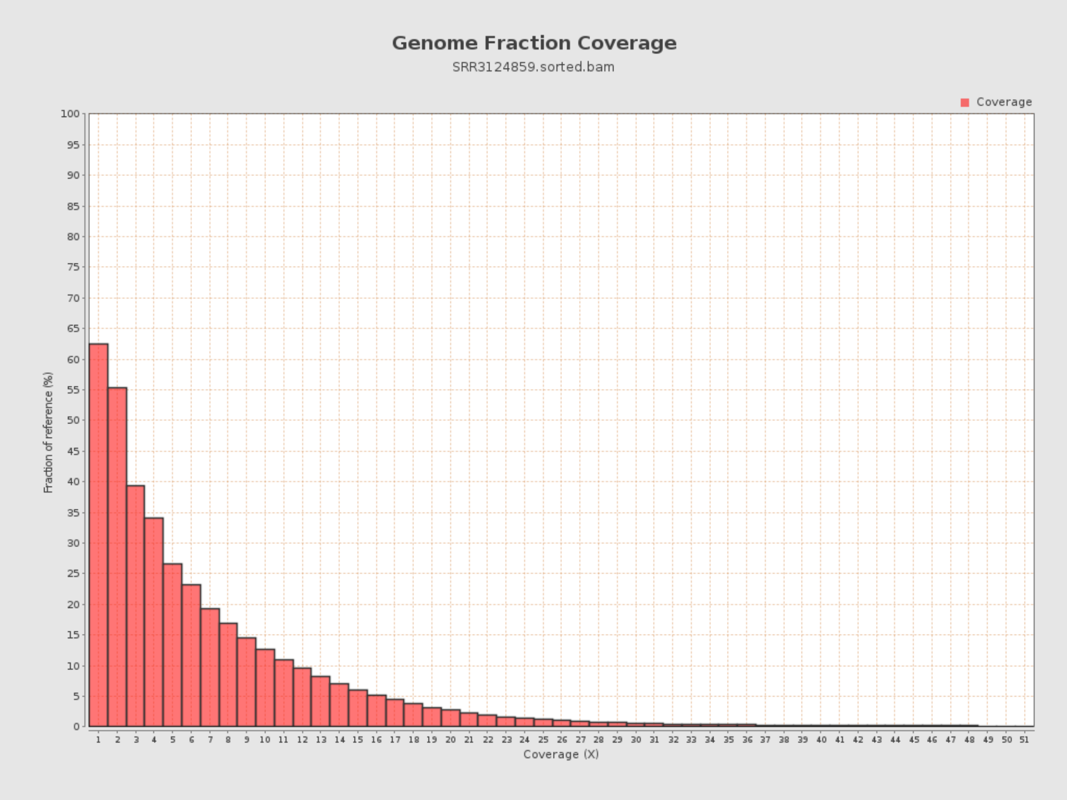
4. Results : Coverage Histogram



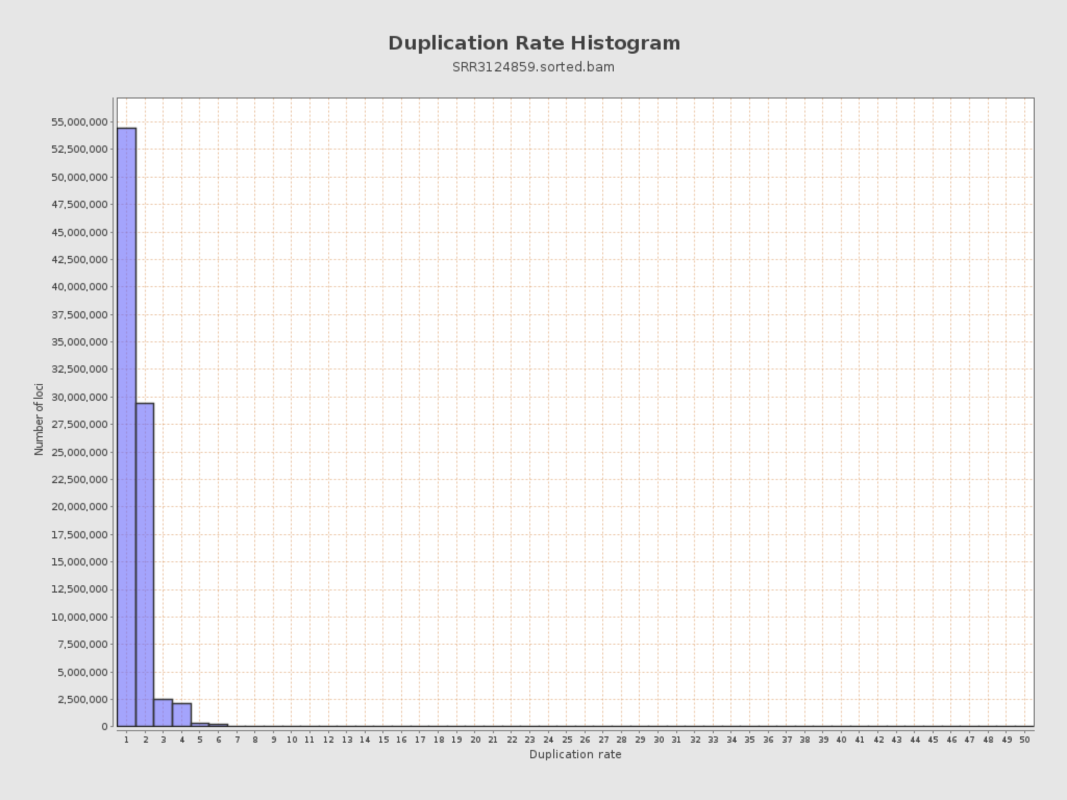
5. Results : Coverage Histogram (0-50X)



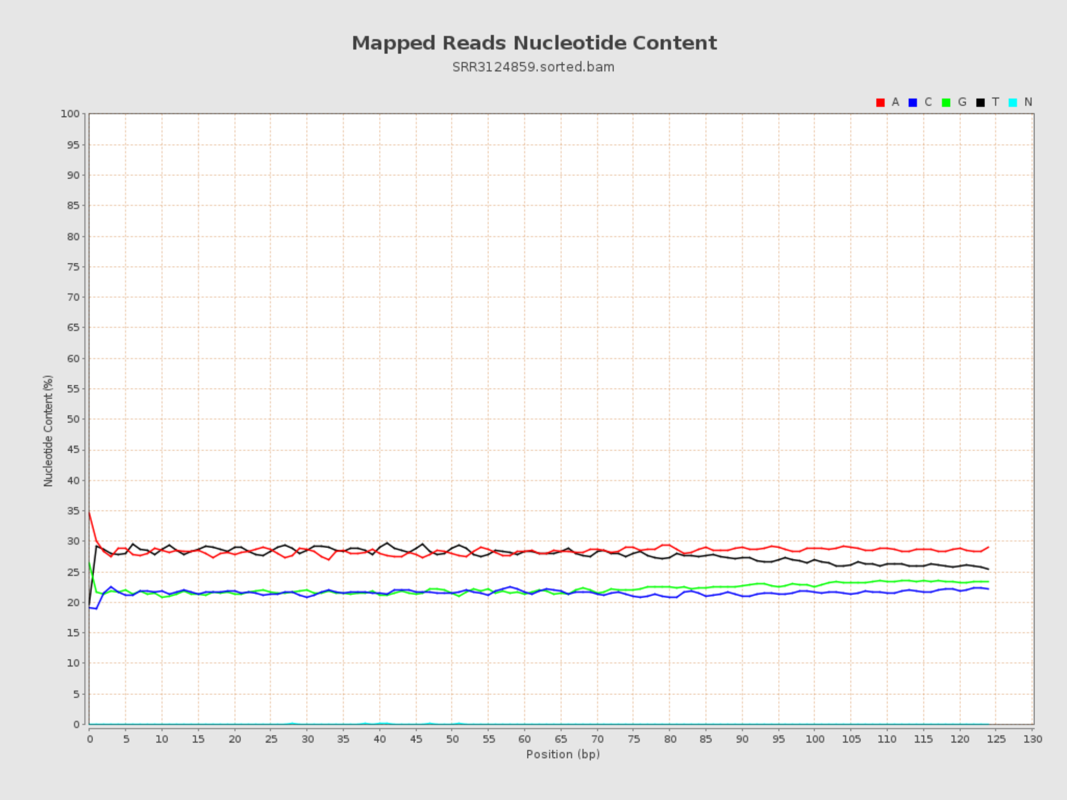
6. Results : Genome Fraction Coverage



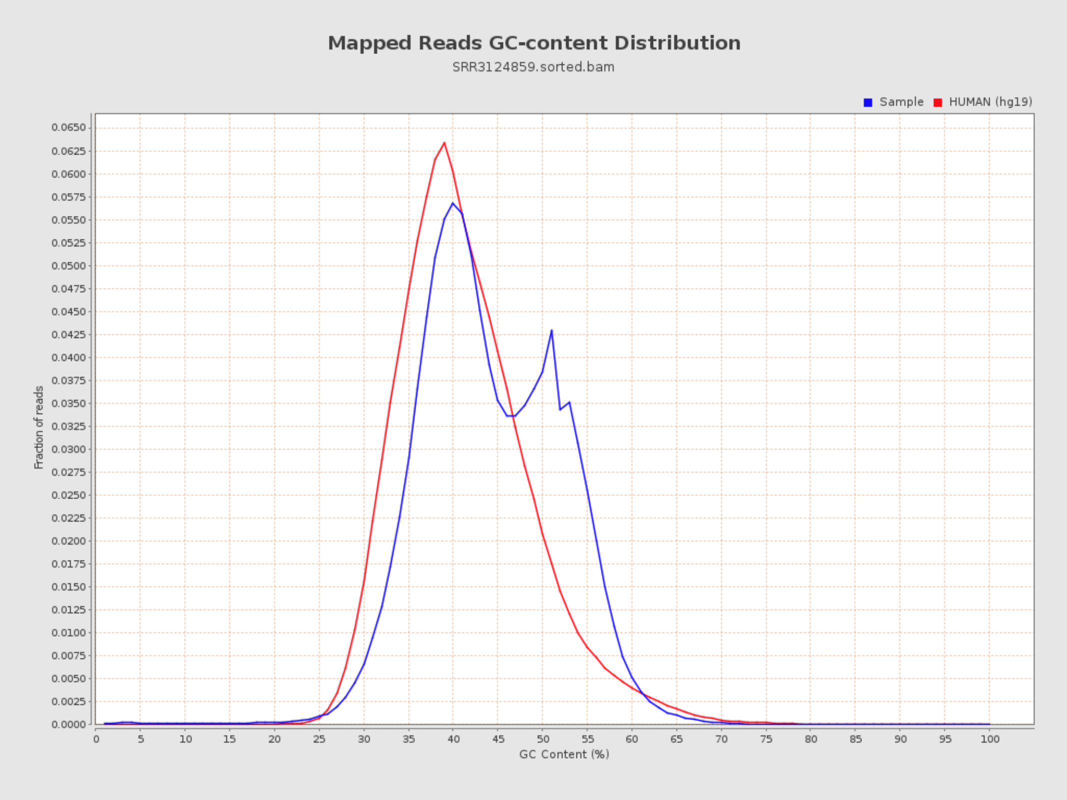
7. Results : Duplication Rate Histogram



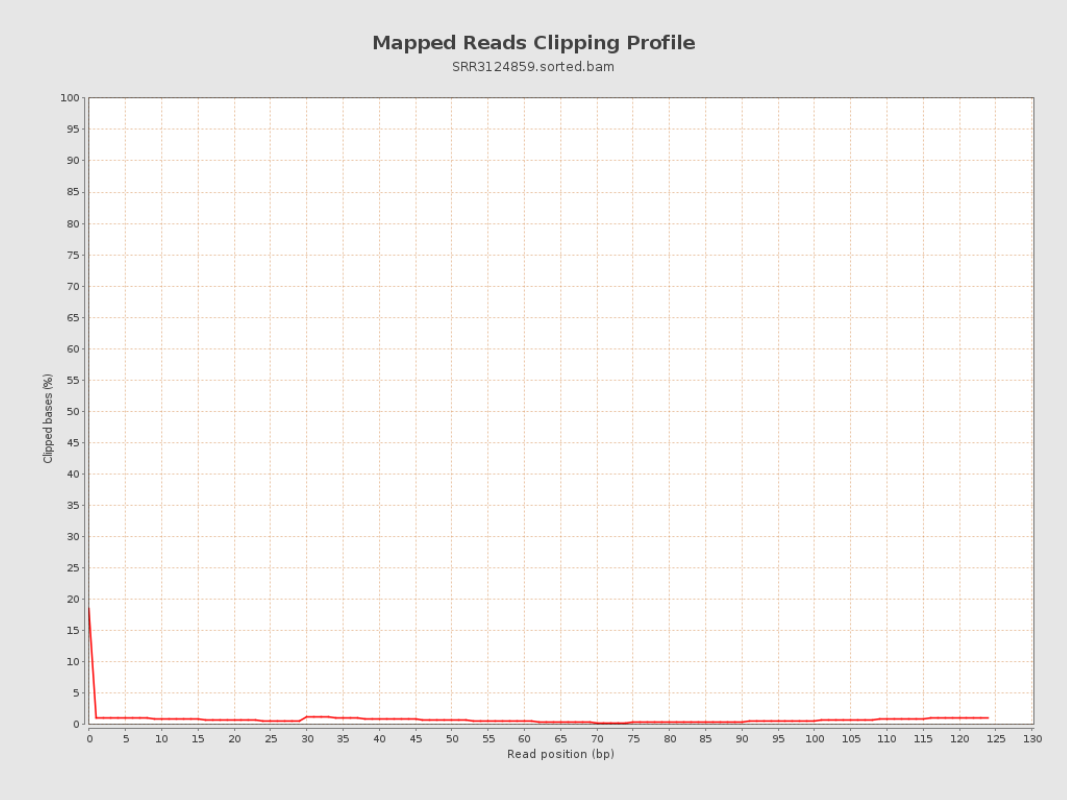
8. Results : Mapped Reads Nucleotide Content



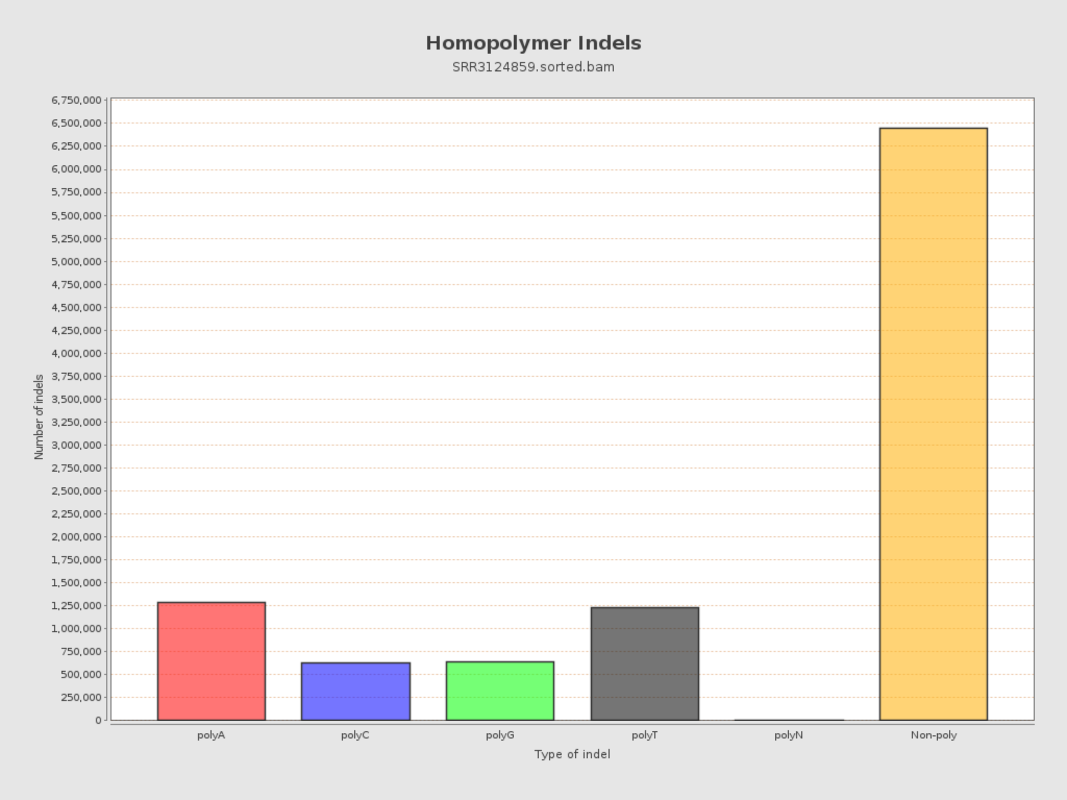
9. Results : Mapped Reads GC-content Distribution



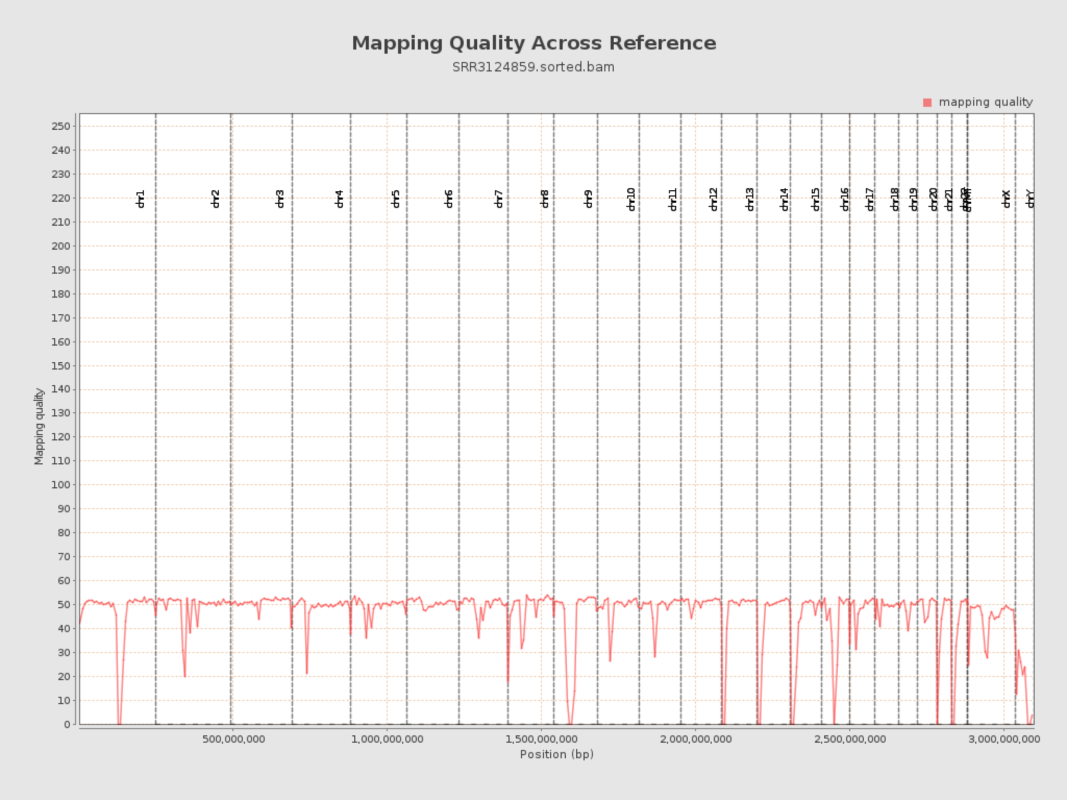
10. Results : Mapped Reads Clipping Profile



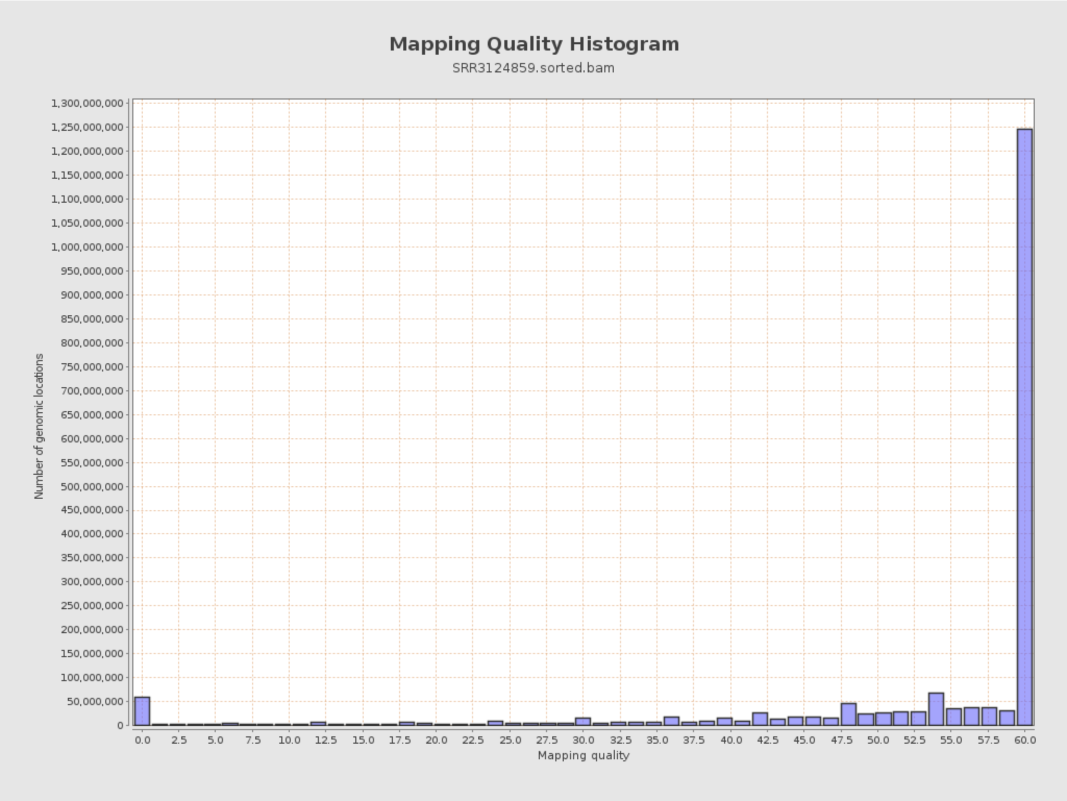
11. Results : Homopolymer Indels



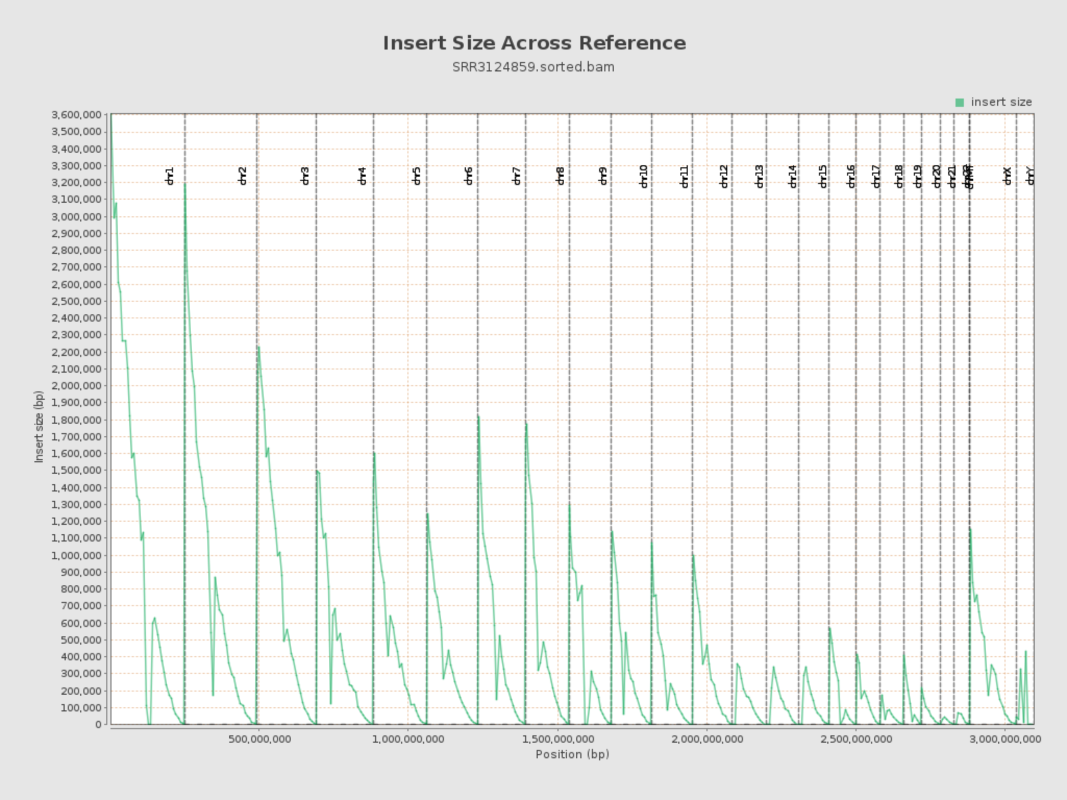
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram