Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 05:10:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124918.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_SRR3124918 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124918_1.fastq.gz SRR3124918_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 05:10:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,254,468
Mapped reads	5,192,656 / 98.82%
Unmapped reads	61,812 / 1.18%
Mapped paired reads	5,192,656 / 98.82%
Mapped reads, first in pair	2,600,308 / 49.49%
Mapped reads, second in pair	2,592,348 / 49.34%
Mapped reads, both in pair	5,172,762 / 98.45%
Mapped reads, singletons	19,894 / 0.38%
Secondary alignments	0
Supplementary alignments	18,526 / 0.35%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	460,737 / 8.77%
Duplication rate	6.27%
Clipped reads	2,501,923 / 47.62%

2.2. ACGT Content

Number/percentage of A's	125,835,640 / 27.97%
Number/percentage of C's	84,312,323 / 18.74%
Number/percentage of T's	133,418,909 / 29.65%
Number/percentage of G's	105,915,535 / 23.54%
Number/percentage of N's	446,001 / 0.1%

GC Percentage	42.28%

2.3. Coverage

Mean	0.1454
Standard Deviation	1.3167

2.4. Mapping Quality

Mean Mapping Quality	52.77

2.5. Insert size

Mean	30,662.81
Standard Deviation	1,634,976.6
P25/Median/P75	141 / 193 / 274

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	3,832,555
Insertions	61,044
Mapped reads with at least one insertion	1.15%
Deletions	144,685
Mapped reads with at least one deletion	2.73%
Homopolymer indels	47.84%

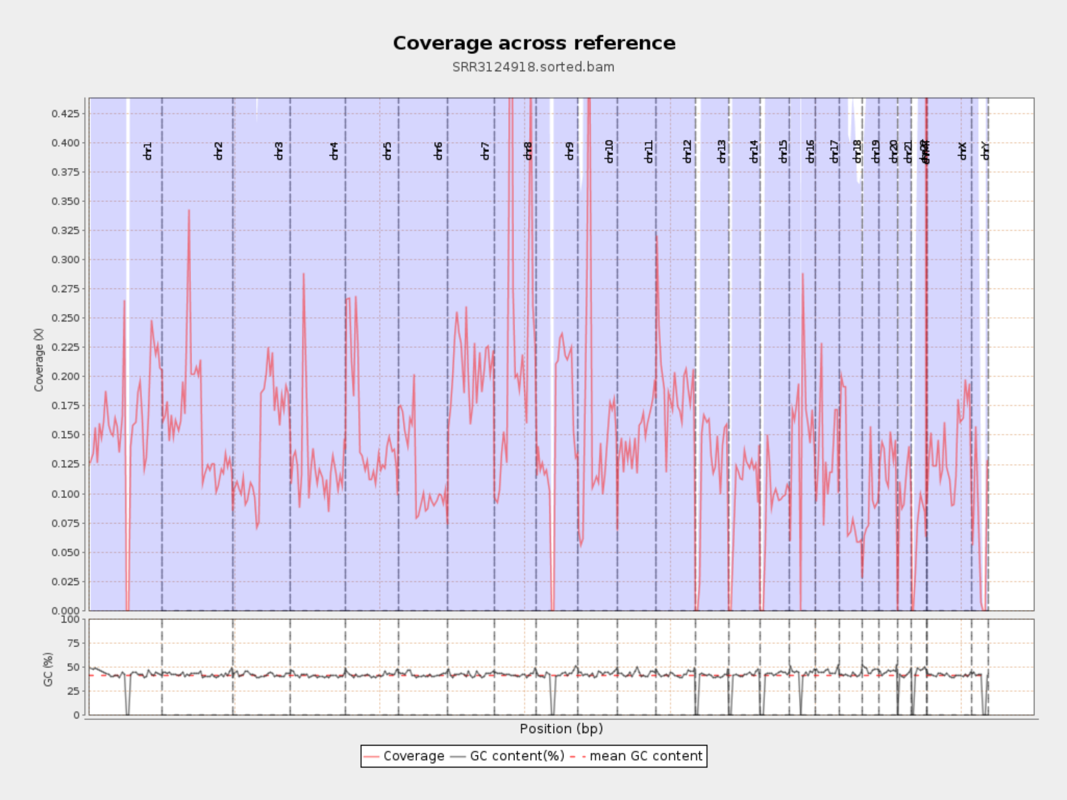
2.7. Chromosome stats

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

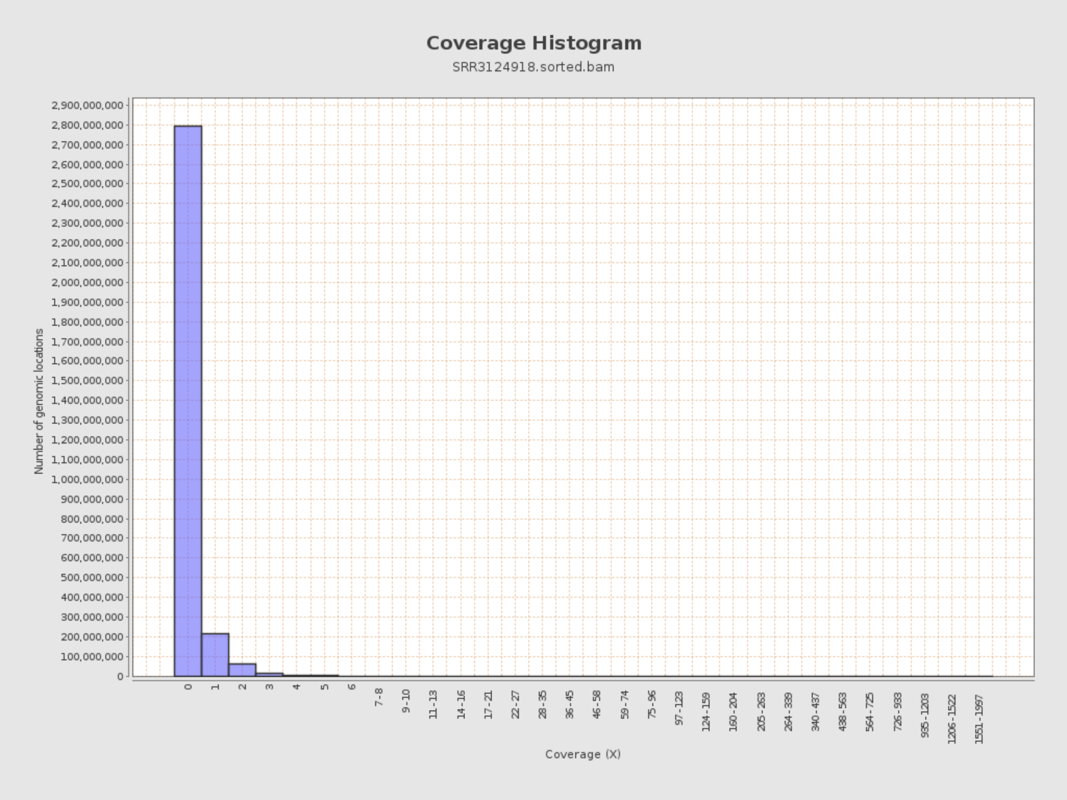
		bases	coverage	deviation
chr1	249250621	39910564	0.1601	1.757
chr2	243199373	38941007	0.1601	1.4584
chr3	198022430	28801018	0.1454	0.5155
chr4	191154276	23918398	0.1251	0.9996
chr5	180915260	28037303	0.155	0.5471
chr6	171115067	20226685	0.1182	0.7641
chr7	159138663	33173500	0.2085	1.9061
chr8	146364022	34772019	0.2376	0.9809
chr9	141213431	21768452	0.1542	1.5369
chr10	135534747	21446662	0.1582	3.1508
chr11	135006516	20004397	0.1482	0.8679
chr12	133851895	25838987	0.193	0.6038
chr13	115169878	13703722	0.119	0.4543
chr14	107349540	10756855	0.1002	0.492
chr15	102531392	8944982	0.0872	0.4076
chr16	90354753	14109080	0.1562	1.3645
chr17	81195210	10684723	0.1316	2.0069
chr18	78077248	8359358	0.1071	1.6347
chr19	59128983	5265224	0.089	1.0861
chr20	63025520	8139117	0.1291	0.5519
chr21	48129895	4769865	0.0991	0.6278
chr22	51304566	3090601	0.0602	0.3437
chrMT	16571	278160	16.786	53.0479
chrX	155270560	21541188	0.1387	0.6736

chrY	59373566	3689048	0.0621	1.4391

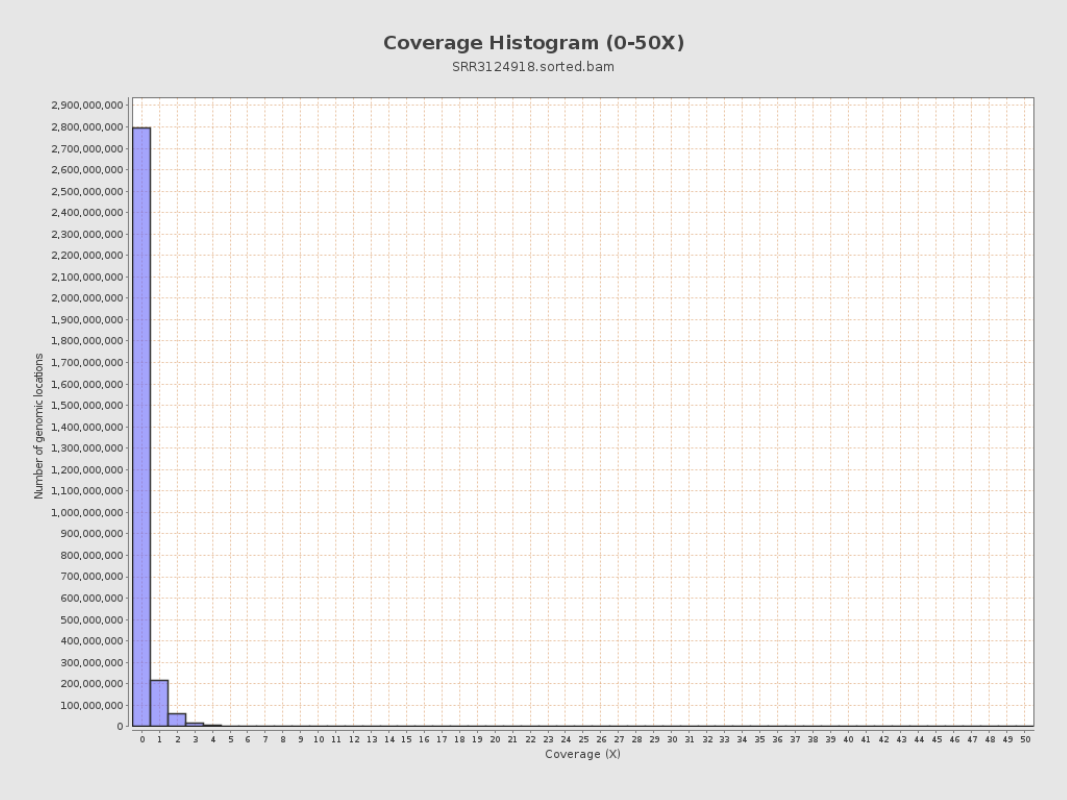
3. Results : Coverage across reference



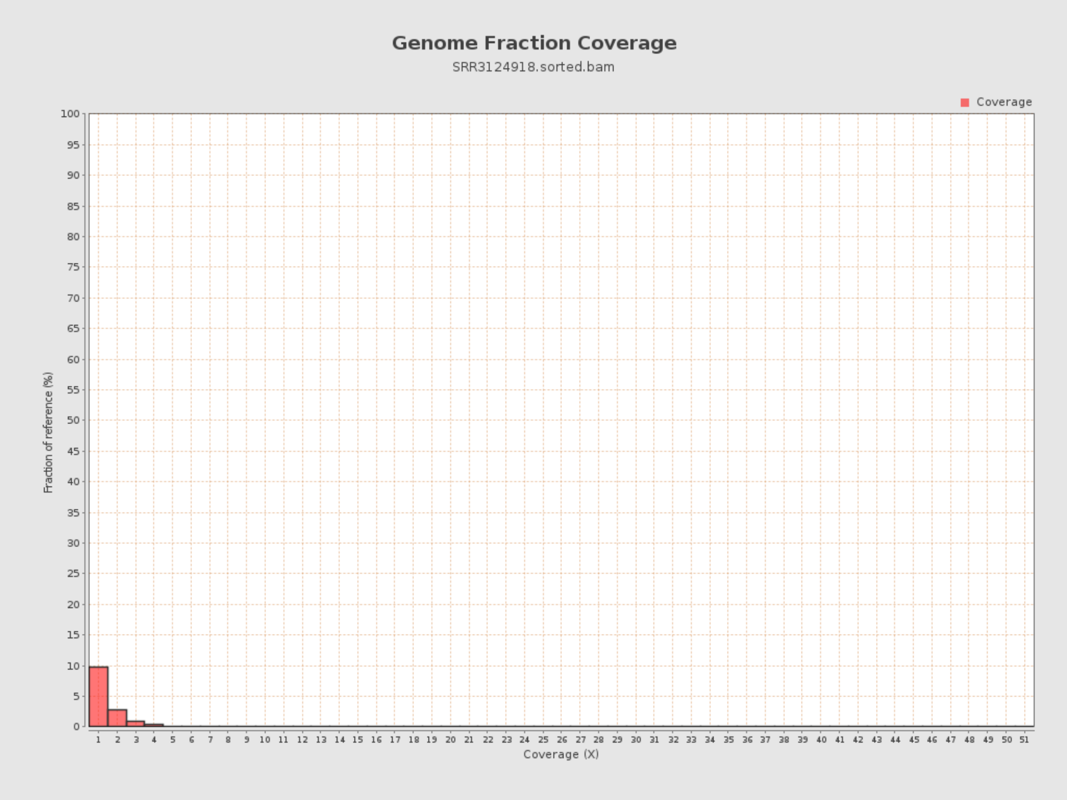
4. Results : Coverage Histogram



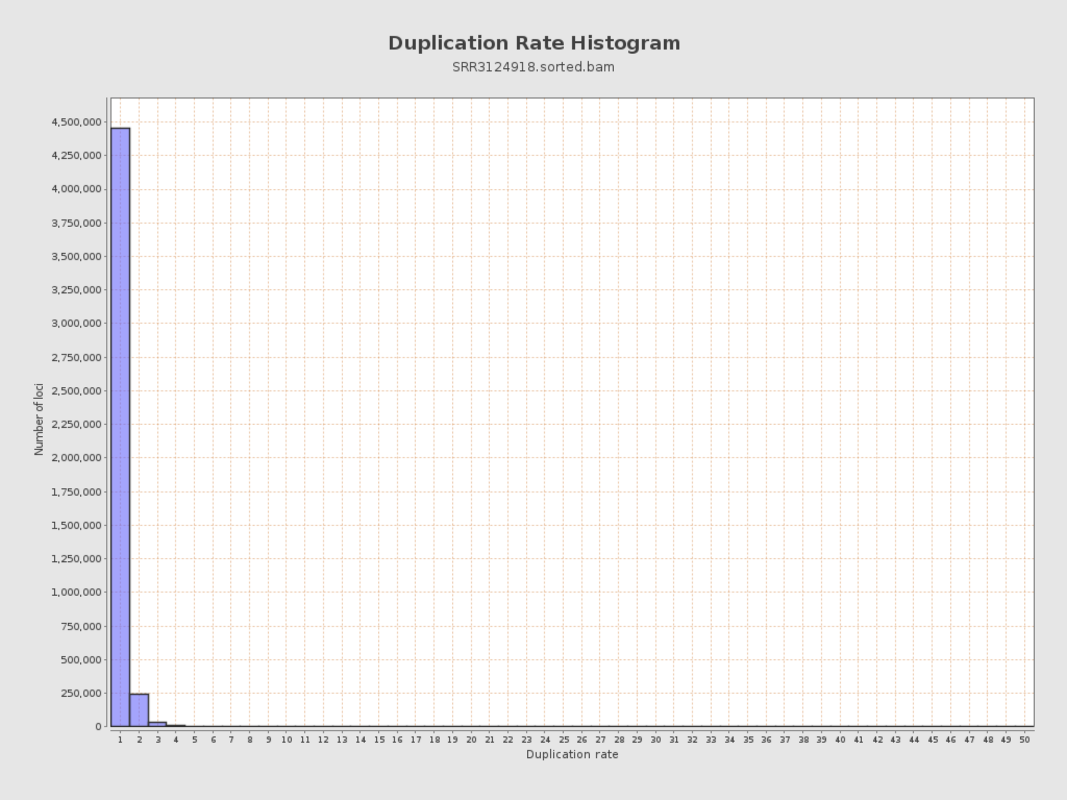
5. Results : Coverage Histogram (0-50X)



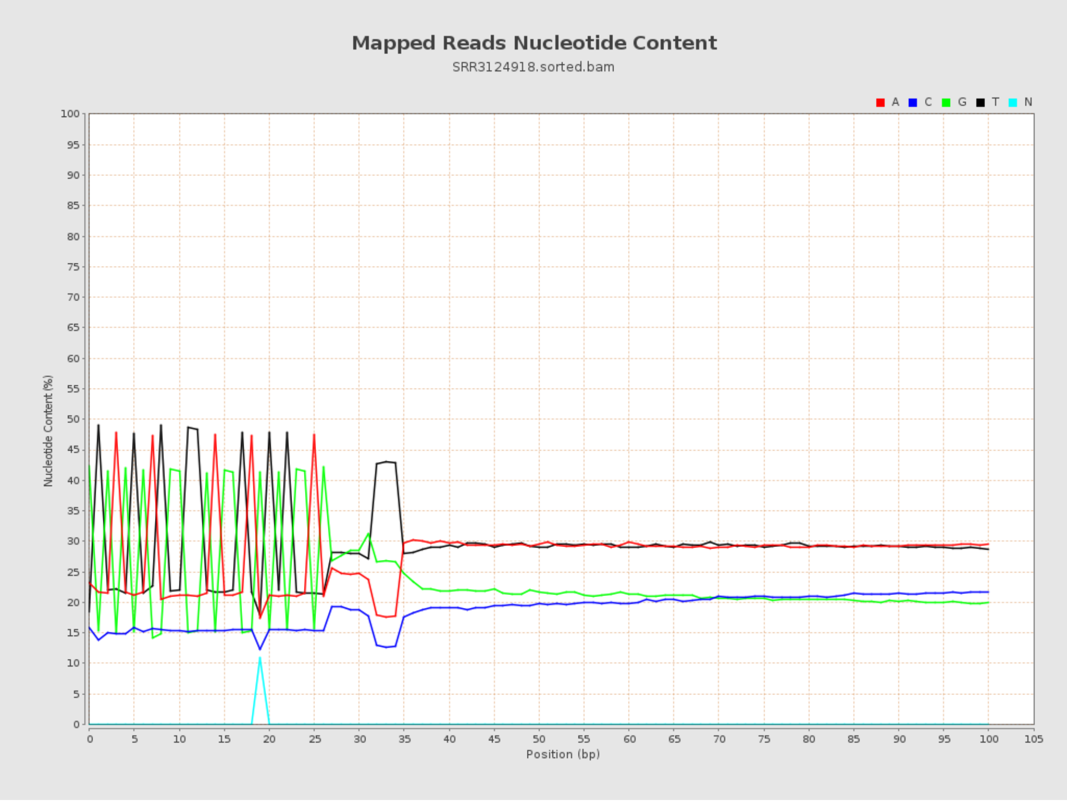
6. Results : Genome Fraction Coverage



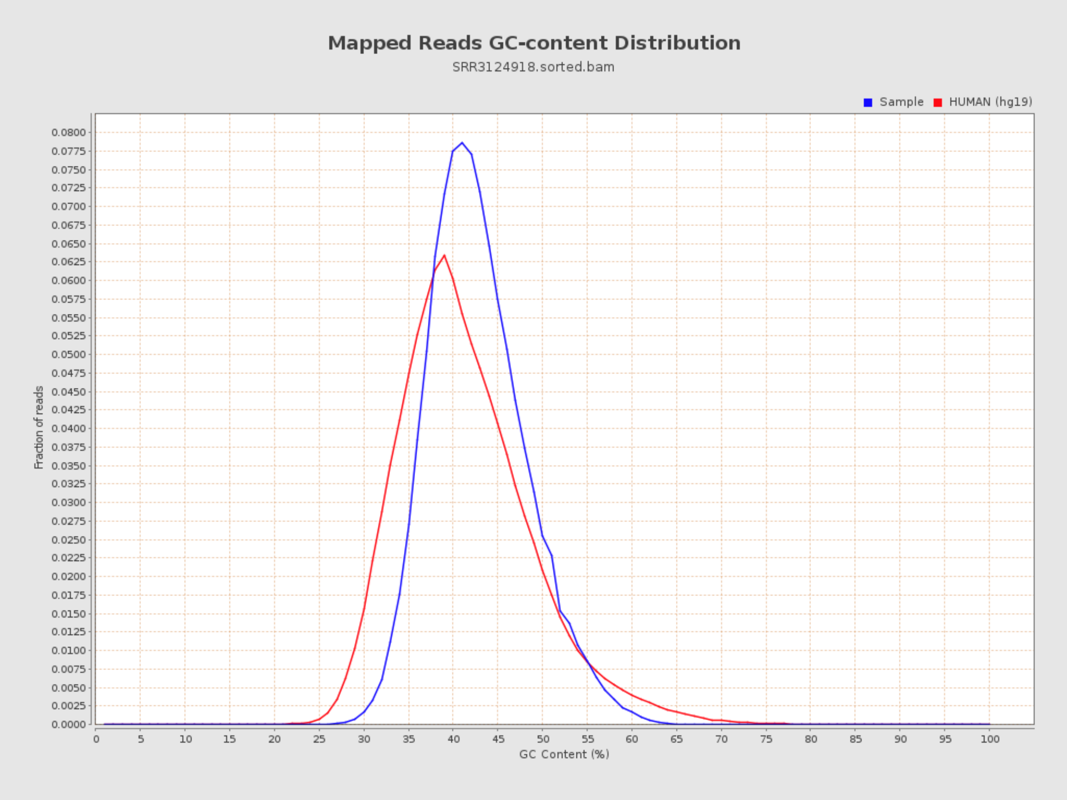
7. Results : Duplication Rate Histogram



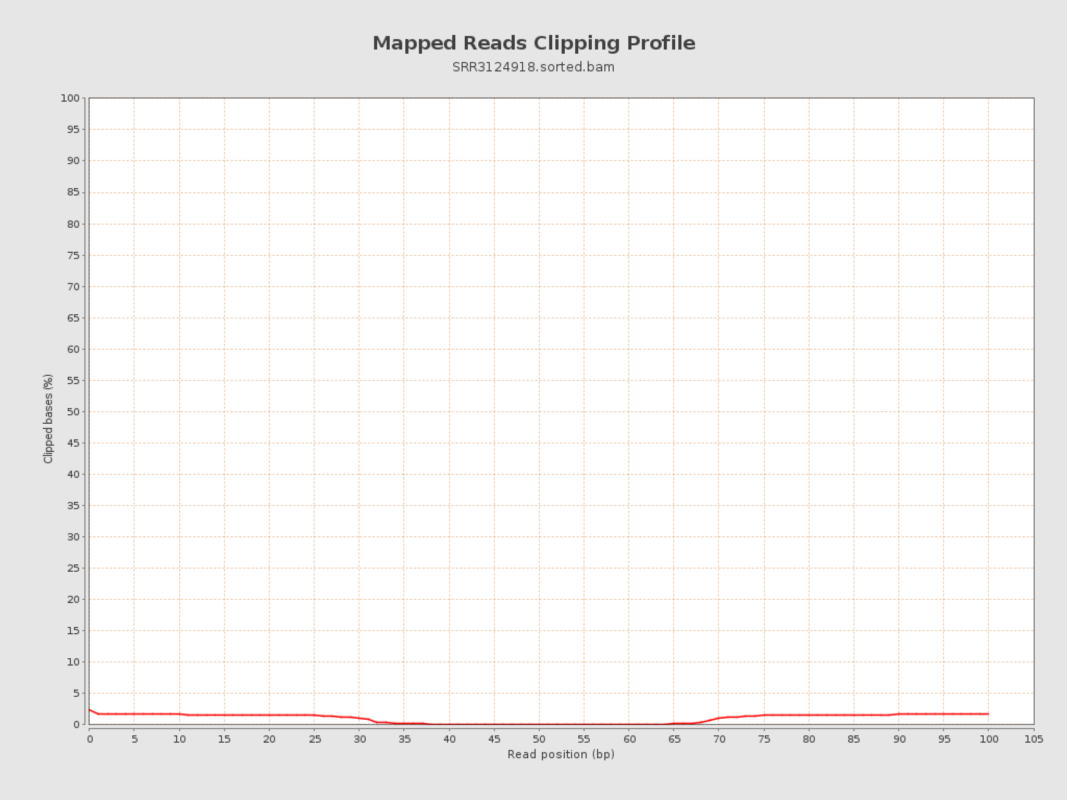
8. Results : Mapped Reads Nucleotide Content



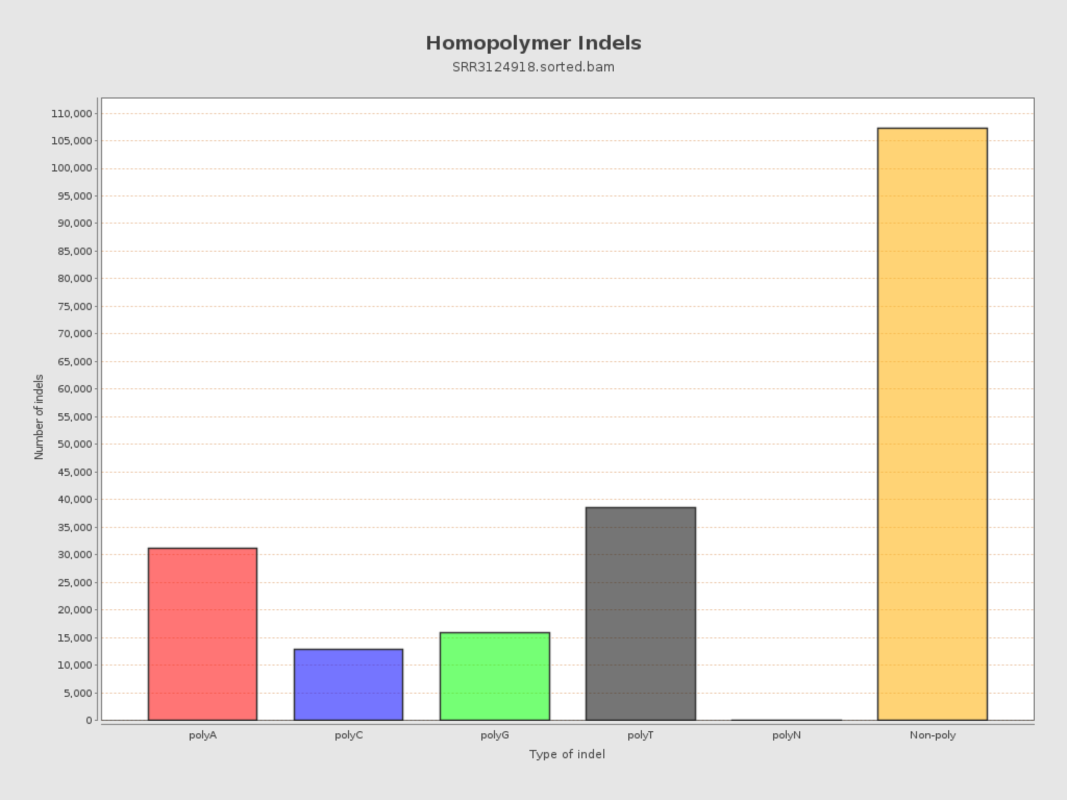
9. Results : Mapped Reads GC-content Distribution



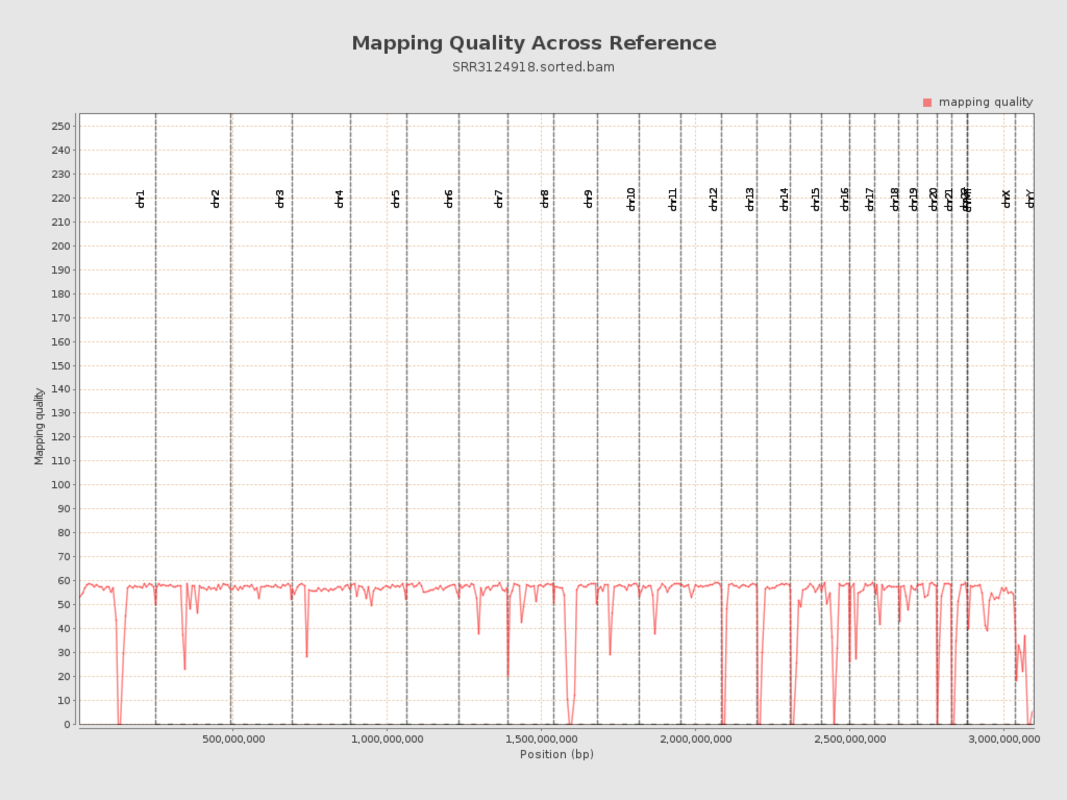
10. Results : Mapped Reads Clipping Profile



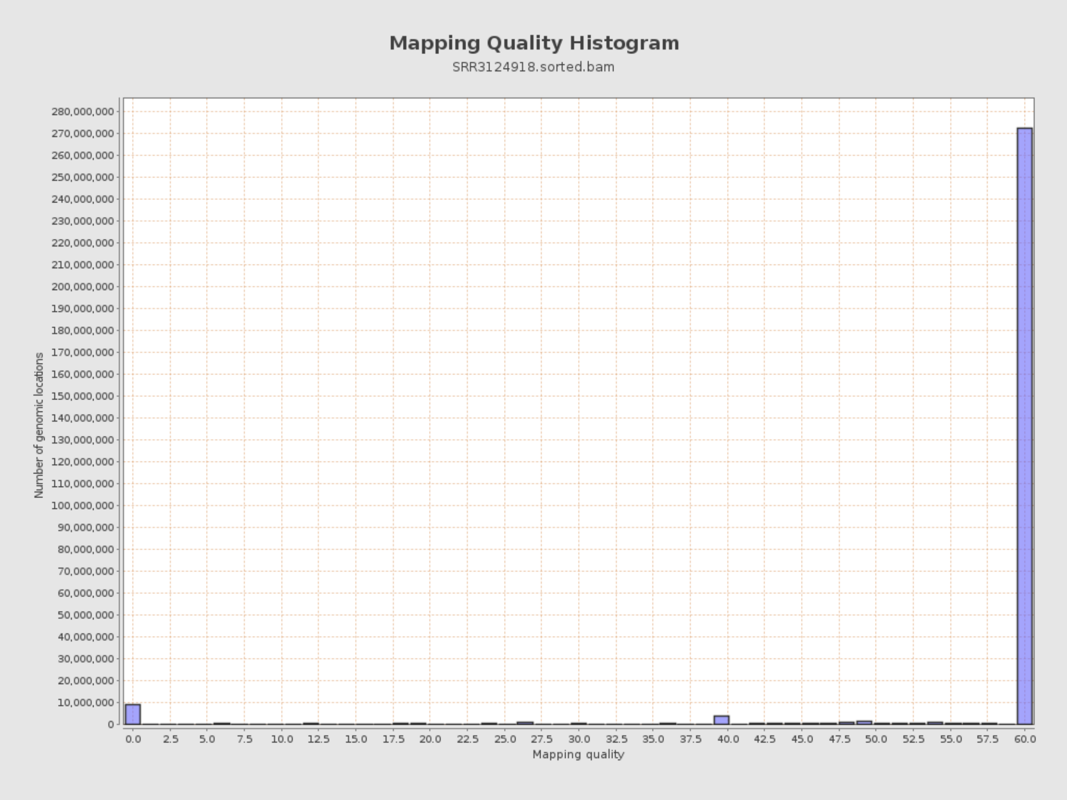
11. Results : Homopolymer Indels



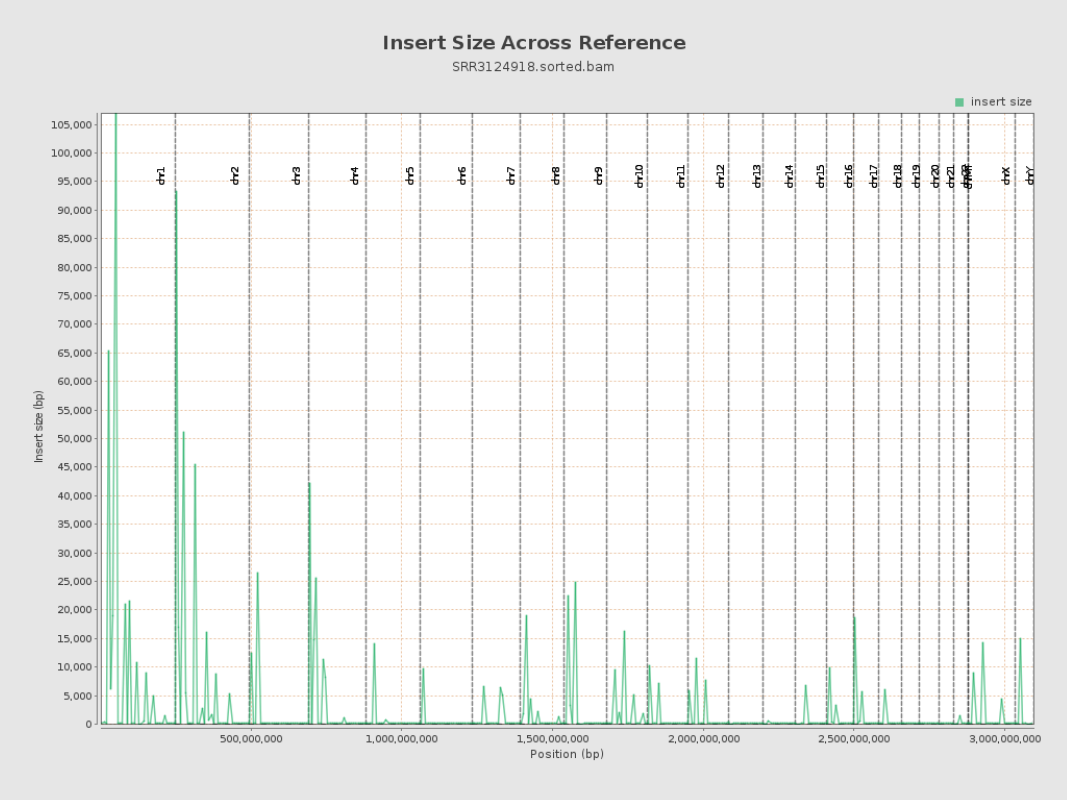
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram