Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 23:50:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124820.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_SRR3124820 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124820_1.fastq.gz SRR3124820_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 23:50:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124820.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,966,532
Mapped reads	23,549,231 / 94.32%
Unmapped reads	1,417,301 / 5.68%
Mapped paired reads	23,549,231 / 94.32%
Mapped reads, first in pair	11,877,812 / 47.57%
Mapped reads, second in pair	11,671,419 / 46.75%
Mapped reads, both in pair	23,106,100 / 92.55%
Mapped reads, singletons	443,131 / 1.77%
Secondary alignments	0
Supplementary alignments	32,824 / 0.13%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	3,243,318 / 12.99%
Duplication rate	8.93%
Clipped reads	8,838,404 / 35.4%

2.2. ACGT Content

Number/percentage of A's	427,644,876 / 28%
Number/percentage of C's	281,307,735 / 18.42%
Number/percentage of T's	454,269,719 / 29.74%
Number/percentage of G's	364,297,298 / 23.85%
Number/percentage of N's	45,928 / 0%

GC Percentage	42.26%

2.3. Coverage

Mean	0.4937
Standard Deviation	2.9832

2.4. Mapping Quality

Mean Mapping Quality	52.03

2.5. Insert size

Mean	37,681.9
Standard Deviation	1,854,691.6
P25/Median/P75	145 / 191 / 262

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	12,397,733
Insertions	183,758
Mapped reads with at least one insertion	0.77%
Deletions	497,438
Mapped reads with at least one deletion	2.09%
Homopolymer indels	48.02%

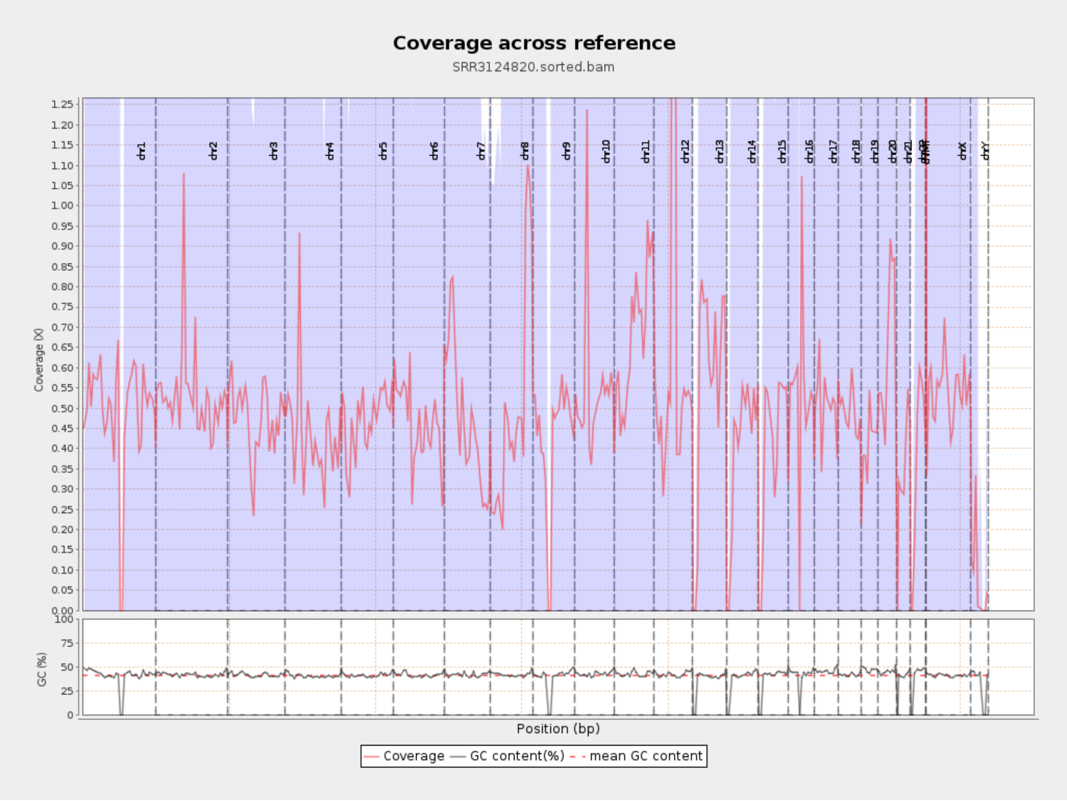
2.7. Chromosome stats

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

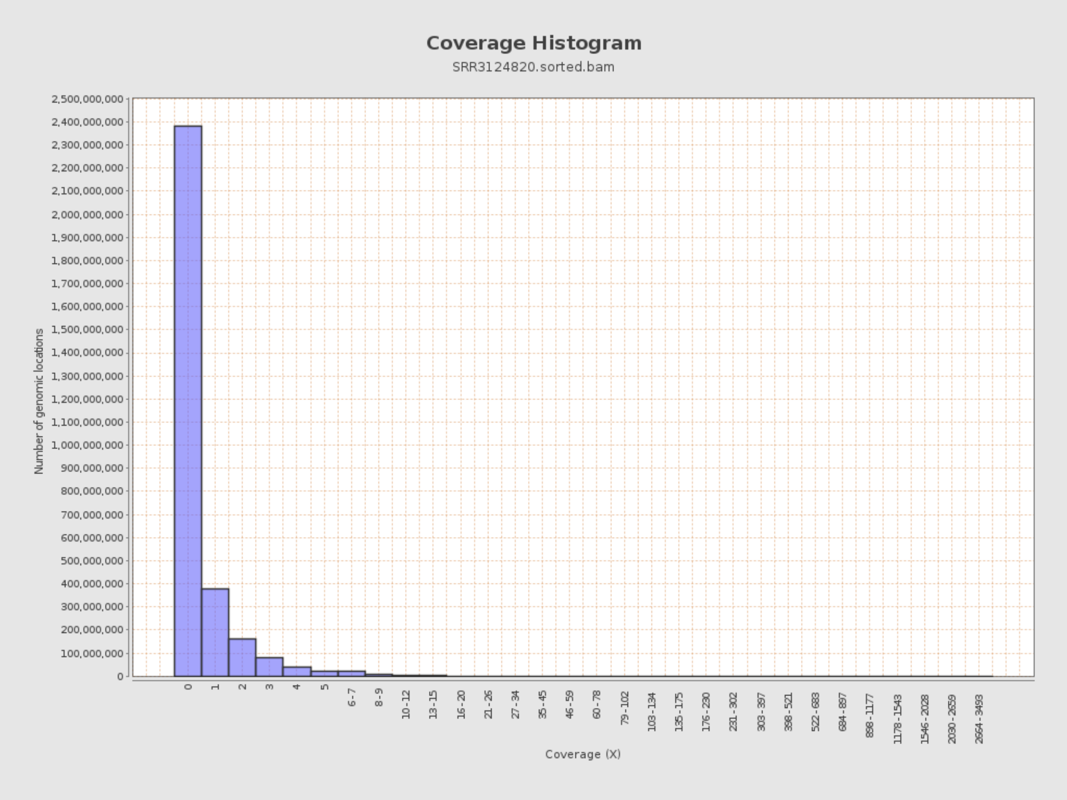
		bases	coverage	deviation
chr1	249250621	123136058	0.494	3.0453
chr2	243199373	130151165	0.5352	4.1924
chr3	198022430	93506470	0.4722	1.1911
chr4	191154276	83653431	0.4376	2.6564
chr5	180915260	85619446	0.4733	1.2086
chr6	171115067	79102830	0.4623	1.9893
chr7	159138663	75204610	0.4726	3.7345
chr8	146364022	72758245	0.4971	1.5969
chr9	141213431	59619400	0.4222	2.8924
chr10	135534747	73324698	0.541	5.5662
chr11	135006516	91301345	0.6763	3.5503
chr12	133851895	92887615	0.694	2.6585
chr13	115169878	65756152	0.5709	1.3628
chr14	107349540	43414620	0.4044	1.3262
chr15	102531392	40623815	0.3962	1.1333
chr16	90354753	47703431	0.528	4.895
chr17	81195210	41739128	0.5141	3.2198
chr18	78077248	38570837	0.494	4.4056
chr19	59128983	24428277	0.4131	2.4291
chr20	63025520	41295329	0.6552	1.6773
chr21	48129895	16884505	0.3508	1.8634
chr22	51304566	18879552	0.368	1.1533
chrMT	16571	237859	14.3539	8.5686
chrX	155270560	84041342	0.5413	2.1172

chrY	59373566	4475634	0.0754	4.5393

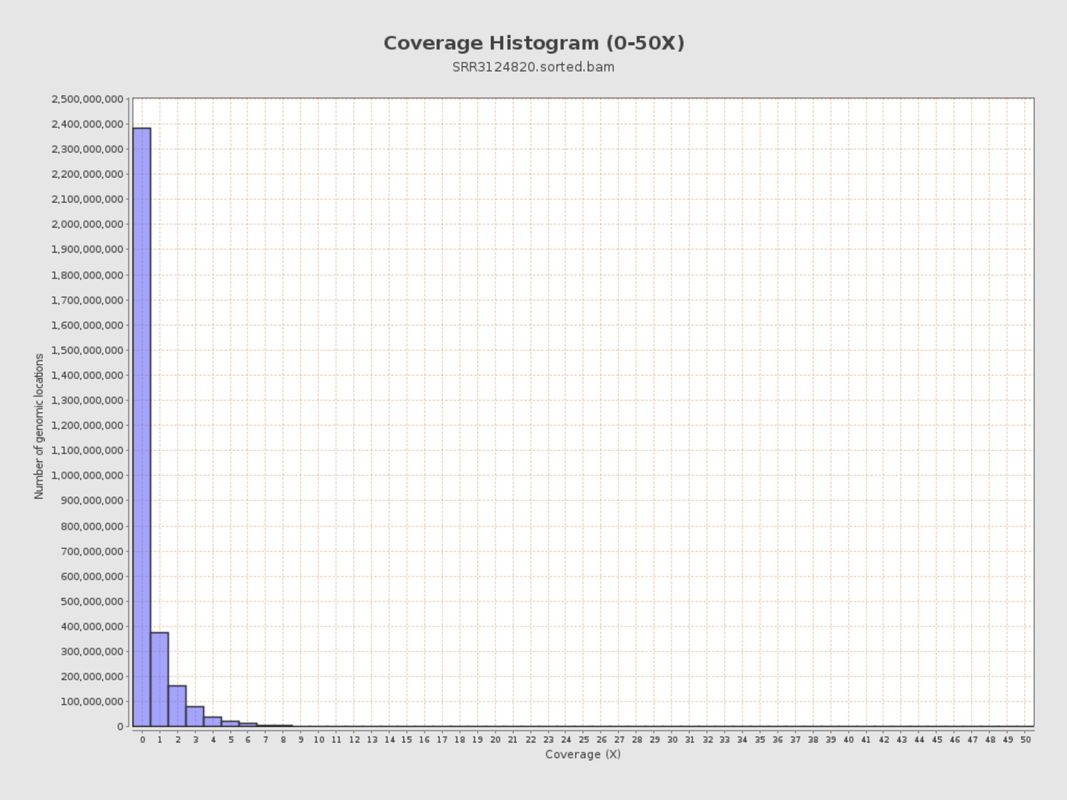
3. Results : Coverage across reference



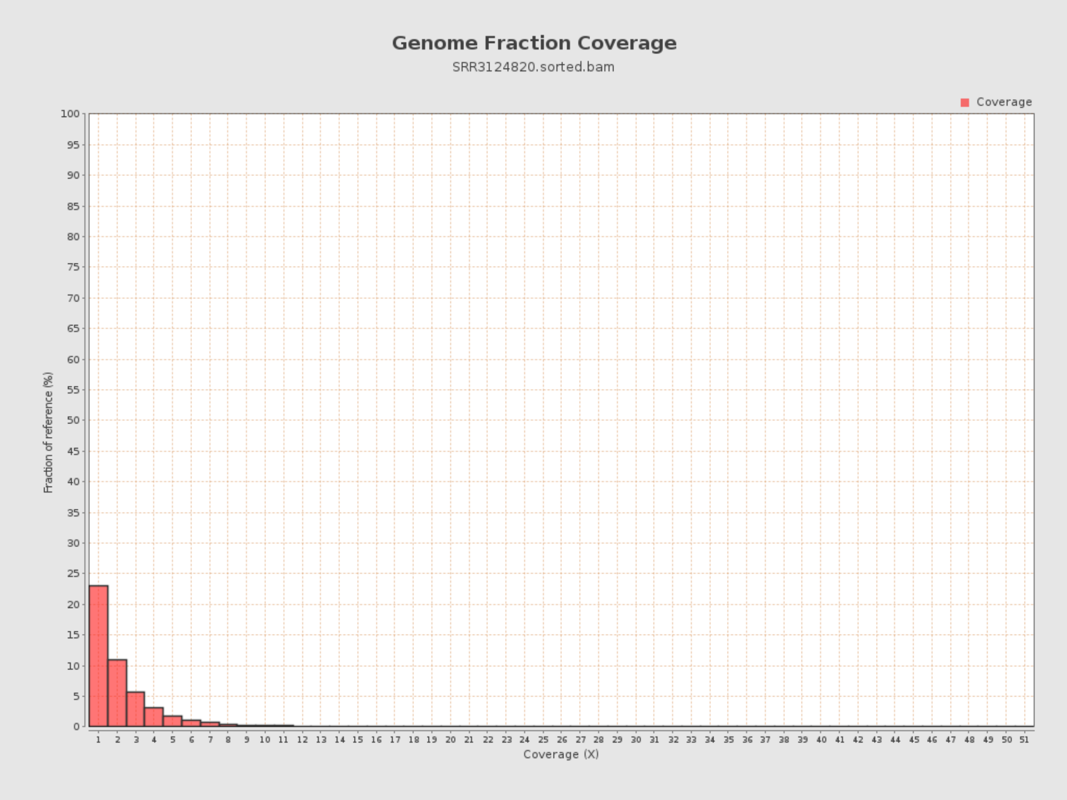
4. Results : Coverage Histogram



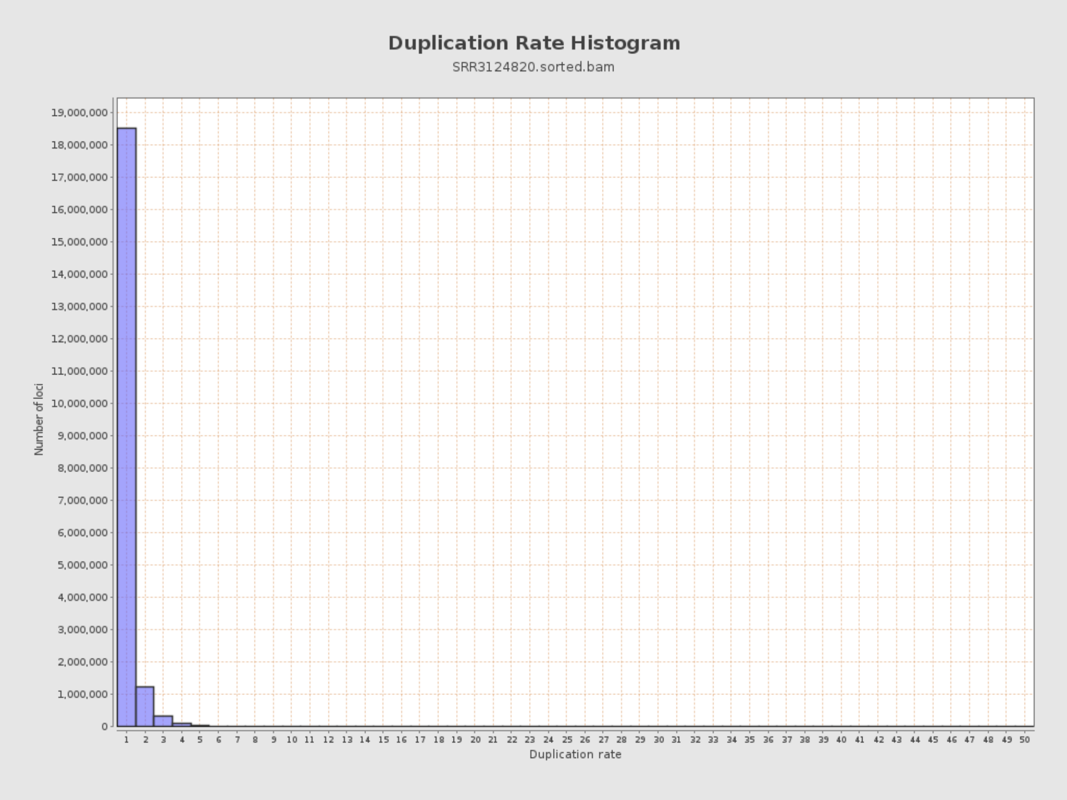
5. Results : Coverage Histogram (0-50X)



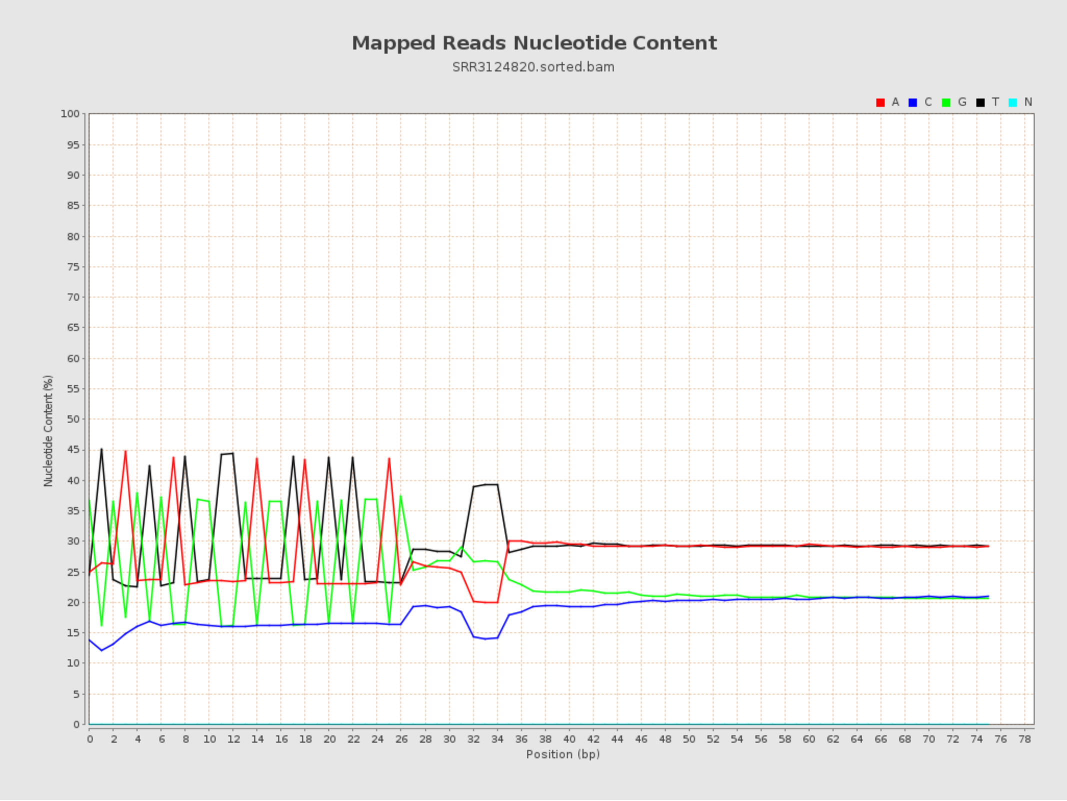
6. Results : Genome Fraction Coverage



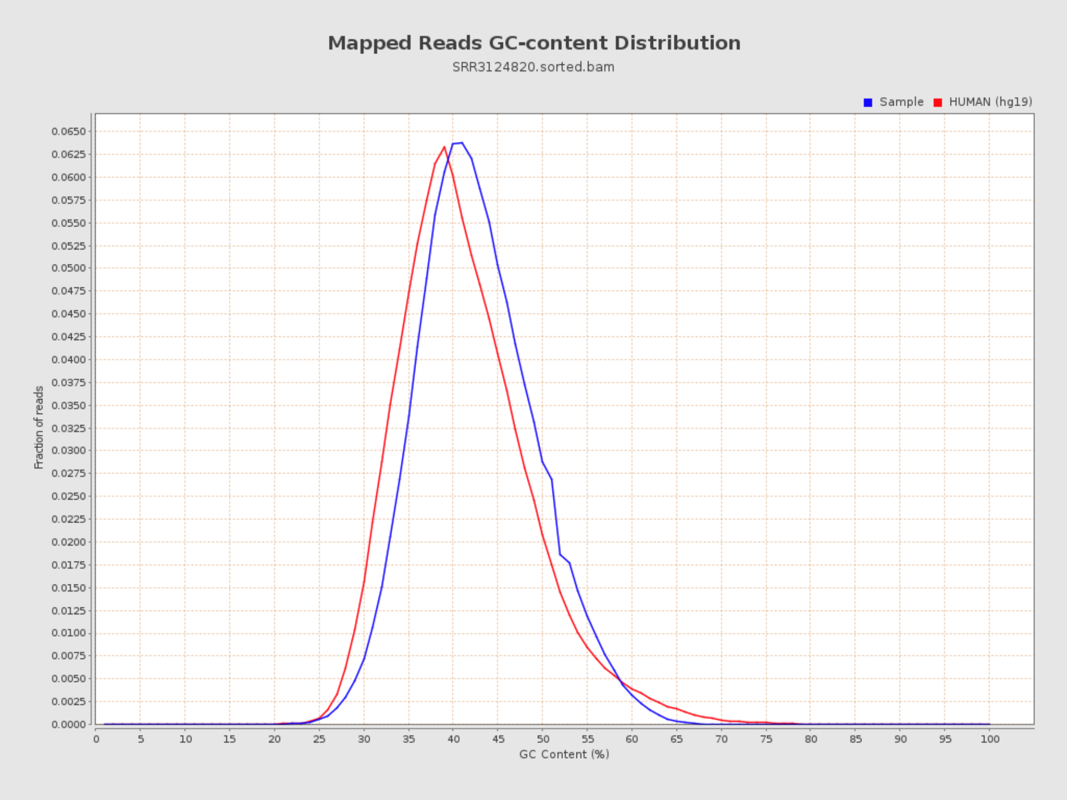
7. Results : Duplication Rate Histogram



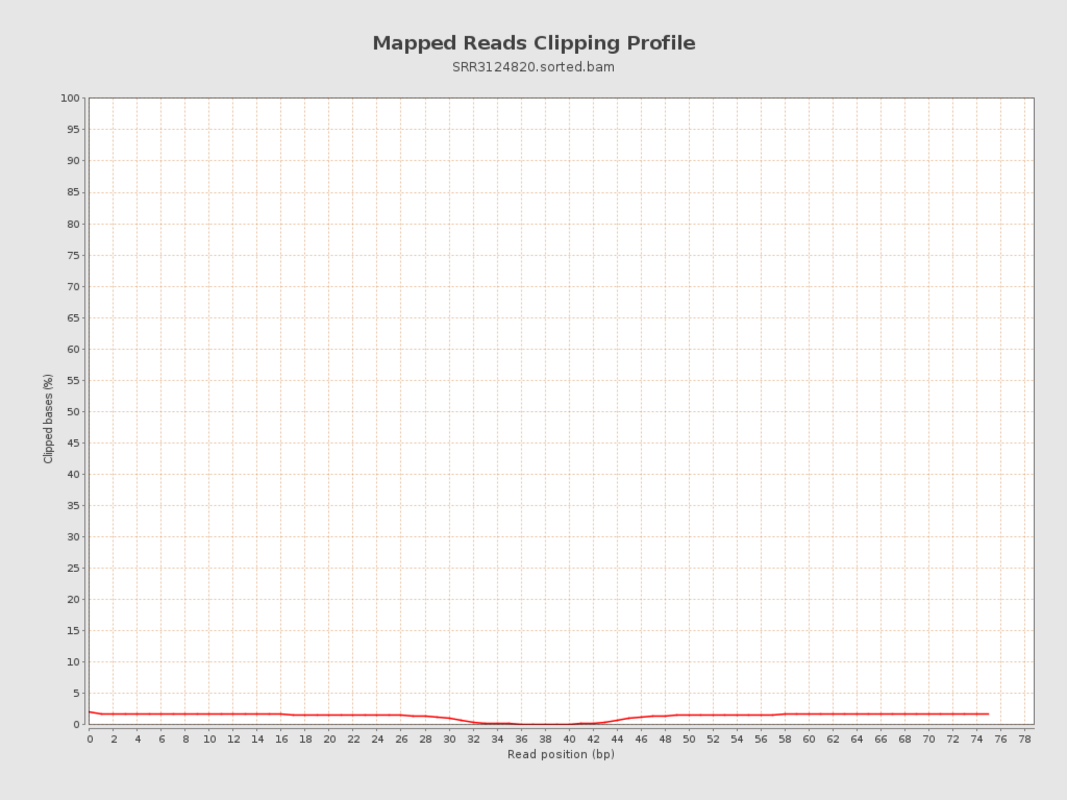
8. Results : Mapped Reads Nucleotide Content



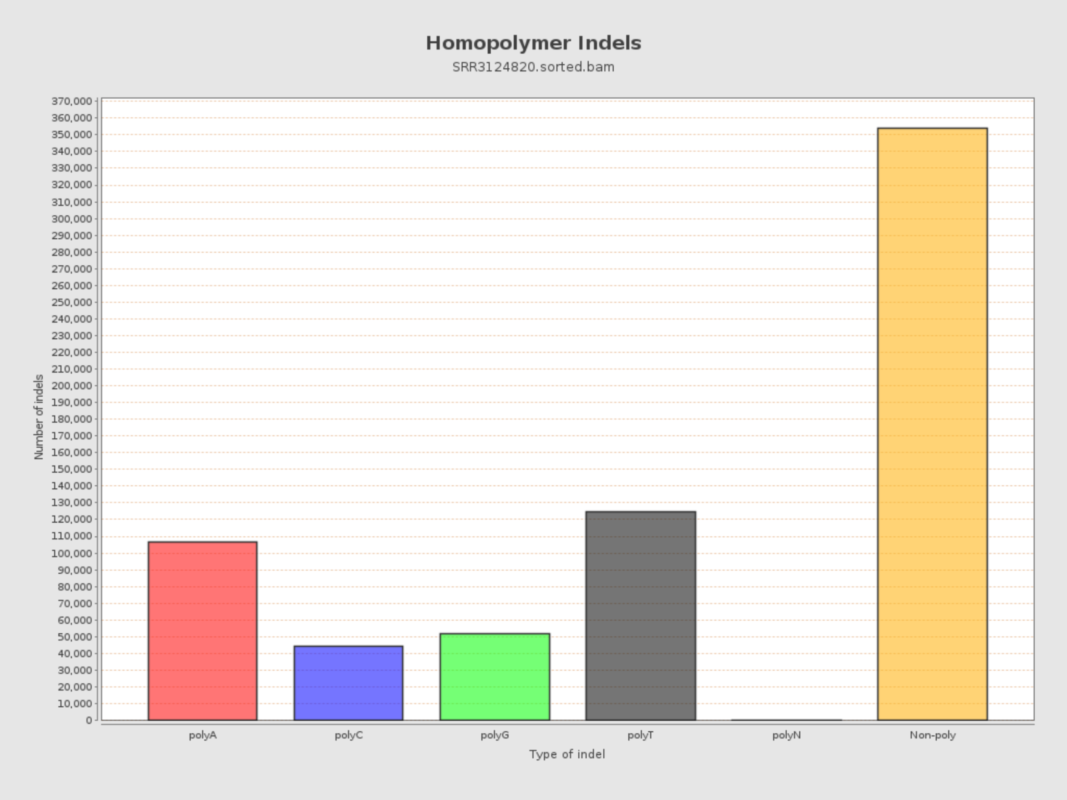
9. Results : Mapped Reads GC-content Distribution



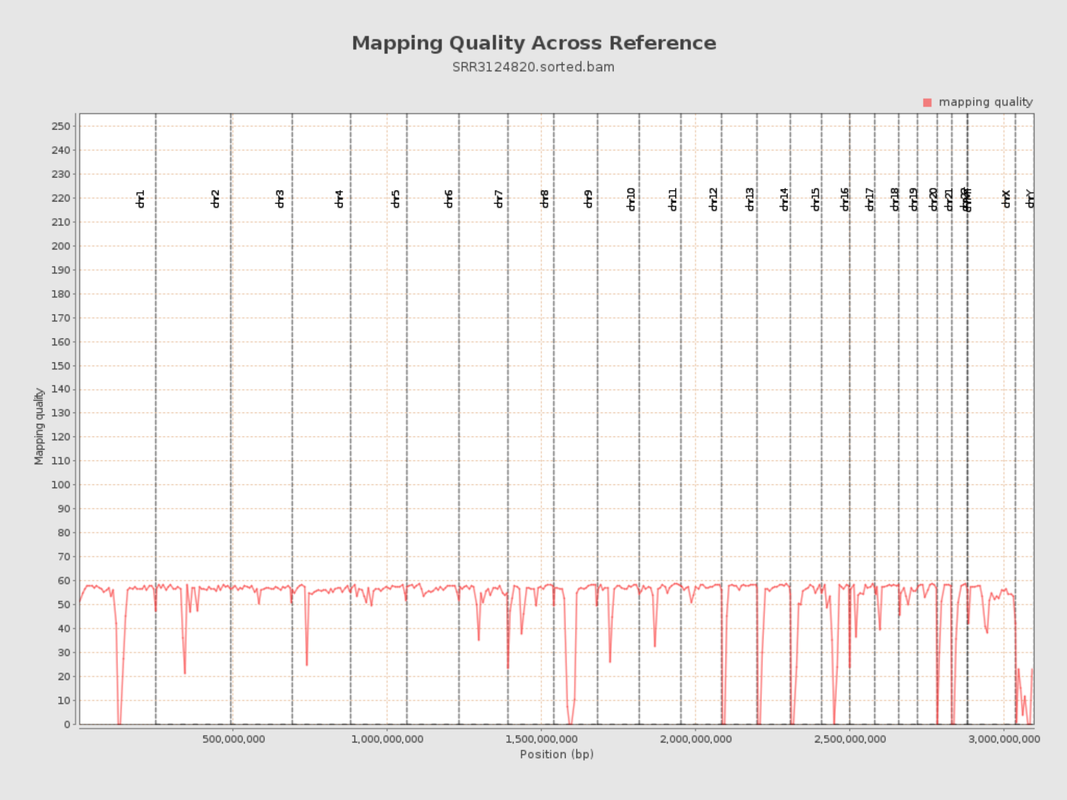
10. Results : Mapped Reads Clipping Profile



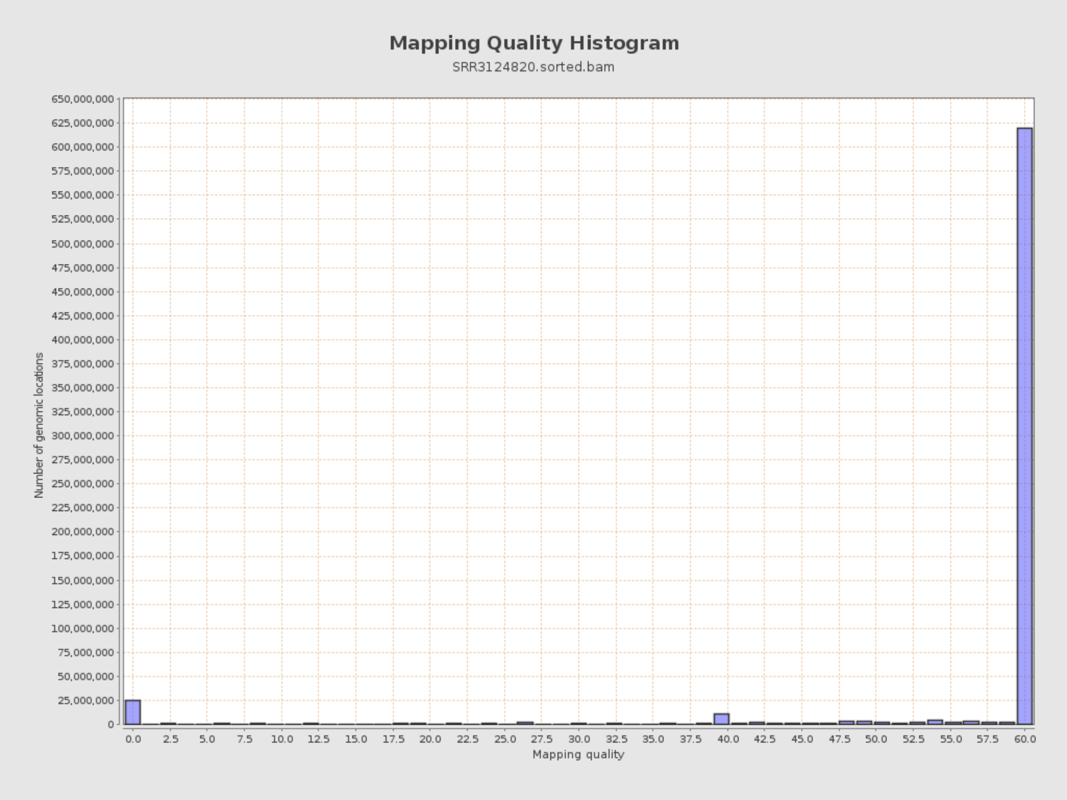
11. Results : Homopolymer Indels



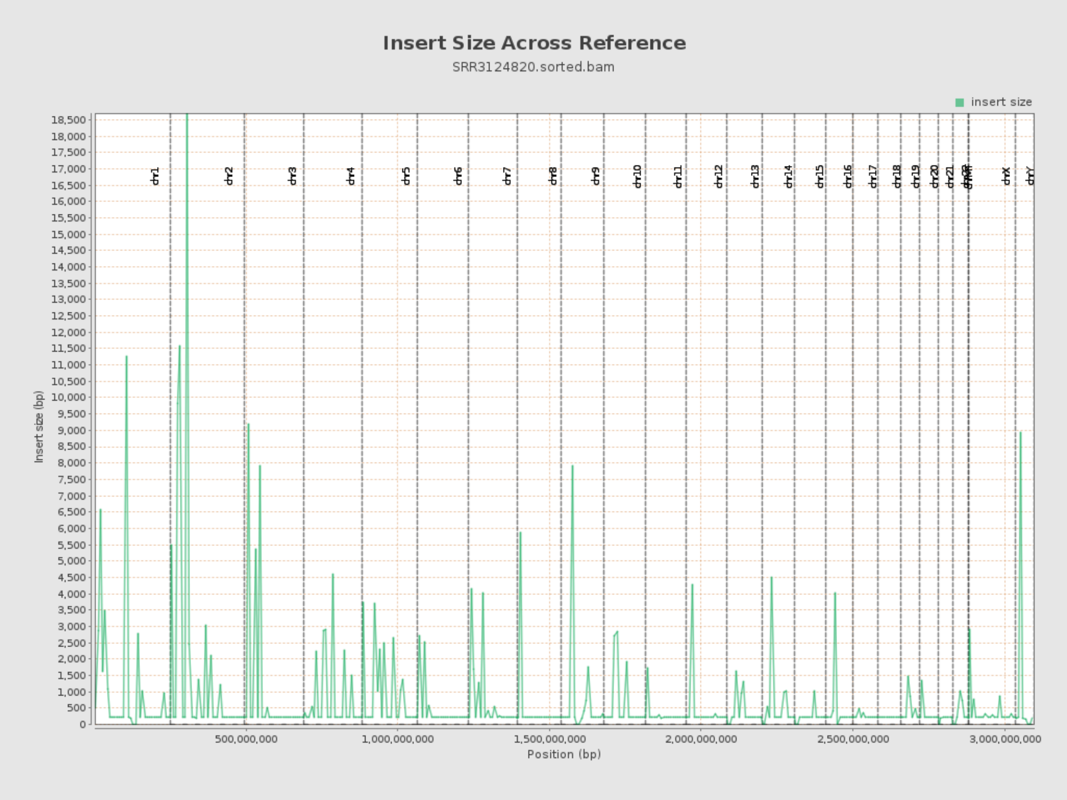
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram