Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 00:23:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124821.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_SRR3124821 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124821_1.fastq.gz SRR3124821_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 00:23:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124821.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,626,840
Mapped reads	29,406,686 / 99.26%
Unmapped reads	220,154 / 0.74%
Mapped paired reads	29,406,686 / 99.26%
Mapped reads, first in pair	14,711,177 / 49.65%
Mapped reads, second in pair	14,695,509 / 49.6%
Mapped reads, both in pair	29,327,488 / 98.99%
Mapped reads, singletons	79,198 / 0.27%
Secondary alignments	0
Supplementary alignments	141,621 / 0.48%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	2,709,223 / 9.14%
Duplication rate	5.3%
Clipped reads	17,394,659 / 58.71%

2.2. ACGT Content

Number/percentage of A's	769,084,879 / 28.51%
Number/percentage of C's	538,879,112 / 19.97%
Number/percentage of T's	791,564,084 / 29.34%
Number/percentage of G's	598,240,812 / 22.18%
Number/percentage of N's	19,673 / 0%

GC Percentage	42.15%

2.3. Coverage

Mean	0.872
Standard Deviation	7.3288

2.4. Mapping Quality

Mean Mapping Quality	52.74

2.5. Insert size

Mean	82,093.62
Standard Deviation	2,763,207.7
P25/Median/P75	139 / 172 / 216

2.6. Mismatches and indels

General error rate	0.73%
Mismatches	18,720,224
Insertions	436,541
Mapped reads with at least one insertion	1.45%
Deletions	896,903
Mapped reads with at least one deletion	2.99%
Homopolymer indels	46.63%

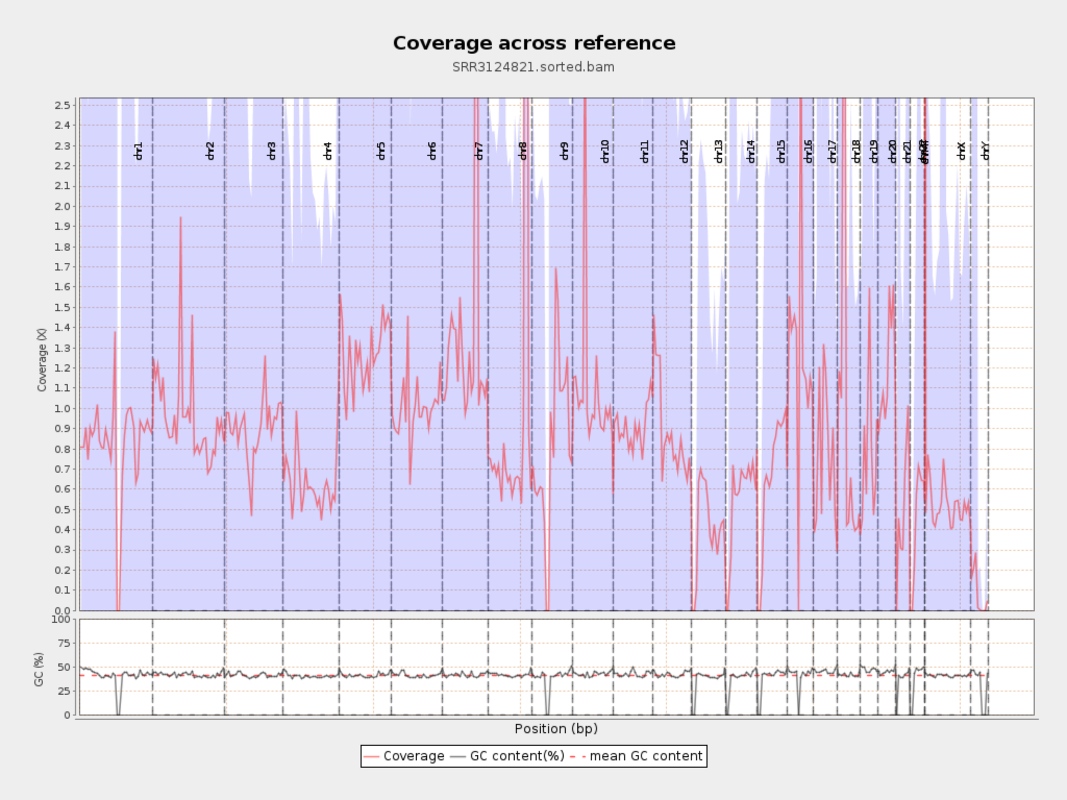
2.7. Chromosome stats

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

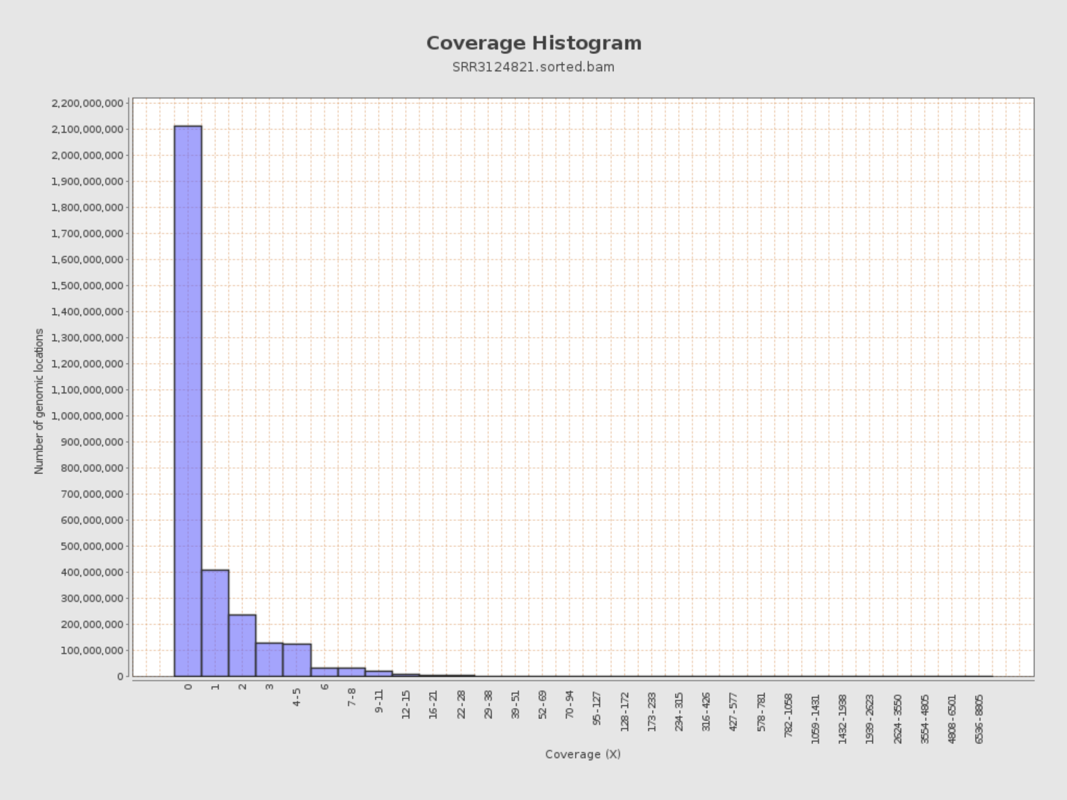
		bases	coverage	deviation
chr1	249250621	205752442	0.8255	9.0666
chr2	243199373	234951491	0.9661	8.049
chr3	198022430	178948147	0.9037	2.0394
chr4	191154276	119338940	0.6243	3.5039
chr5	180915260	229992069	1.2713	2.3811
chr6	171115067	171981421	1.0051	5.9251
chr7	159138663	217951082	1.3696	11.1449
chr8	146364022	153129943	1.0462	6.2493
chr9	141213431	114138620	0.8083	8.5501
chr10	135534747	152494860	1.1251	18.2466
chr11	135006516	121303126	0.8985	4.0374
chr12	133851895	118532595	0.8856	1.896
chr13	115169878	46479520	0.4036	1.1214
chr14	107349540	58257584	0.5427	1.8537
chr15	102531392	66184516	0.6455	1.5364
chr16	90354753	115790566	1.2815	14.1829
chr17	81195210	61833749	0.7615	8.774
chr18	78077248	77419267	0.9916	8.8149
chr19	59128983	45171744	0.764	5.0418
chr20	63025520	75273274	1.1943	2.4422
chr21	48129895	25115691	0.5218	1.9782
chr22	51304566	22637906	0.4412	1.5252
chrMT	16571	286131	17.267	10.1493
chrX	155270560	81186453	0.5229	2.3454

chrY	59373566	5169226	0.0871	5.3201

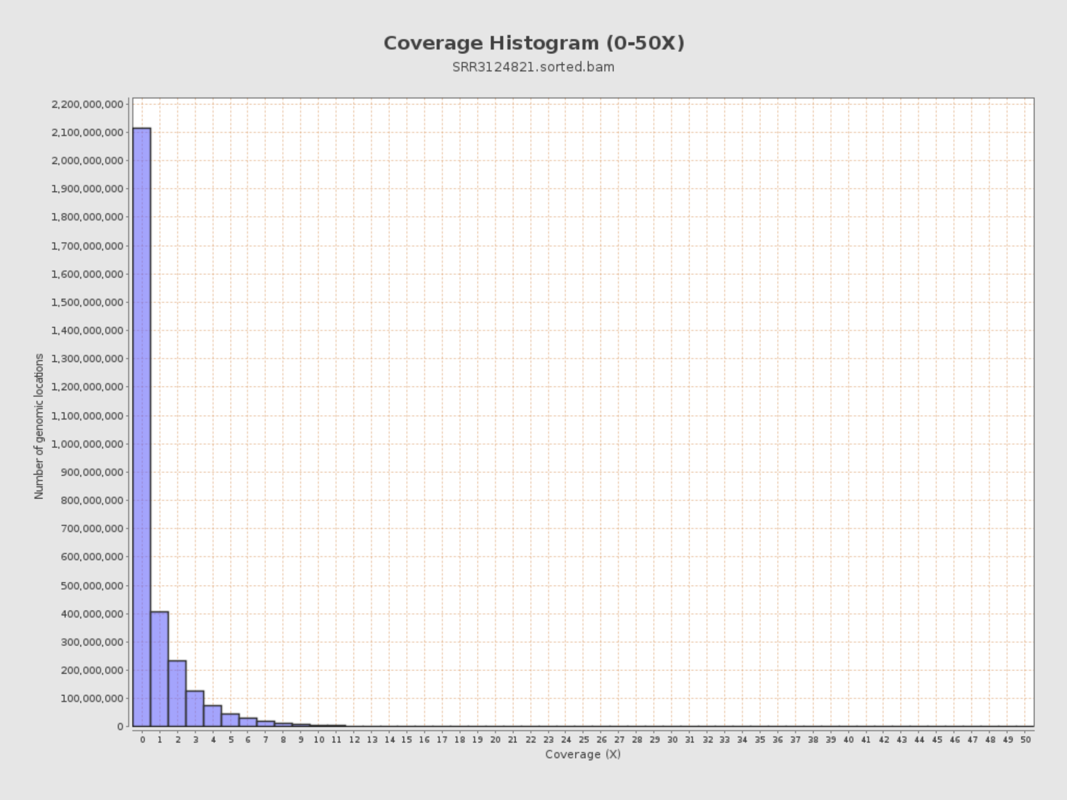
3. Results : Coverage across reference



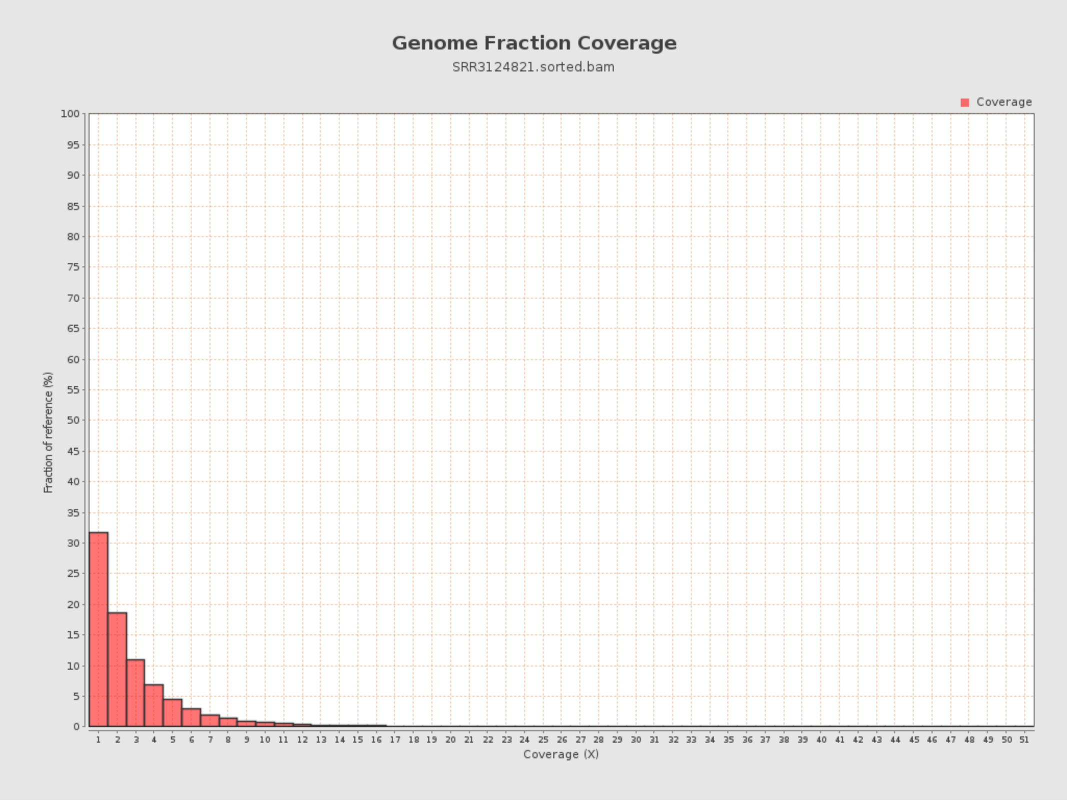
4. Results : Coverage Histogram



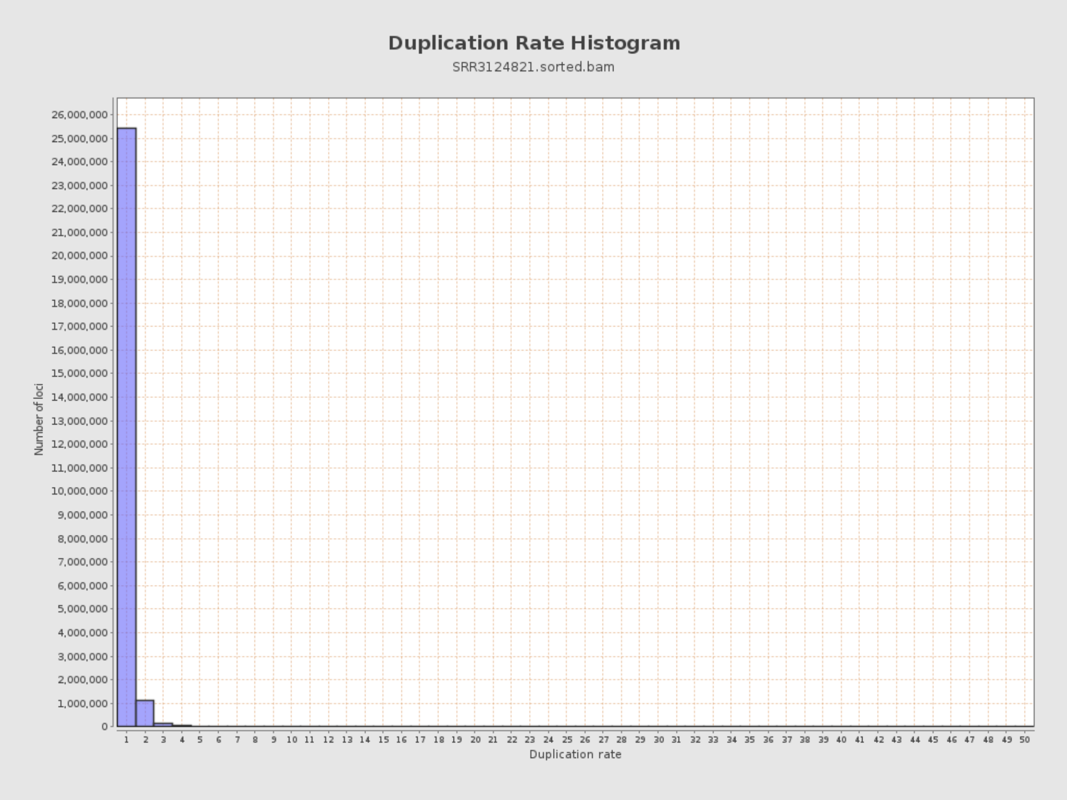
5. Results : Coverage Histogram (0-50X)



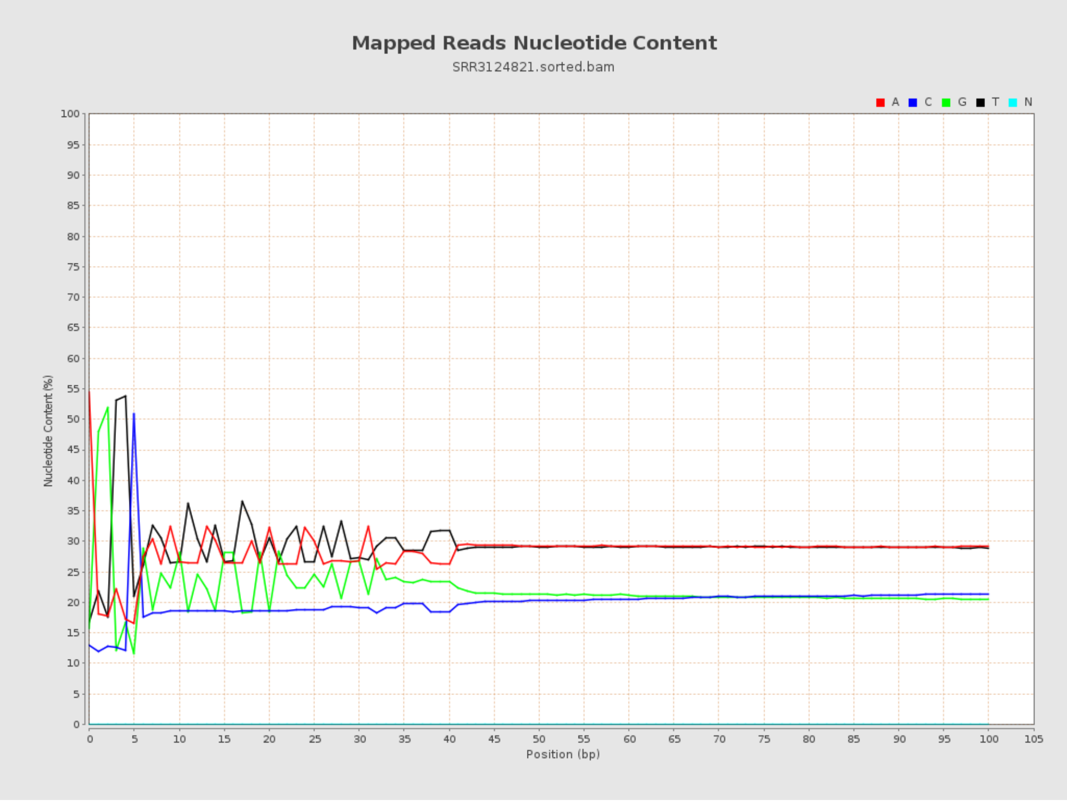
6. Results : Genome Fraction Coverage



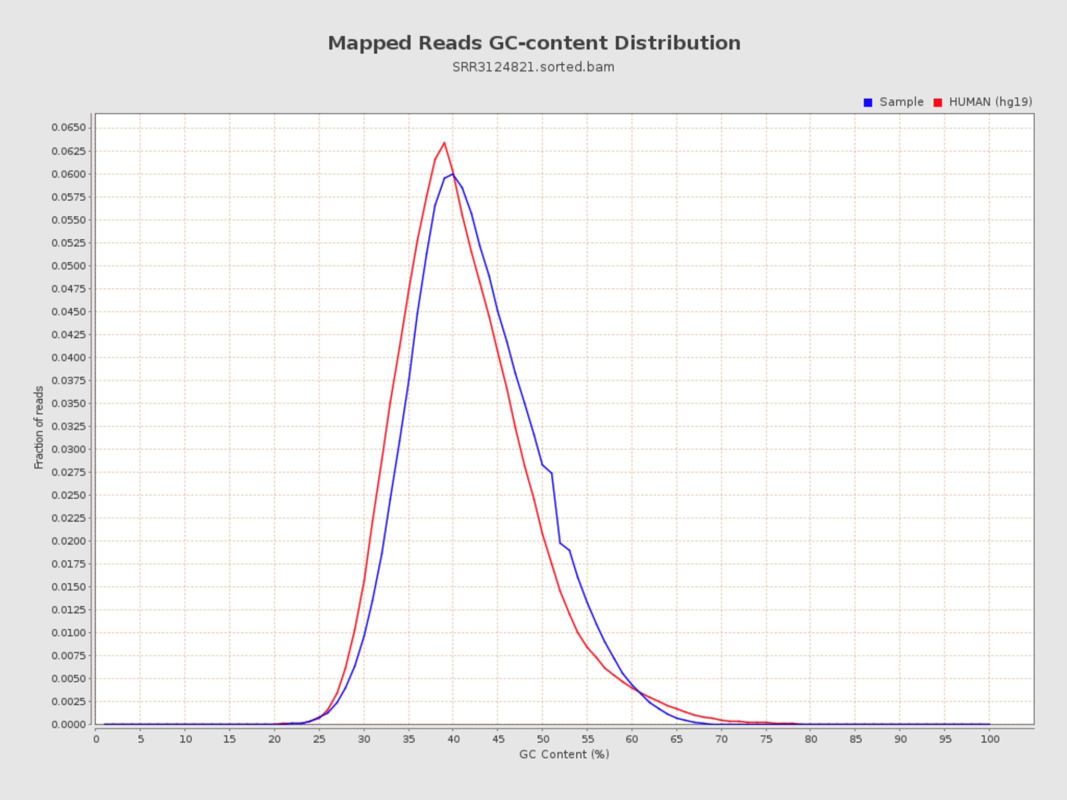
7. Results : Duplication Rate Histogram



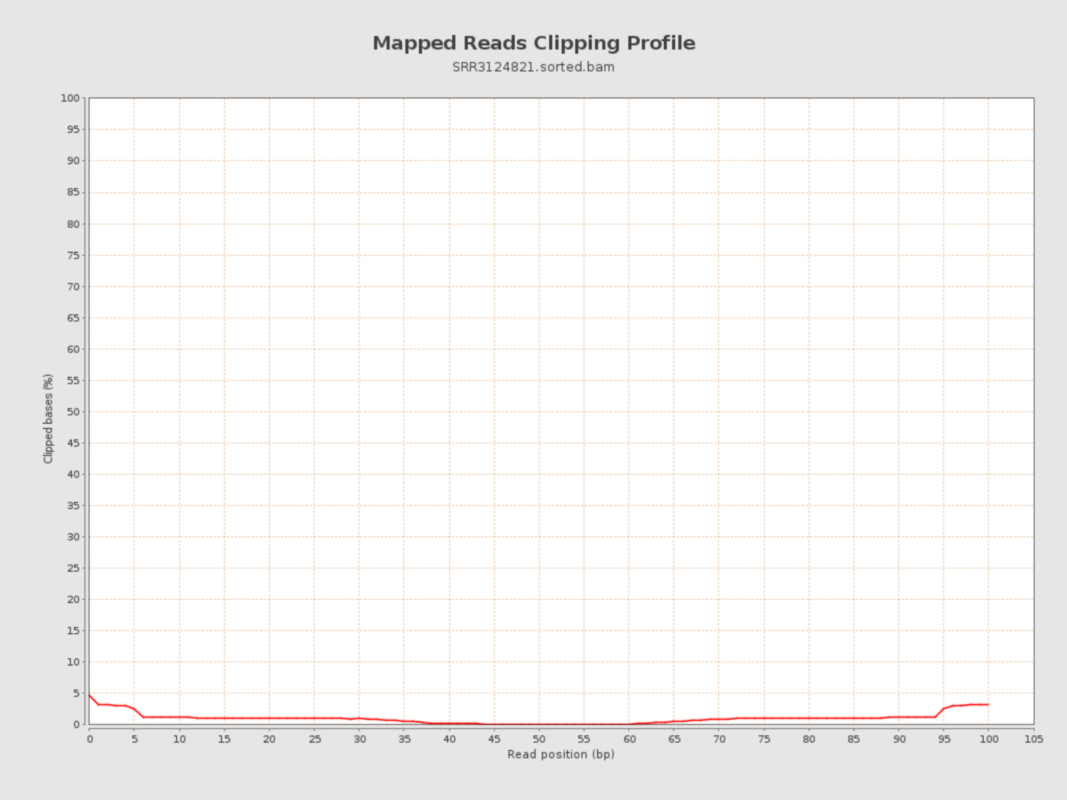
8. Results : Mapped Reads Nucleotide Content



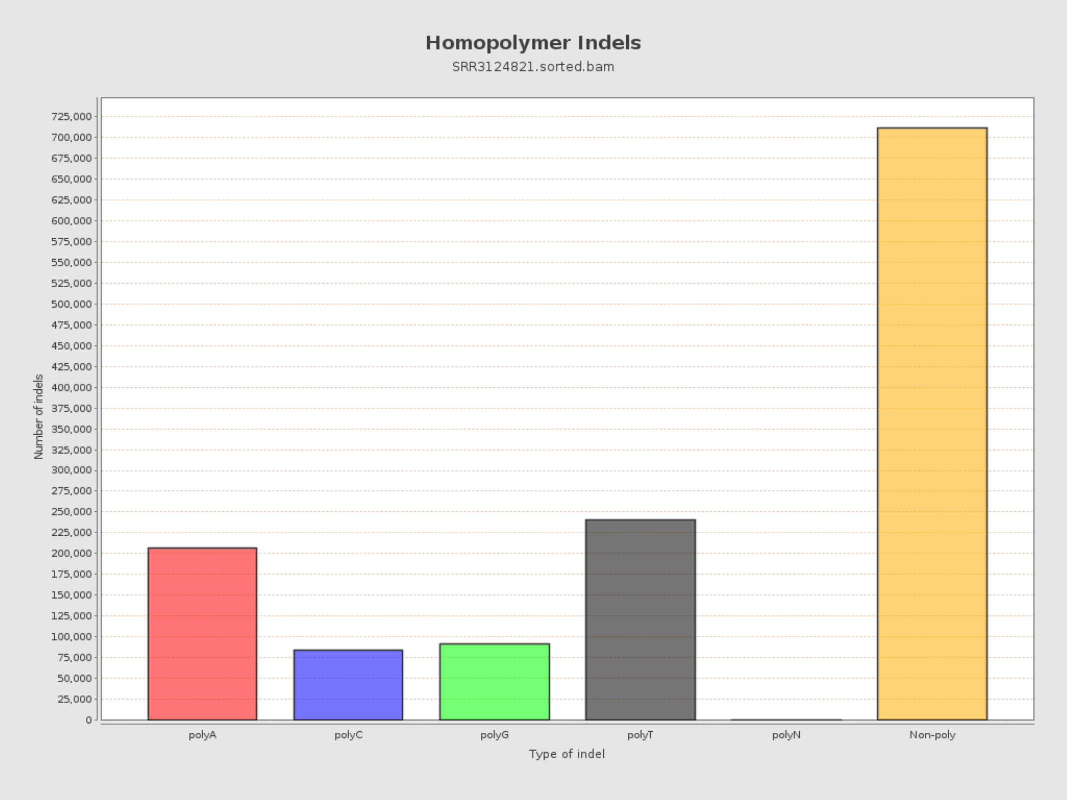
9. Results : Mapped Reads GC-content Distribution



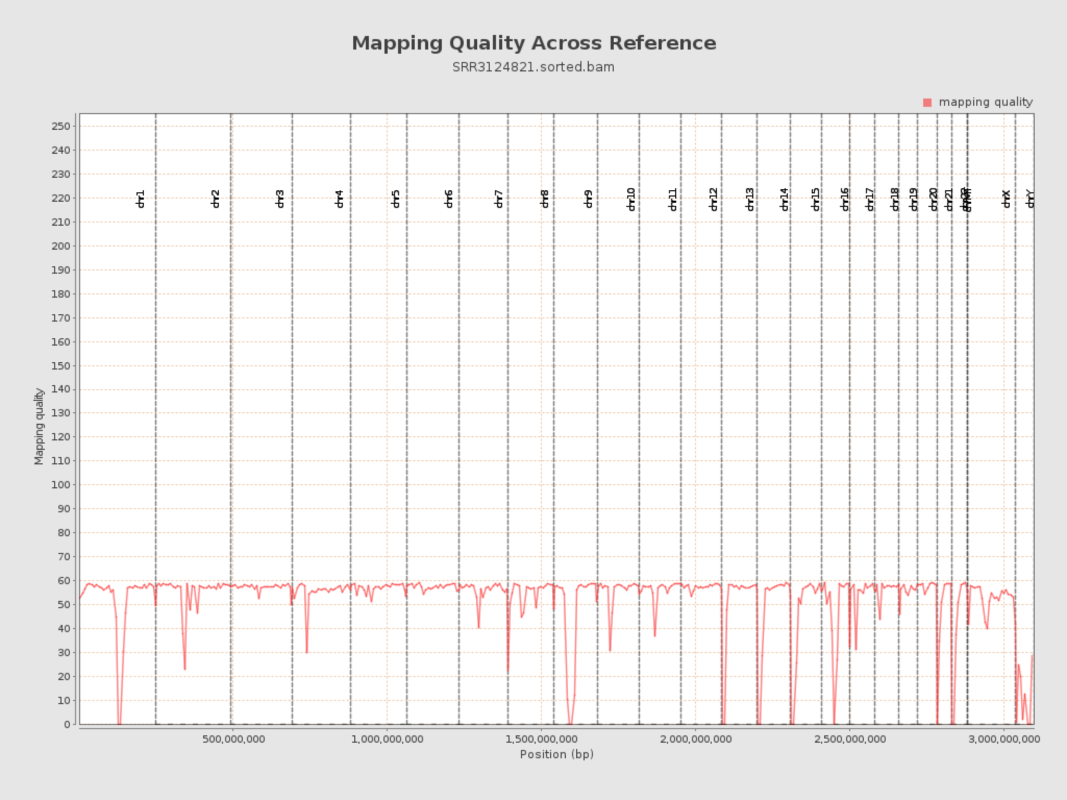
10. Results : Mapped Reads Clipping Profile



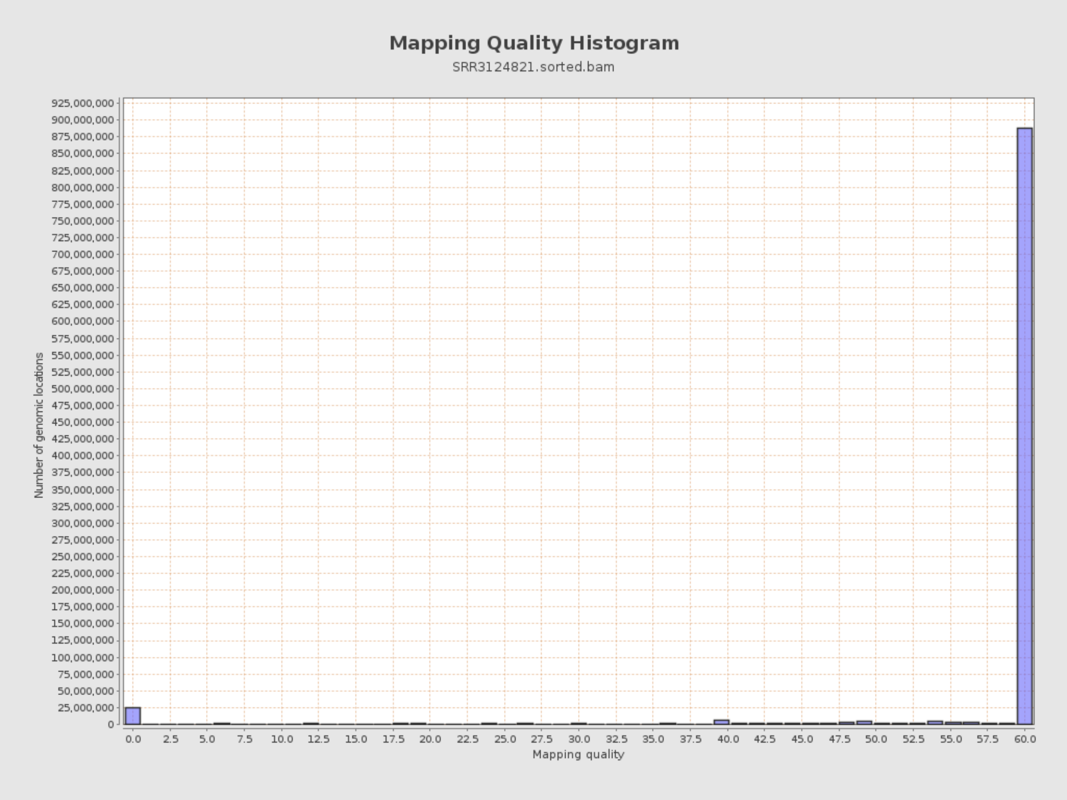
11. Results : Homopolymer Indels



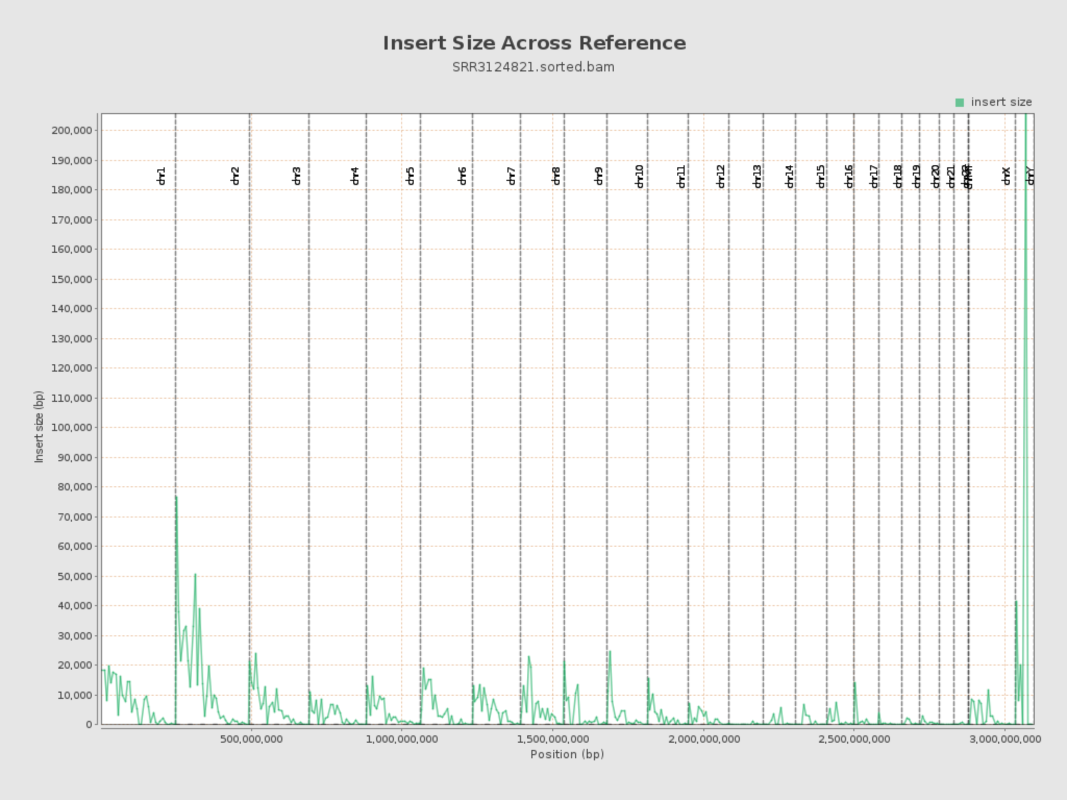
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram