Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 19:50:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124835.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_SRR3124835 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124835_1.fastq.gz SRR3124835_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 19:50:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124835.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	603,465,272
Mapped reads	598,645,038 / 99.2%
Unmapped reads	4,820,234 / 0.8%
Mapped paired reads	598,645,038 / 99.2%
Mapped reads, first in pair	300,366,112 / 49.77%
Mapped reads, second in pair	298,278,926 / 49.43%
Mapped reads, both in pair	595,851,052 / 98.74%
Mapped reads, singletons	2,793,986 / 0.46%
Secondary alignments	0
Supplementary alignments	5,420,843 / 0.9%
Read min/max/mean length	30 / 150 / 150.42
Duplicated reads (estimated)	139,647,062 / 23.14%
Duplication rate	17.72%
Clipped reads	60,968,428 / 10.1%

2.2. ACGT Content

Number/percentage of A's	25,852,512,940 / 29.42%
Number/percentage of C's	18,081,122,433 / 20.58%
Number/percentage of T's	25,821,157,079 / 29.39%
Number/percentage of G's	18,103,424,432 / 20.6%
Number/percentage of N's	2,330,003 / 0%

GC Percentage	41.18%

2.3. Coverage

Mean	28.3932
Standard Deviation	400.3034

2.4. Mapping Quality

Mean Mapping Quality	54.28

2.5. Insert size

Mean	51,283.79
Standard Deviation	2,162,758.03
P25/Median/P75	254 / 319 / 404

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	705,092,914
Insertions	10,853,372
Mapped reads with at least one insertion	1.69%
Deletions	11,617,973
Mapped reads with at least one deletion	1.83%
Homopolymer indels	40.54%

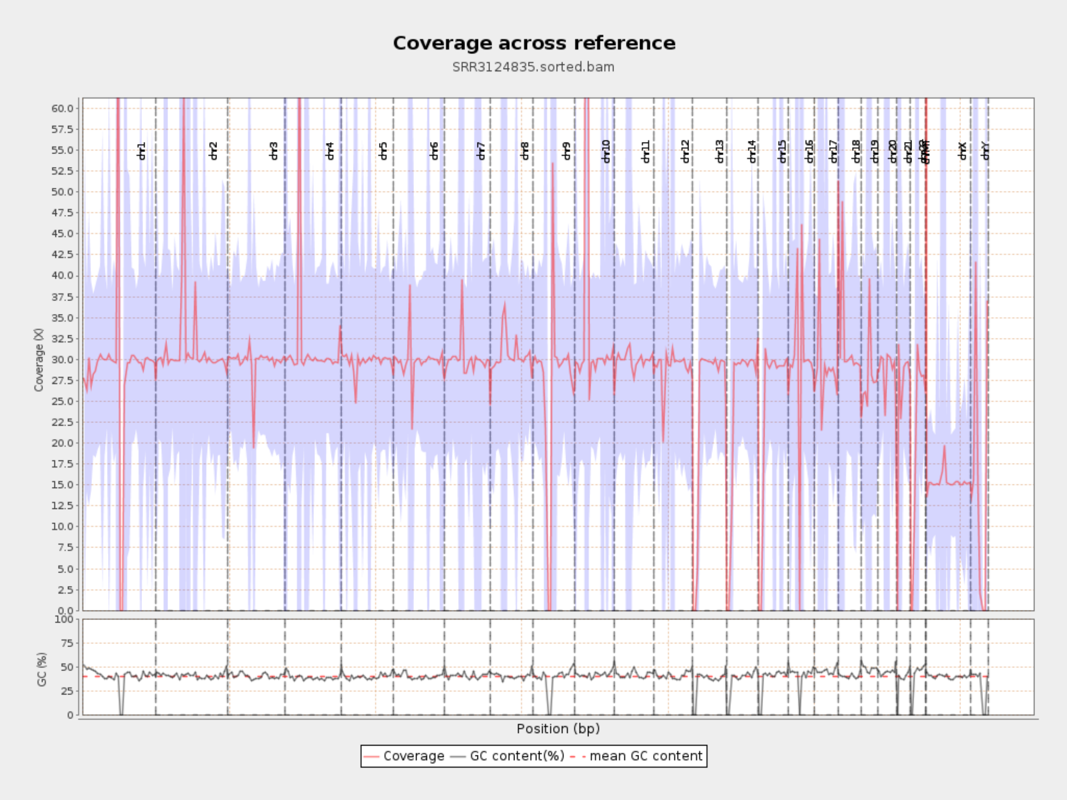
2.7. Chromosome stats

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

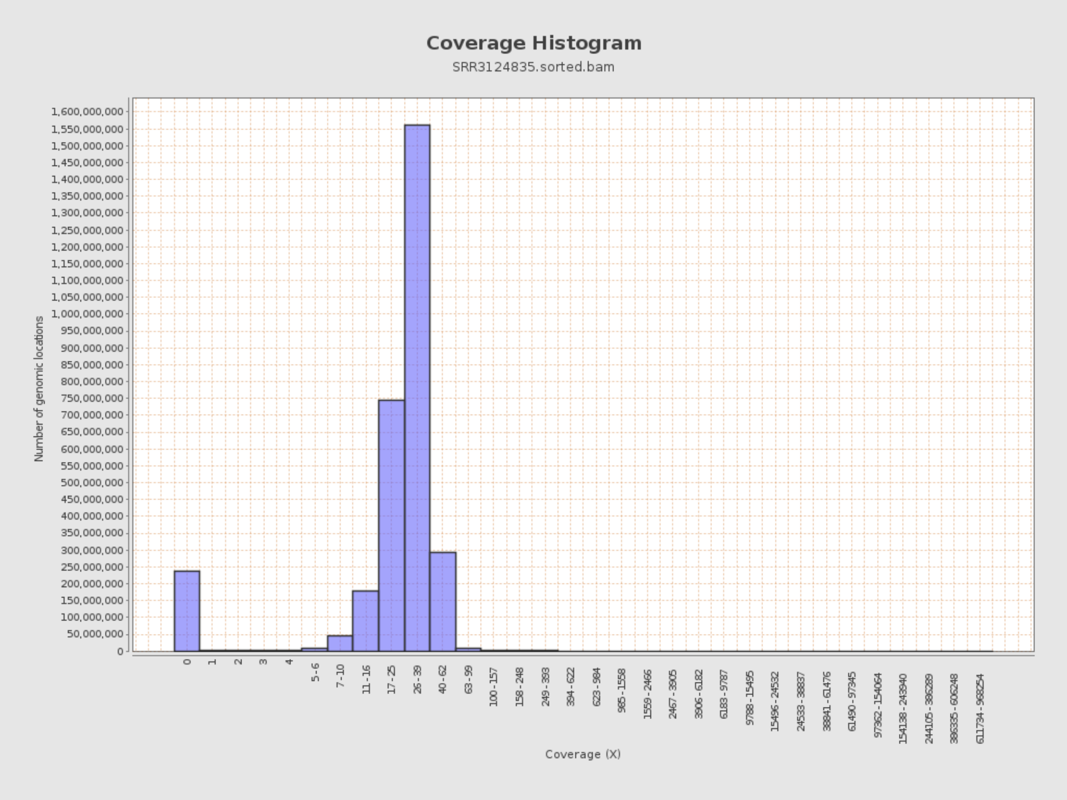
		bases	**coverage**	**deviation**
chr1	249250621	7243166929	29.0598	997.2243
chr2	243199373	7688240768	31.6129	198.4888
chr3	198022430	5879965600	29.6934	21.1529
chr4	191154276	6058969879	31.6968	336.7464
chr5	180915260	5376410663	29.7178	25.7051
chr6	171115067	5111778378	29.8733	112.2572
chr7	159138663	4789969369	30.0993	221.2899
chr8	146364022	4482379773	30.6249	379.1522
chr9	141213431	3827566989	27.1048	509.9296
chr10	135534747	4816130777	35.5343	848.9817
chr11	135006516	4038051331	29.91	160.1561
chr12	133851895	3898580934	29.1261	94.7117
chr13	115169878	2849401580	24.7409	14.9346
chr14	107349540	2647389005	24.6614	20.4399
chr15	102531392	2487549489	24.2613	53.5712
chr16	90354753	2657835574	29.4156	160.7845
chr17	81195210	2370617053	29.1965	205.5208
chr18	78077248	2548583776	32.6418	486.5573
chr19	59128983	1664151385	28.1444	436.0518
chr20	63025520	1815745937	28.8097	103.7989
chr21	48129895	1245326842	25.8743	169.3131
chr22	51304566	1032372705	20.1224	71.7388
chrMT	16571	32270610	1,947.4148	187.2301
chrX	155270560	2396348509	15.4334	54.188

chrY	59373566	937926033	15.797	364.9473

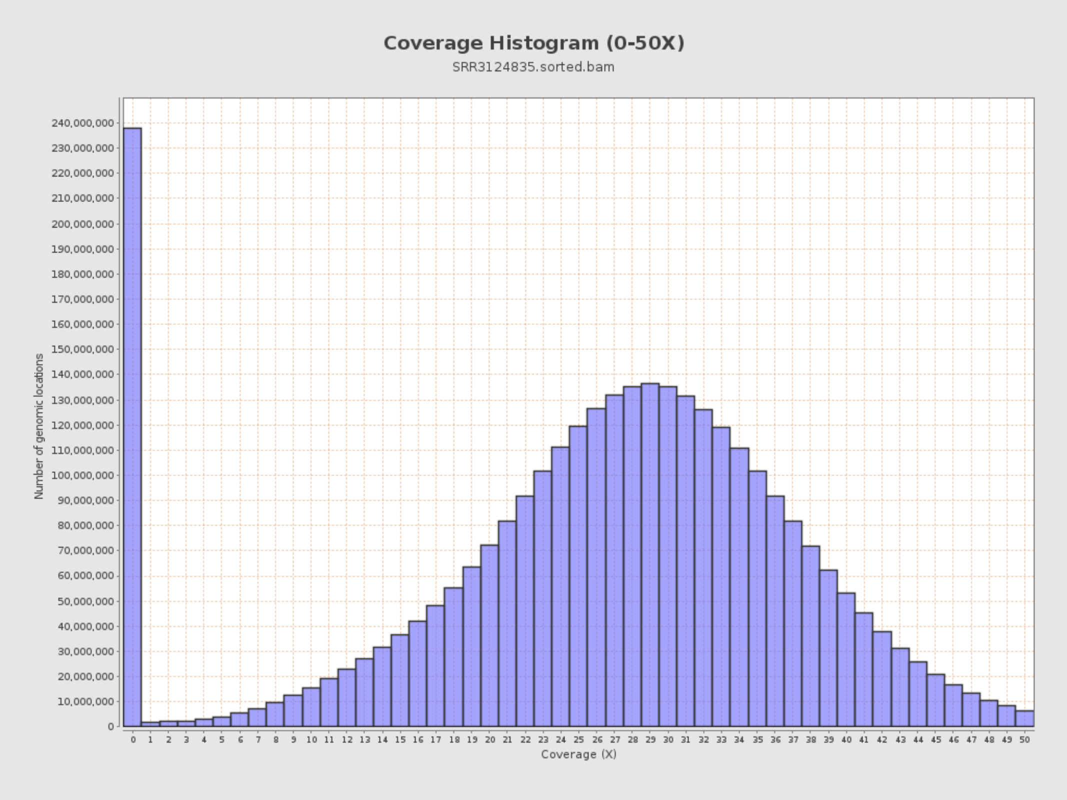
3. Results : Coverage across reference



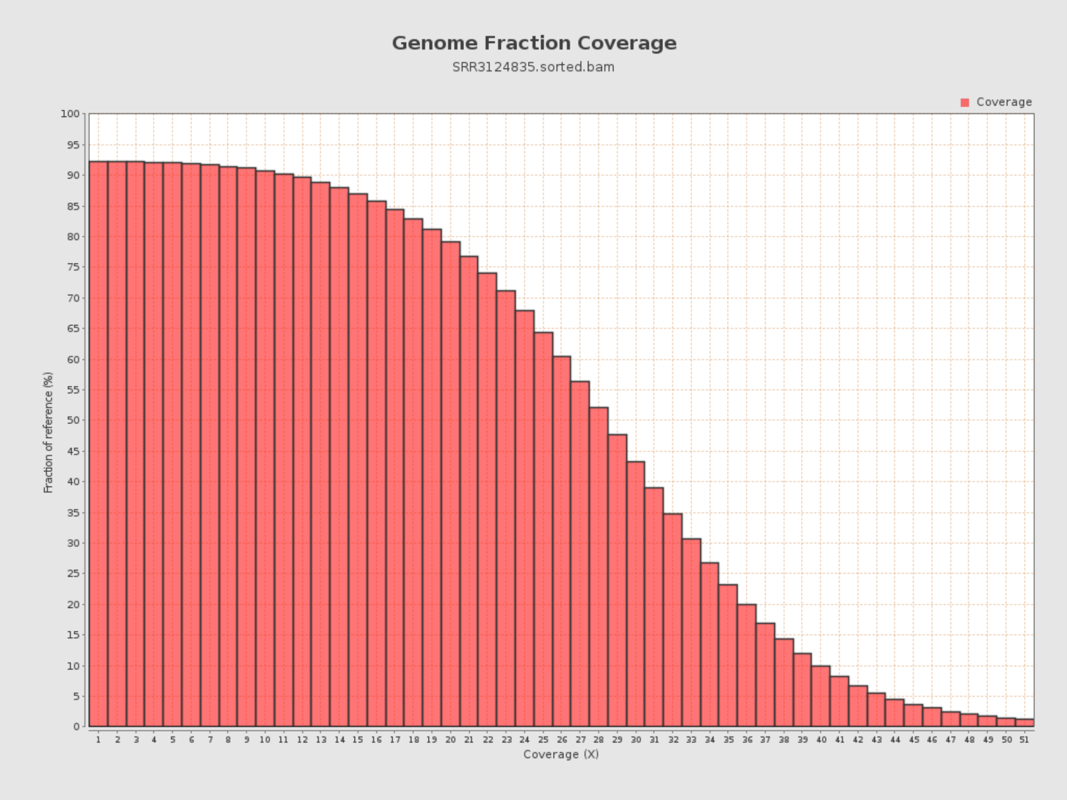
4. Results : Coverage Histogram



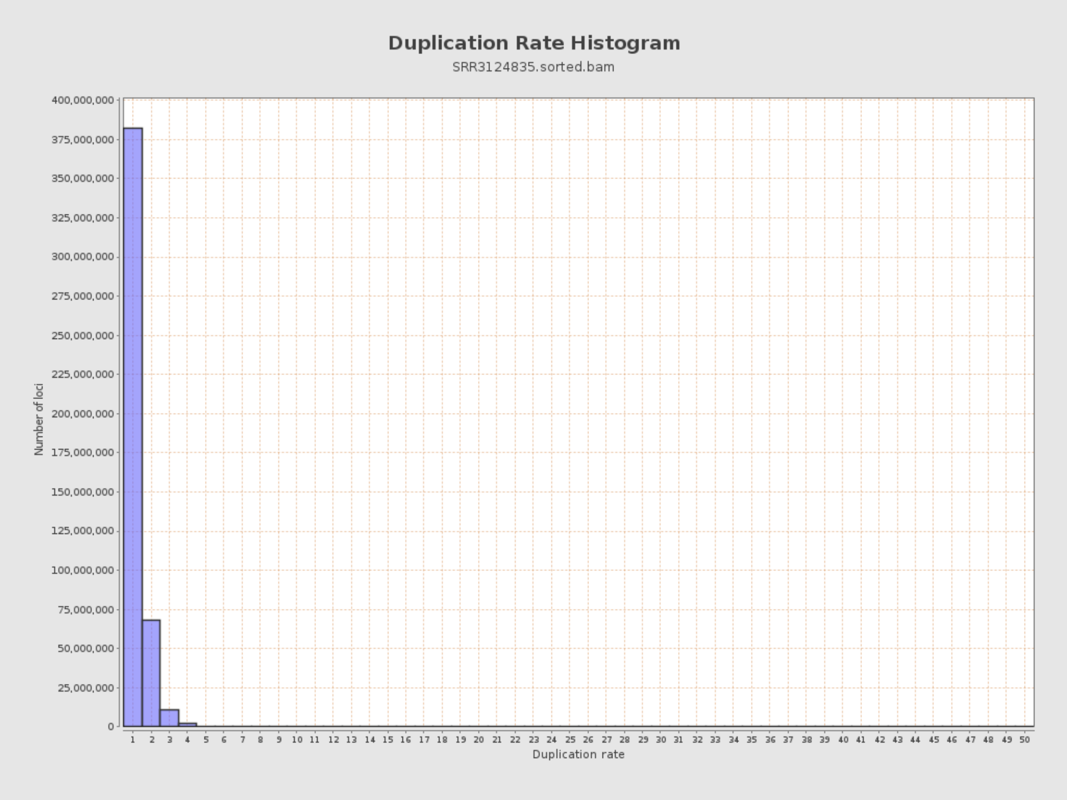
5. Results : Coverage Histogram (0-50X)



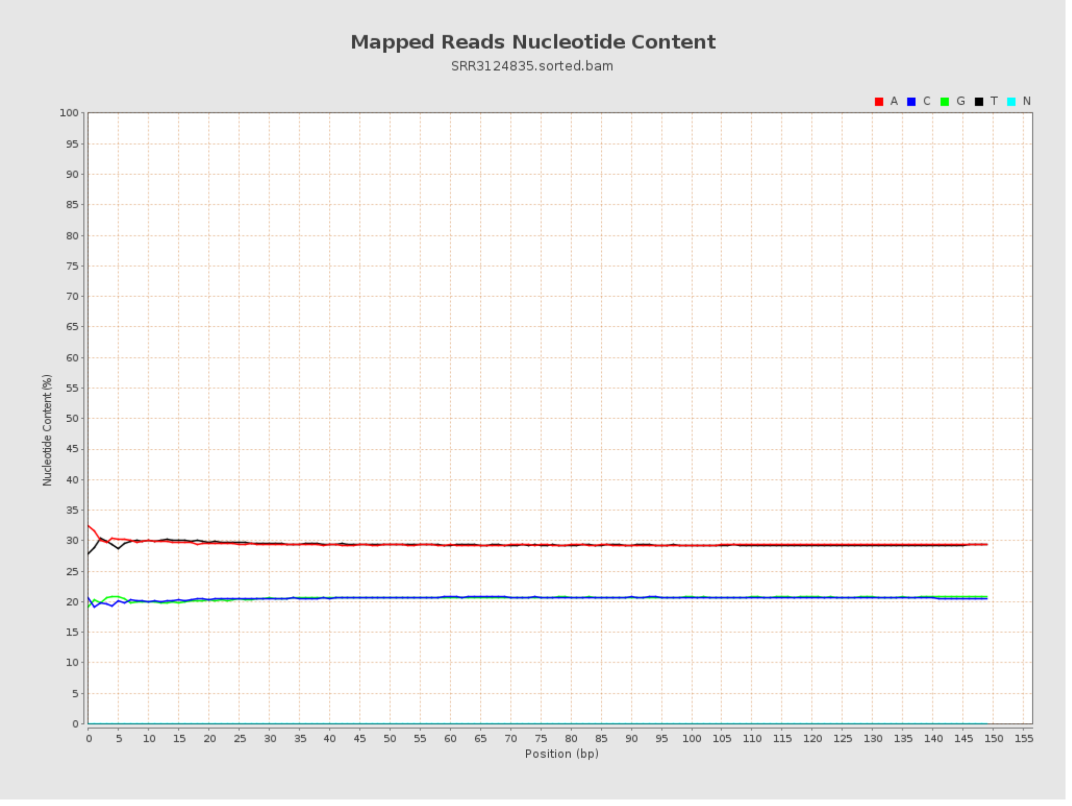
6. Results : Genome Fraction Coverage



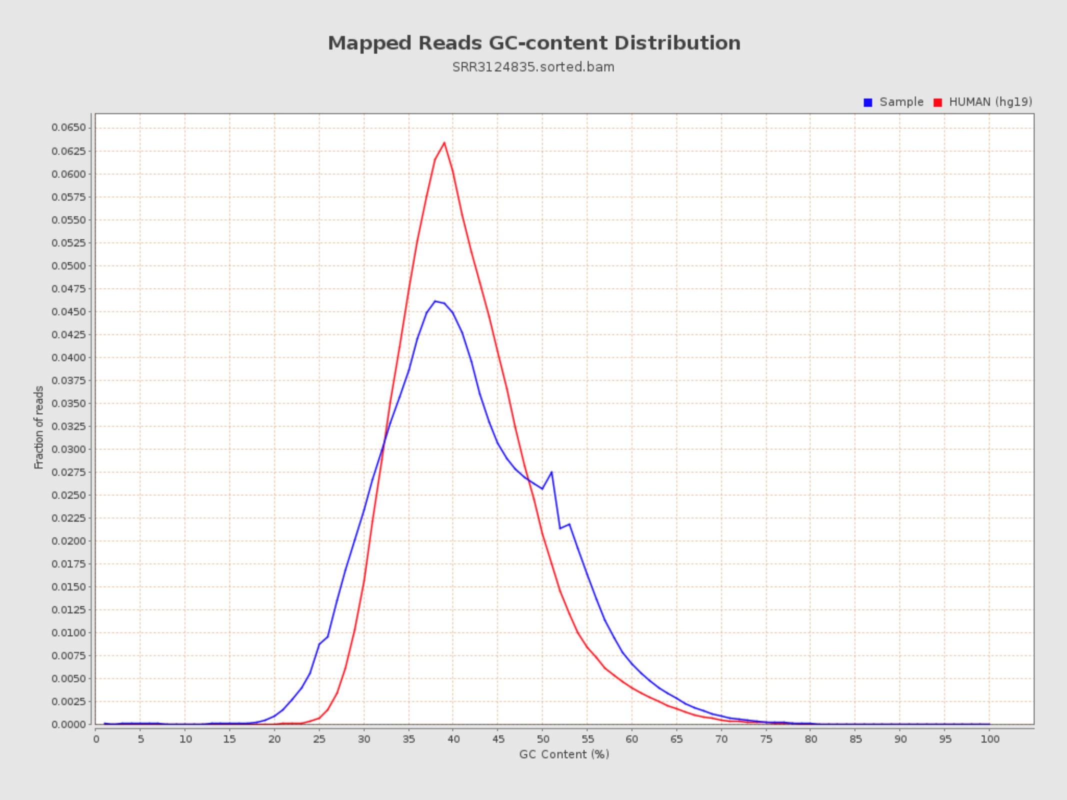
7. Results : Duplication Rate Histogram



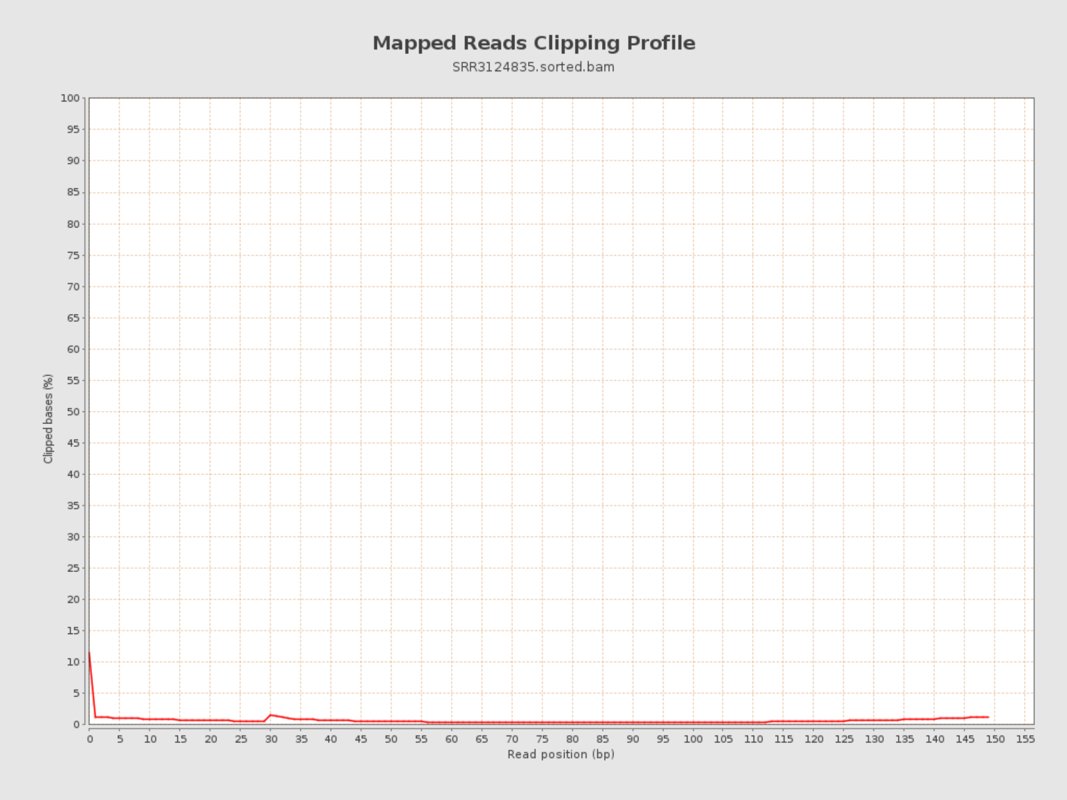
8. Results : Mapped Reads Nucleotide Content



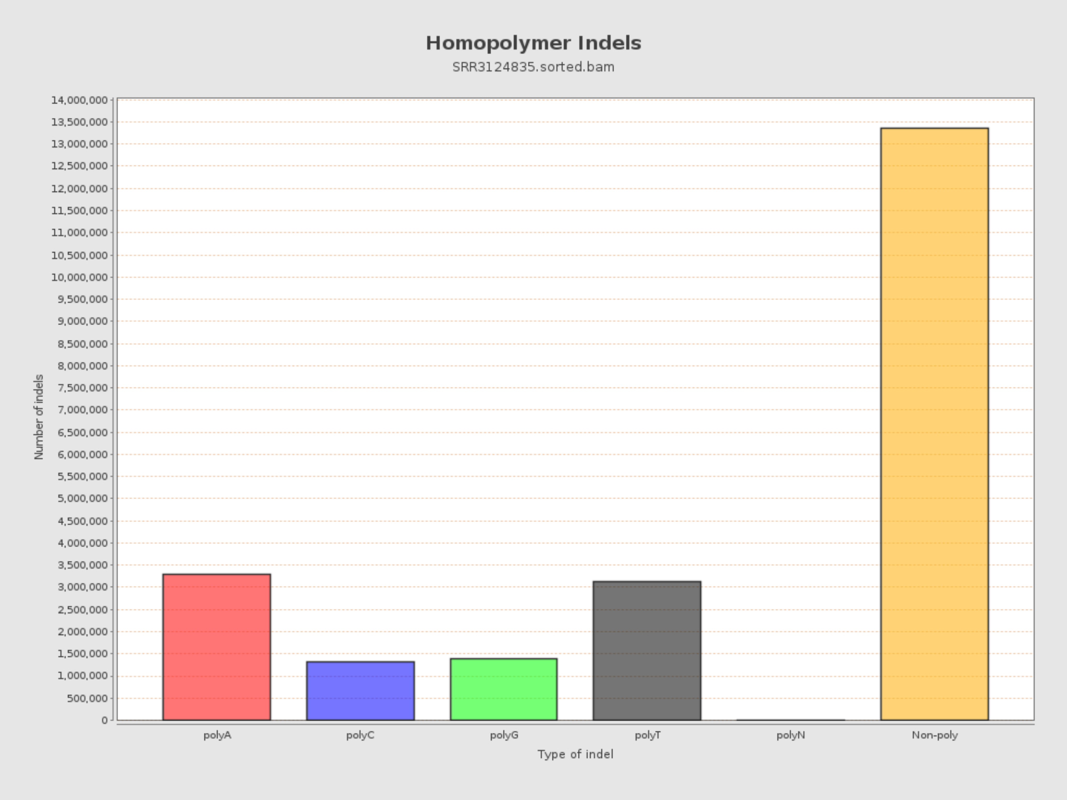
9. Results : Mapped Reads GC-content Distribution



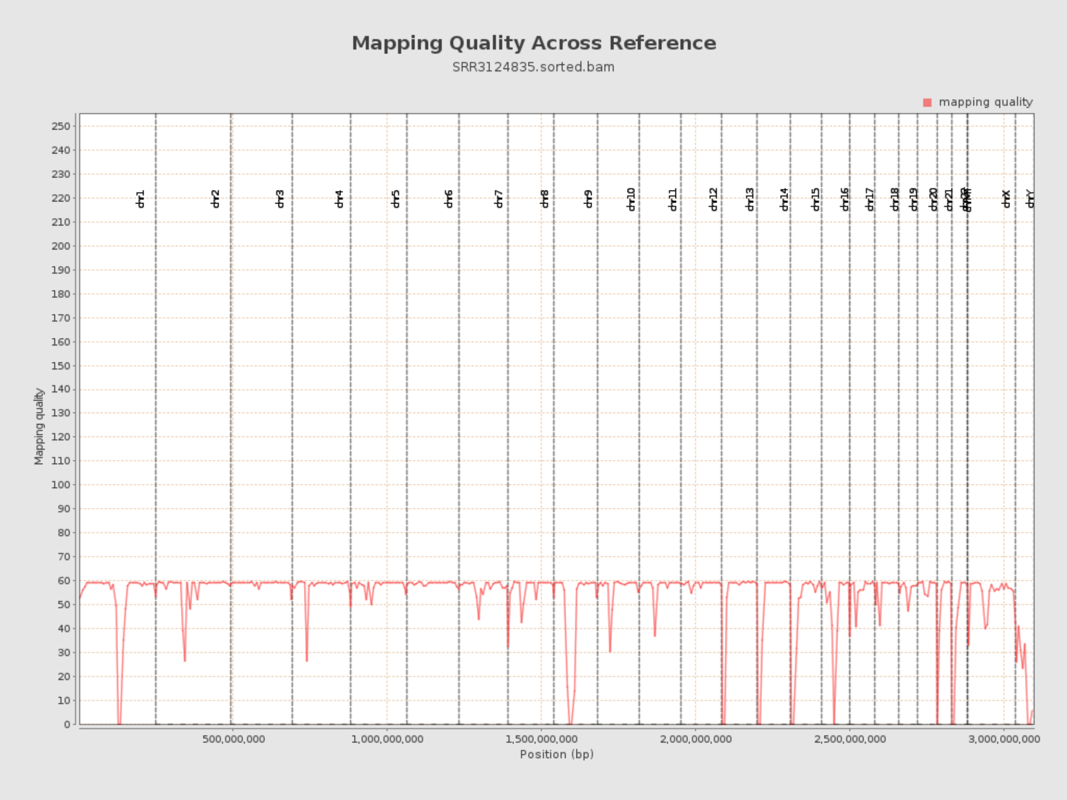
10. Results : Mapped Reads Clipping Profile



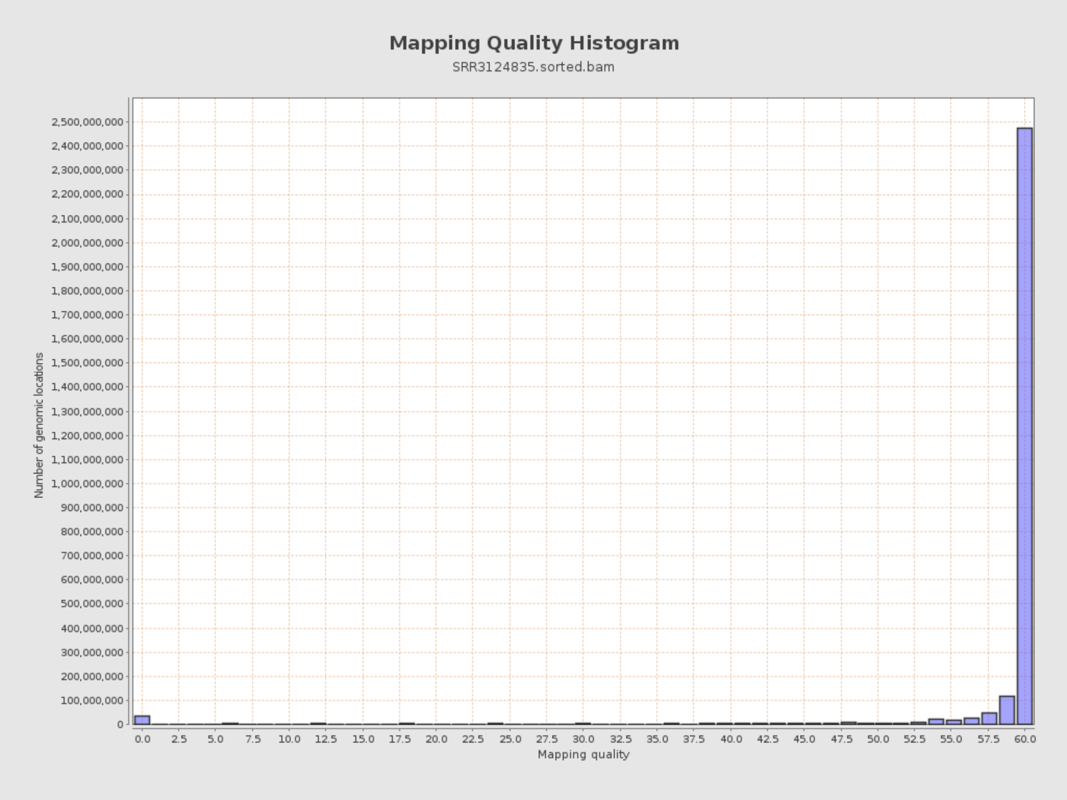
11. Results : Homopolymer Indels



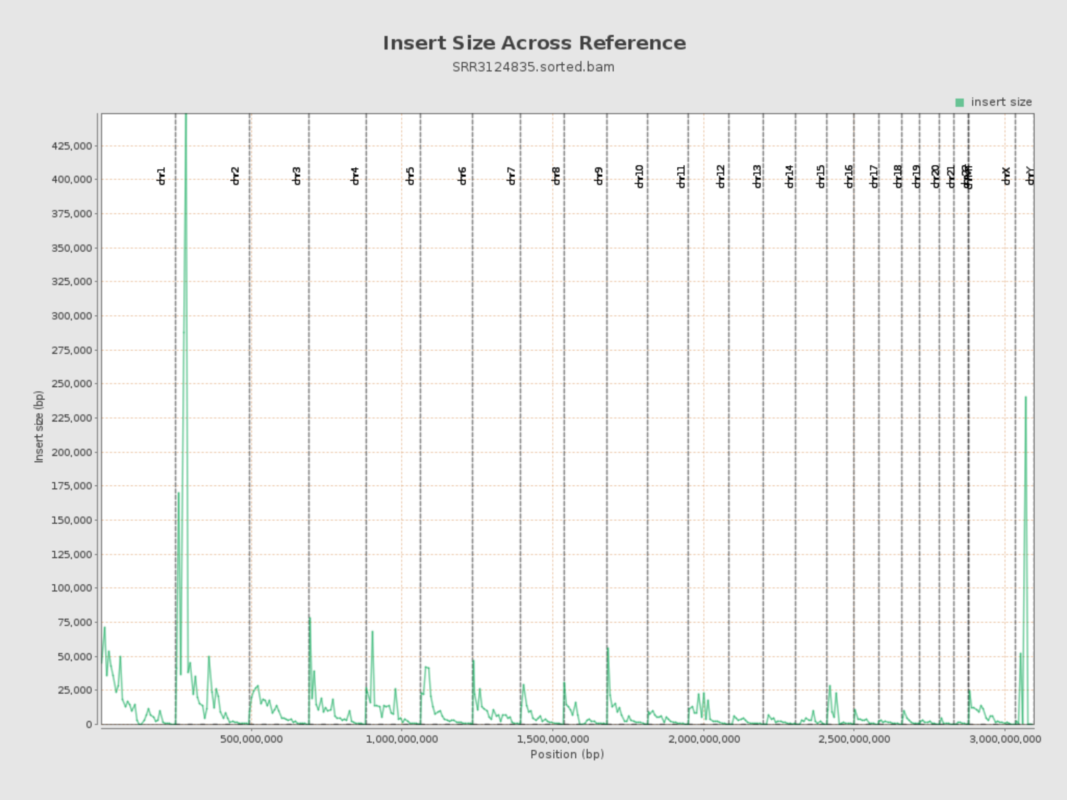
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram