Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 22:16:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124817.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_SRR3124817 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124817_1.fastq.gz SRR3124817_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 22:16:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124817.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,143,050
Mapped reads	27,884,201 / 99.08%
Unmapped reads	258,849 / 0.92%
Mapped paired reads	27,884,201 / 99.08%
Mapped reads, first in pair	13,967,605 / 49.63%
Mapped reads, second in pair	13,916,596 / 49.45%
Mapped reads, both in pair	27,789,924 / 98.75%
Mapped reads, singletons	94,277 / 0.33%
Secondary alignments	0
Supplementary alignments	81,487 / 0.29%
Read min/max/mean length	30 / 101 / 101.11
Duplicated reads (estimated)	4,790,923 / 17.02%
Duplication rate	11.7%
Clipped reads	13,007,235 / 46.22%

2.2. ACGT Content

Number/percentage of A's	678,099,186 / 27.92%
Number/percentage of C's	457,148,792 / 18.82%
Number/percentage of T's	716,201,394 / 29.49%
Number/percentage of G's	577,514,499 / 23.78%
Number/percentage of N's	22,450 / 0%

GC Percentage	42.6%

2.3. Coverage

Mean	0.785
Standard Deviation	5.7207

2.4. Mapping Quality

Mean Mapping Quality	53.1

2.5. Insert size

Mean	27,517.36
Standard Deviation	1,568,897.74
P25/Median/P75	154 / 206 / 282

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	17,489,592
Insertions	306,490
Mapped reads with at least one insertion	1.08%
Deletions	754,624
Mapped reads with at least one deletion	2.66%
Homopolymer indels	48.81%

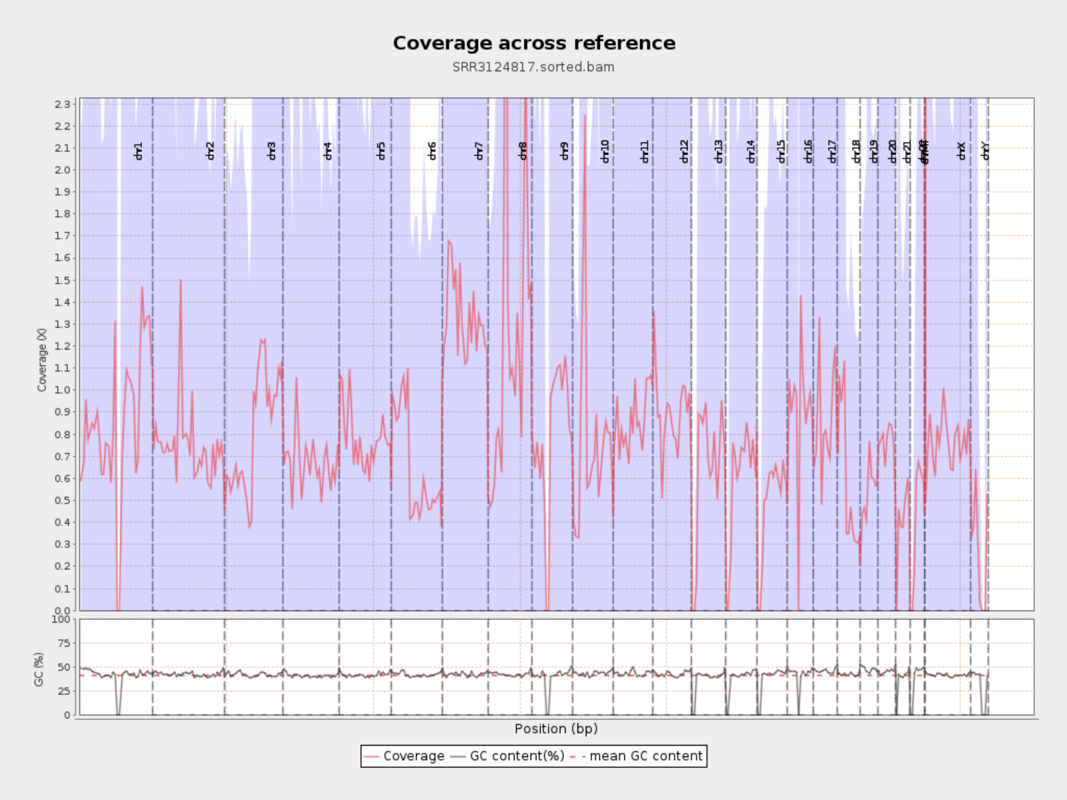
2.7. Chromosome stats

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

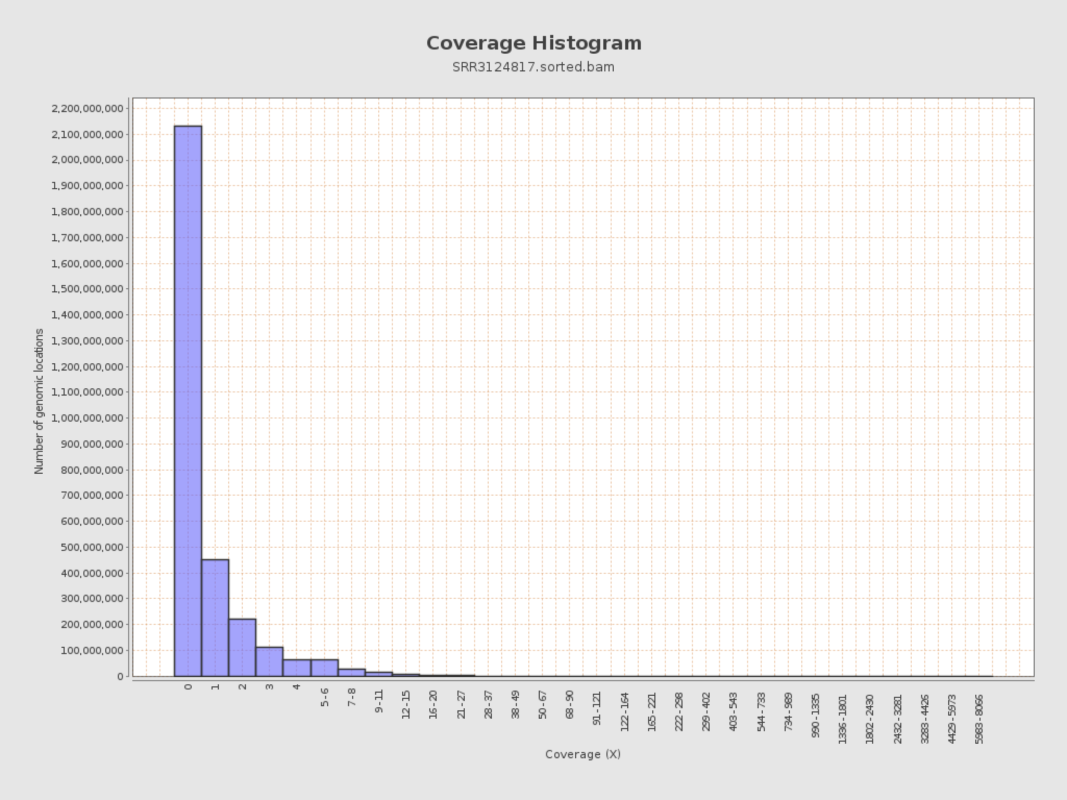
		bases	coverage	deviation
chr1	249250621	214000791	0.8586	8.0822
chr2	243199373	183755030	0.7556	5.7389
chr3	198022430	160283962	0.8094	1.7661
chr4	191154276	127764360	0.6684	3.4627
chr5	180915260	141612350	0.7828	1.7597
chr6	171115067	111672817	0.6526	3.5525
chr7	159138663	211102913	1.3265	10.6038
chr8	146364022	187311624	1.2798	4.0224
chr9	141213431	110659866	0.7836	6.8417
chr10	135534747	107943758	0.7964	12.4071
chr11	135006516	115419199	0.8549	4.1149
chr12	133851895	120414411	0.8996	1.9064
chr13	115169878	74406836	0.6461	1.5343
chr14	107349540	63332721	0.59	1.7692
chr15	102531392	49270022	0.4805	1.3637
chr16	90354753	80672728	0.8928	6.1509
chr17	81195210	68622036	0.8451	10.21
chr18	78077248	45111851	0.5778	6.9376
chr19	59128983	31585463	0.5342	4.6801
chr20	63025520	48293395	0.7663	1.9332
chr21	48129895	20253277	0.4208	1.9235
chr22	51304566	21388719	0.4169	1.3319
chrMT	16571	813958	49.1194	30.6429
chrX	155270560	118043878	0.7602	2.856

chrY	59373566	16479010	0.2775	4.4568

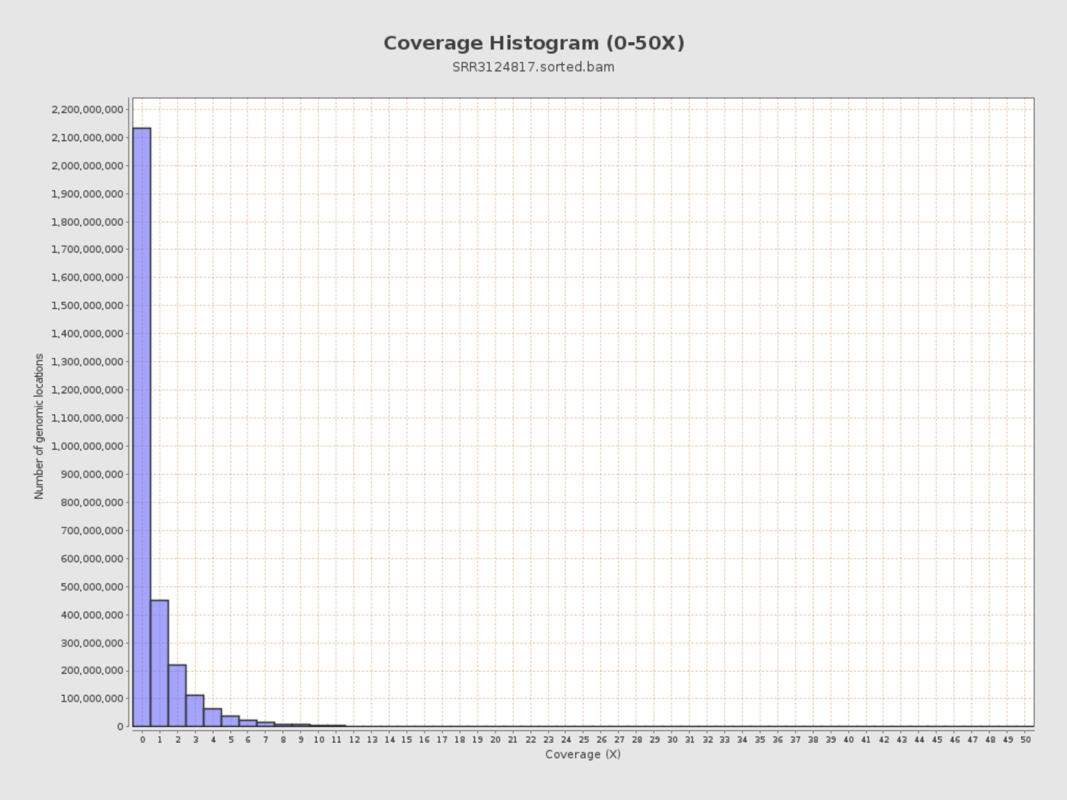
3. Results : Coverage across reference



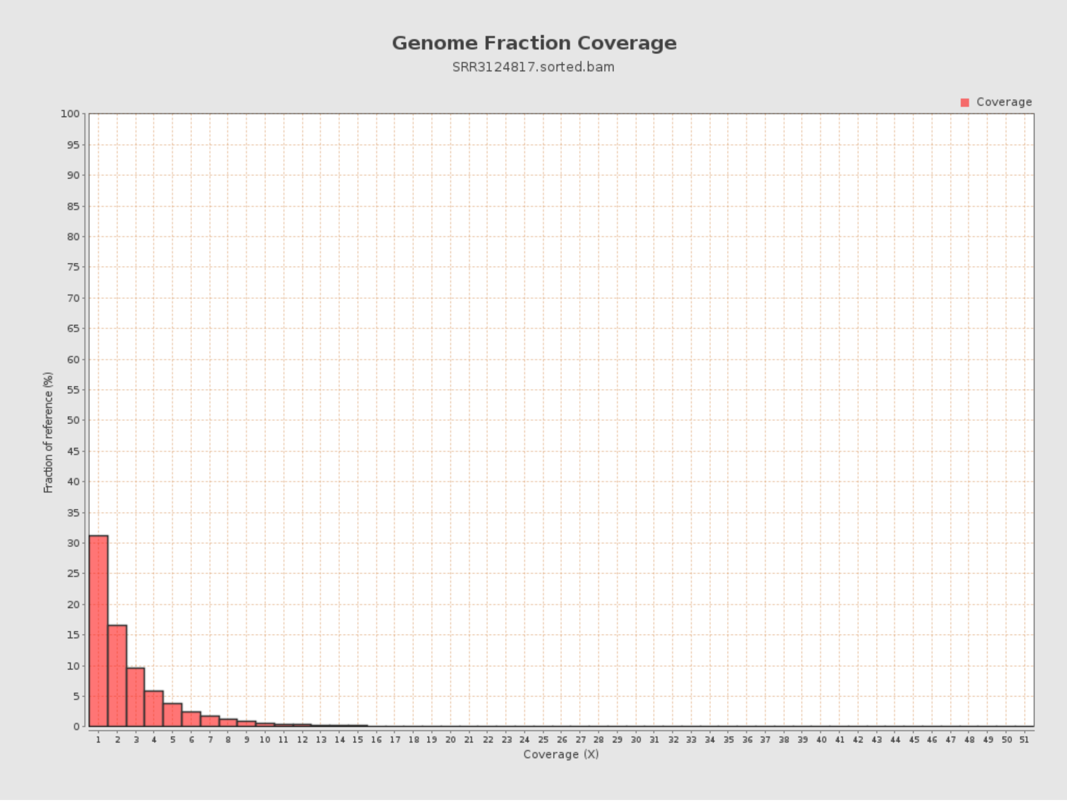
4. Results : Coverage Histogram



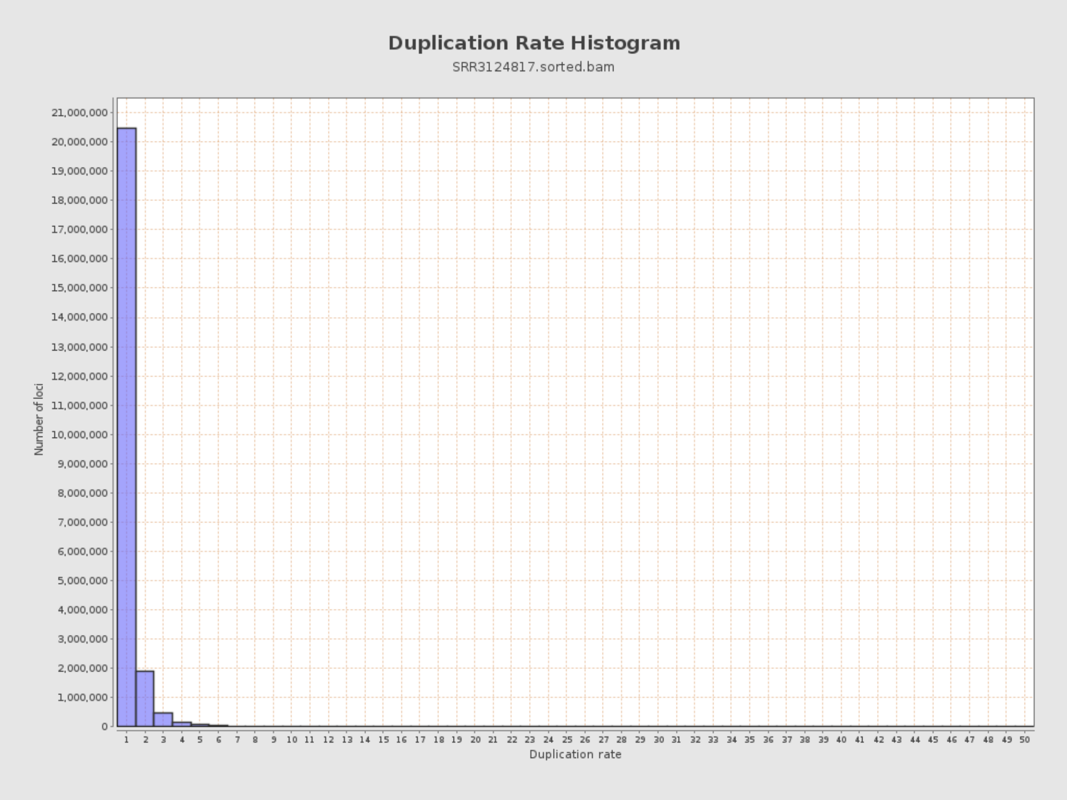
5. Results : Coverage Histogram (0-50X)



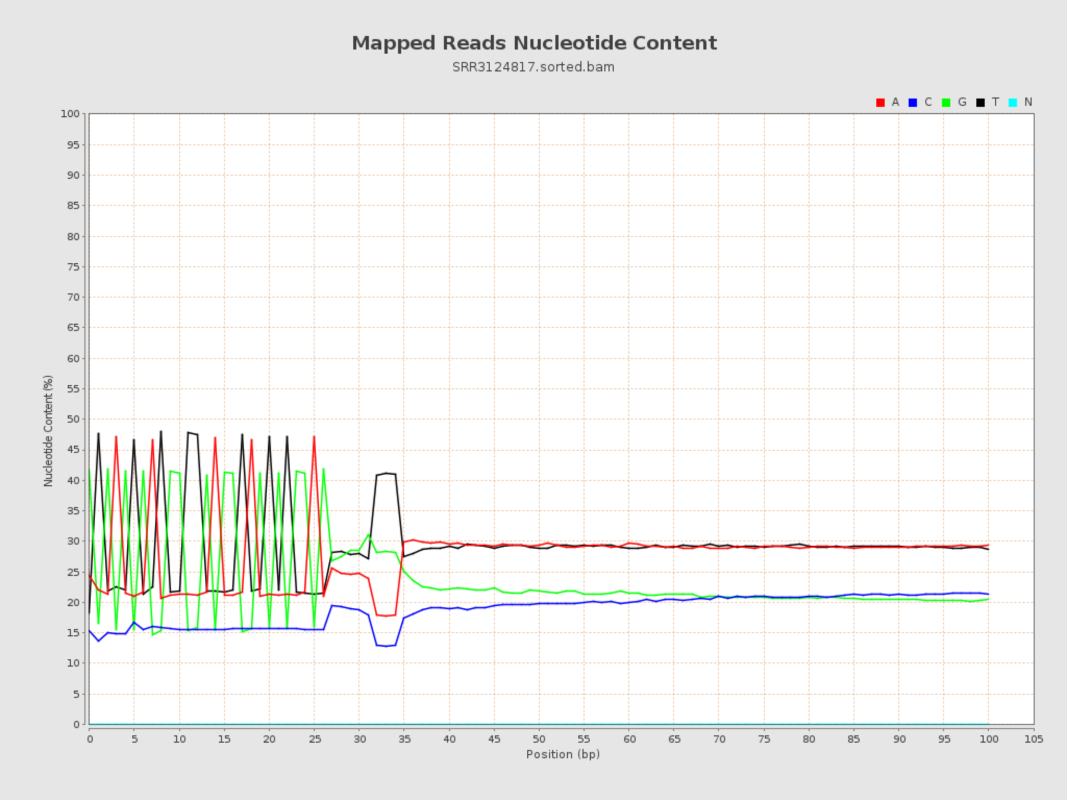
6. Results : Genome Fraction Coverage



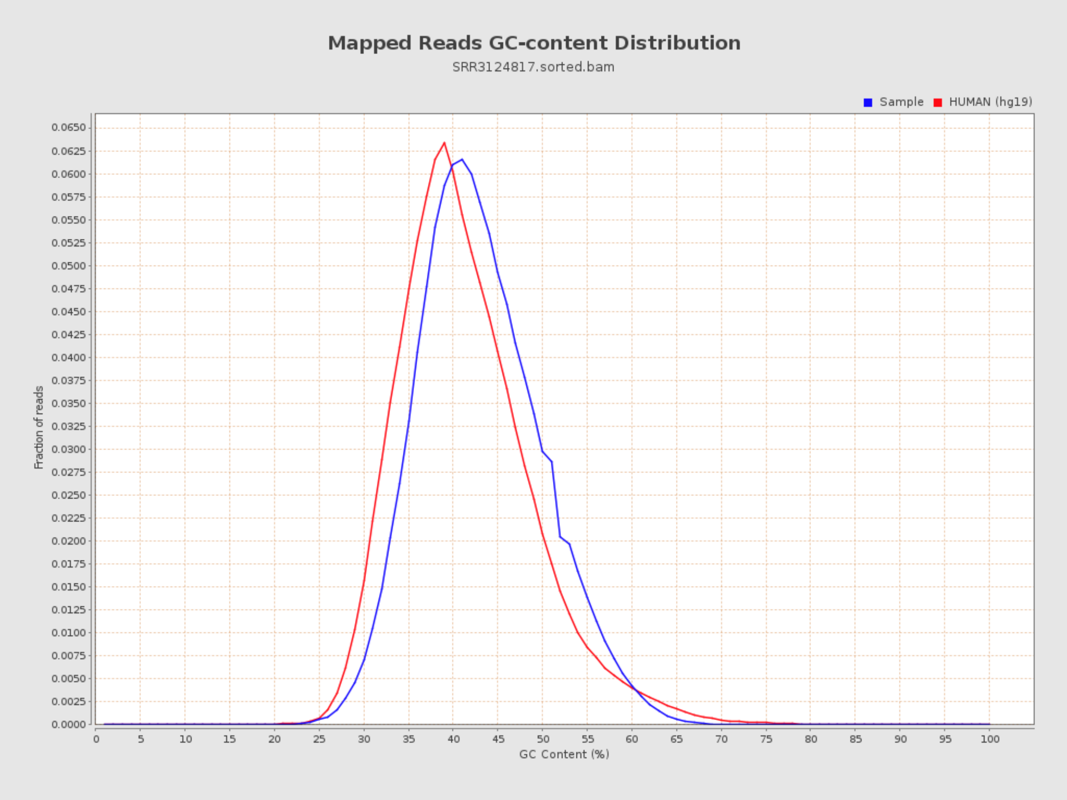
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

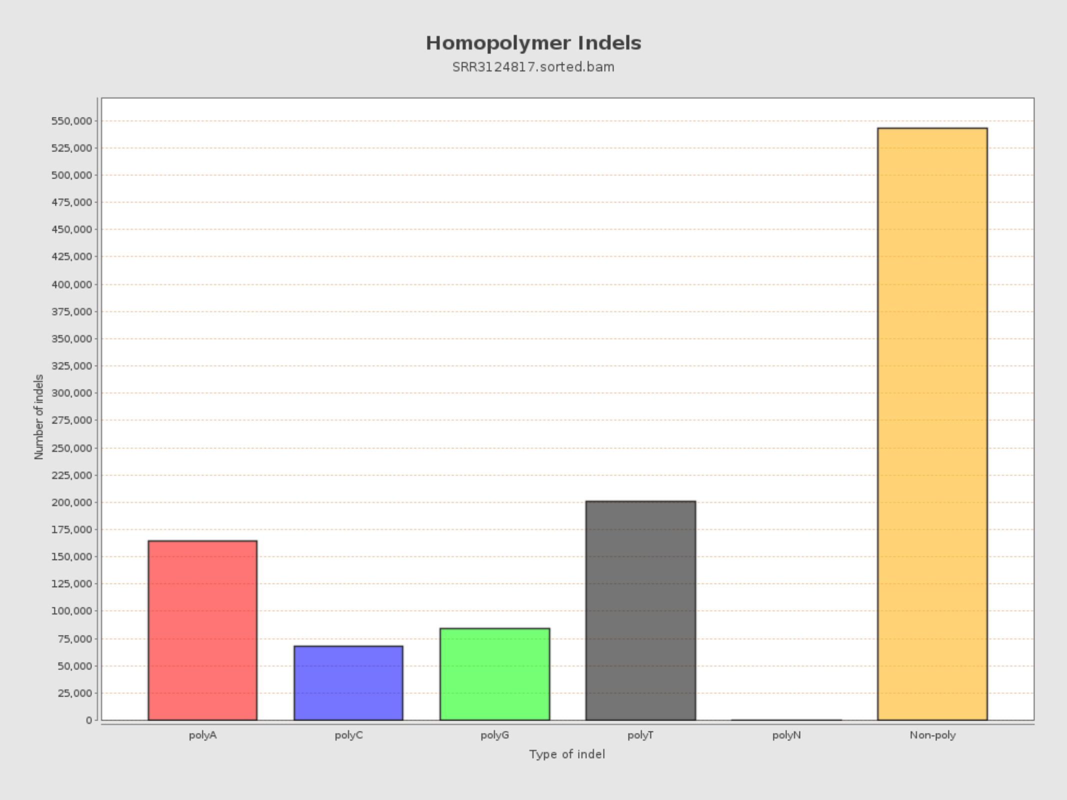


9. Results : Mapped Reads GC-content Distribution

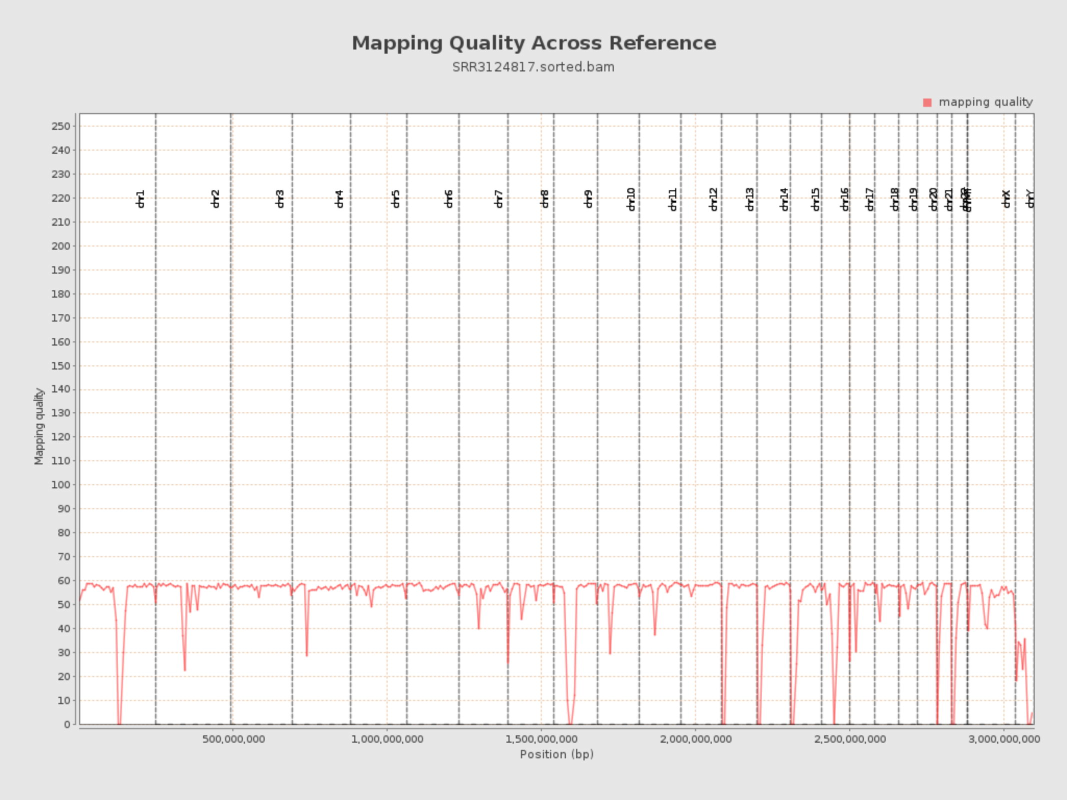


10. Results : Mapped Reads Clipping Profile

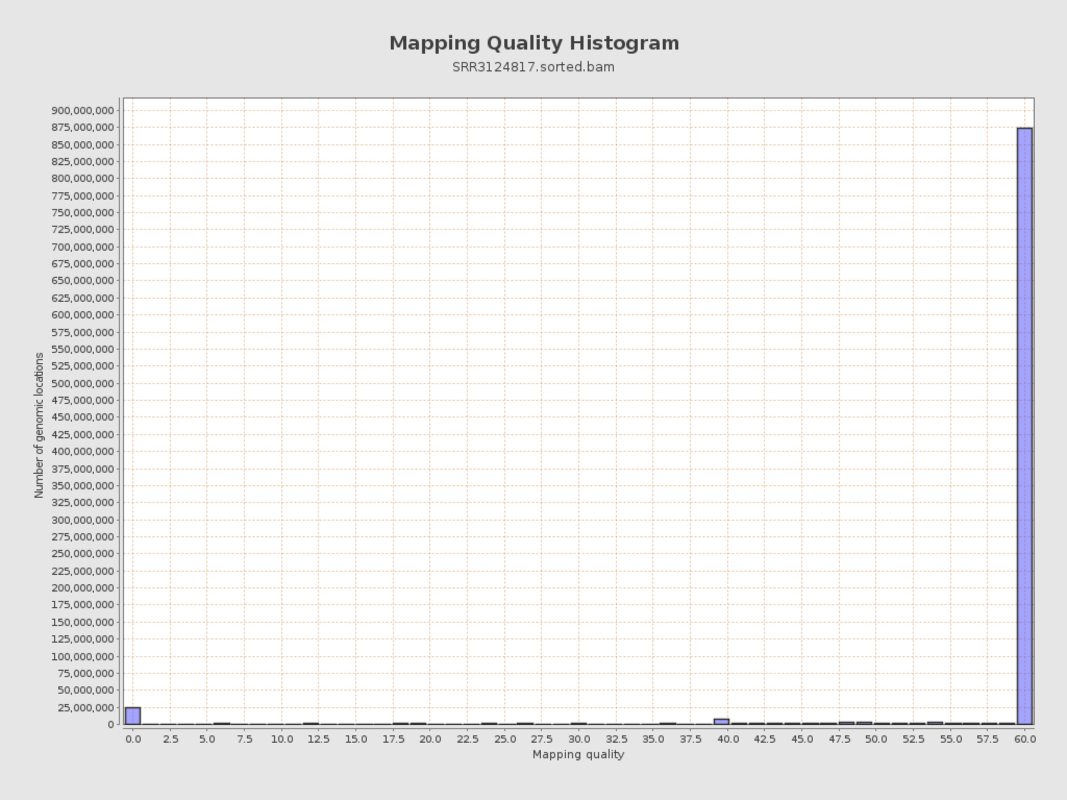
11. Results : Homopolymer Indels



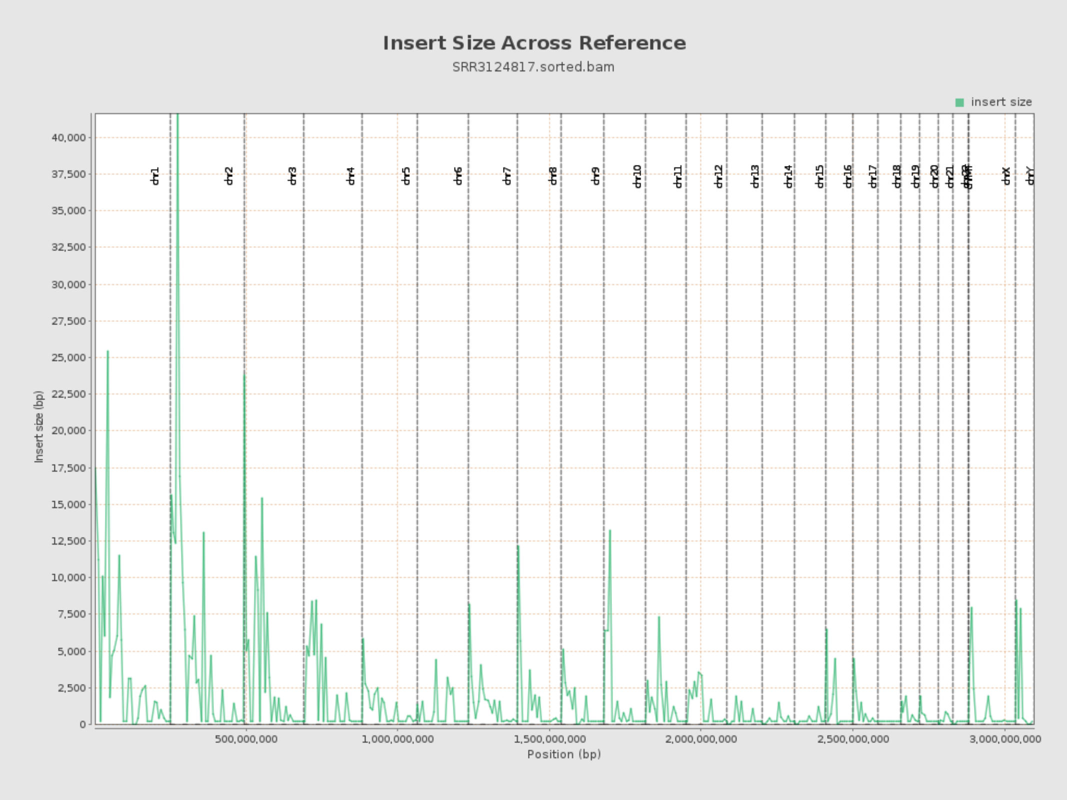
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram