Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 21:44:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124816.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_SRR3124816 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124816_1.fastq.gz SRR3124816_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 21:44:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124816.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,898,334
Mapped reads	22,402,100 / 97.83%
Unmapped reads	496,234 / 2.17%
Mapped paired reads	22,402,100 / 97.83%
Mapped reads, first in pair	11,289,053 / 49.3%
Mapped reads, second in pair	11,113,047 / 48.53%
Mapped reads, both in pair	22,138,376 / 96.68%
Mapped reads, singletons	263,724 / 1.15%
Secondary alignments	0
Supplementary alignments	96,693 / 0.42%
Read min/max/mean length	30 / 101 / 91.98
Duplicated reads (estimated)	2,613,421 / 11.41%
Duplication rate	6.5%
Clipped reads	12,756,428 / 55.71%

2.2. ACGT Content

Number/percentage of A's	515,250,150 / 28.61%
Number/percentage of C's	341,068,353 / 18.94%
Number/percentage of T's	542,067,236 / 30.1%
Number/percentage of G's	402,301,888 / 22.34%
Number/percentage of N's	12,788 / 0%

GC Percentage	41.28%

2.3. Coverage

Mean	0.582
Standard Deviation	6.3382

2.4. Mapping Quality

Mean Mapping Quality	52.1

2.5. Insert size

Mean	79,656.15
Standard Deviation	2,706,149.93
P25/Median/P75	137 / 174 / 226

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	13,915,160
Insertions	280,984
Mapped reads with at least one insertion	1.23%
Deletions	586,367
Mapped reads with at least one deletion	2.57%
Homopolymer indels	46.97%

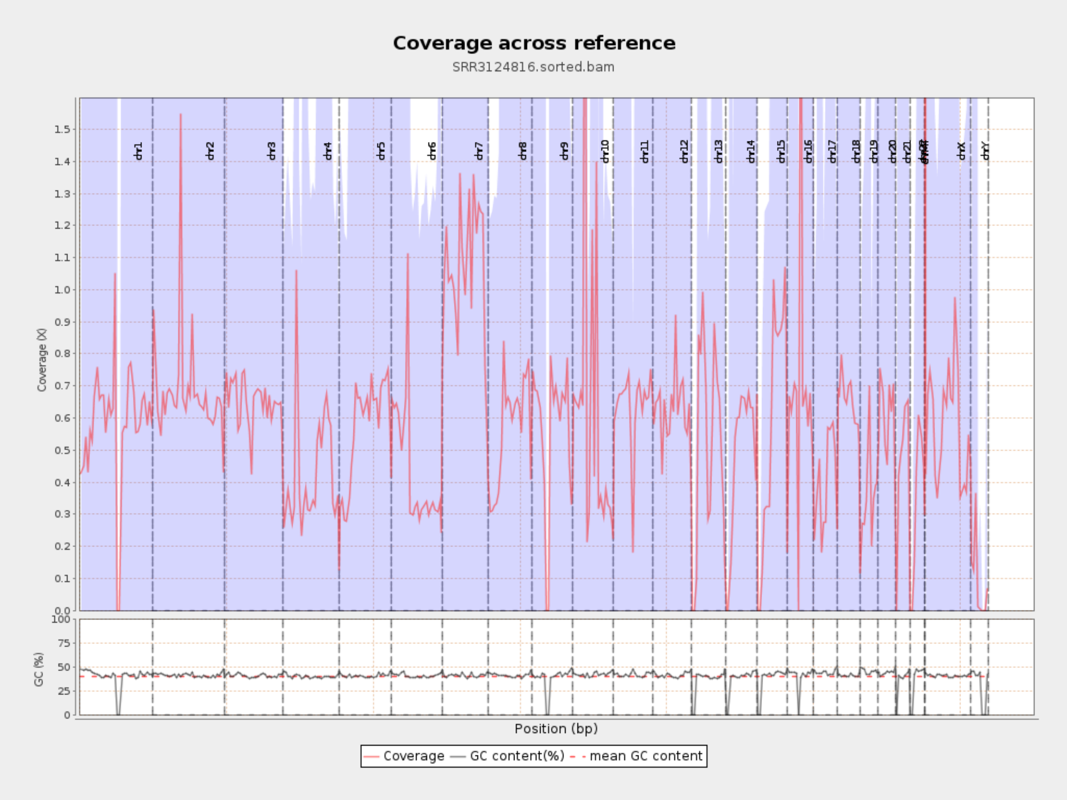
2.7. Chromosome stats

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

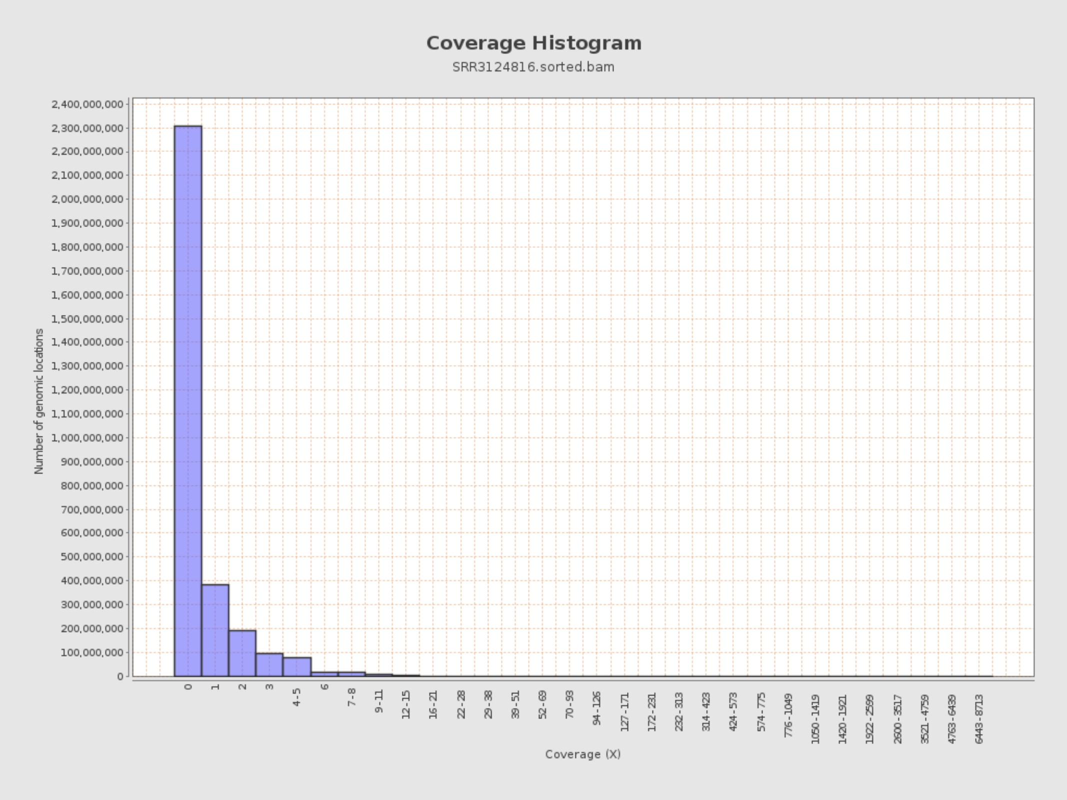
		bases	coverage	deviation
chr1	249250621	145172251	0.5824	7.8262
chr2	243199373	167800677	0.69	6.363
chr3	198022430	129026642	0.6516	1.689
chr4	191154276	81545884	0.4266	4.0042
chr5	180915260	103028304	0.5695	1.3772
chr6	171115067	75463407	0.441	5.654
chr7	159138663	169868807	1.0674	10.0057
chr8	146364022	82545800	0.564	2.2862
chr9	141213431	78025172	0.5525	7.3258
chr10	135534747	89633773	0.6613	17.0555
chr11	135006516	84475619	0.6257	4.3008
chr12	133851895	84004746	0.6276	1.4295
chr13	115169878	59584242	0.5174	1.2872
chr14	107349540	51168305	0.4767	1.6928
chr15	102531392	59286936	0.5782	1.5049
chr16	90354753	64358157	0.7123	11.6237
chr17	81195210	31698024	0.3904	3.4384
chr18	78077248	51357971	0.6578	8.2331
chr19	59128983	20688453	0.3499	4.5188
chr20	63025520	38208991	0.6062	1.7201
chr21	48129895	22883155	0.4754	2.0792
chr22	51304566	17551909	0.3421	1.1416
chrMT	16571	531477	32.0727	21.0649
chrX	155270560	88489297	0.5699	2.5198

chrY	59373566	5265021	0.0887	4.8322

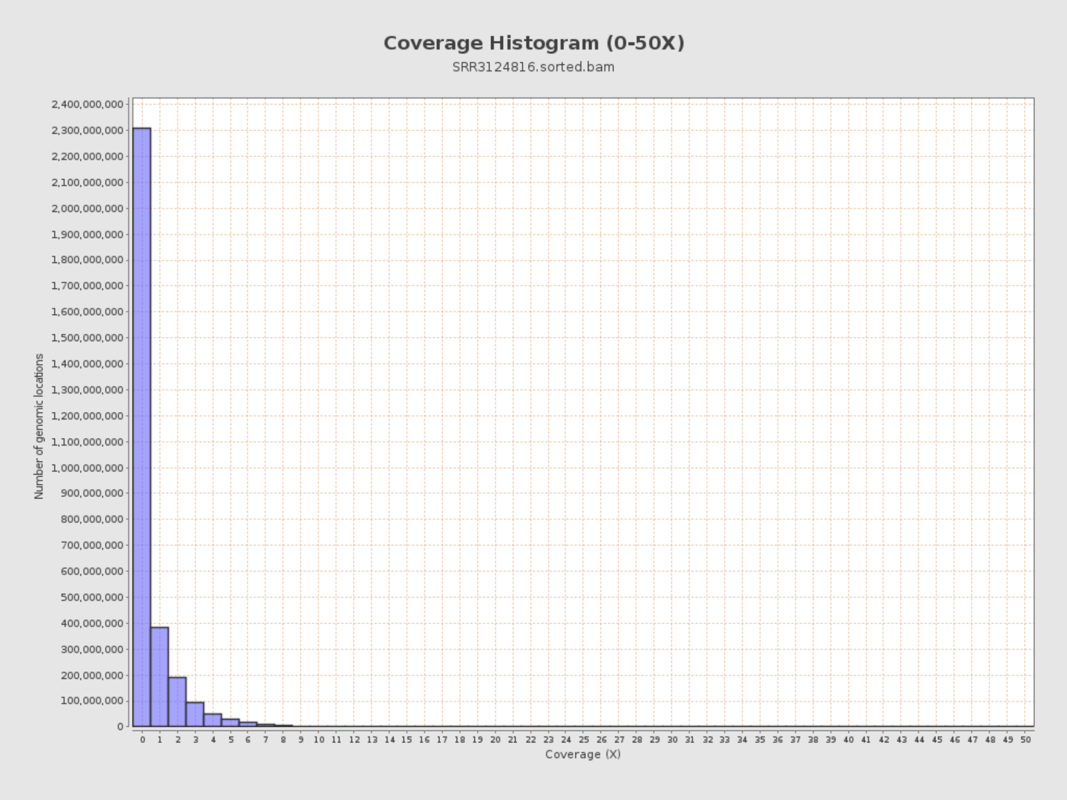
3. Results : Coverage across reference



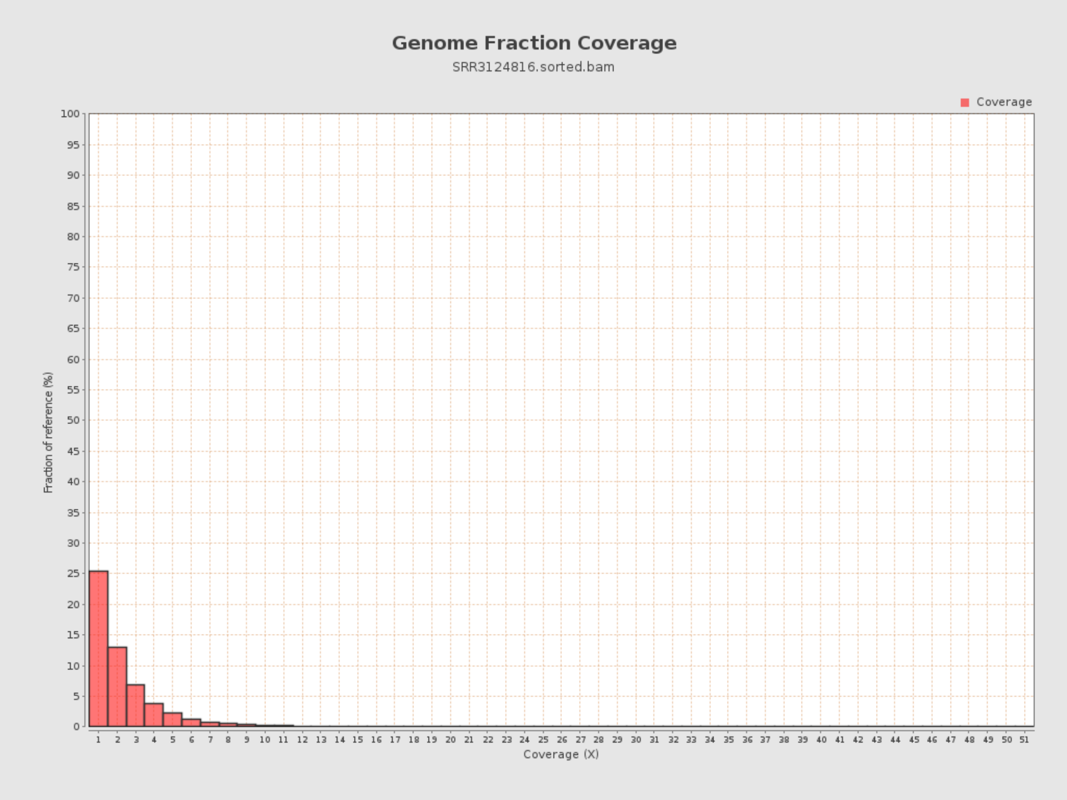
4. Results : Coverage Histogram



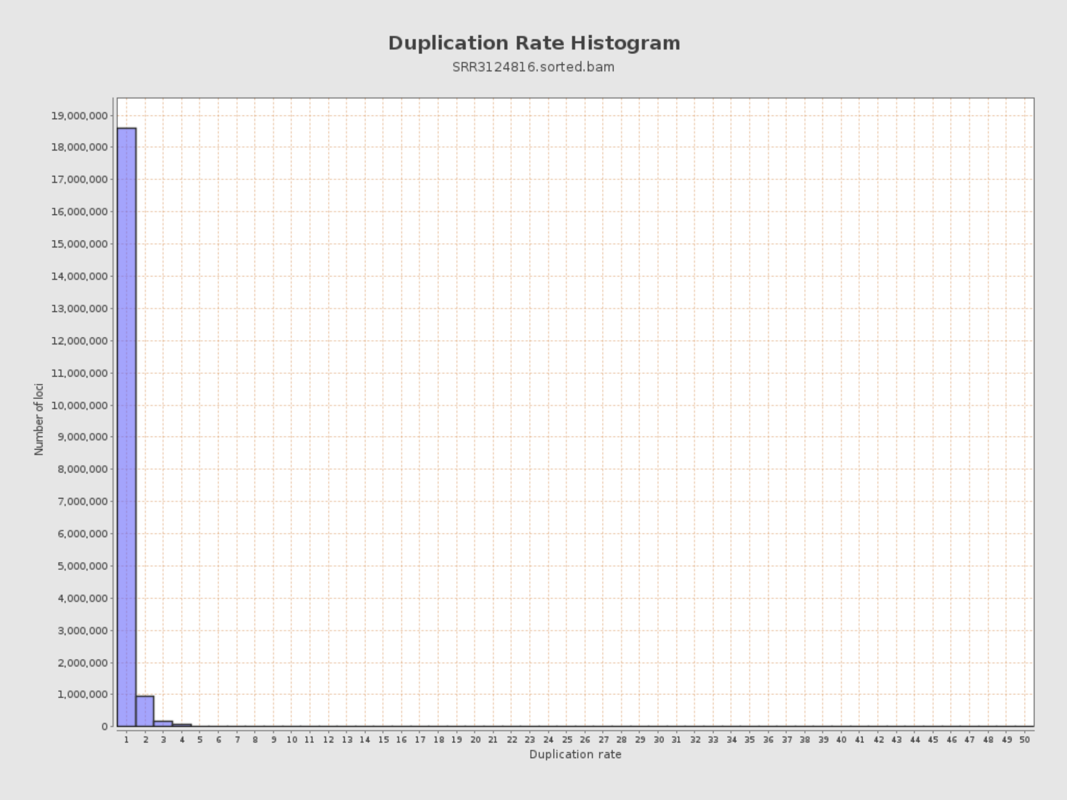
5. Results : Coverage Histogram (0-50X)



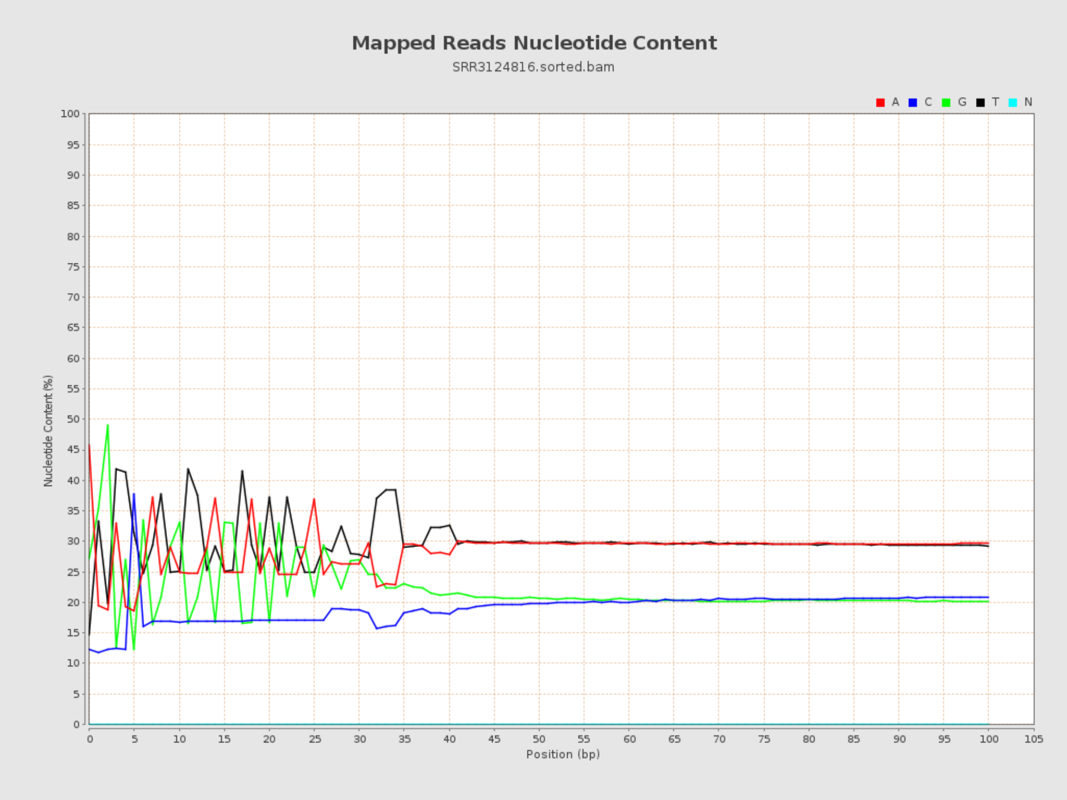
6. Results : Genome Fraction Coverage



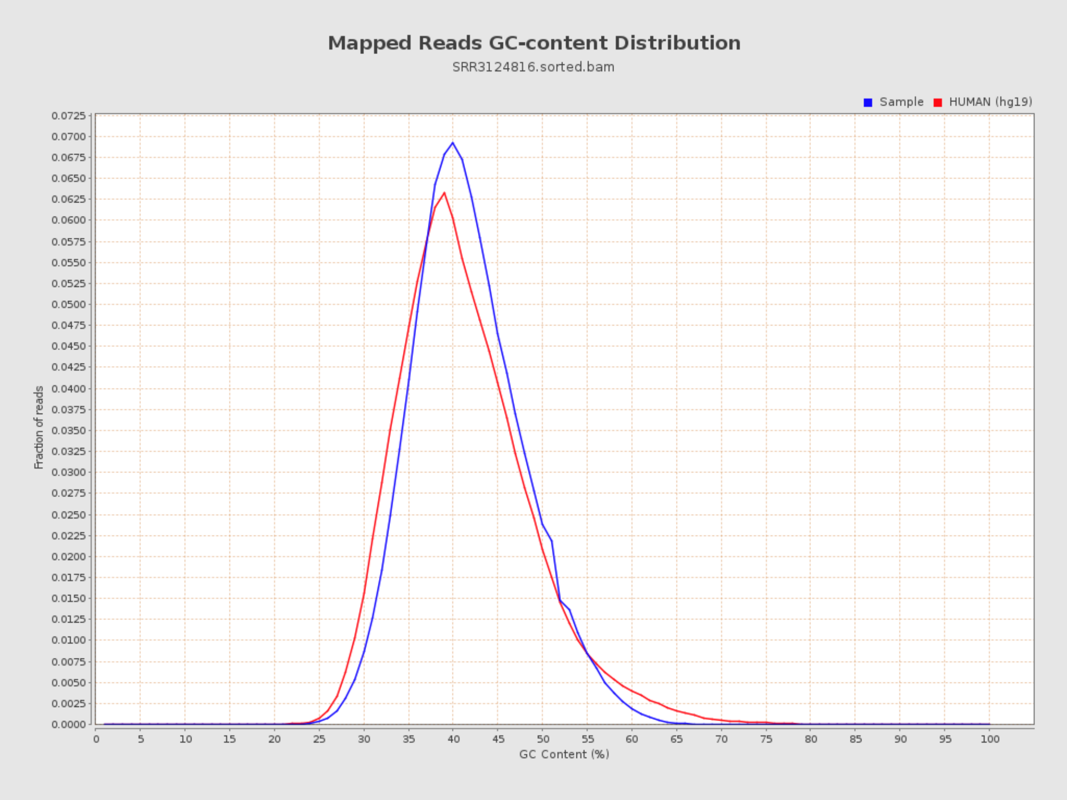
7. Results : Duplication Rate Histogram



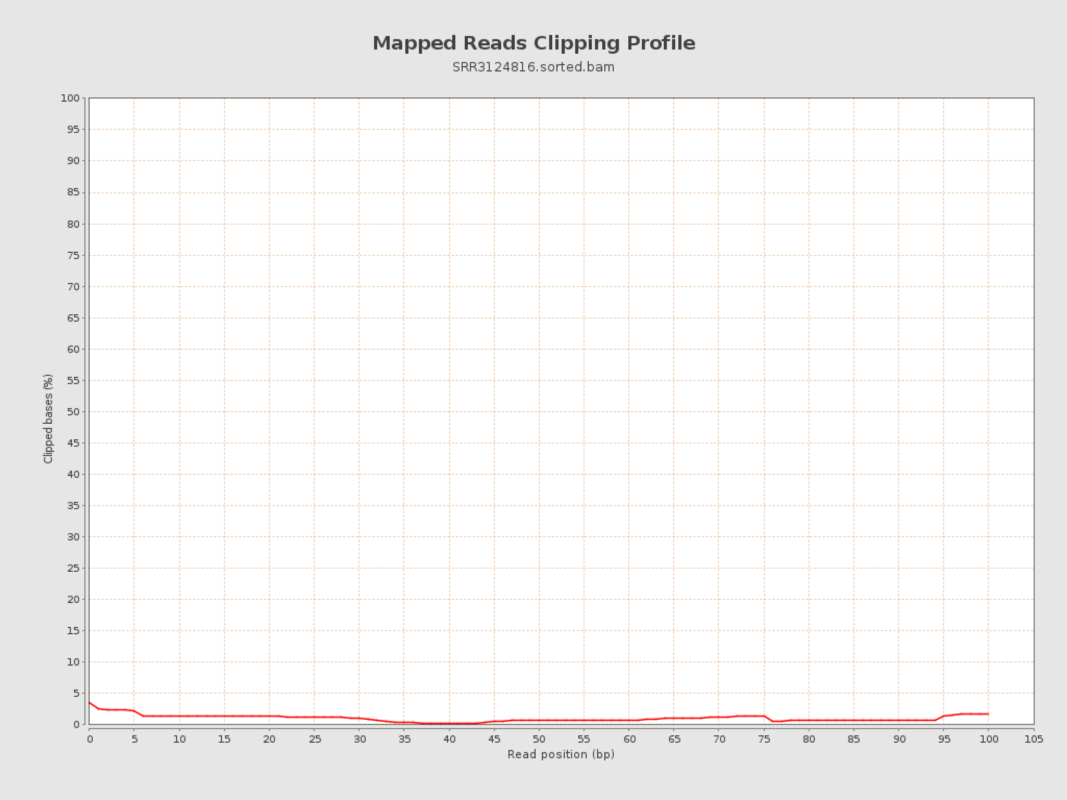
8. Results : Mapped Reads Nucleotide Content



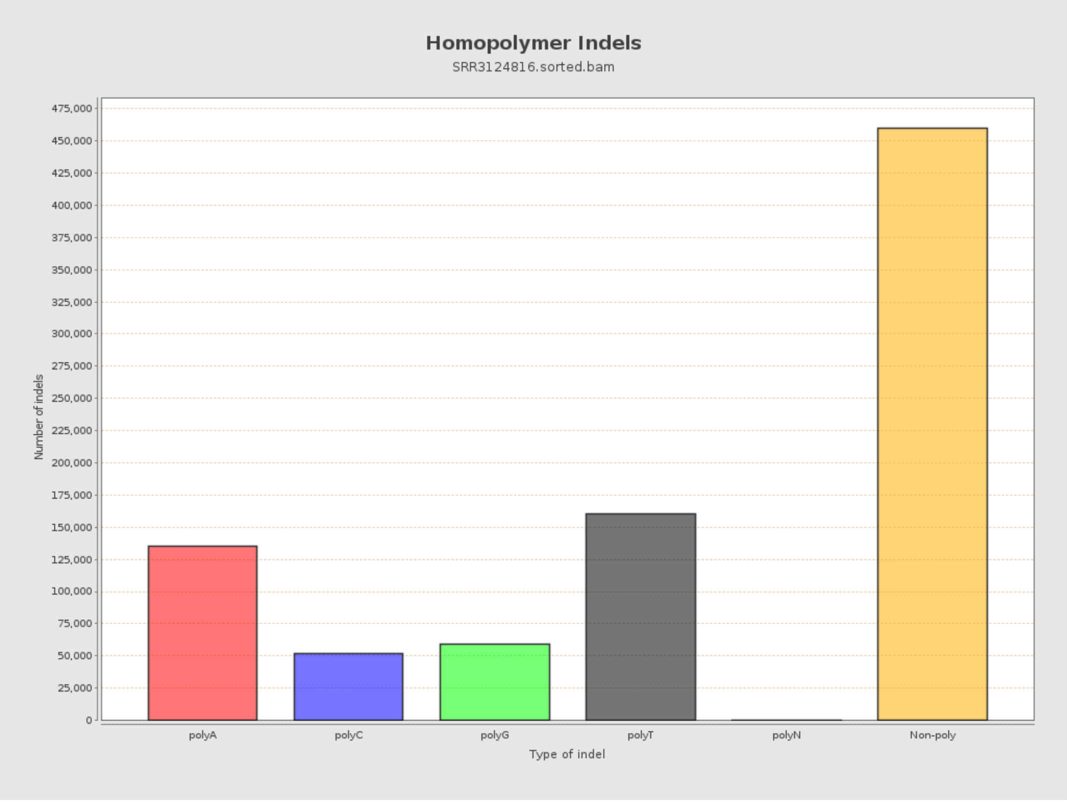
9. Results : Mapped Reads GC-content Distribution



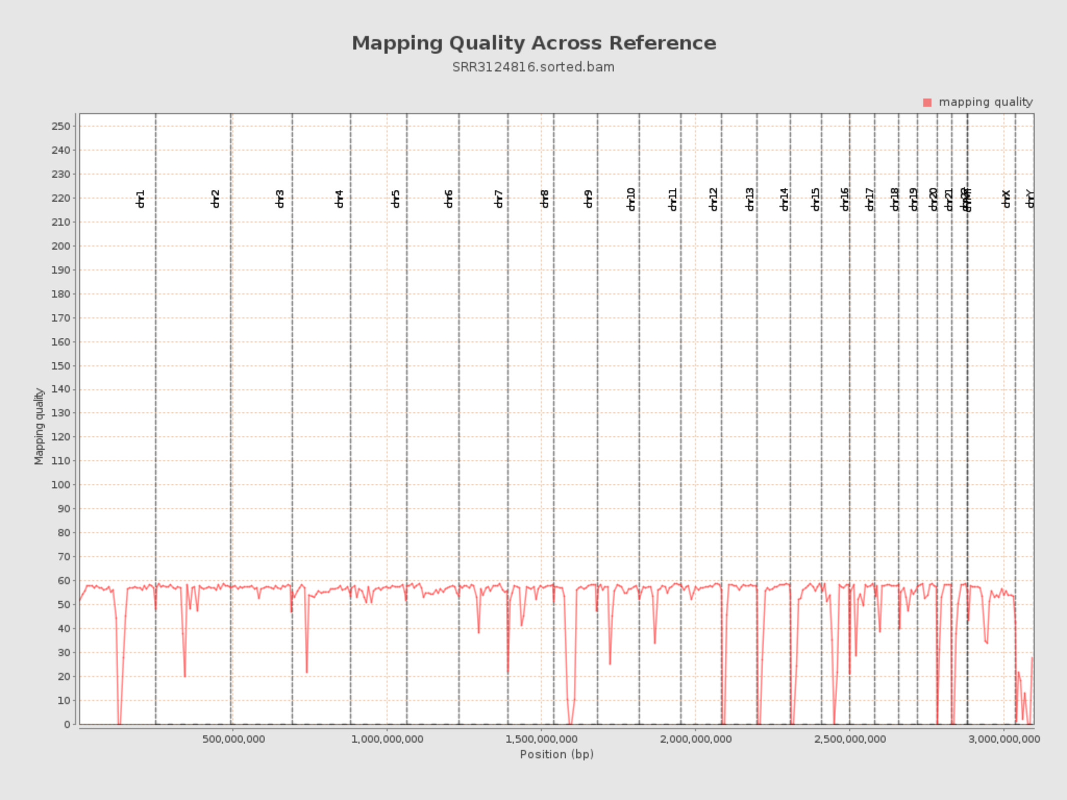
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



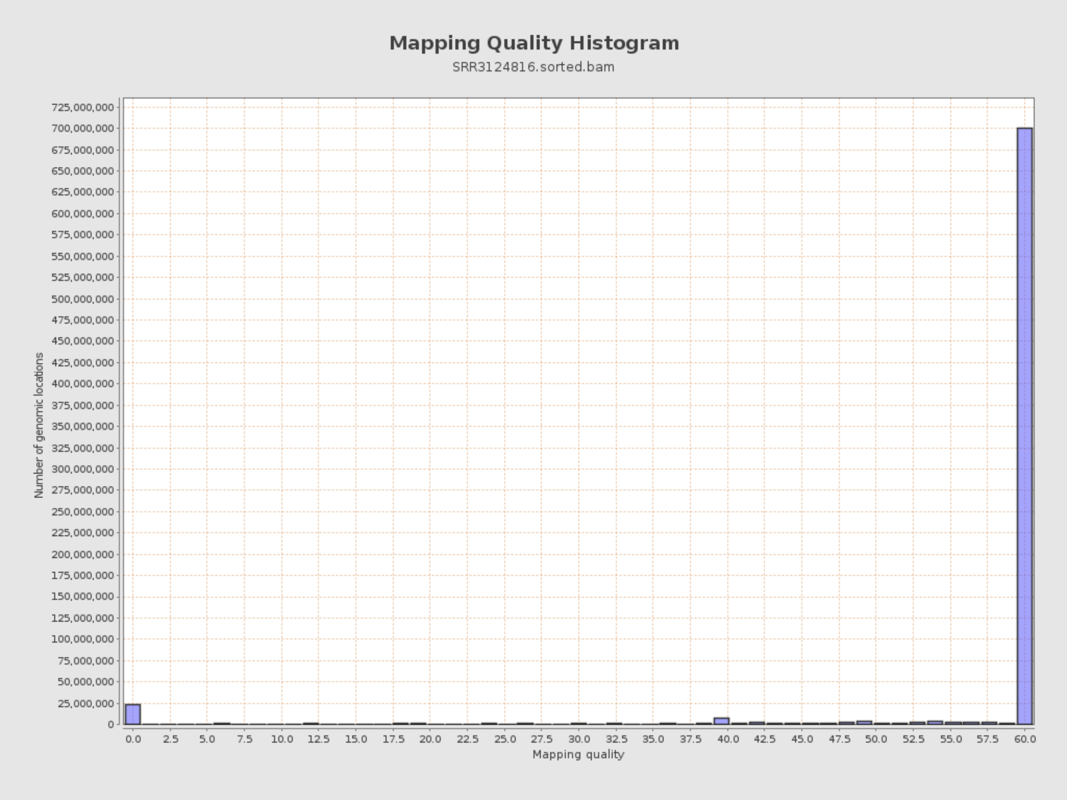
12. Results : Mapping Quality Across Reference



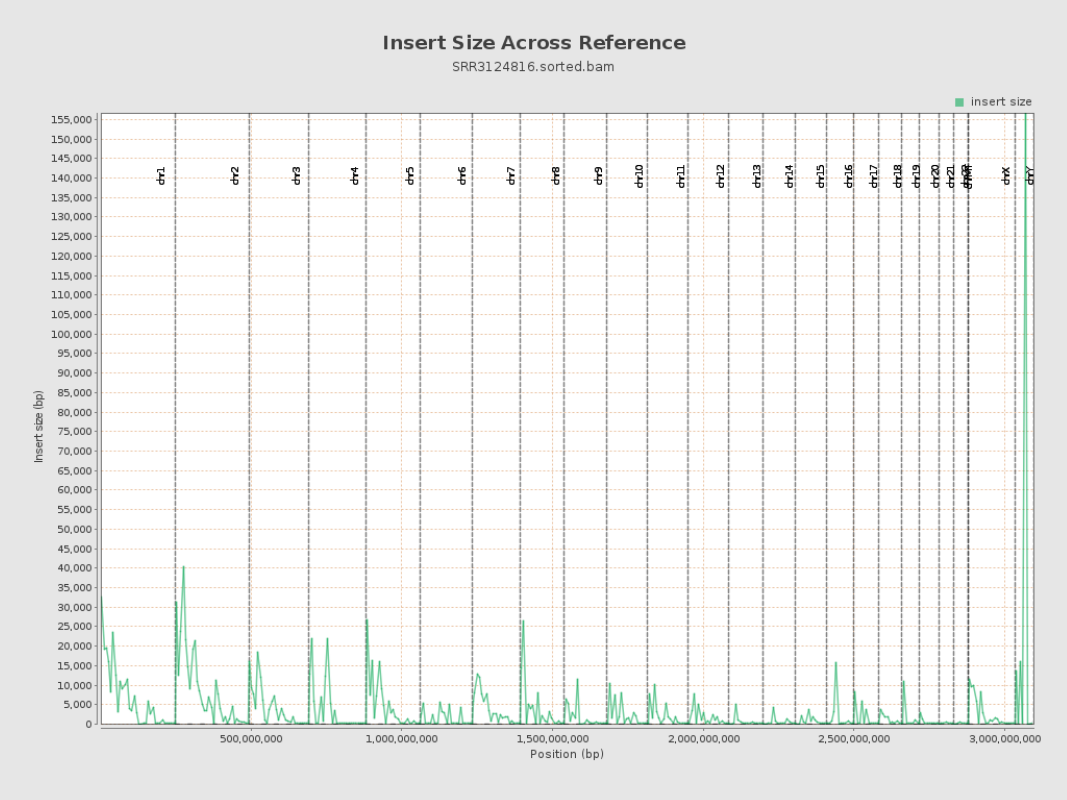
Mapping Quality Across Reference

SRR3124816.sorted.bam

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram