Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 03:54:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124826.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_SRR3124826 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124826_1.fastq.gz SRR3124826_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 03:54:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124826.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,363,196
Mapped reads	30,128,659 / 99.23%
Unmapped reads	234,537 / 0.77%
Mapped paired reads	30,128,659 / 99.23%
Mapped reads, first in pair	15,073,207 / 49.64%
Mapped reads, second in pair	15,055,452 / 49.58%
Mapped reads, both in pair	30,031,026 / 98.91%
Mapped reads, singletons	97,633 / 0.32%
Secondary alignments	0
Supplementary alignments	130,037 / 0.43%
Read min/max/mean length	30 / 101 / 101.17
Duplicated reads (estimated)	2,857,884 / 9.41%
Duplication rate	5.09%
Clipped reads	18,089,639 / 59.58%

2.2. ACGT Content

Number/percentage of A's	806,064,007 / 29.28%
Number/percentage of C's	550,450,093 / 20%
Number/percentage of T's	806,731,212 / 29.3%
Number/percentage of G's	589,630,584 / 21.42%
Number/percentage of N's	20,580 / 0%

GC Percentage	41.41%

2.3. Coverage

Mean	0.8898
Standard Deviation	8.6815

2.4. Mapping Quality

Mean Mapping Quality	52.52

2.5. Insert size

Mean	64,911.56
Standard Deviation	2,411,077.24
P25/Median/P75	137 / 171 / 218

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	19,684,058
Insertions	476,981
Mapped reads with at least one insertion	1.55%
Deletions	887,039
Mapped reads with at least one deletion	2.88%
Homopolymer indels	46.99%

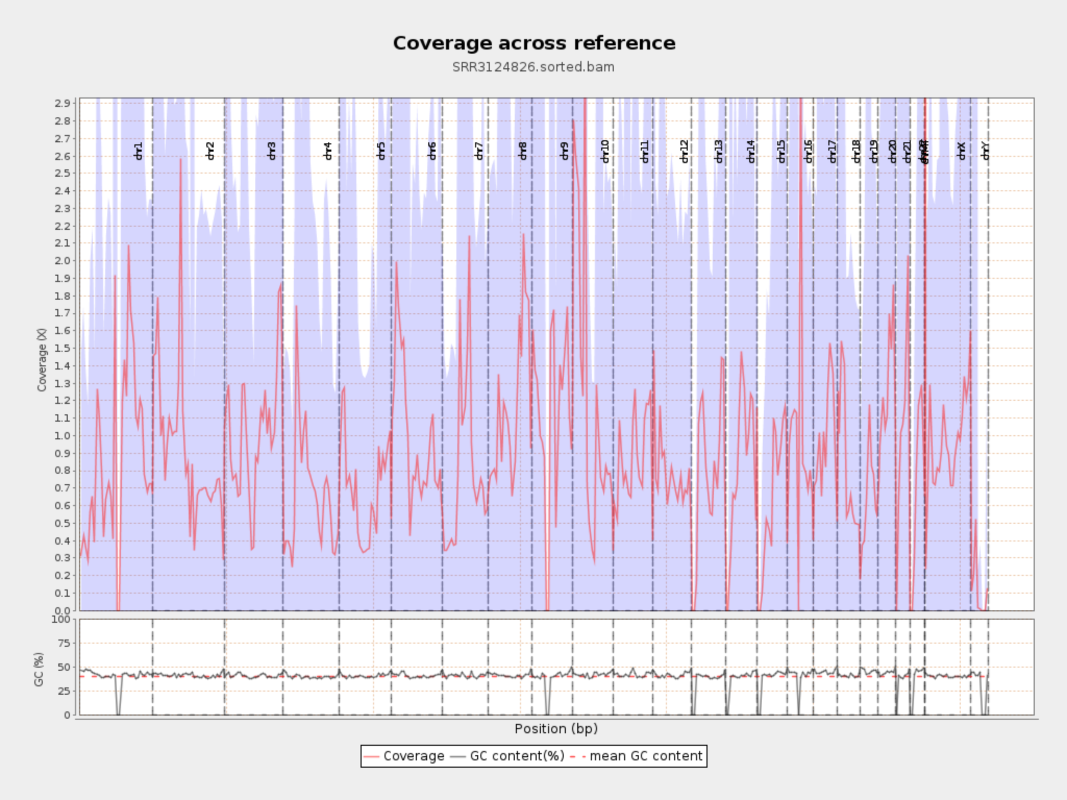
2.7. Chromosome stats

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

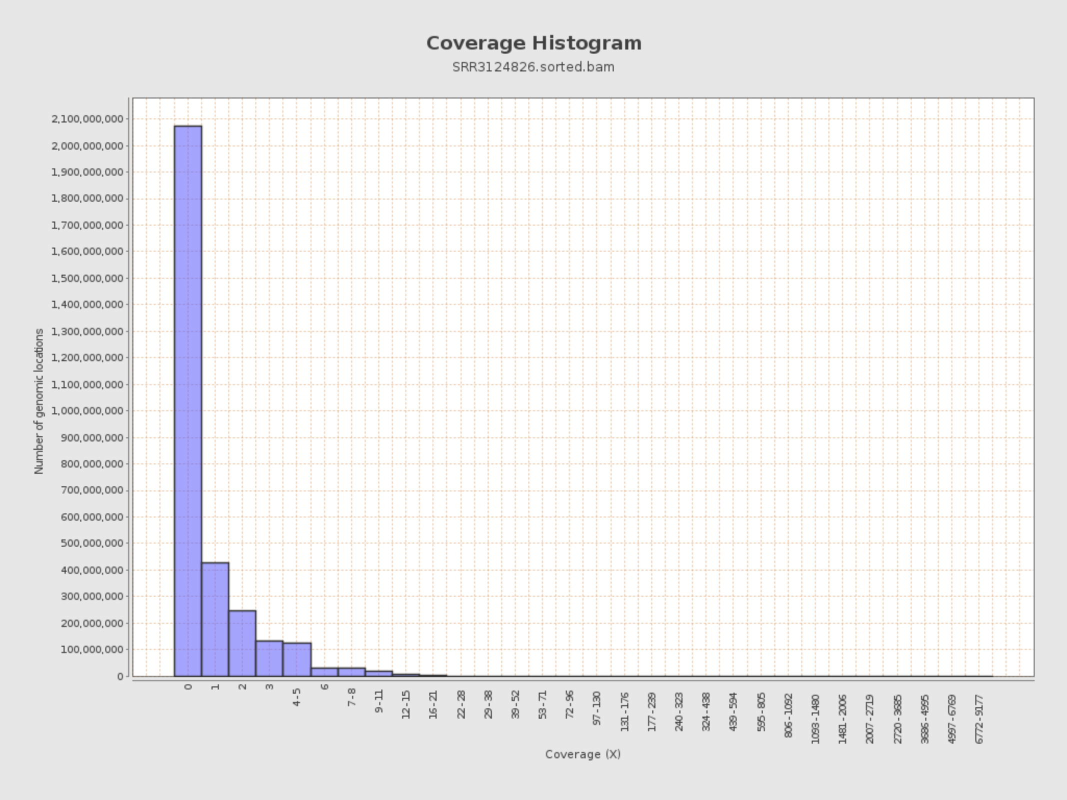
		bases	coverage	deviation
chr1	249250621	214478315	0.8605	8.723
chr2	243199373	224651190	0.9237	10.2954
chr3	198022430	203109595	1.0257	2.2145
chr4	191154276	125436723	0.6562	8.4158
chr5	180915260	126661160	0.7001	1.7445
chr6	171115067	172215503	1.0064	4.4629
chr7	159138663	127795483	0.803	15.6348
chr8	146364022	171391634	1.171	3.84
chr9	141213431	155952711	1.1044	12.7058
chr10	135534747	170401823	1.2573	20.4061
chr11	135006516	120261844	0.8908	3.5368
chr12	133851895	106187974	0.7933	1.7358
chr13	115169878	92067105	0.7994	1.7234
chr14	107349540	87219461	0.8125	2.3481
chr15	102531392	64164143	0.6258	1.5576
chr16	90354753	89914652	0.9951	14.895
chr17	81195210	79659660	0.9811	7.0077
chr18	78077248	63154322	0.8089	13.1058
chr19	59128983	38489513	0.6509	5.0188
chr20	63025520	79850351	1.267	3.0977
chr21	48129895	50814589	1.0558	4.1112
chr22	51304566	35852740	0.6988	1.8199
chrMT	16571	699933	42.2384	23.5538
chrX	155270560	146666734	0.9446	3.1002

chrY	59373566	7335685	0.1236	8.5683

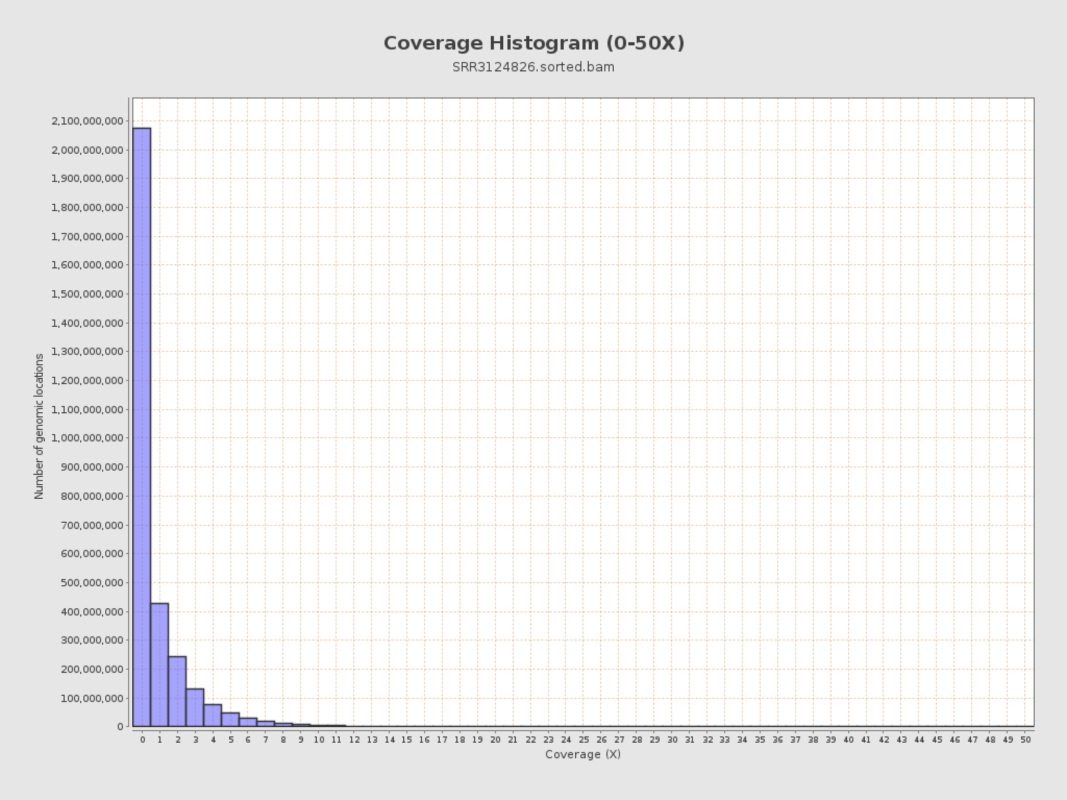
3. Results : Coverage across reference



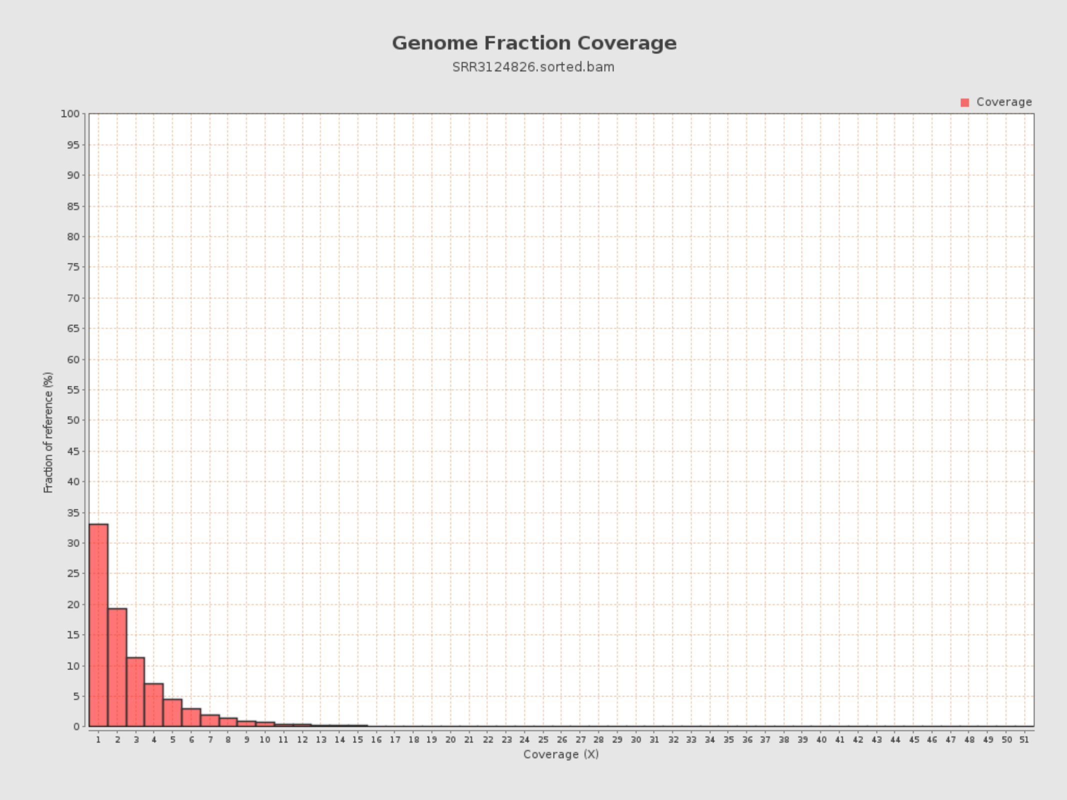
4. Results : Coverage Histogram



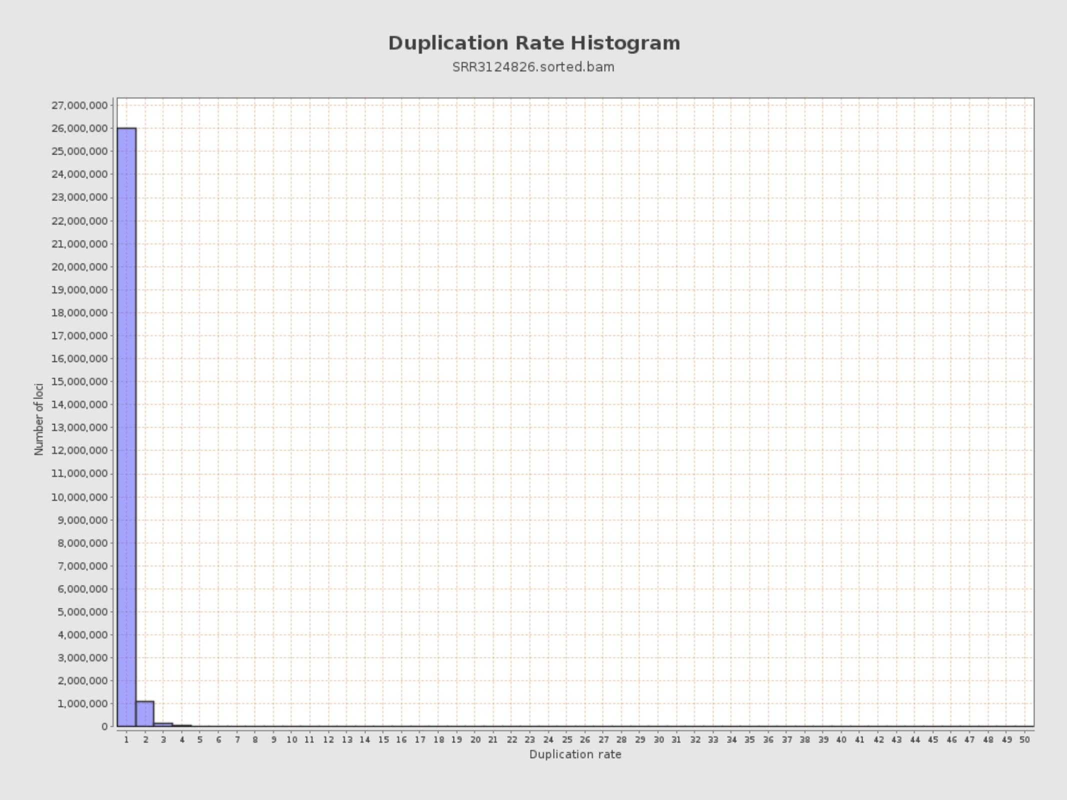
5. Results : Coverage Histogram (0-50X)



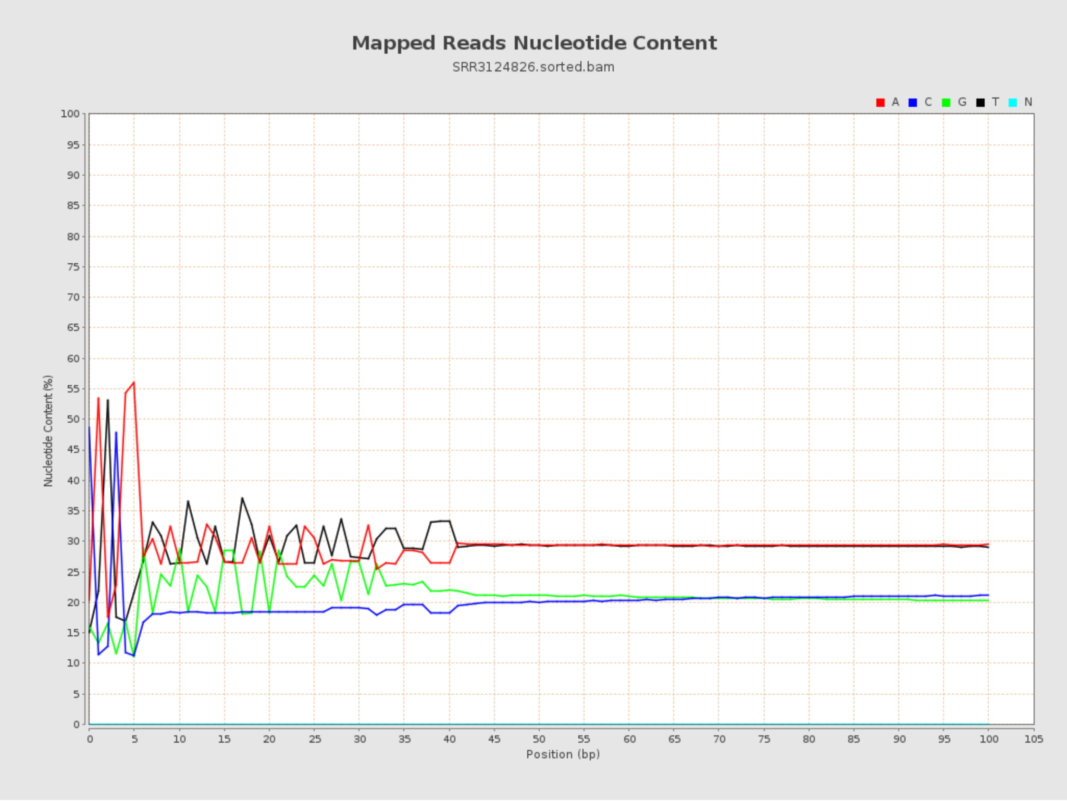
6. Results : Genome Fraction Coverage



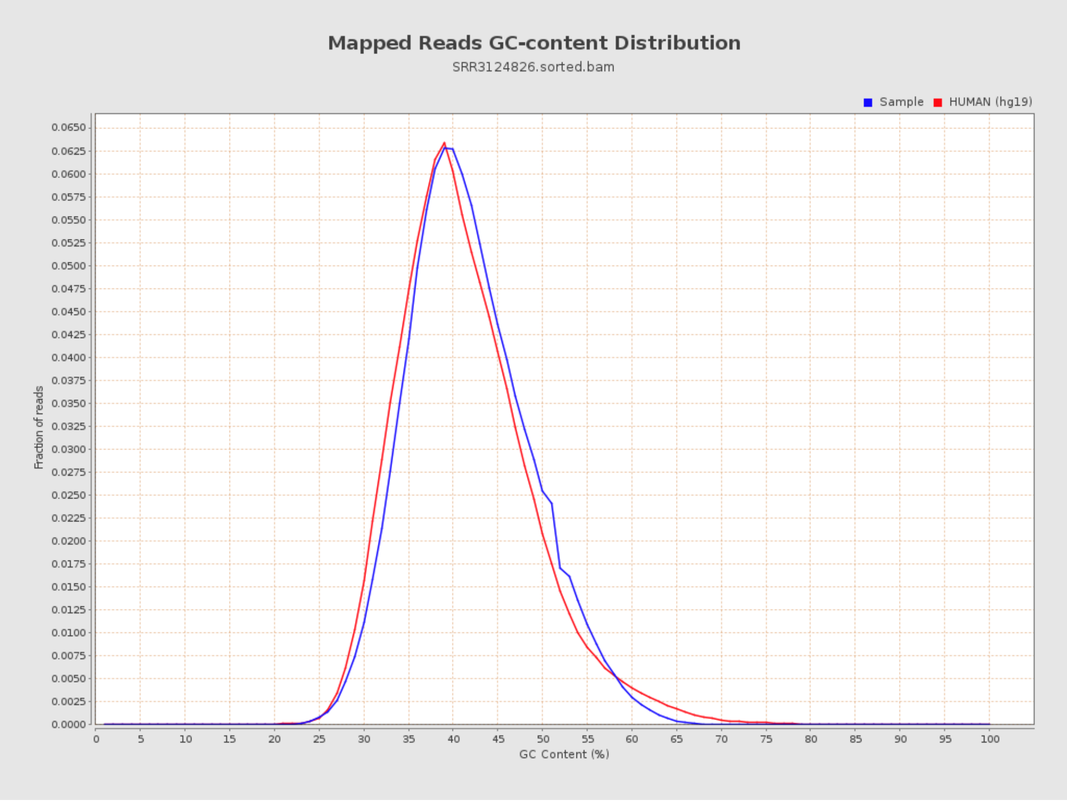
7. Results : Duplication Rate Histogram



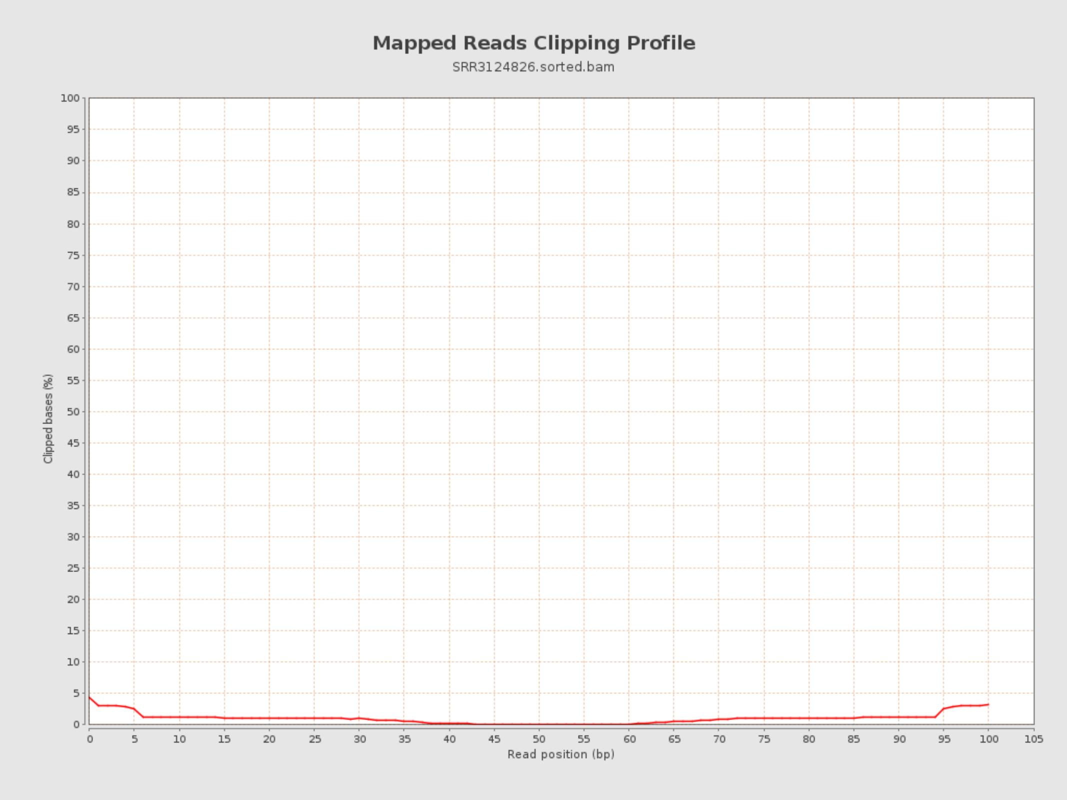
8. Results : Mapped Reads Nucleotide Content



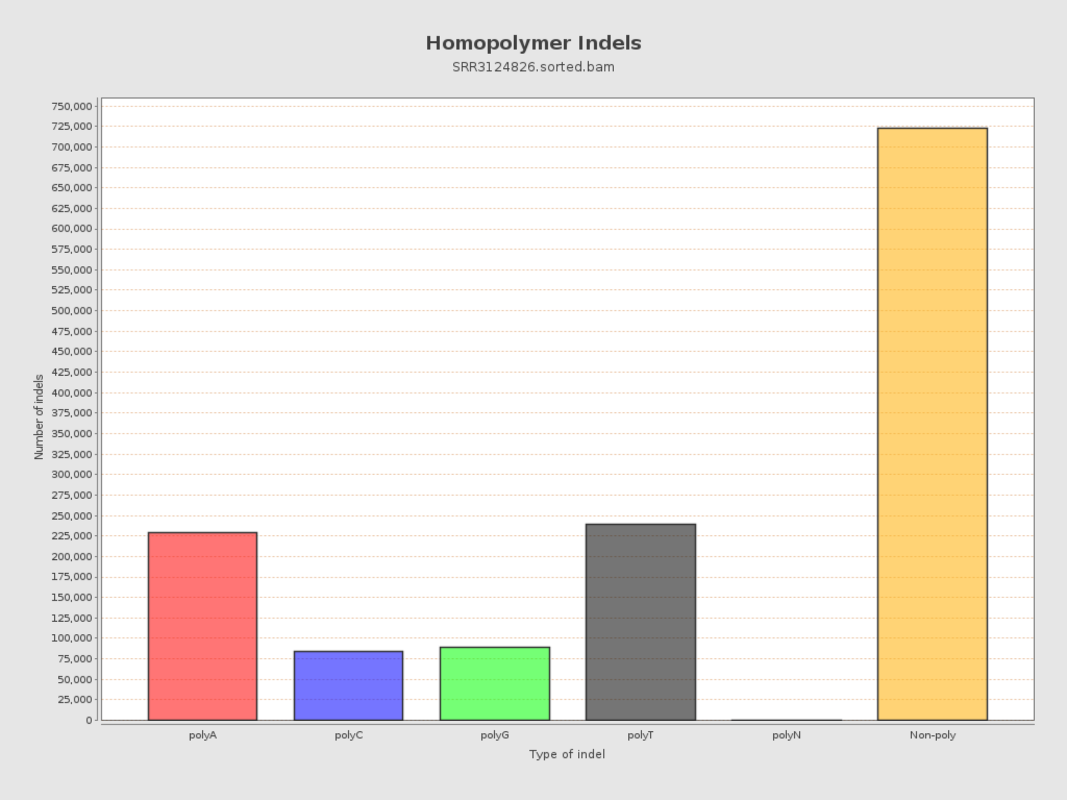
9. Results : Mapped Reads GC-content Distribution



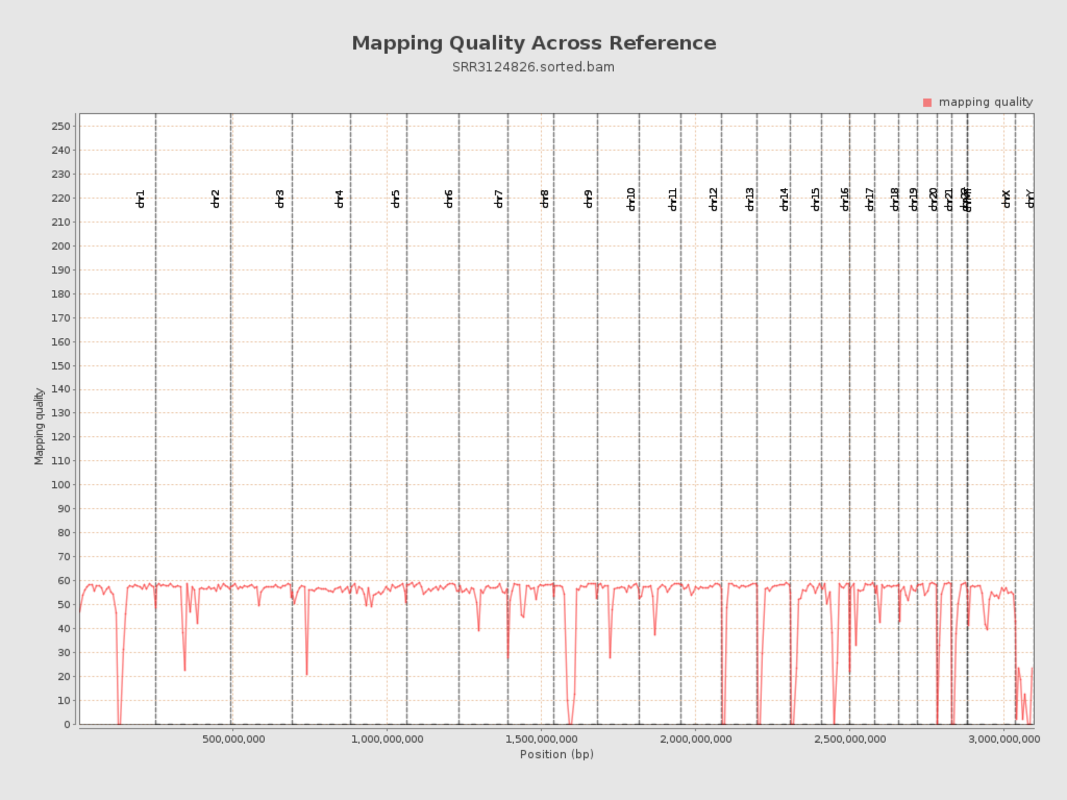
10. Results : Mapped Reads Clipping Profile



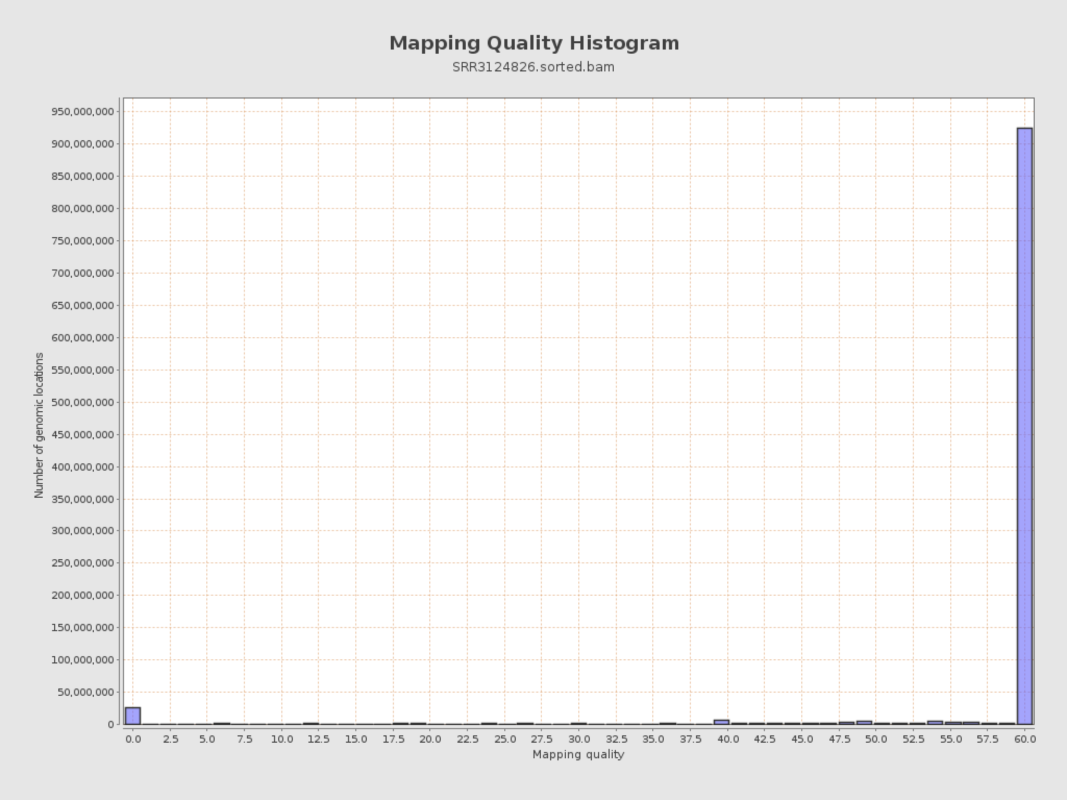
11. Results : Homopolymer Indels



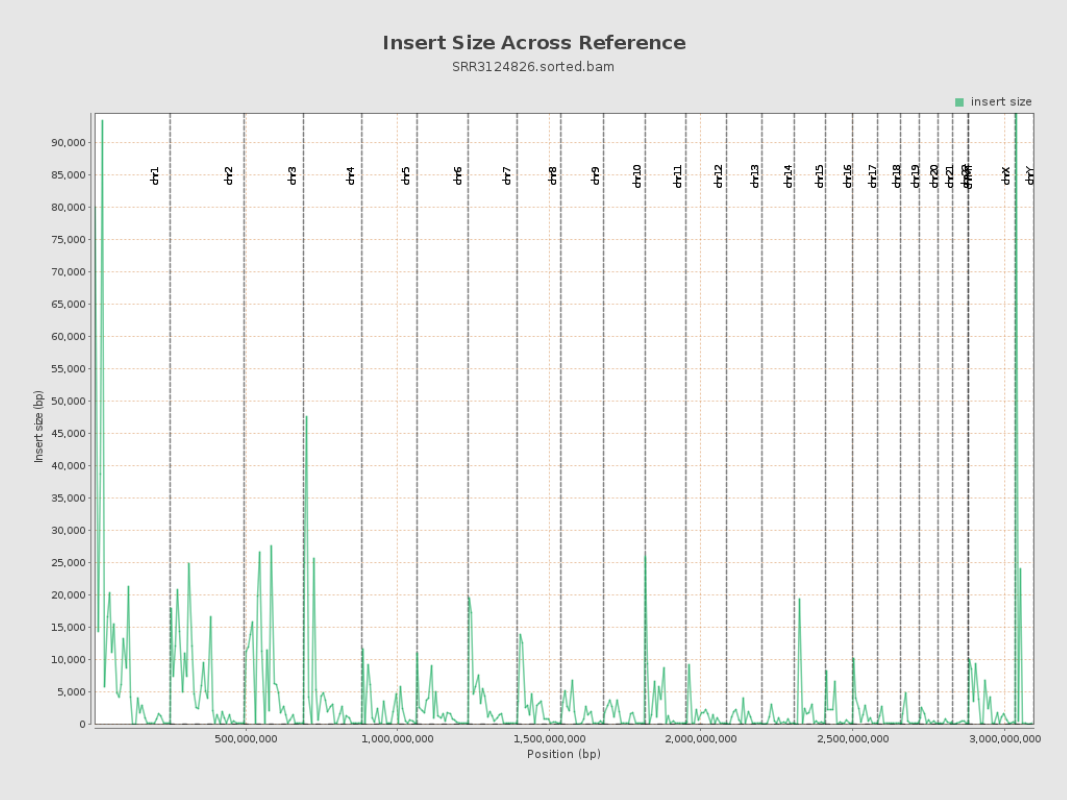
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram