Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 05:01:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124917.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_SRR3124917 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124917_1.fastq.gz SRR3124917_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 05:01:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,536,394
Mapped reads	6,464,681 / 98.9%
Unmapped reads	71,713 / 1.1%
Mapped paired reads	6,464,681 / 98.9%
Mapped reads, first in pair	3,234,866 / 49.49%
Mapped reads, second in pair	3,229,815 / 49.41%
Mapped reads, both in pair	6,440,912 / 98.54%
Mapped reads, singletons	23,769 / 0.36%
Secondary alignments	0
Supplementary alignments	29,762 / 0.46%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	405,458 / 6.2%
Duplication rate	3.59%
Clipped reads	3,873,039 / 59.25%

2.2. ACGT Content

Number/percentage of A's	169,145,527 / 28.89%
Number/percentage of C's	116,389,905 / 19.88%
Number/percentage of T's	170,156,898 / 29.07%
Number/percentage of G's	129,693,841 / 22.15%
Number/percentage of N's	9,625 / 0%

GC Percentage	42.04%

2.3. Coverage

Mean	0.1892
Standard Deviation	1.8519

2.4. Mapping Quality

Mean Mapping Quality	52.74

2.5. Insert size

Mean	81,909.56
Standard Deviation	2,723,402.54
P25/Median/P75	137 / 170 / 215

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	4,284,208
Insertions	96,130
Mapped reads with at least one insertion	1.44%
Deletions	191,736
Mapped reads with at least one deletion	2.9%
Homopolymer indels	45.46%

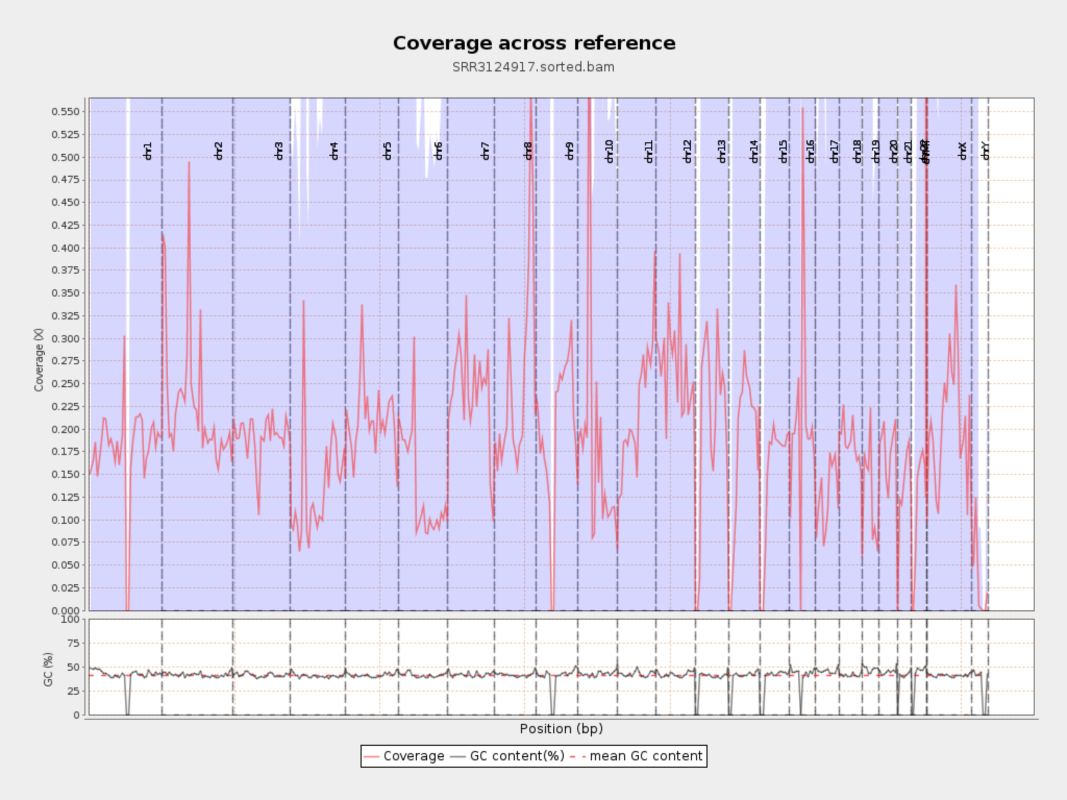
2.7. Chromosome stats

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

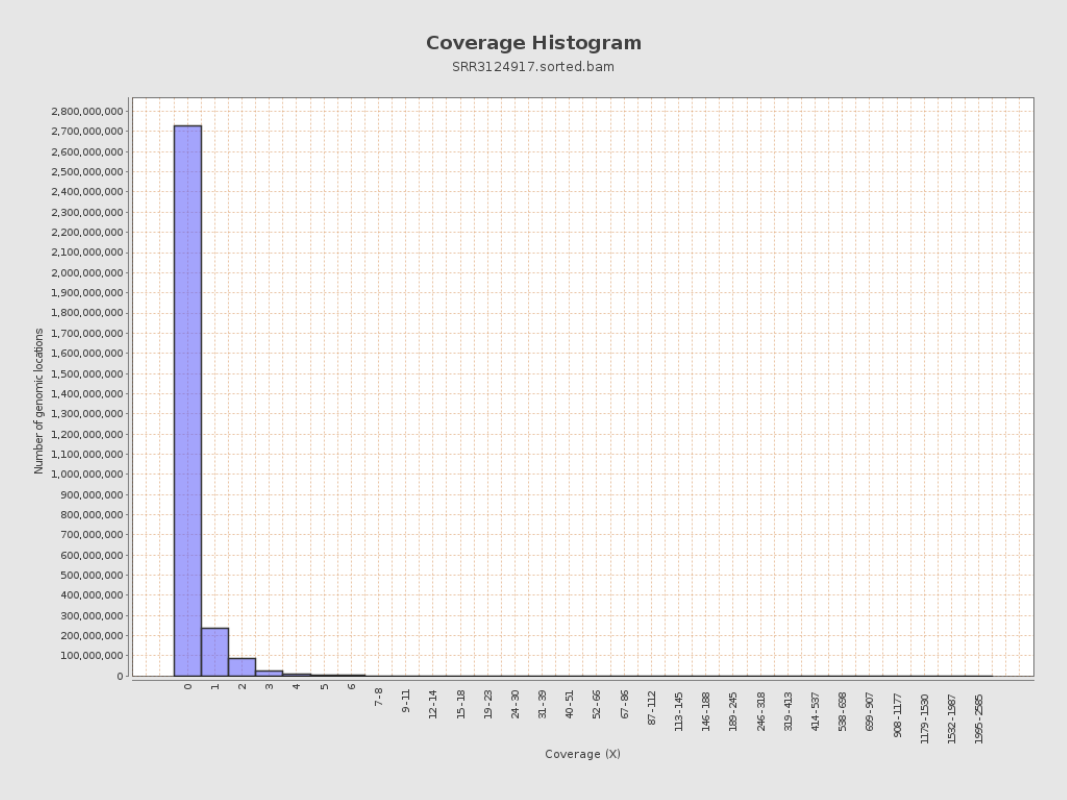
		bases	coverage	deviation
chr1	249250621	44056576	0.1768	2.5589
chr2	243199373	55804966	0.2295	2.3058
chr3	198022430	37985126	0.1918	0.6301
chr4	191154276	25542944	0.1336	1.5802
chr5	180915260	37944365	0.2097	0.6589
chr6	171115067	23240335	0.1358	1.4018
chr7	159138663	38812630	0.2439	2.5173
chr8	146364022	37102630	0.2535	0.9271
chr9	141213431	28037502	0.1985	2.1485
chr10	135534747	24411780	0.1801	4.4955
chr11	135006516	30003756	0.2222	1.1981
chr12	133851895	36054852	0.2694	0.7328
chr13	115169878	23267139	0.202	0.6314
chr14	107349540	19288331	0.1797	0.6757
chr15	102531392	15300081	0.1492	0.5272
chr16	90354753	18870523	0.2088	2.75
chr17	81195210	10169898	0.1253	1.0803
chr18	78077248	14594684	0.1869	2.2685
chr19	59128983	7753695	0.1311	1.46
chr20	63025520	11085068	0.1759	0.7068
chr21	48129895	6396743	0.1329	0.8187
chr22	51304566	5702288	0.1111	0.5122
chrMT	16571	155062	9.3574	6.7084
chrX	155270560	32323589	0.2082	1.0492

chrY	59373566	1826040	0.0308	2.0249

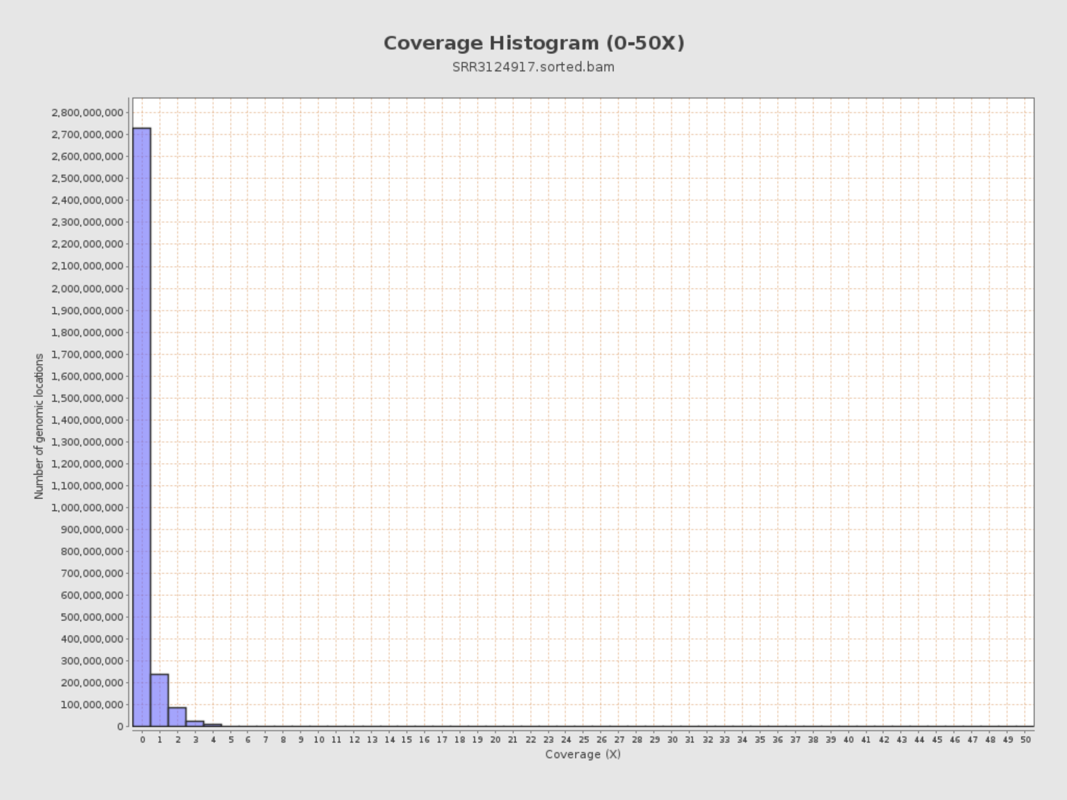
3. Results : Coverage across reference



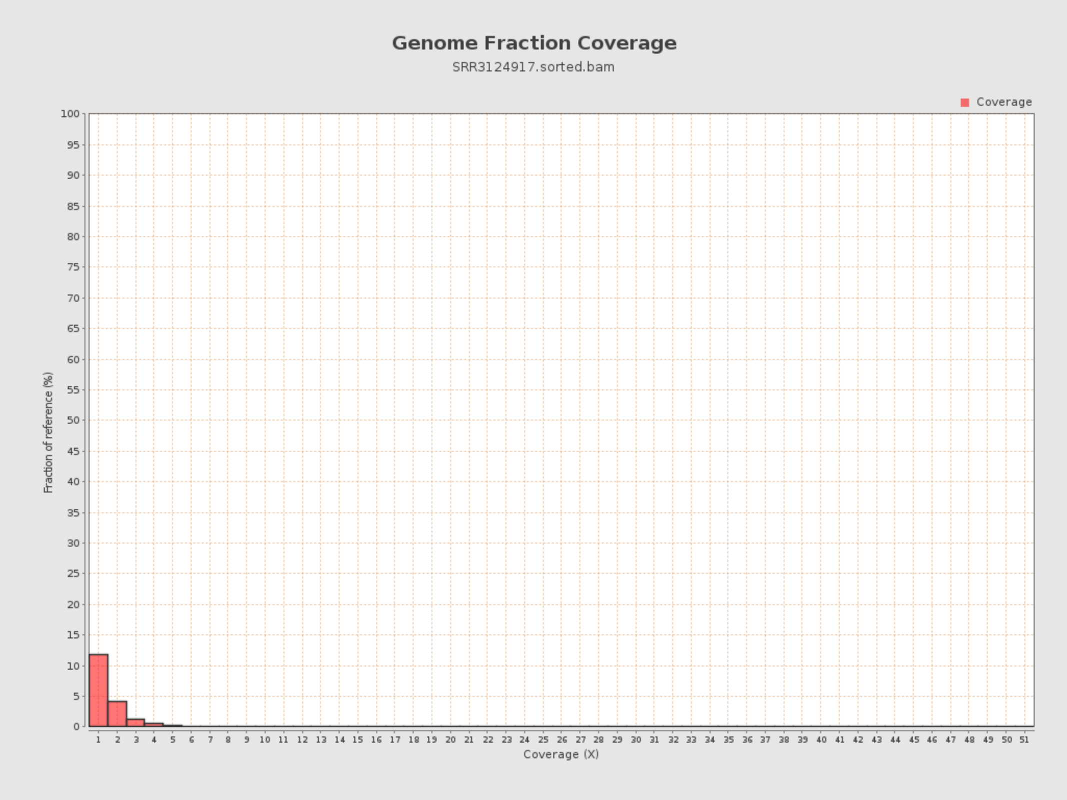
4. Results : Coverage Histogram



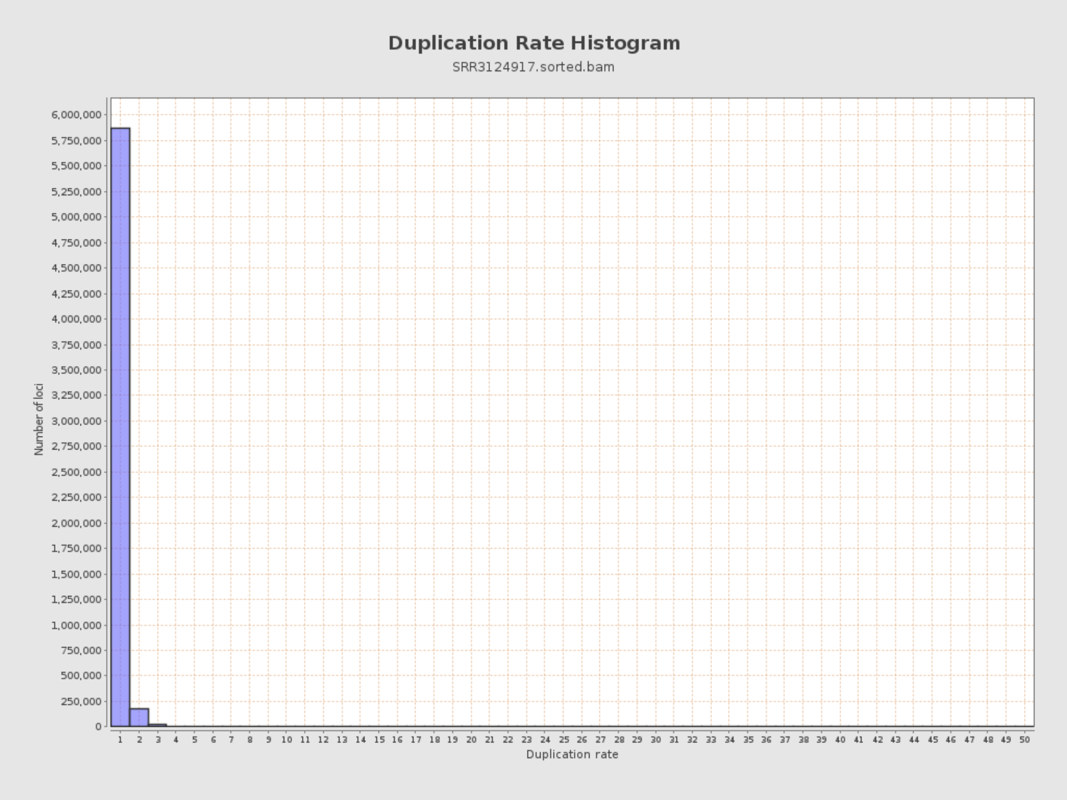
5. Results : Coverage Histogram (0-50X)



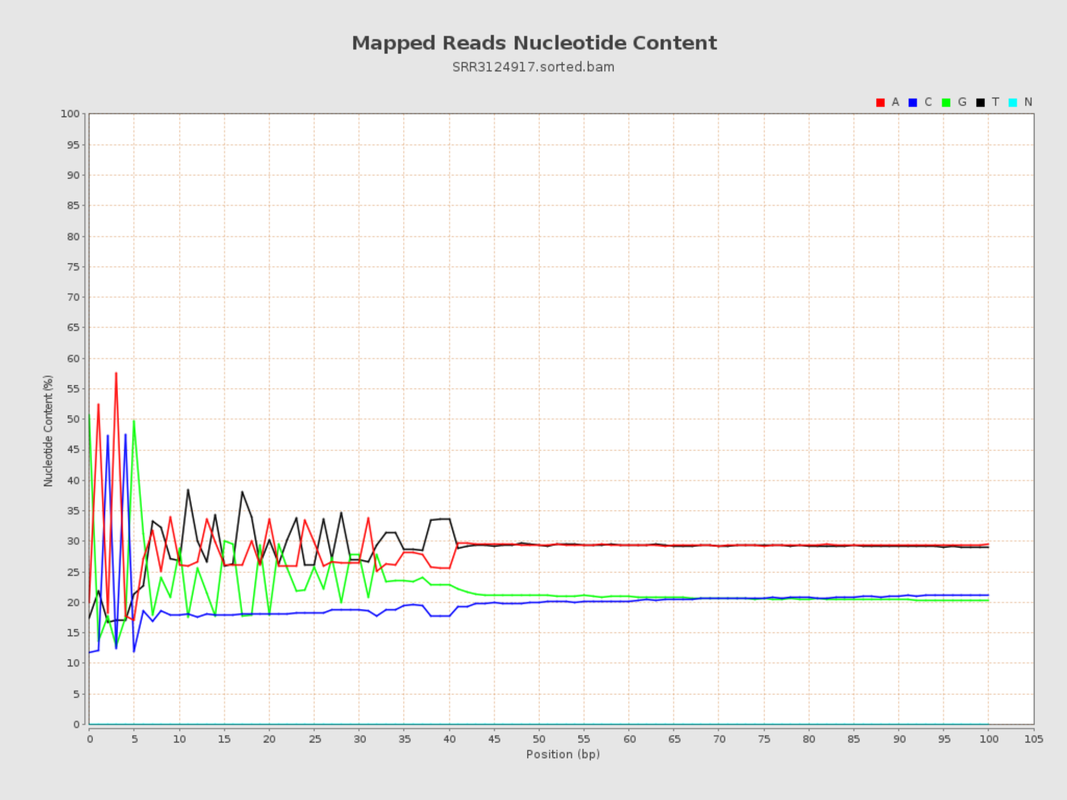
6. Results : Genome Fraction Coverage



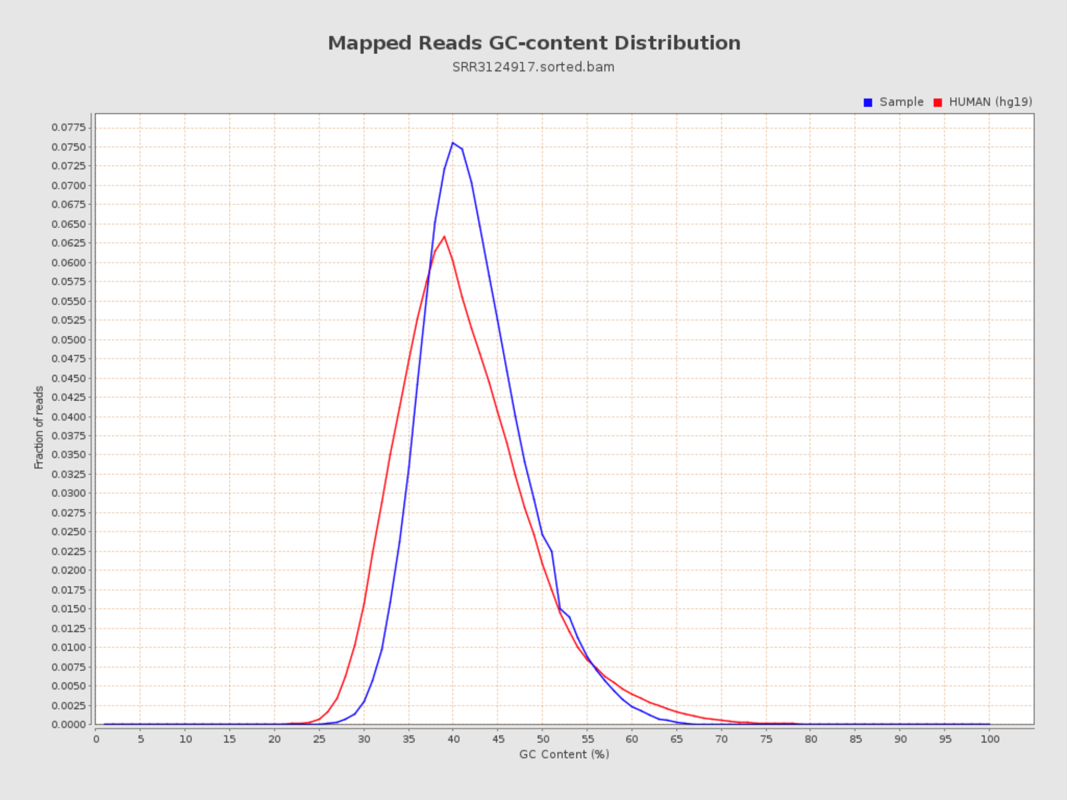
7. Results : Duplication Rate Histogram



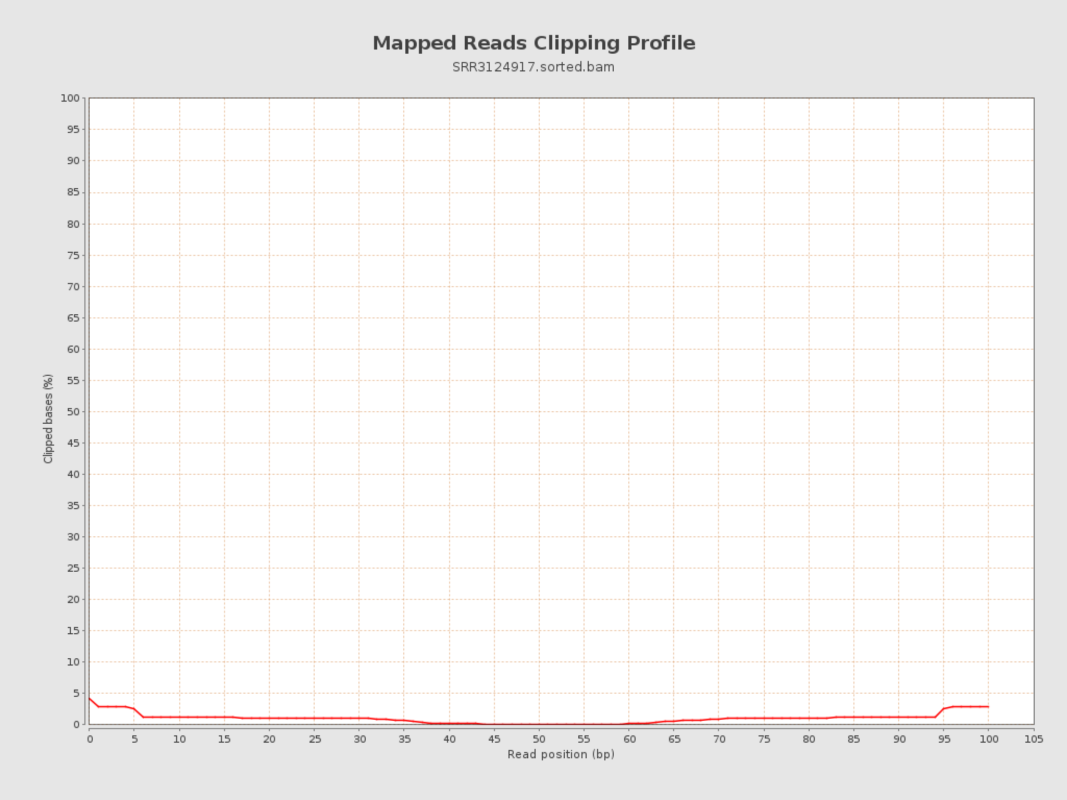
8. Results : Mapped Reads Nucleotide Content



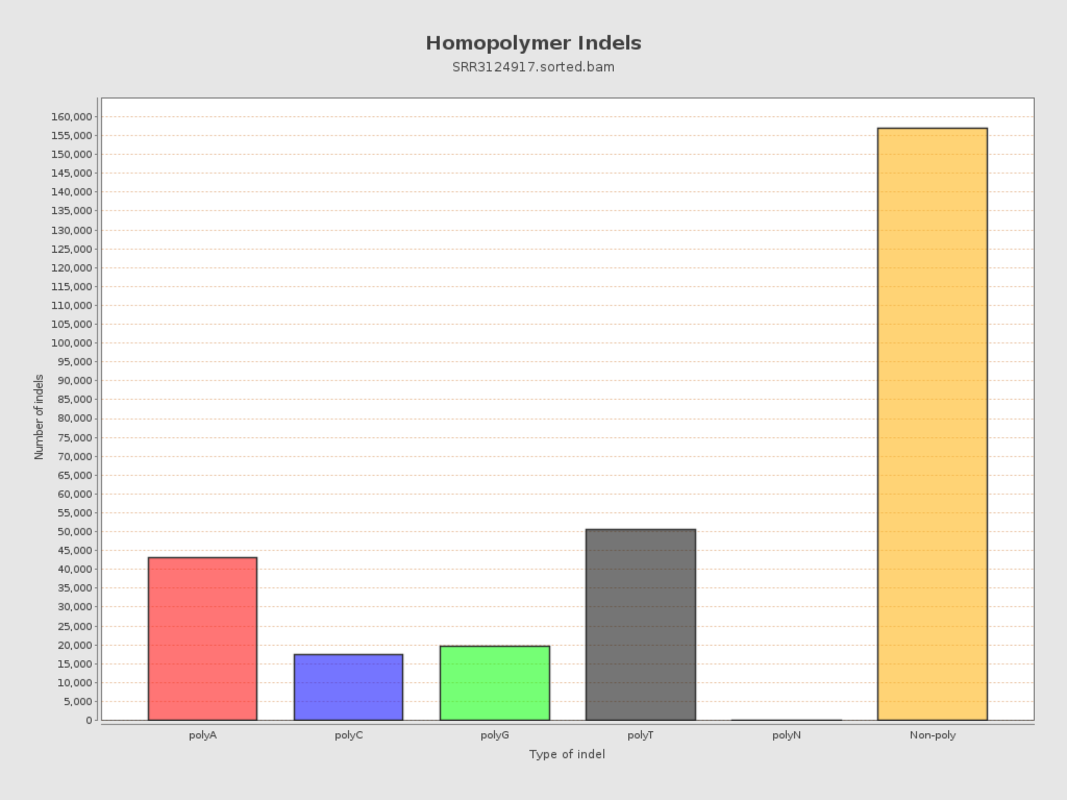
9. Results : Mapped Reads GC-content Distribution



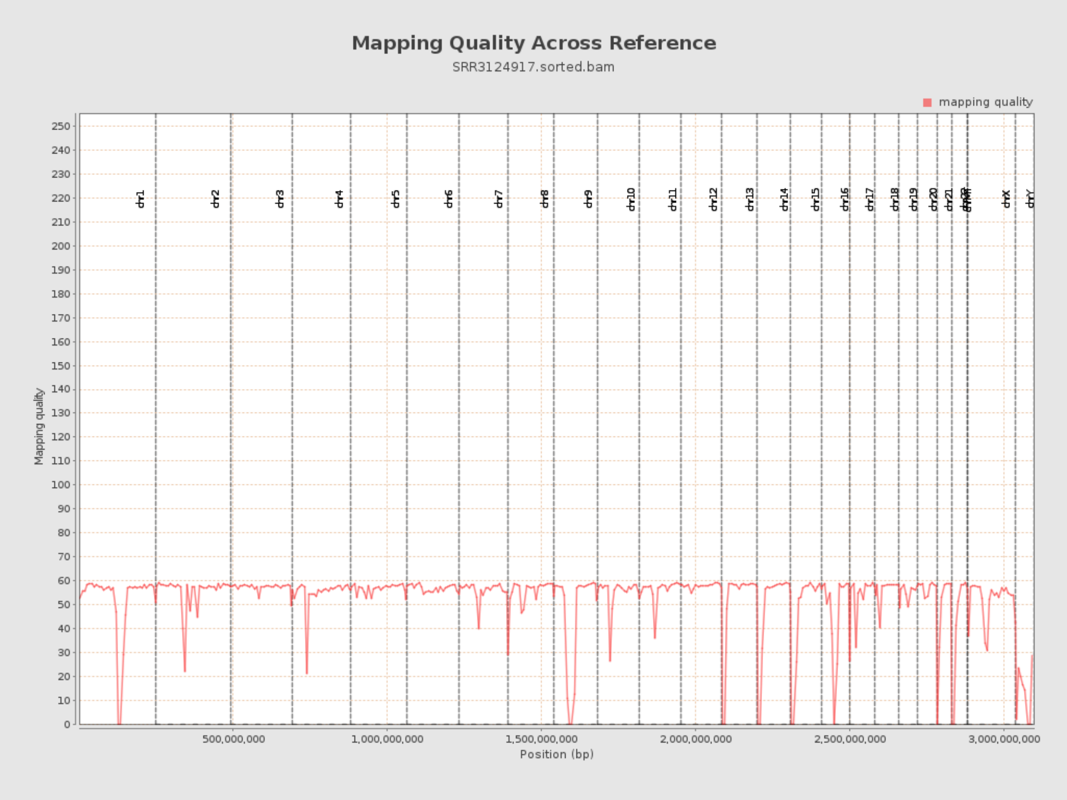
10. Results : Mapped Reads Clipping Profile



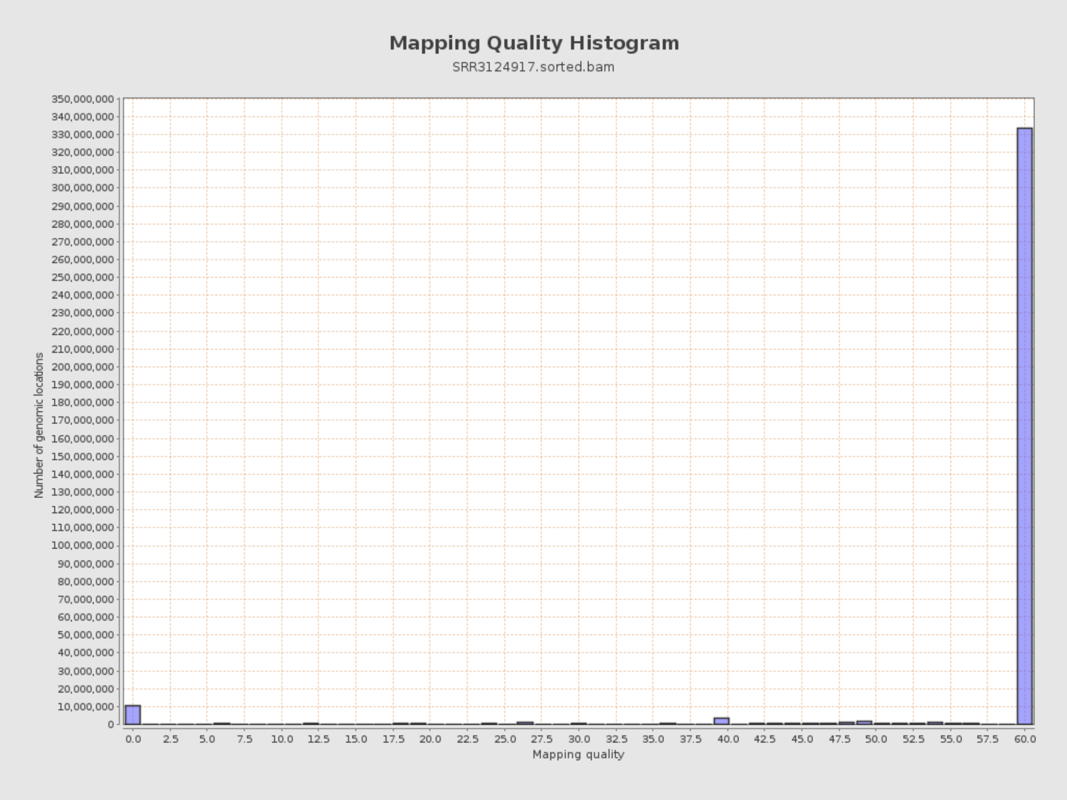
11. Results : Homopolymer Indels



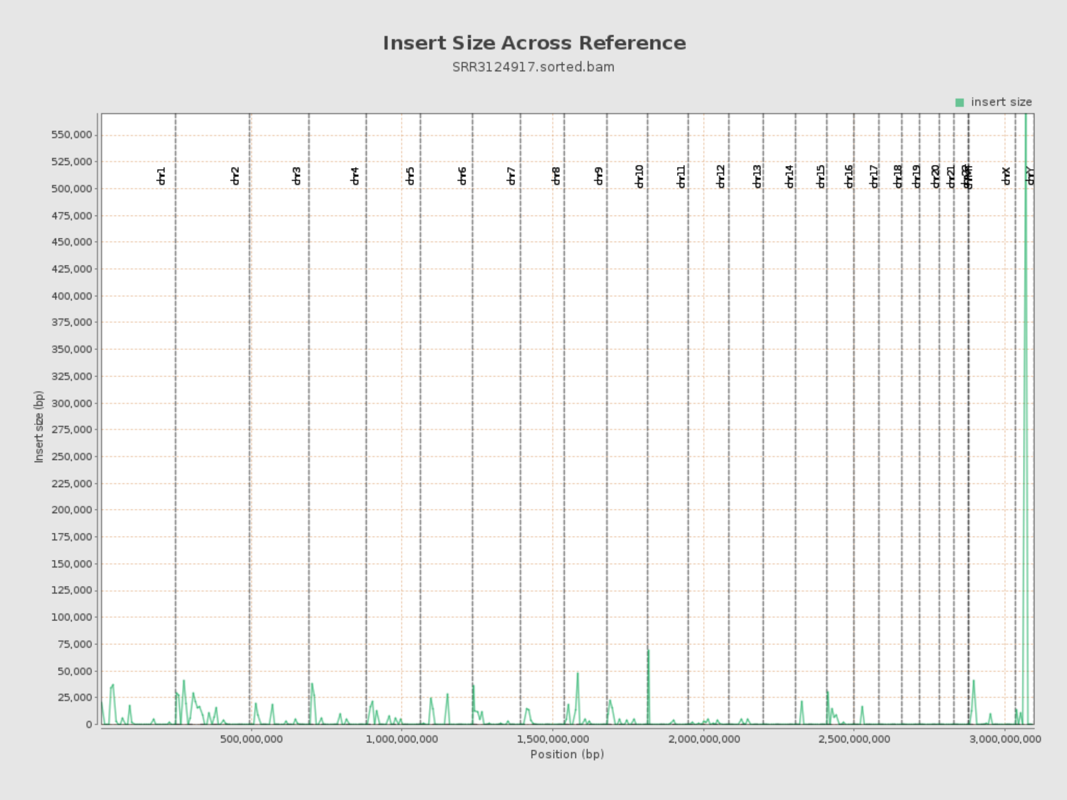
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram