Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 13:25:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124984.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_SRR3124984 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124984_1.fastq.gz SRR3124984_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 13:25:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124984.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,743,892
Mapped reads	2,706,343 / 98.63%
Unmapped reads	37,549 / 1.37%
Mapped paired reads	2,706,343 / 98.63%
Mapped reads, first in pair	1,360,064 / 49.57%
Mapped reads, second in pair	1,346,279 / 49.06%
Mapped reads, both in pair	2,690,328 / 98.05%
Mapped reads, singletons	16,015 / 0.58%
Secondary alignments	0
Supplementary alignments	63,870 / 2.33%
Read min/max/mean length	30 / 151 / 152.13
Duplicated reads (estimated)	494,031 / 18%
Duplication rate	16.4%
Clipped reads	1,942,552 / 70.8%

2.2. ACGT Content

Number/percentage of A's	98,933,288 / 29.08%
Number/percentage of C's	67,093,739 / 19.72%
Number/percentage of T's	100,696,696 / 29.6%
Number/percentage of G's	73,476,522 / 21.6%
Number/percentage of N's	2,577 / 0%

GC Percentage	41.32%

2.3. Coverage

Mean	0.11
Standard Deviation	1.7417

2.4. Mapping Quality

Mean Mapping Quality	53.2

2.5. Insert size

Mean	98,016.95
Standard Deviation	3,003,517.32
P25/Median/P75	122 / 167 / 235

2.6. Mismatches and indels

General error rate	1%
Mismatches	3,203,904
Insertions	69,988
Mapped reads with at least one insertion	2.39%
Deletions	122,792
Mapped reads with at least one deletion	4.33%
Homopolymer indels	44.62%

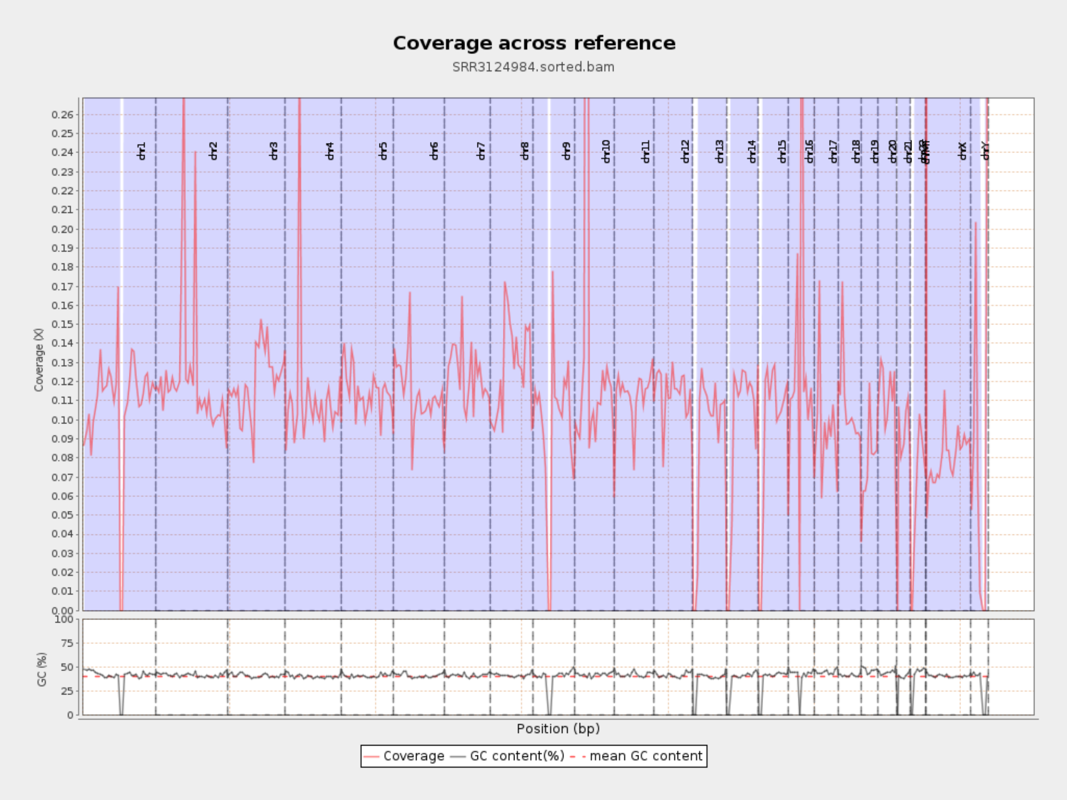
2.7. Chromosome stats

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

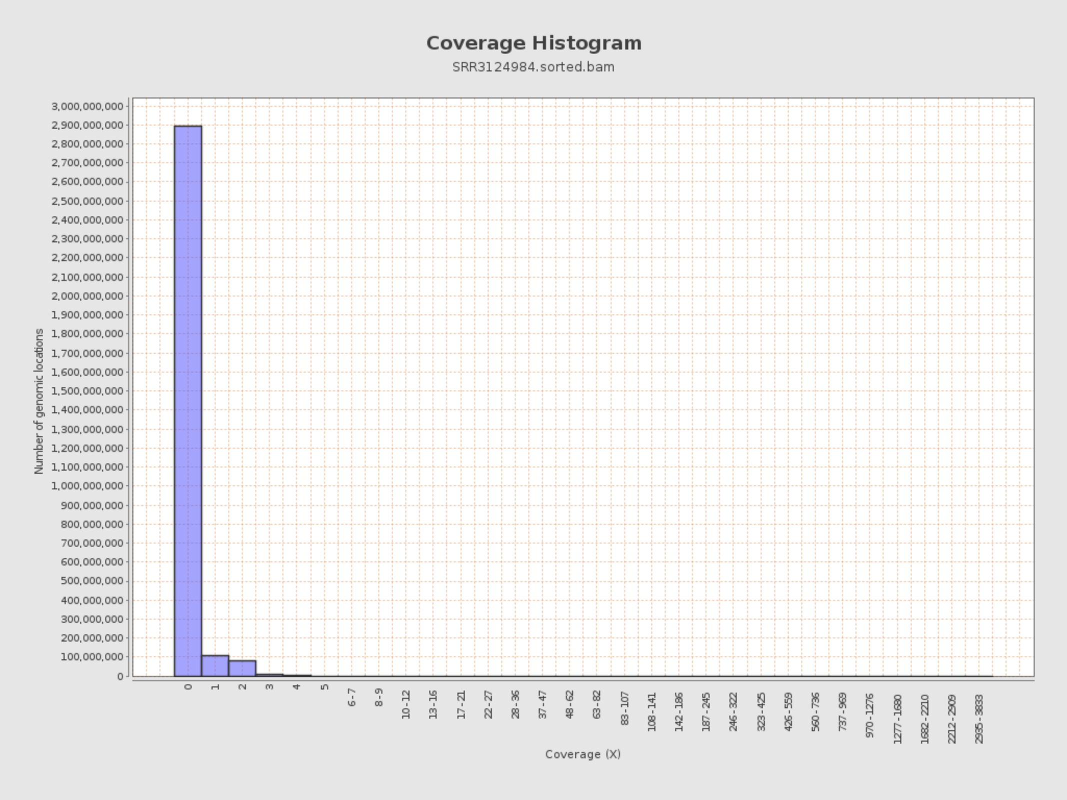
		bases	**coverage**	**deviation**
chr1	249250621	26998251	0.1083	1.1255
chr2	243199373	30117280	0.1238	1.9586
chr3	198022430	23792751	0.1202	0.5131
chr4	191154276	21552229	0.1127	1.427
chr5	180915260	20785164	0.1149	0.4864
chr6	171115067	19637252	0.1148	0.6662
chr7	159138663	19489824	0.1225	1.0923
chr8	146364022	18711721	0.1278	0.6259
chr9	141213431	13665251	0.0968	1.6951
chr10	135534747	19582655	0.1445	6.1841
chr11	135006516	15221443	0.1127	0.8204
chr12	133851895	15304567	0.1143	0.4682
chr13	115169878	10409767	0.0904	0.4114
chr14	107349540	10301606	0.096	0.4586
chr15	102531392	9594026	0.0936	0.4304
chr16	90354753	11849644	0.1311	2.4971
chr17	81195210	7895728	0.0972	1.4064
chr18	78077248	8441093	0.1081	1.8618
chr19	59128983	4674926	0.0791	0.7109
chr20	63025520	7167319	0.1137	0.6489
chr21	48129895	4185415	0.087	0.8966
chr22	51304566	3180552	0.062	0.3841
chrMT	16571	75405	4.5504	3.7287
chrX	155270560	12460379	0.0802	0.4873

chrY	59373566	5383543	0.0907	2.6884

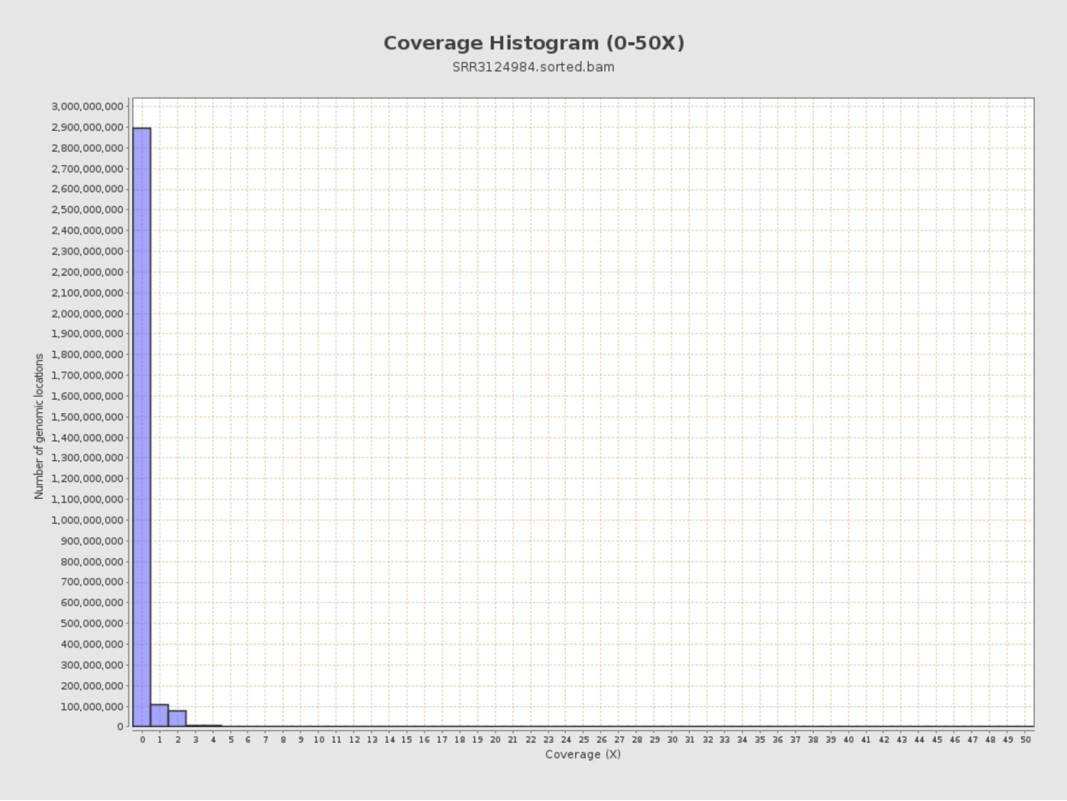
3. Results : Coverage across reference



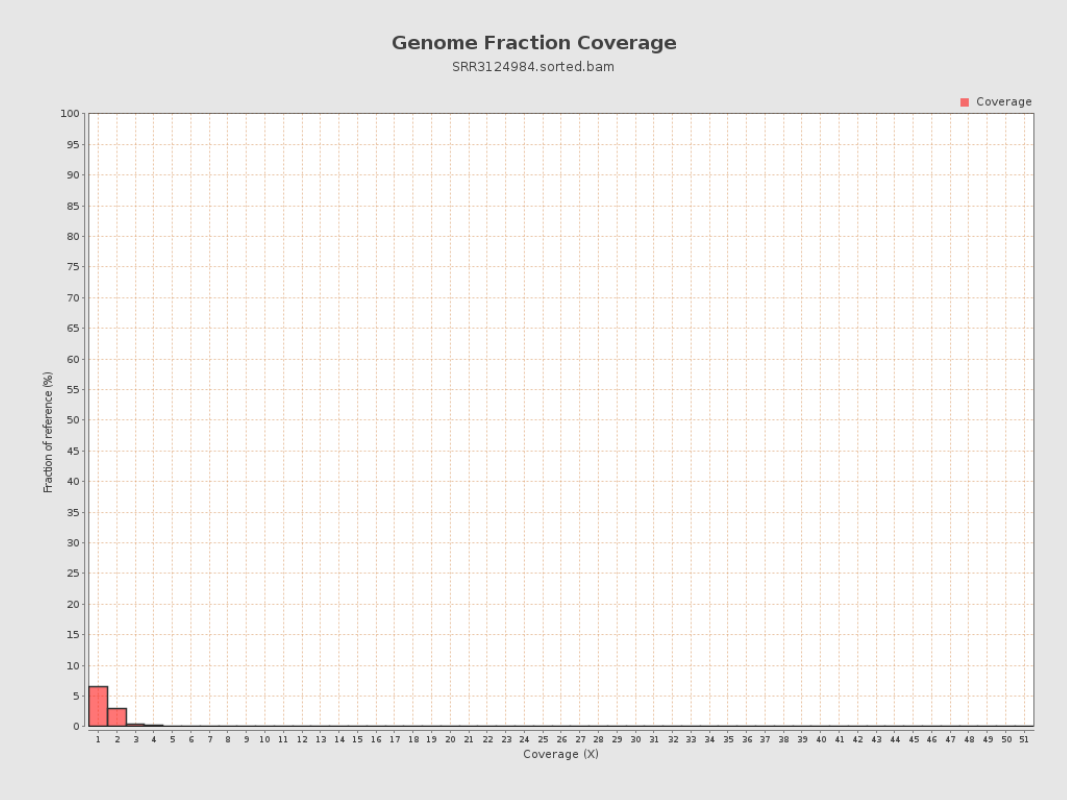
4. Results : Coverage Histogram



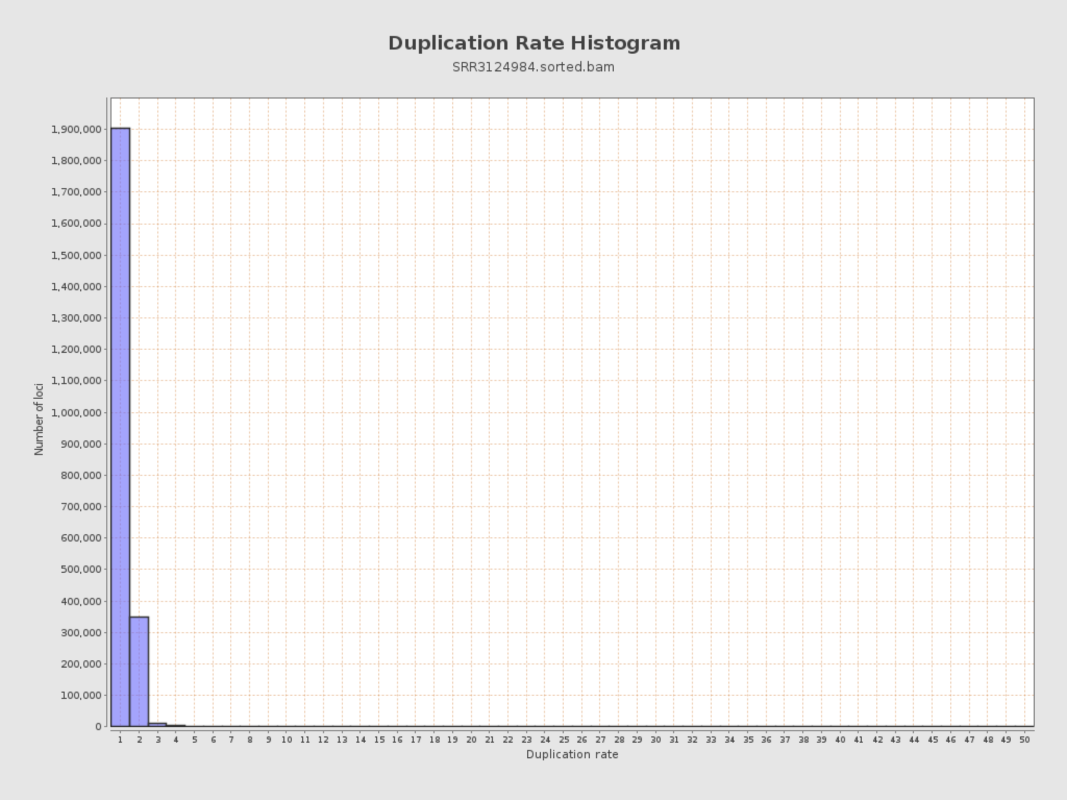
5. Results : Coverage Histogram (0-50X)



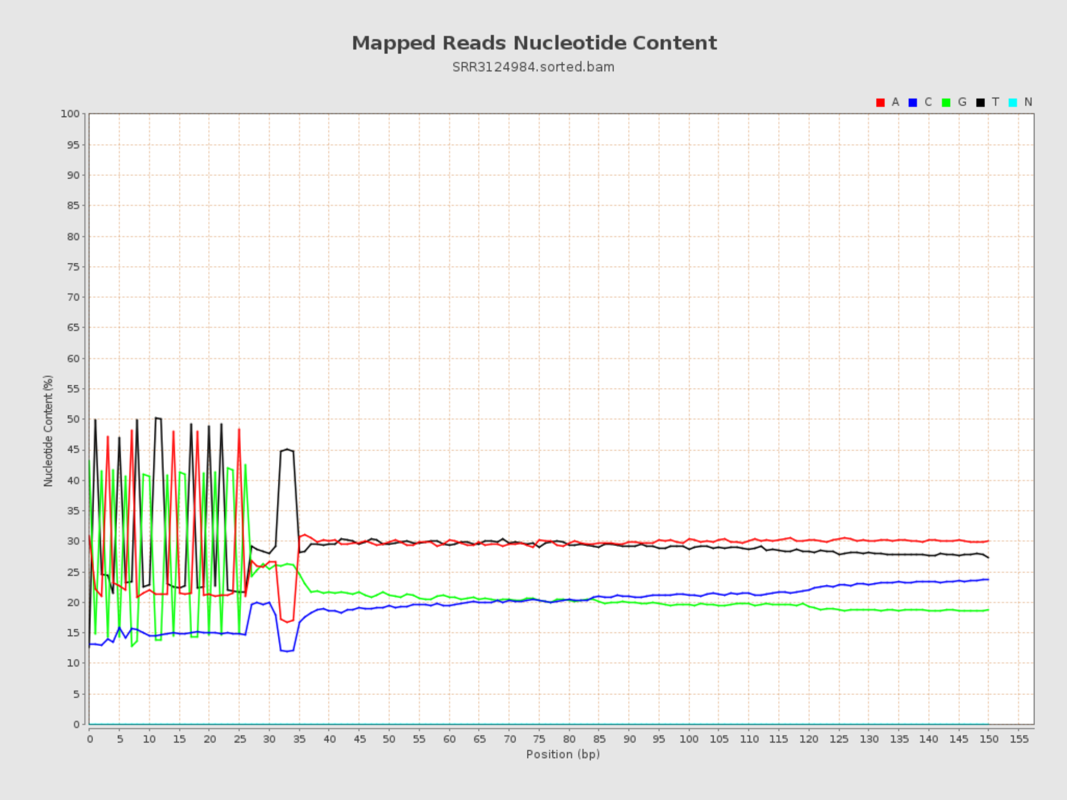
6. Results : Genome Fraction Coverage



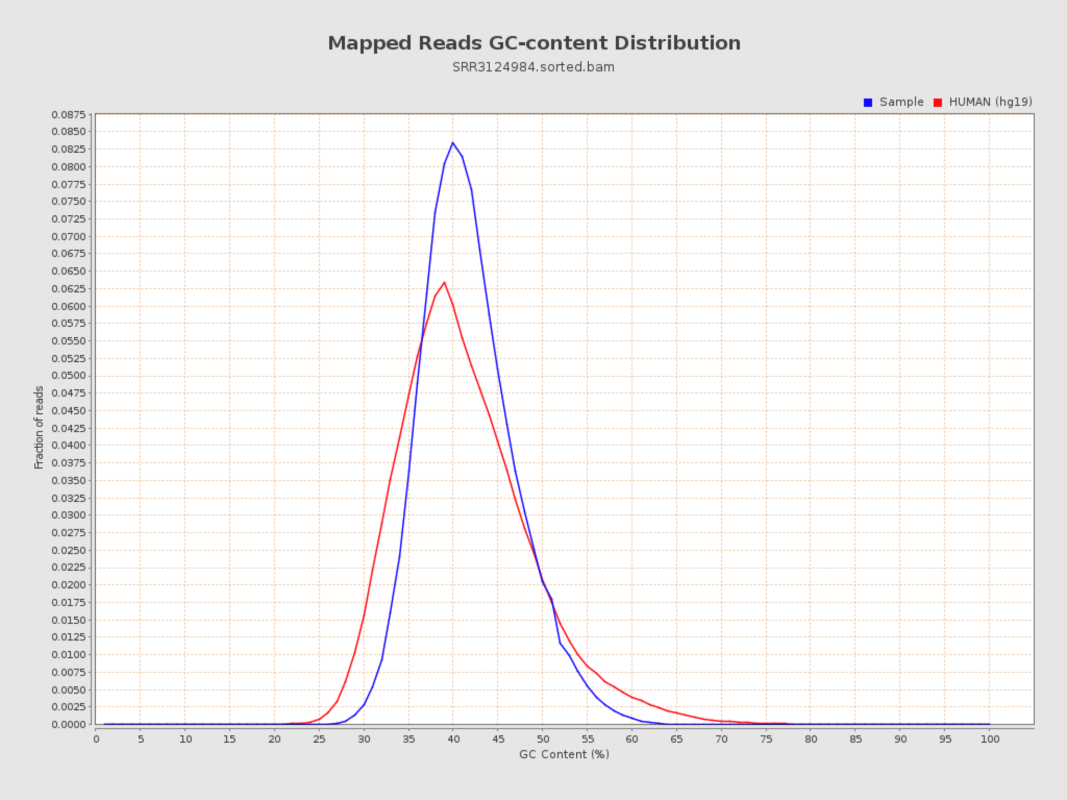
7. Results : Duplication Rate Histogram



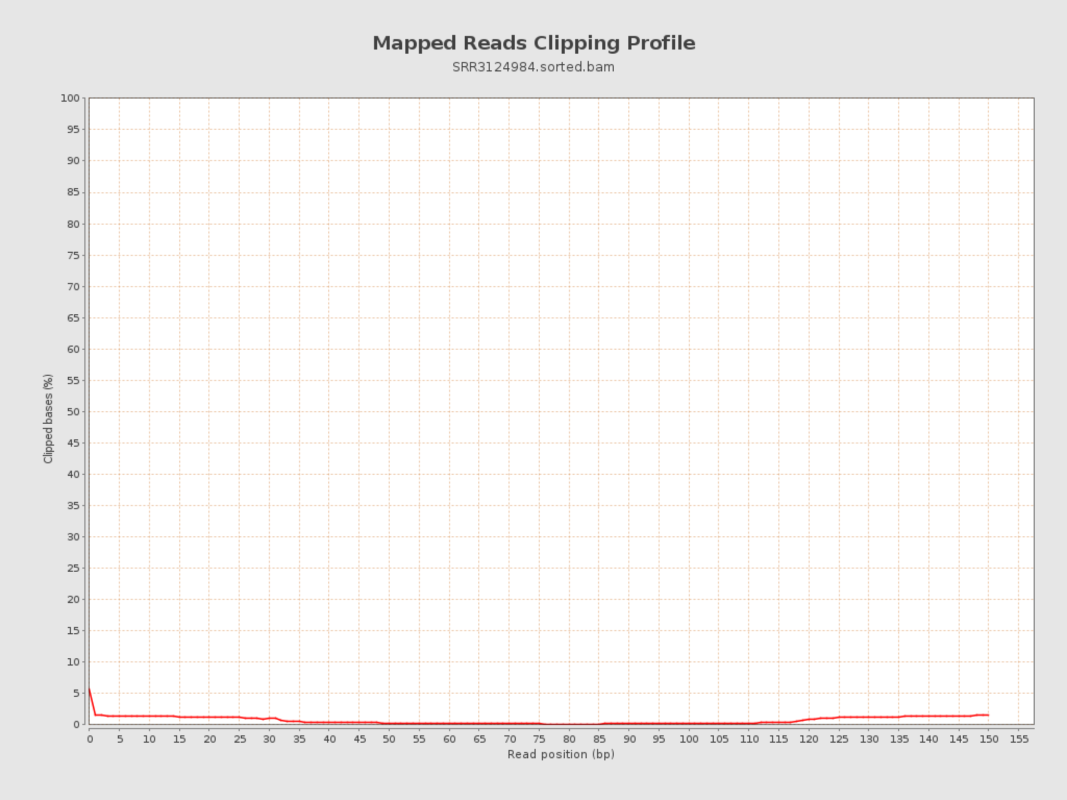
8. Results : Mapped Reads Nucleotide Content



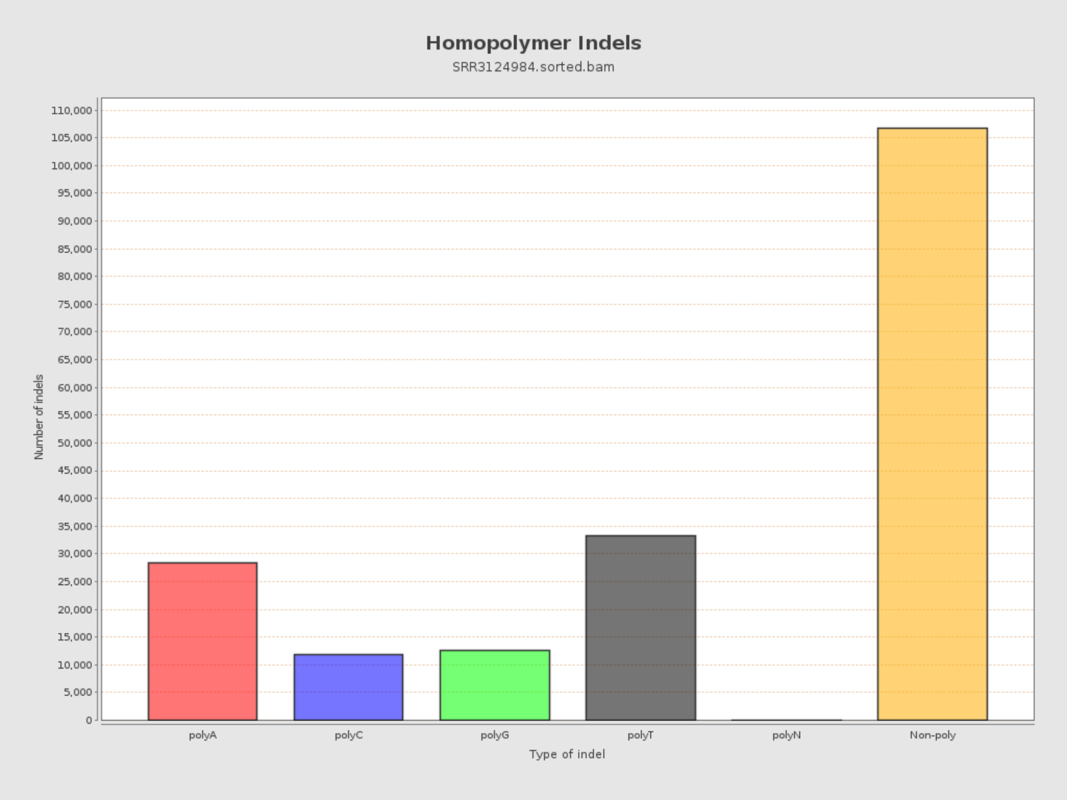
9. Results : Mapped Reads GC-content Distribution



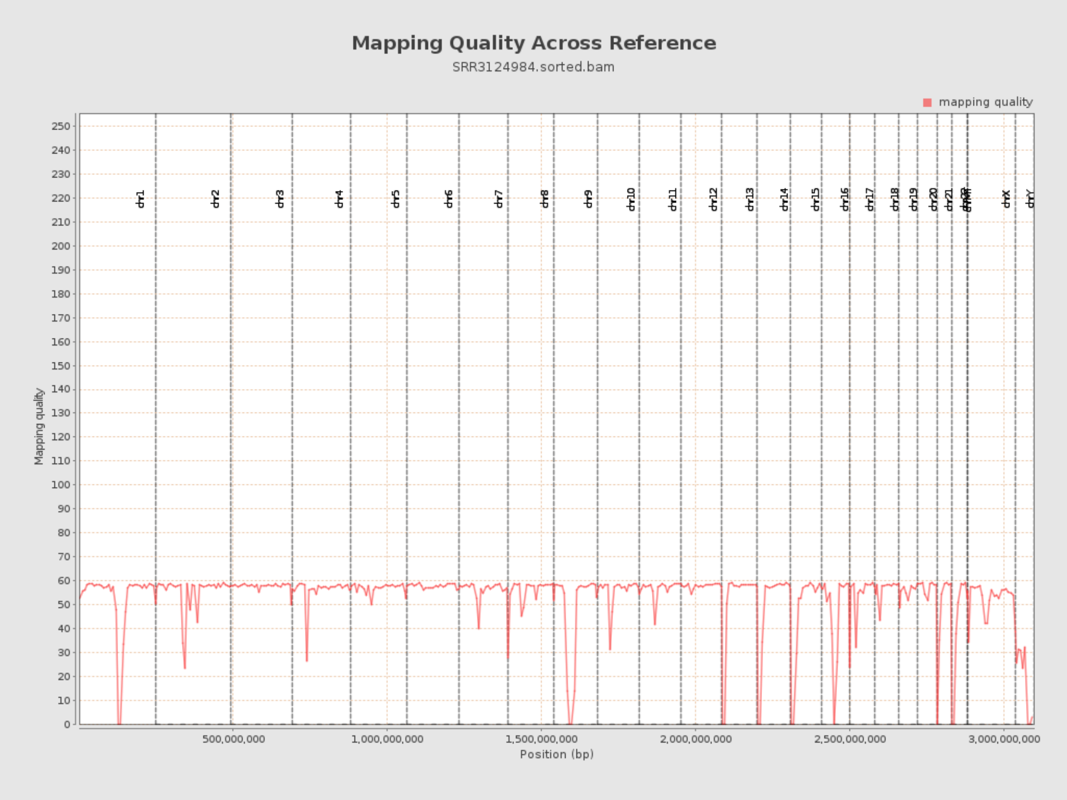
10. Results : Mapped Reads Clipping Profile



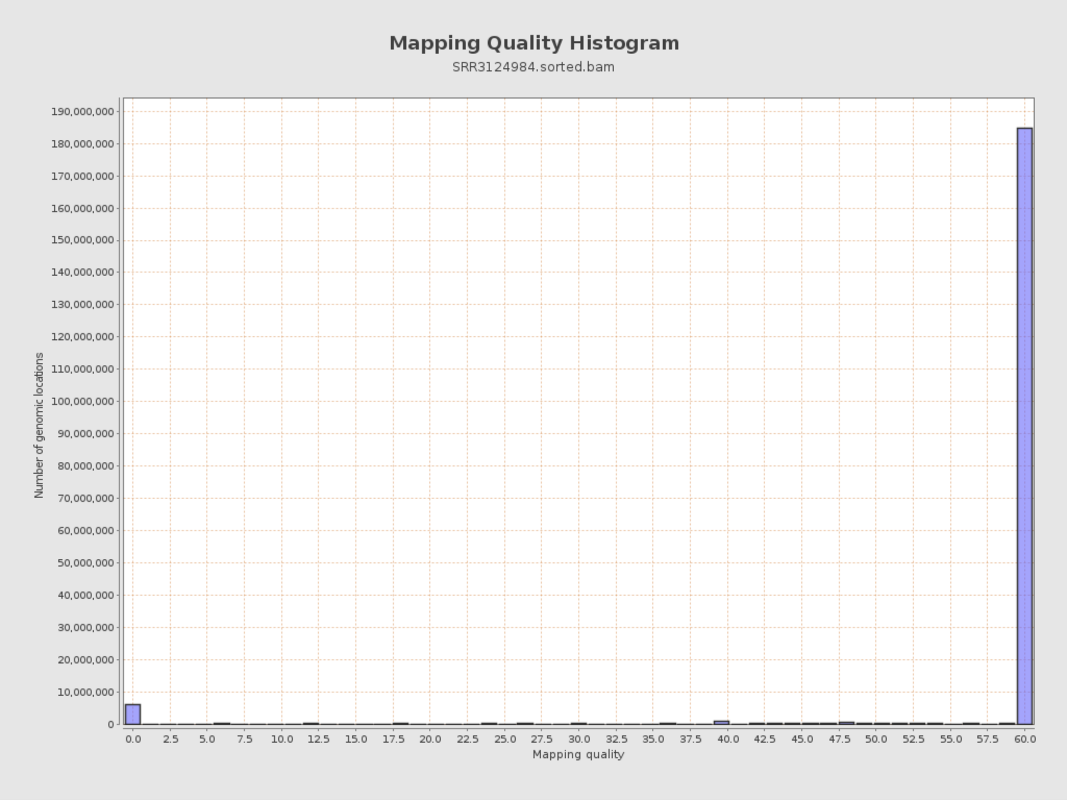
11. Results : Homopolymer Indels



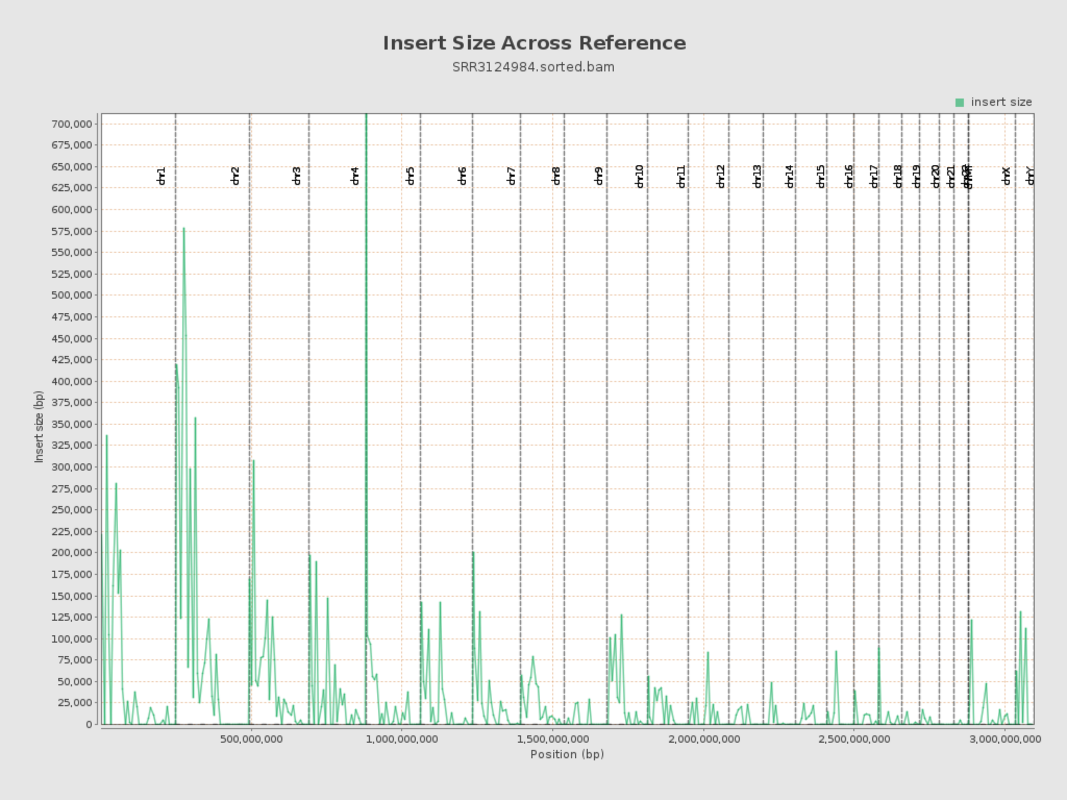
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram