Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/08 11:53:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124851.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_SRR3124851 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124851_1.fastq.gz SRR3124851_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 08 11:53:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124851.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	139,184,794
Mapped reads	134,676,192 / 96.76%
Unmapped reads	4,508,602 / 3.24%
Mapped paired reads	134,676,192 / 96.76%
Mapped reads, first in pair	68,041,508 / 48.89%
Mapped reads, second in pair	66,634,684 / 47.87%
Mapped reads, both in pair	132,652,322 / 95.31%
Mapped reads, singletons	2,023,870 / 1.45%
Secondary alignments	0
Supplementary alignments	2,409,945 / 1.73%
Read min/max/mean length	30 / 150 / 150.85
Duplicated reads (estimated)	56,976,218 / 40.94%
Duplication rate	28.8%
Clipped reads	64,965,154 / 46.68%

2.2. ACGT Content

Number/percentage of A's	5,211,777,147 / 28.76%
Number/percentage of C's	3,591,170,943 / 19.82%
Number/percentage of T's	5,280,031,937 / 29.14%
Number/percentage of G's	4,038,383,188 / 22.29%
Number/percentage of N's	39,867 / 0%

GC Percentage	42.1%

2.3. Coverage

Mean	5.8591
Standard Deviation	86.9844

2.4. Mapping Quality

Mean Mapping Quality	53.72

2.5. Insert size

Mean	54,065.3
Standard Deviation	2,187,695.9
P25/Median/P75	191 / 250 / 318

2.6. Mismatches and indels

General error rate	1.42%
Mismatches	244,831,132
Insertions	3,961,445
Mapped reads with at least one insertion	2.69%
Deletions	7,408,656
Mapped reads with at least one deletion	5.23%
Homopolymer indels	44.31%

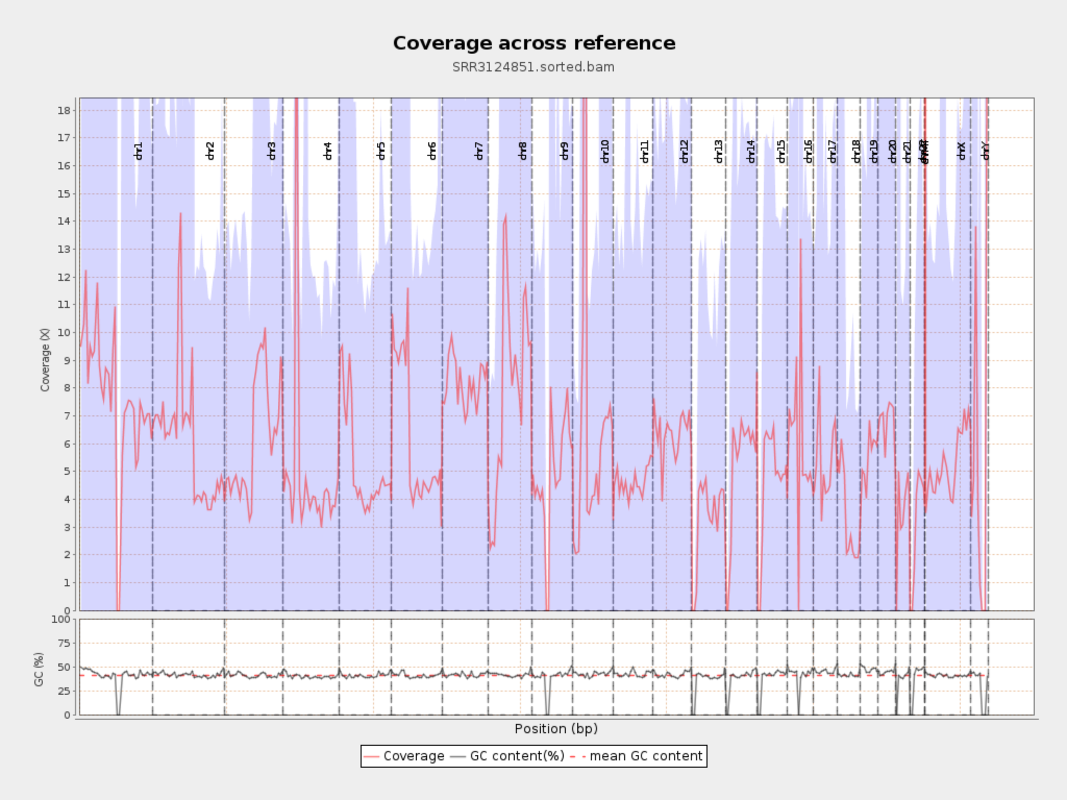
2.7. Chromosome stats

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

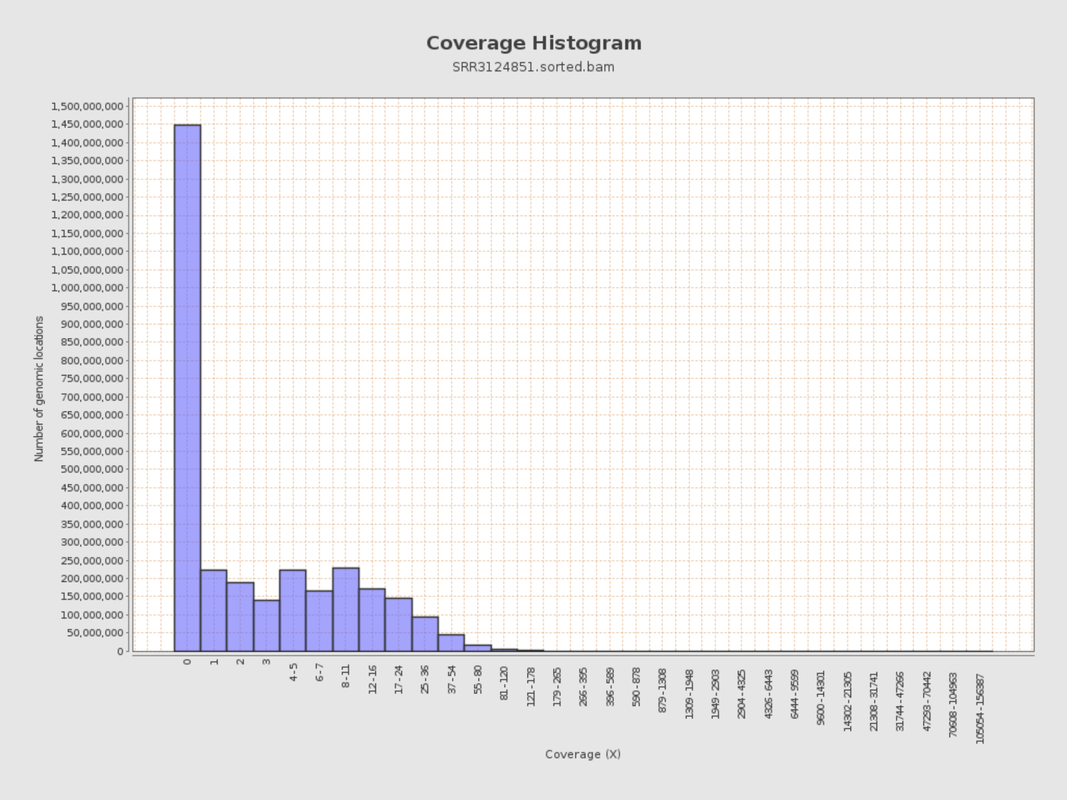
		bases	coverage	deviation
chr1	249250621	1896643846	7.6094	53.8655
chr2	243199373	1490779560	6.1299	77.3454
chr3	198022430	1237966726	6.2516	12.6403
chr4	191154276	919939376	4.8125	140.8197
chr5	180915260	956507327	5.287	11.3613
chr6	171115067	1073433723	6.2732	31.5173
chr7	159138663	1308865973	8.2247	46.1436
chr8	146364022	1180349806	8.0645	23.2151
chr9	141213431	677287273	4.7962	71.9281
chr10	135534747	980808853	7.2366	301.3812
chr11	135006516	620807381	4.5984	19.1827
chr12	133851895	853226400	6.3744	11.4593
chr13	115169878	381668325	3.314	7.3563
chr14	107349540	553644762	5.1574	11.8098
chr15	102531392	467585139	4.5604	9.2666
chr16	90354753	541210042	5.9898	67.1719
chr17	81195210	427217956	5.2616	70.7539
chr18	78077248	253508408	3.2469	56.134
chr19	59128983	322044446	5.4465	26.0407
chr20	63025520	431490955	6.8463	44.9052
chr21	48129895	176277441	3.6625	61.3672
chr22	51304566	160262173	3.1237	9.6719
chrMT	16571	30753080	1,855.8373	767.8708
chrX	155270560	816785689	5.2604	15.4778

chrY	59373566	379007222	6.3834	190.3014

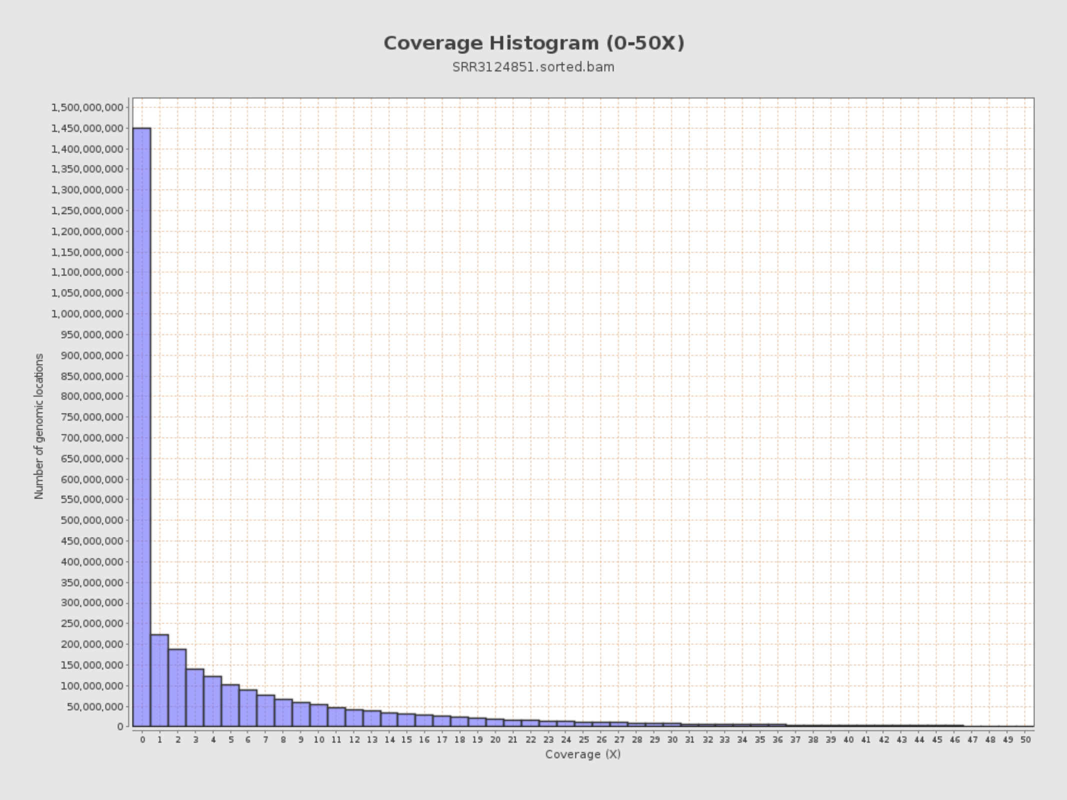
3. Results : Coverage across reference



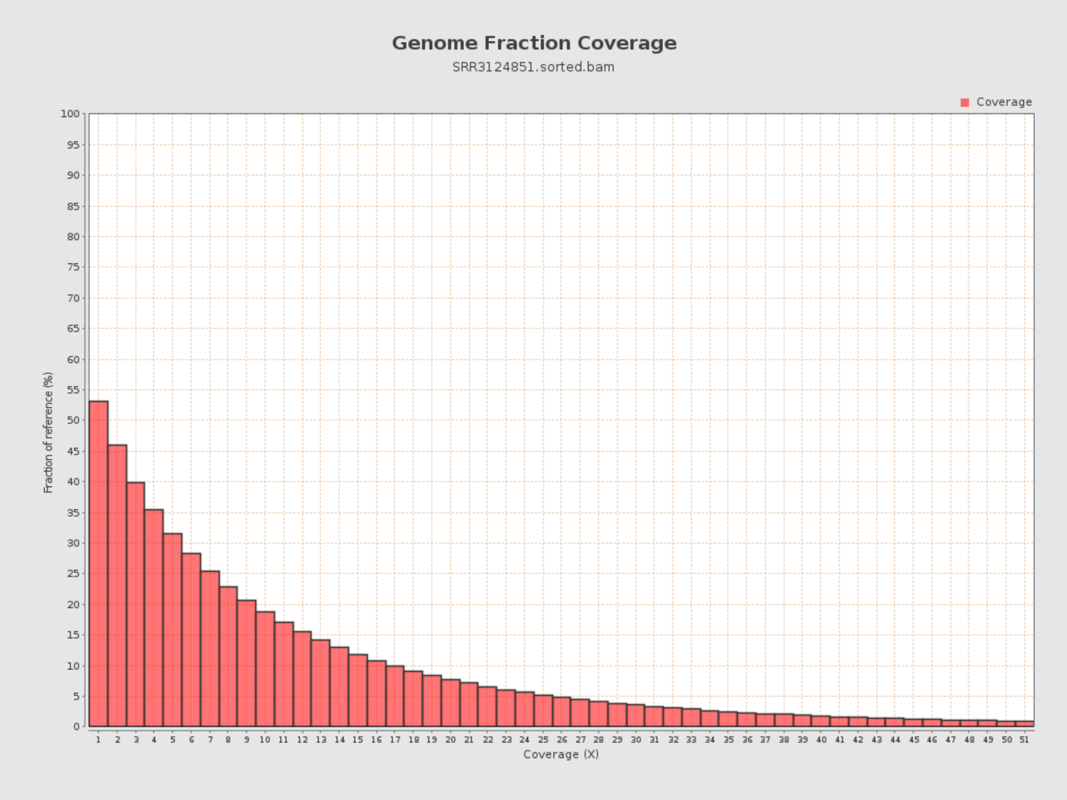
4. Results : Coverage Histogram



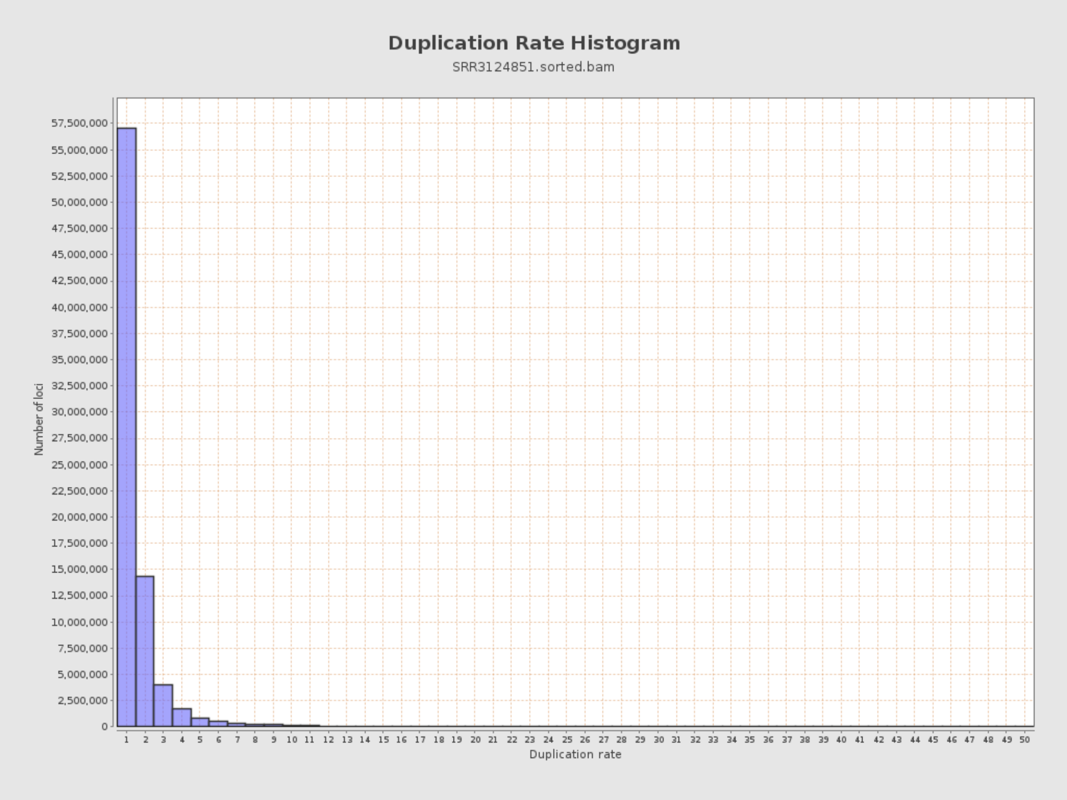
5. Results : Coverage Histogram (0-50X)



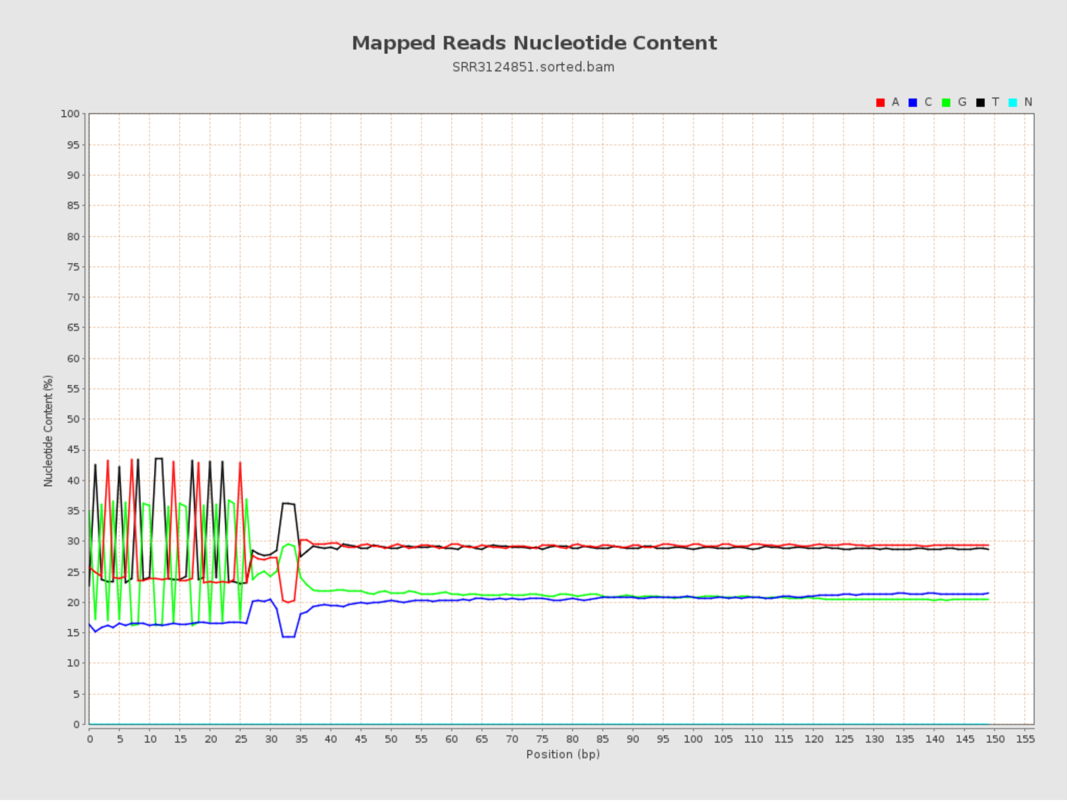
6. Results : Genome Fraction Coverage



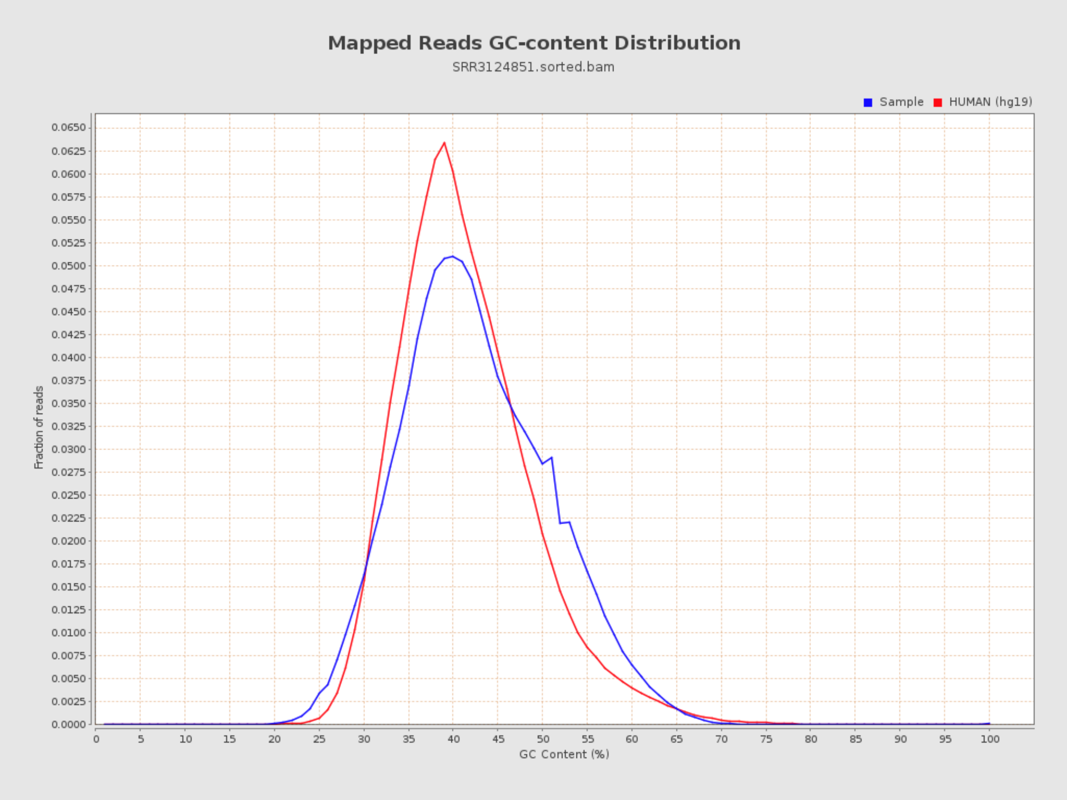
7. Results : Duplication Rate Histogram



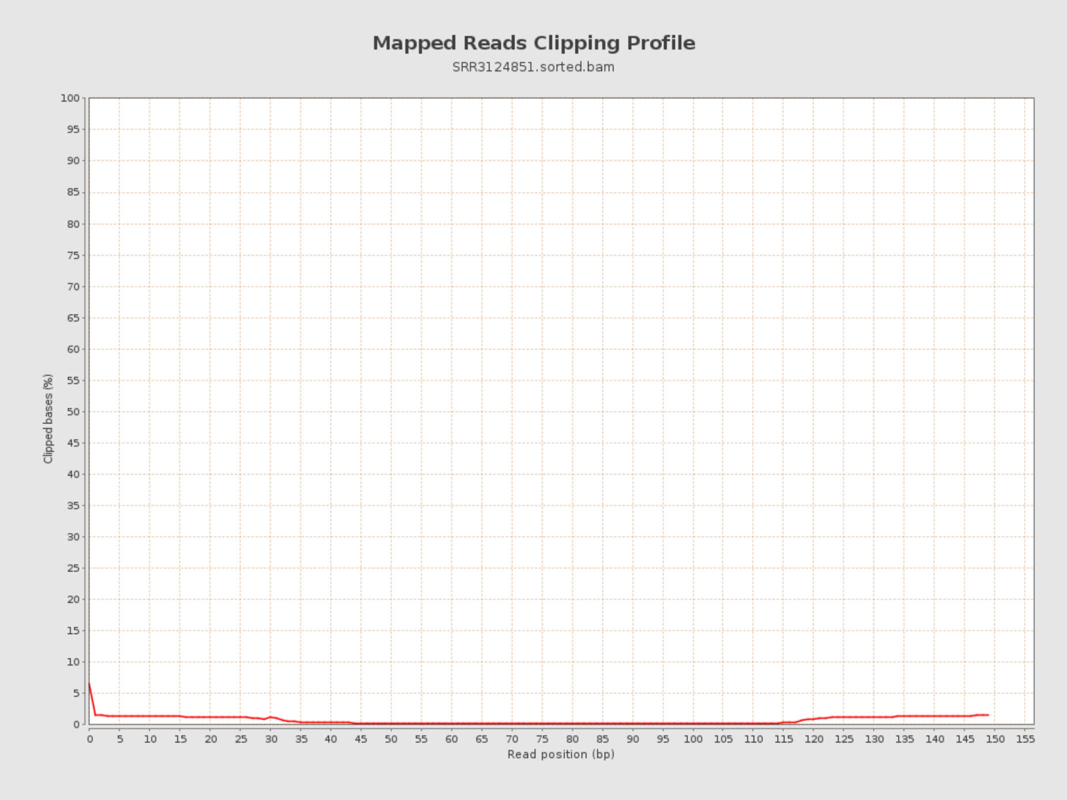
8. Results : Mapped Reads Nucleotide Content



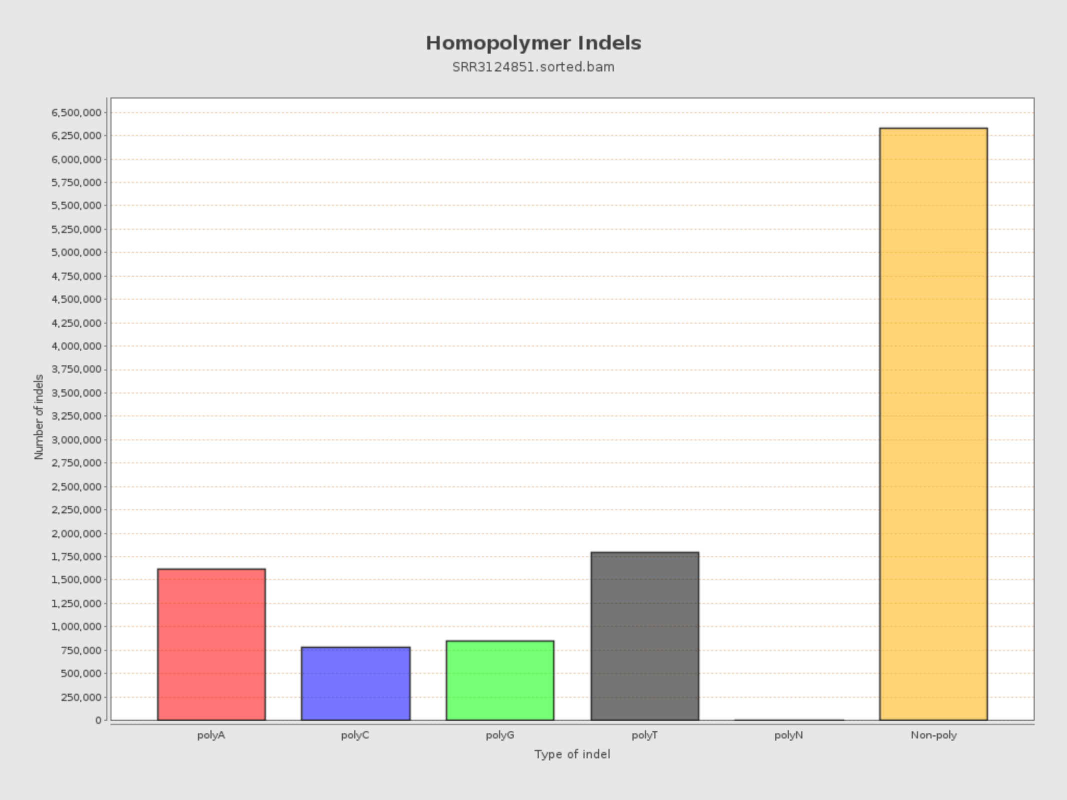
9. Results : Mapped Reads GC-content Distribution



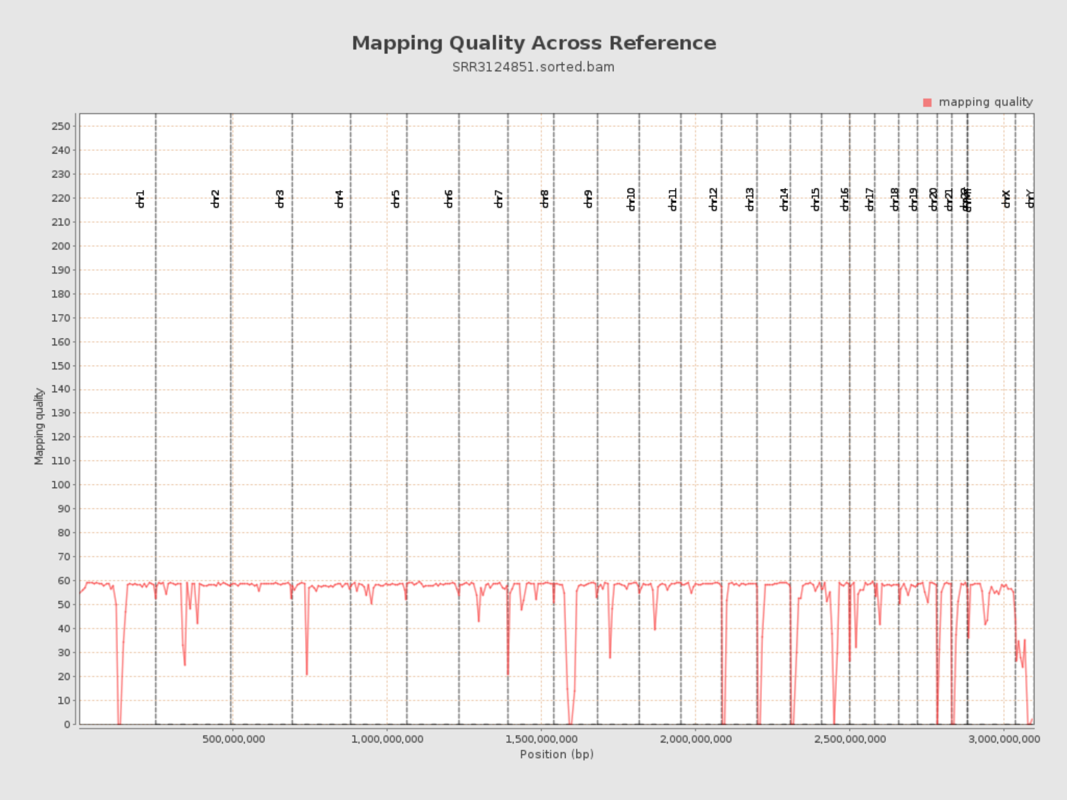
10. Results : Mapped Reads Clipping Profile



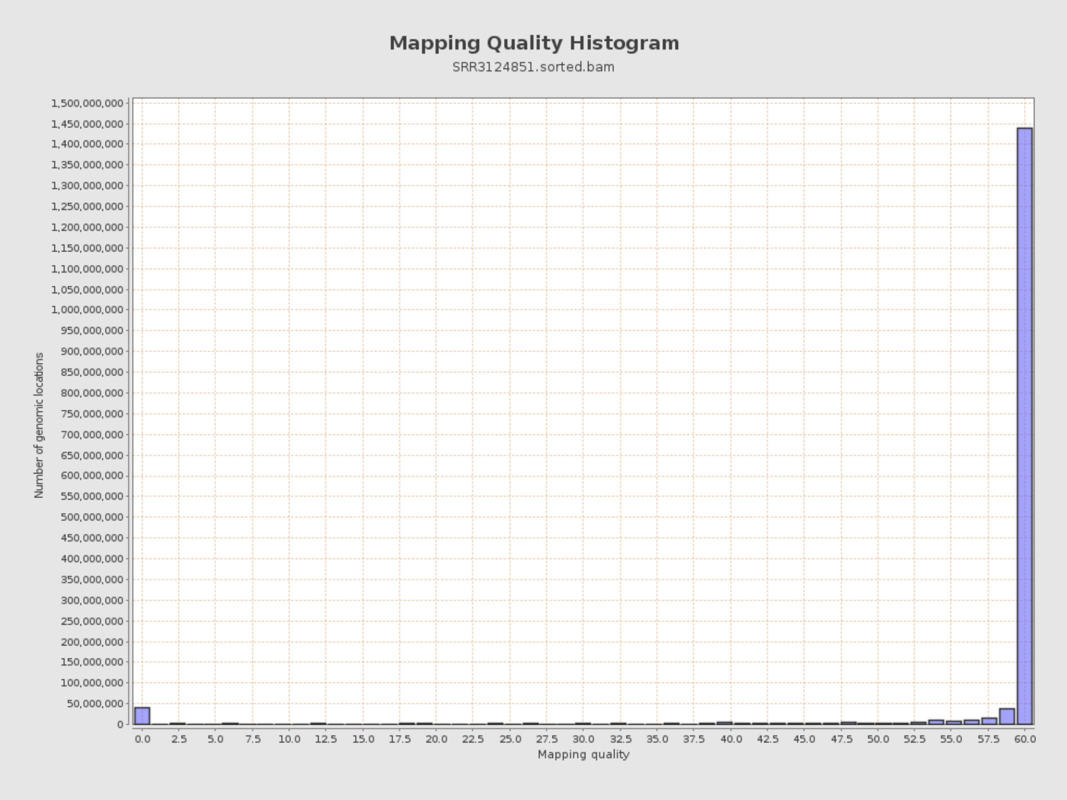
11. Results : Homopolymer Indels



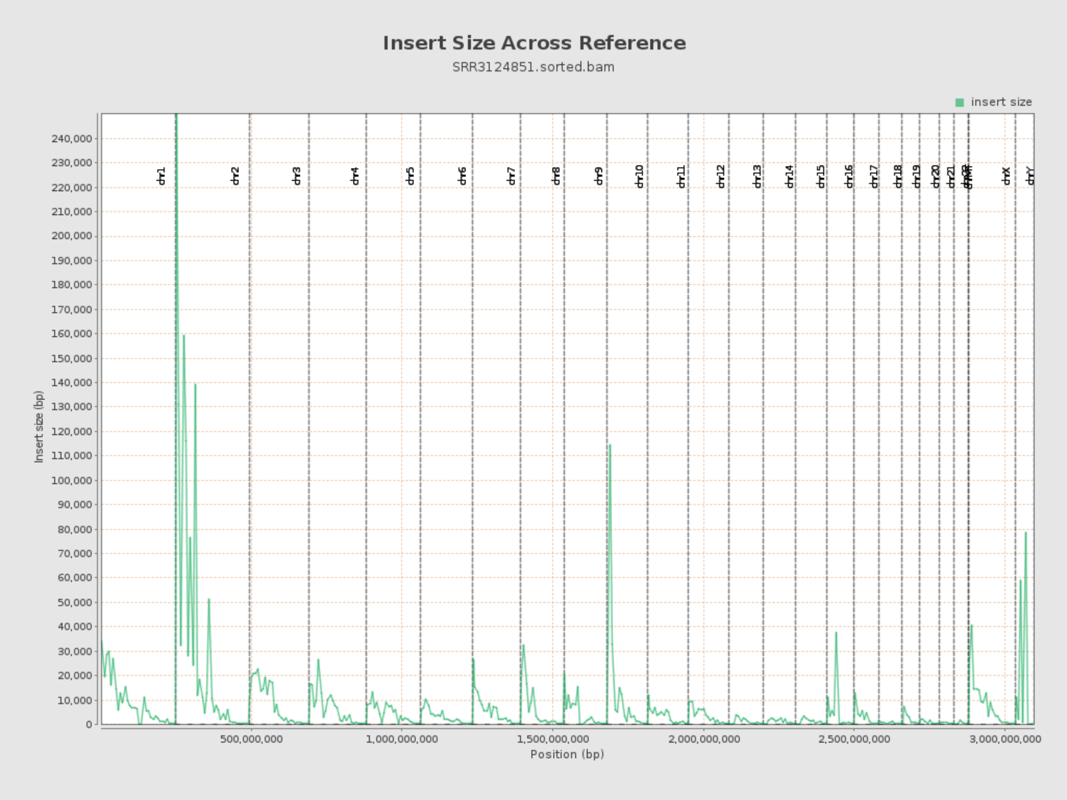
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram