Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 01:38:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124890.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_SRR3124890 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124890_1.fastq.gz SRR3124890_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 01:38:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124890.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,817,770
Mapped reads	1,783,986 / 98.14%
Unmapped reads	33,784 / 1.86%
Mapped paired reads	1,783,986 / 98.14%
Mapped reads, first in pair	892,876 / 49.12%
Mapped reads, second in pair	891,110 / 49.02%
Mapped reads, both in pair	1,778,040 / 97.81%
Mapped reads, singletons	5,946 / 0.33%
Secondary alignments	0
Supplementary alignments	14,277 / 0.79%
Read min/max/mean length	30 / 151 / 151.38
Duplicated reads (estimated)	265,186 / 14.59%
Duplication rate	14.8%
Clipped reads	1,316,561 / 72.43%

2.2. ACGT Content

Number/percentage of A's	70,040,368 / 29.05%
Number/percentage of C's	48,886,104 / 20.28%
Number/percentage of T's	70,777,583 / 29.36%
Number/percentage of G's	51,359,789 / 21.3%
Number/percentage of N's	24,620 / 0.01%

GC Percentage	41.58%

2.3. Coverage

Mean	0.0779
Standard Deviation	0.9393

2.4. Mapping Quality

Mean Mapping Quality	53.68

2.5. Insert size

Mean	61,555.34
Standard Deviation	2,424,422.12
P25/Median/P75	141 / 176 / 224

2.6. Mismatches and indels

General error rate	1.21%
Mismatches	2,840,101
Insertions	37,040
Mapped reads with at least one insertion	2%
Deletions	83,426
Mapped reads with at least one deletion	4.54%
Homopolymer indels	49.33%

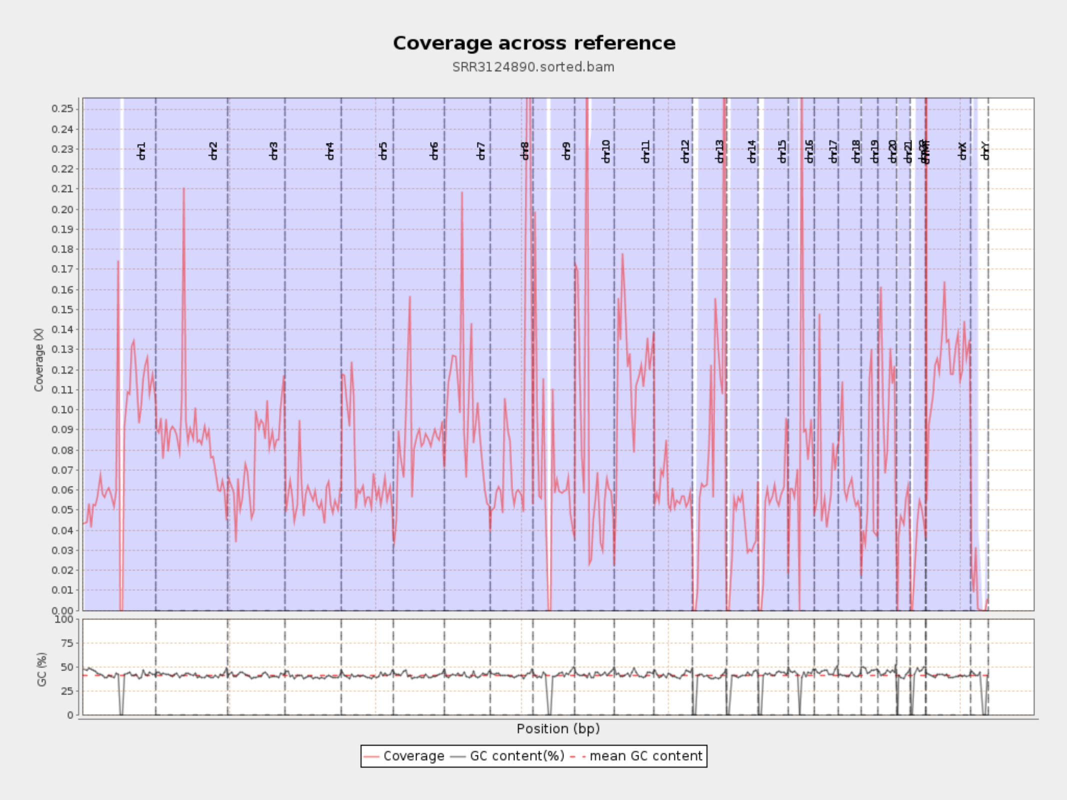
2.7. Chromosome stats

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

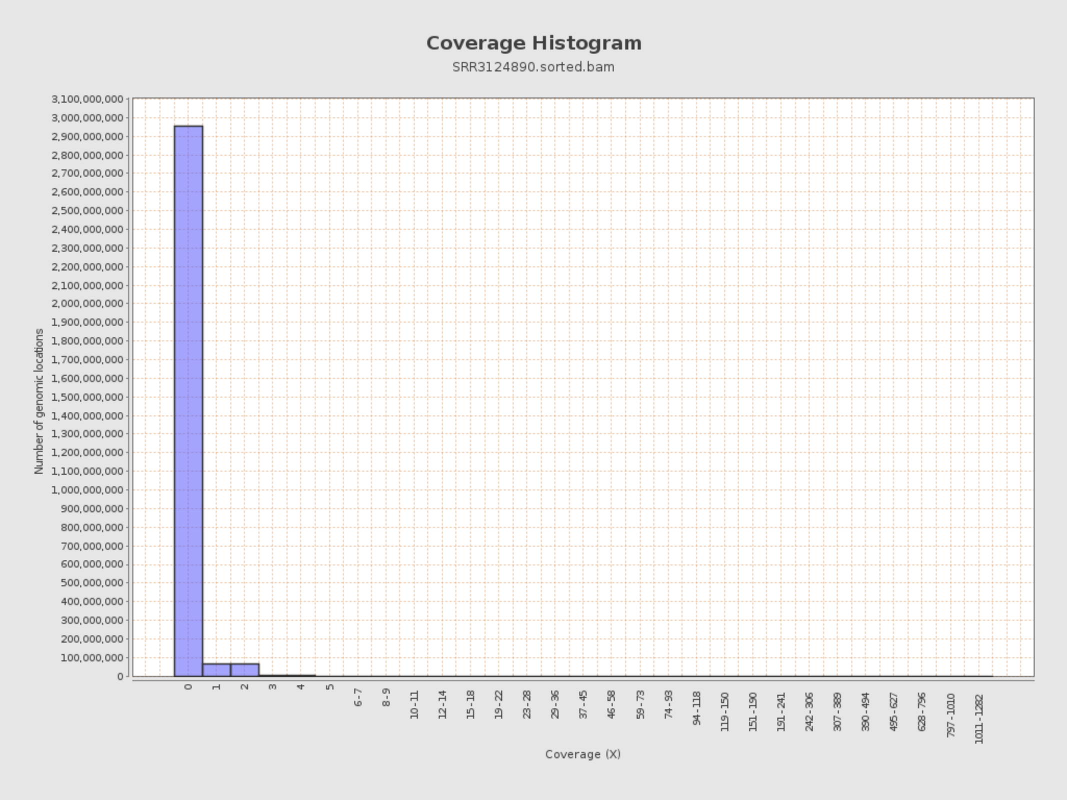
		bases	coverage	deviation
chr1	249250621	20139818	0.0808	1.1258
chr2	243199373	21150749	0.087	0.8572
chr3	198022430	14986451	0.0757	0.3869
chr4	191154276	10844164	0.0567	0.4757
chr5	180915260	12838236	0.071	0.3684
chr6	171115067	14655300	0.0856	0.6648
chr7	159138663	15956325	0.1003	1.4276
chr8	146364022	14176316	0.0969	0.4905
chr9	141213431	9396355	0.0665	1.104
chr10	135534747	11037918	0.0814	2.554
chr11	135006516	16289969	0.1207	0.9011
chr12	133851895	7748352	0.0579	0.3293
chr13	115169878	10960450	0.0952	0.4737
chr14	107349540	3922075	0.0365	0.2707
chr15	102531392	5098522	0.0497	0.3048
chr16	90354753	7460910	0.0826	1.3626
chr17	81195210	5414837	0.0667	1.0306
chr18	78077248	5267605	0.0675	1.1557
chr19	59128983	3577047	0.0605	0.6684
chr20	63025520	6941592	0.1101	0.4806
chr21	48129895	2067418	0.043	0.3322
chr22	51304566	1718891	0.0335	0.2511
chrMT	16571	119802	7.2296	4.9776
chrX	155270560	18988598	0.1223	0.5945

chrY	59373566	477917	0.008	0.498

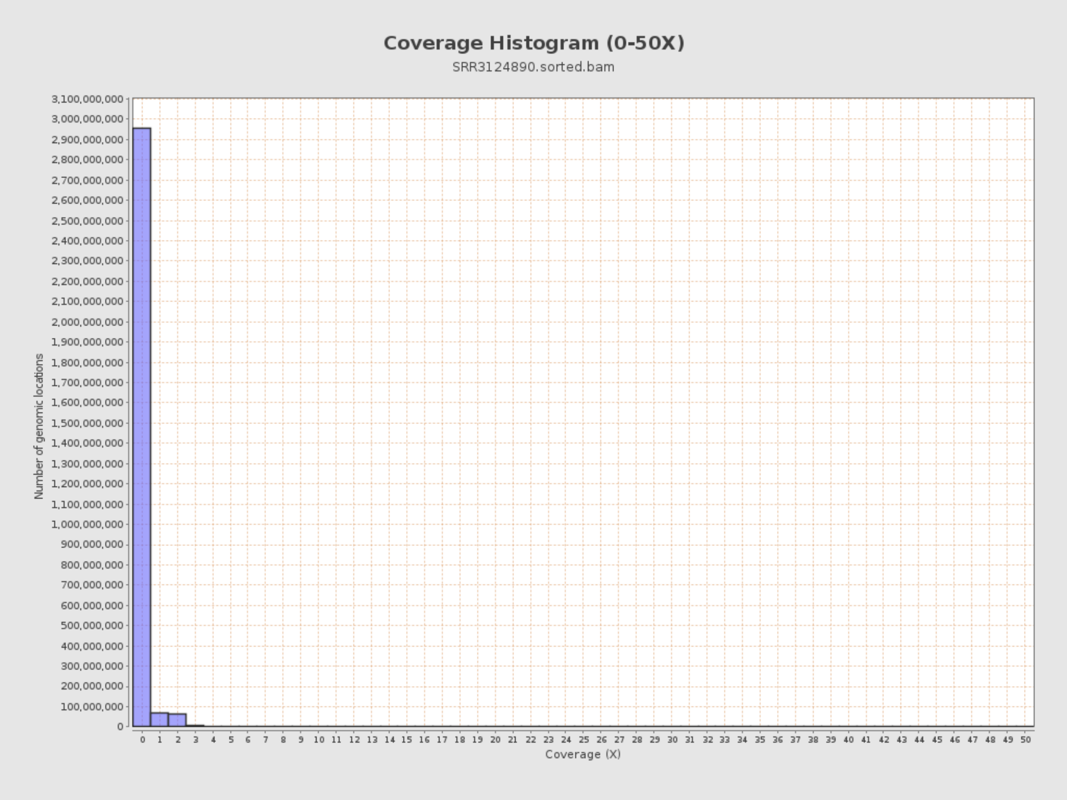
3. Results : Coverage across reference



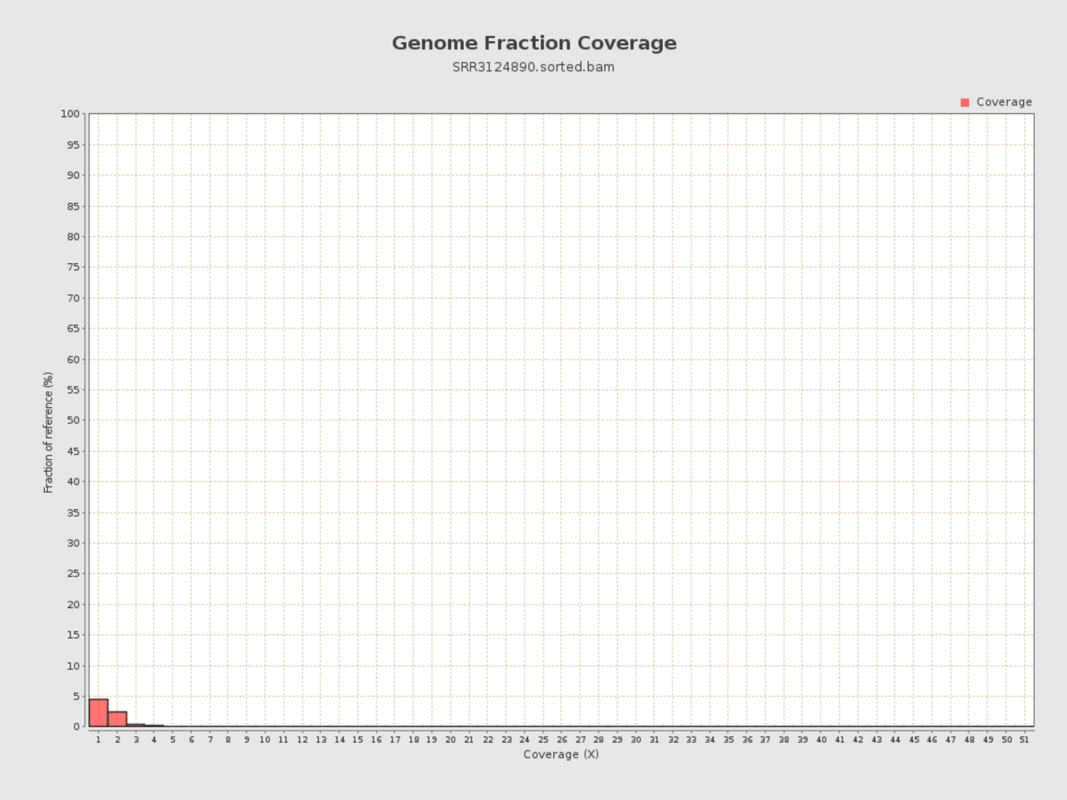
4. Results : Coverage Histogram



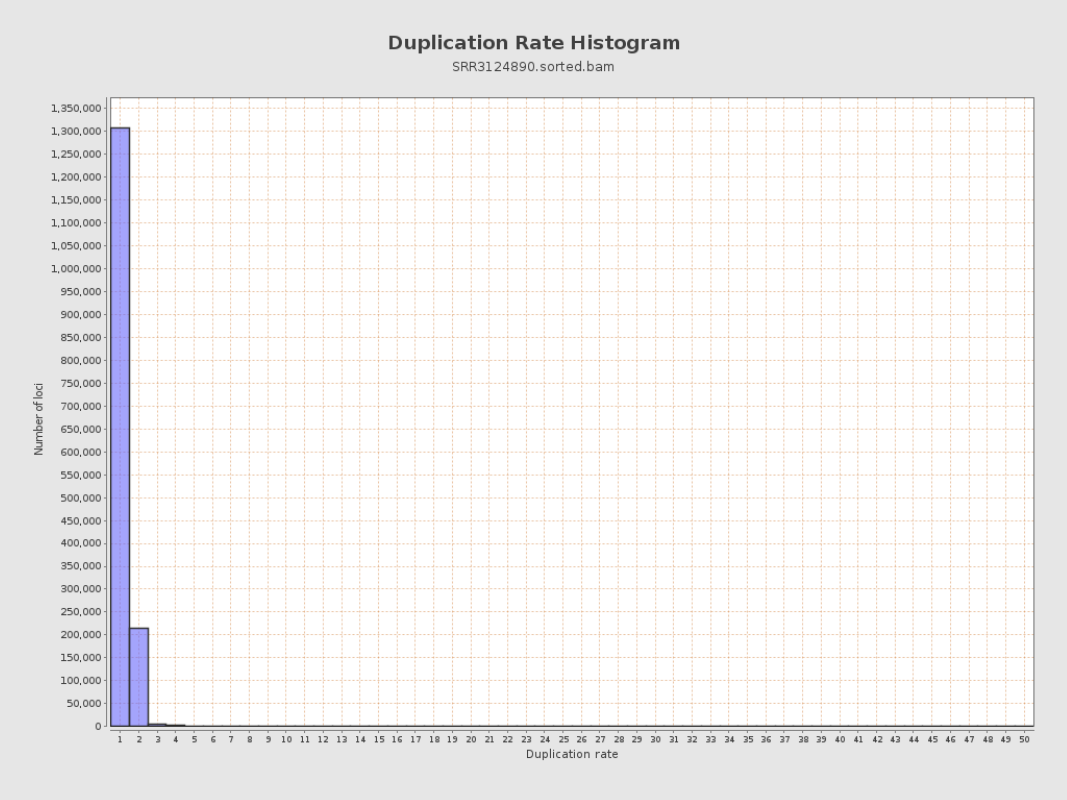
5. Results : Coverage Histogram (0-50X)



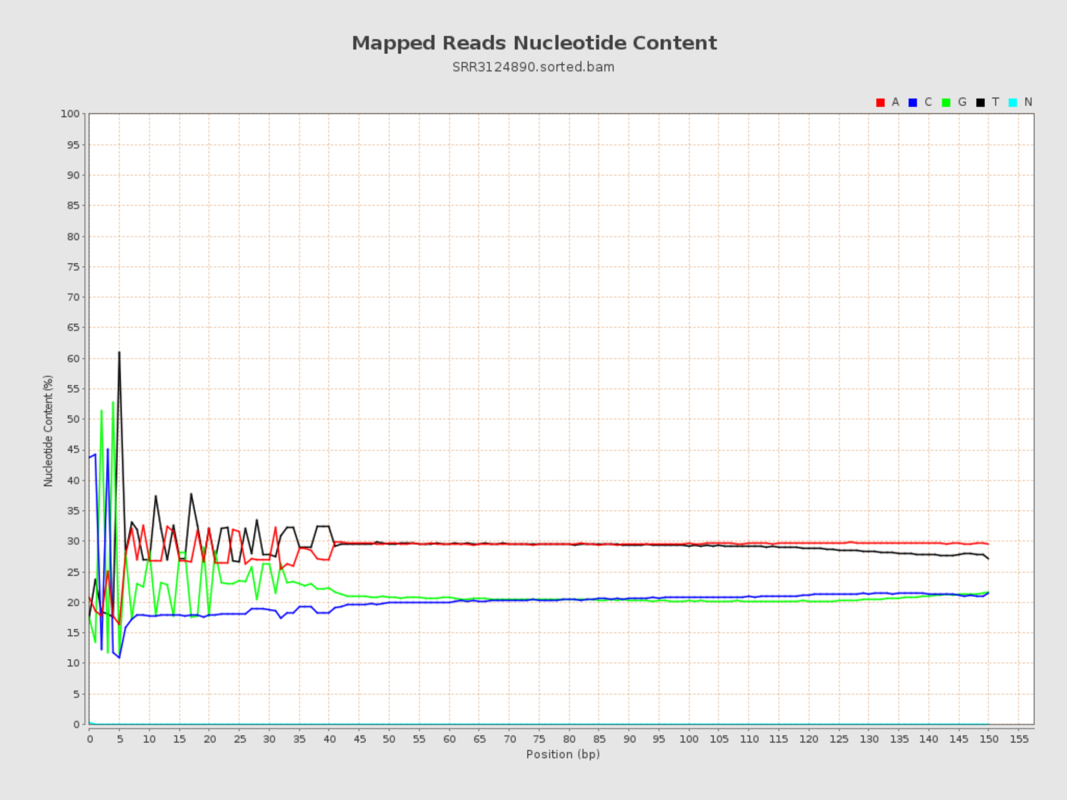
6. Results : Genome Fraction Coverage



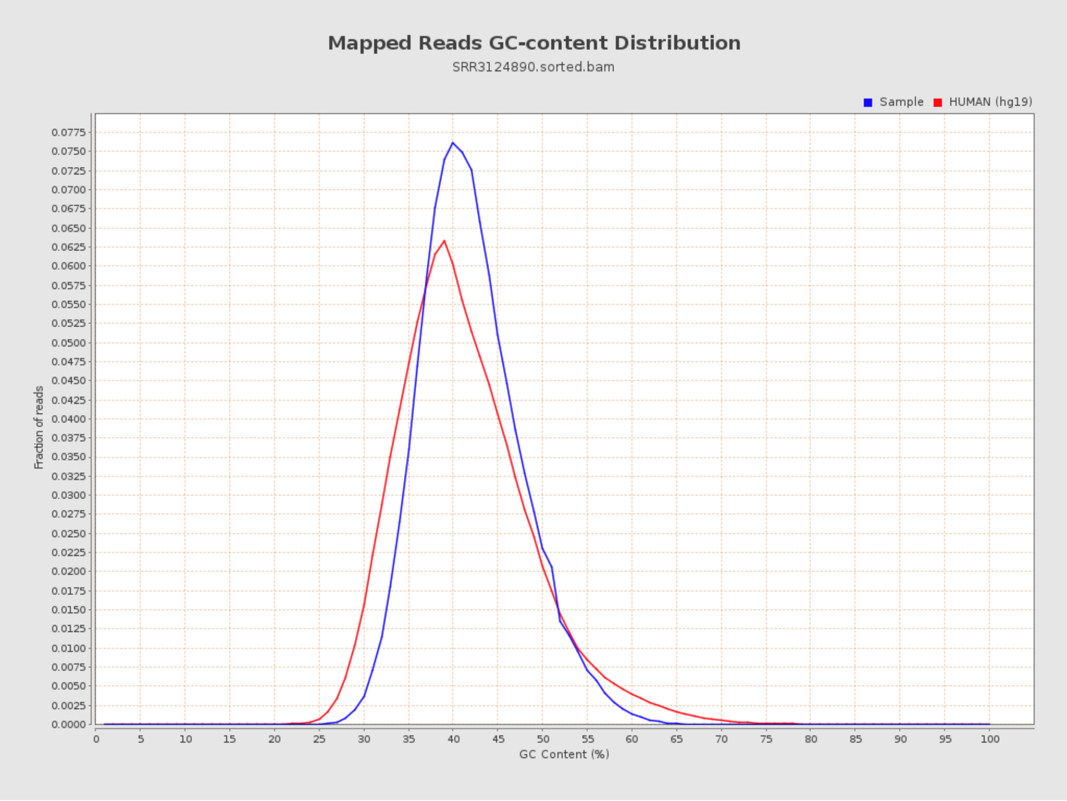
7. Results : Duplication Rate Histogram



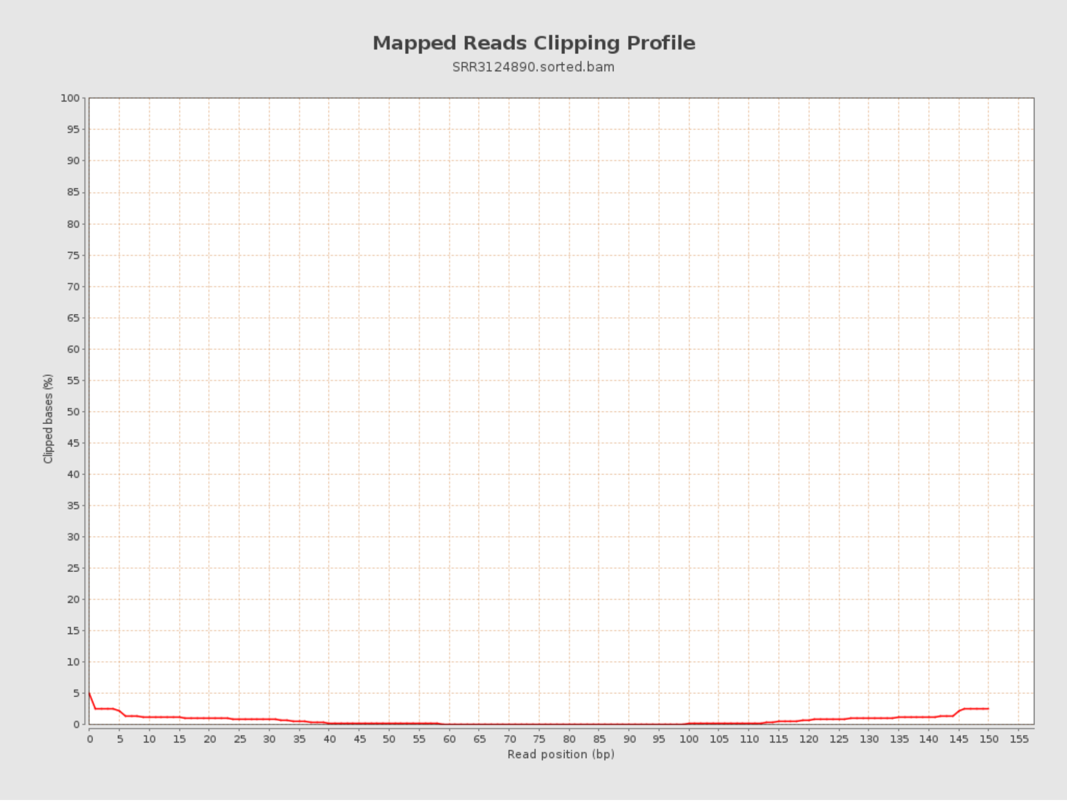
8. Results : Mapped Reads Nucleotide Content



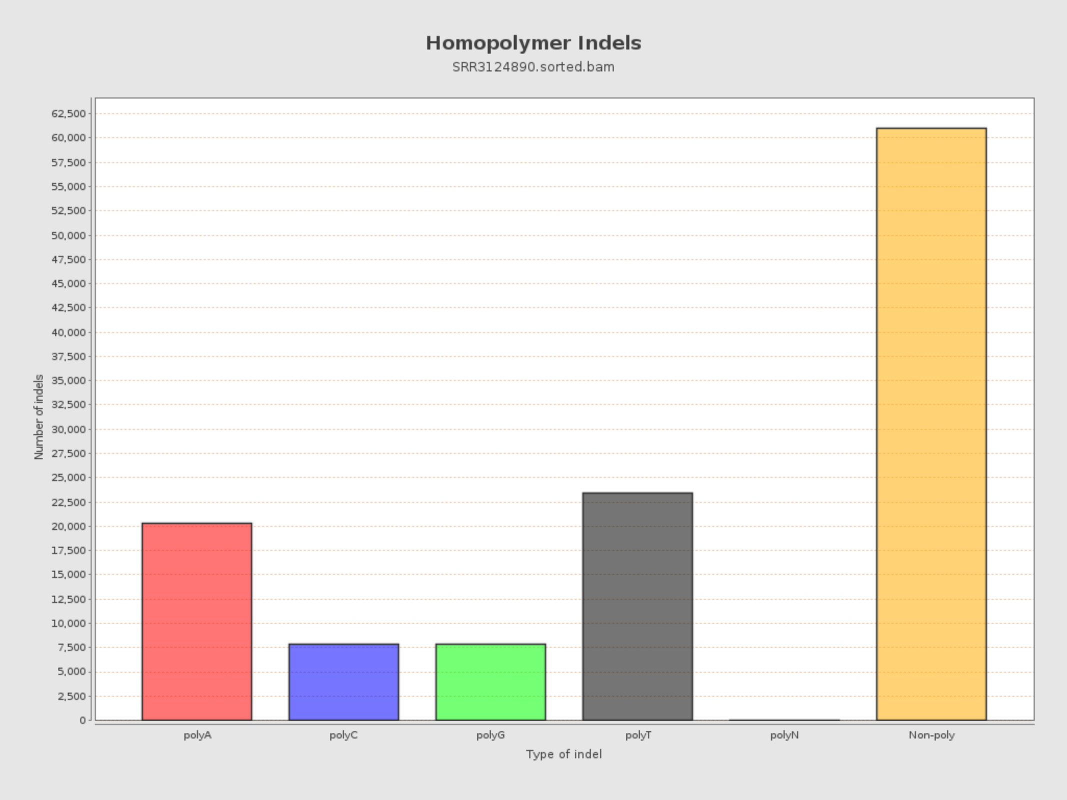
9. Results : Mapped Reads GC-content Distribution



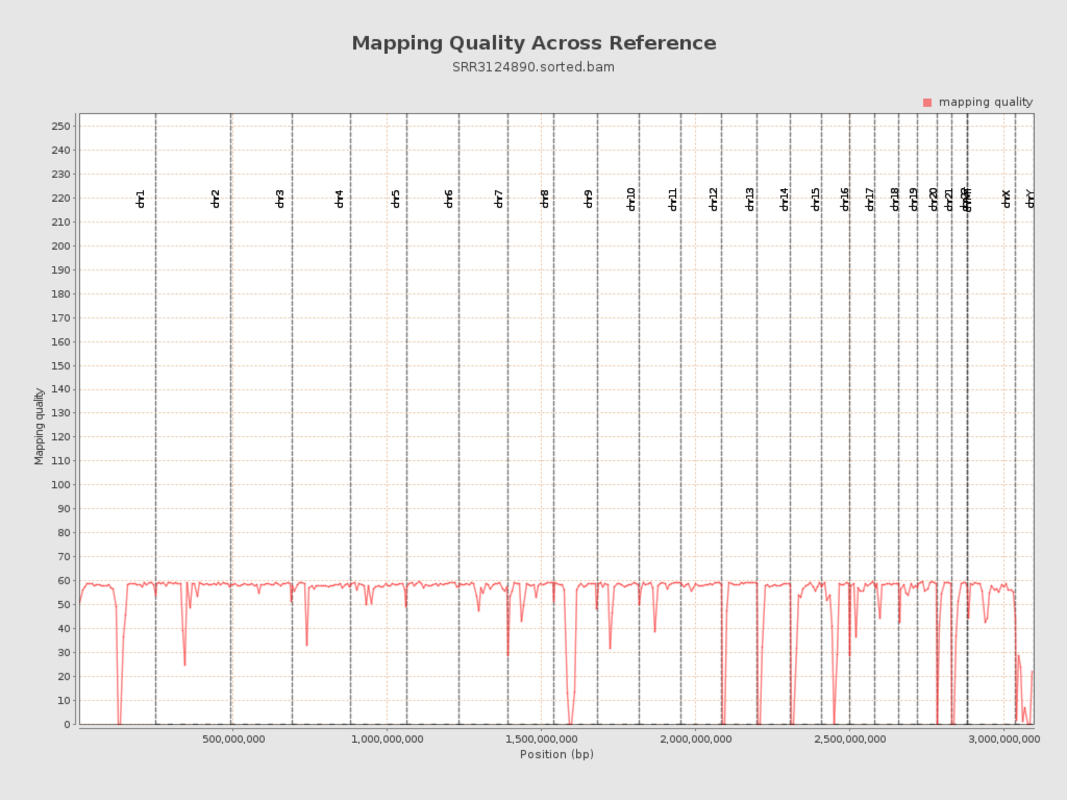
10. Results : Mapped Reads Clipping Profile



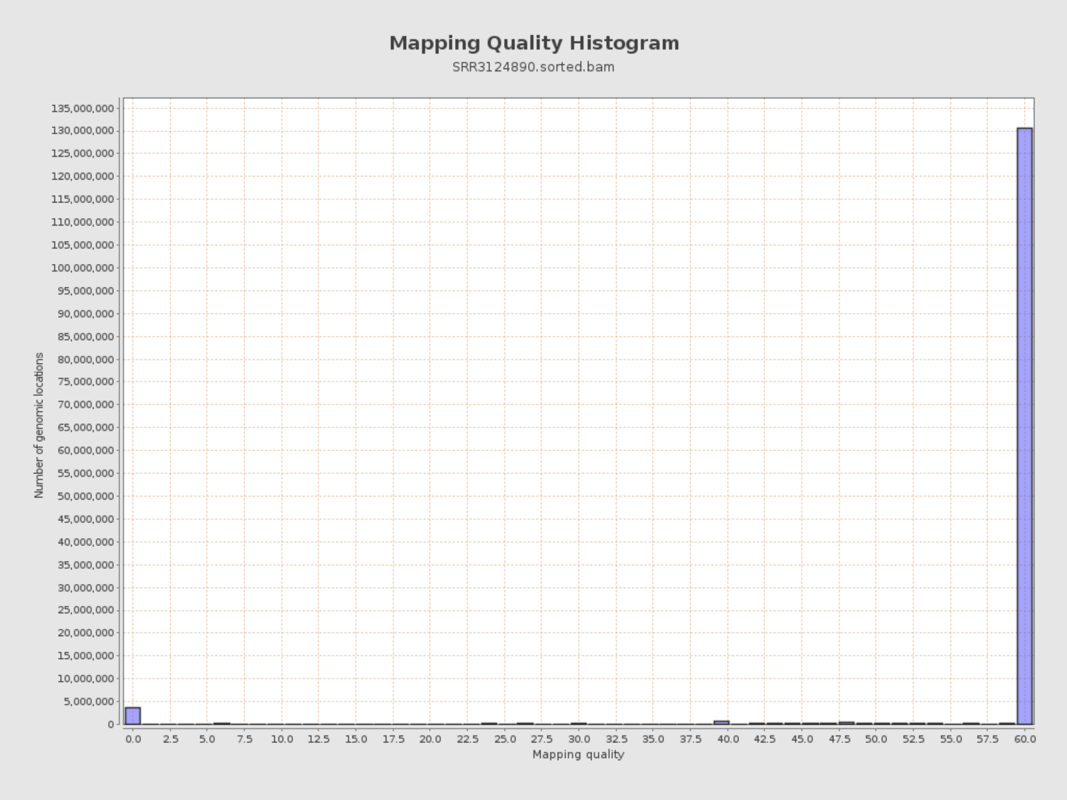
11. Results : Homopolymer Indels



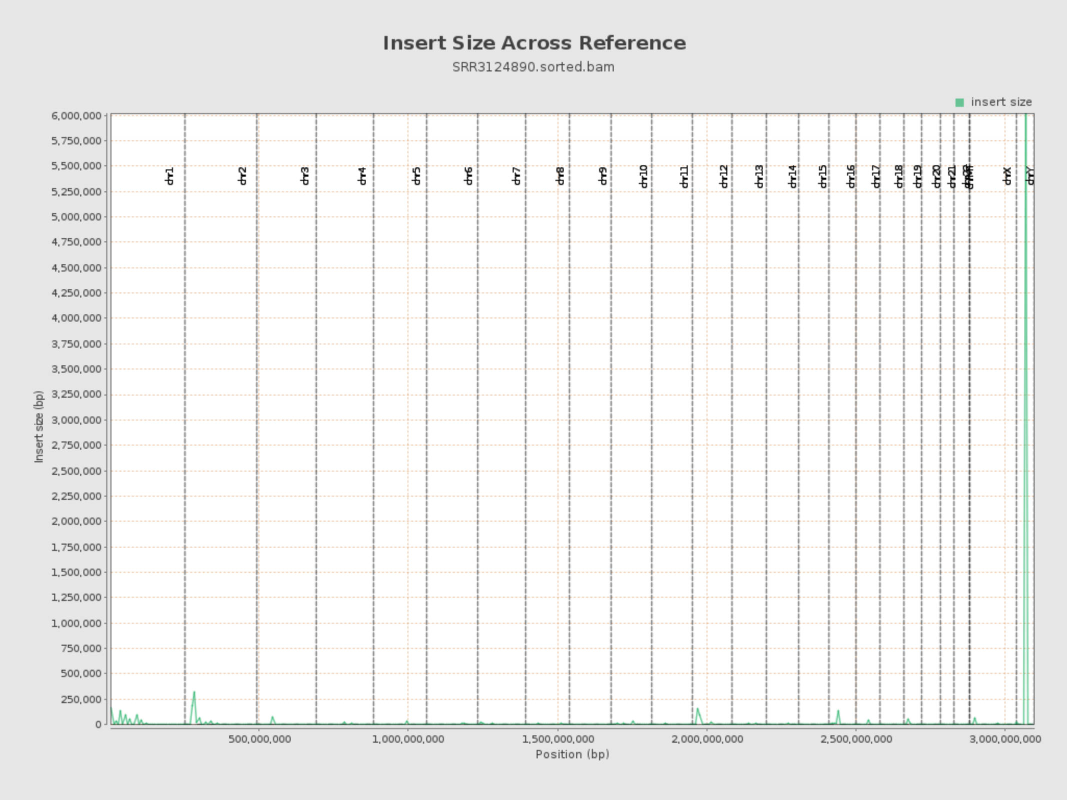
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram