Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 00:50:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124883.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_SRR3124883 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124883_1.fastq.gz SRR3124883_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 00:50:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124883.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,585,196
Mapped reads	3,553,936 / 99.13%
Unmapped reads	31,260 / 0.87%
Mapped paired reads	3,553,936 / 99.13%
Mapped reads, first in pair	1,784,217 / 49.77%
Mapped reads, second in pair	1,769,719 / 49.36%
Mapped reads, both in pair	3,537,240 / 98.66%
Mapped reads, singletons	16,696 / 0.47%
Secondary alignments	0
Supplementary alignments	45,902 / 1.28%
Read min/max/mean length	30 / 151 / 151.67
Duplicated reads (estimated)	461,429 / 12.87%
Duplication rate	10.8%
Clipped reads	1,259,417 / 35.13%

2.2. ACGT Content

Number/percentage of A's	148,204,757 / 29.09%
Number/percentage of C's	105,254,958 / 20.66%
Number/percentage of T's	146,666,608 / 28.79%
Number/percentage of G's	109,301,403 / 21.45%
Number/percentage of N's	47,198 / 0.01%

GC Percentage	42.11%

2.3. Coverage

Mean	0.1647
Standard Deviation	2.4027

2.4. Mapping Quality

Mean Mapping Quality	53.78

2.5. Insert size

Mean	97,843.46
Standard Deviation	3,020,549.26
P25/Median/P75	151 / 184 / 238

2.6. Mismatches and indels

General error rate	0.85%
Mismatches	4,165,068
Insertions	70,465
Mapped reads with at least one insertion	1.89%
Deletions	150,744
Mapped reads with at least one deletion	4.1%
Homopolymer indels	49.15%

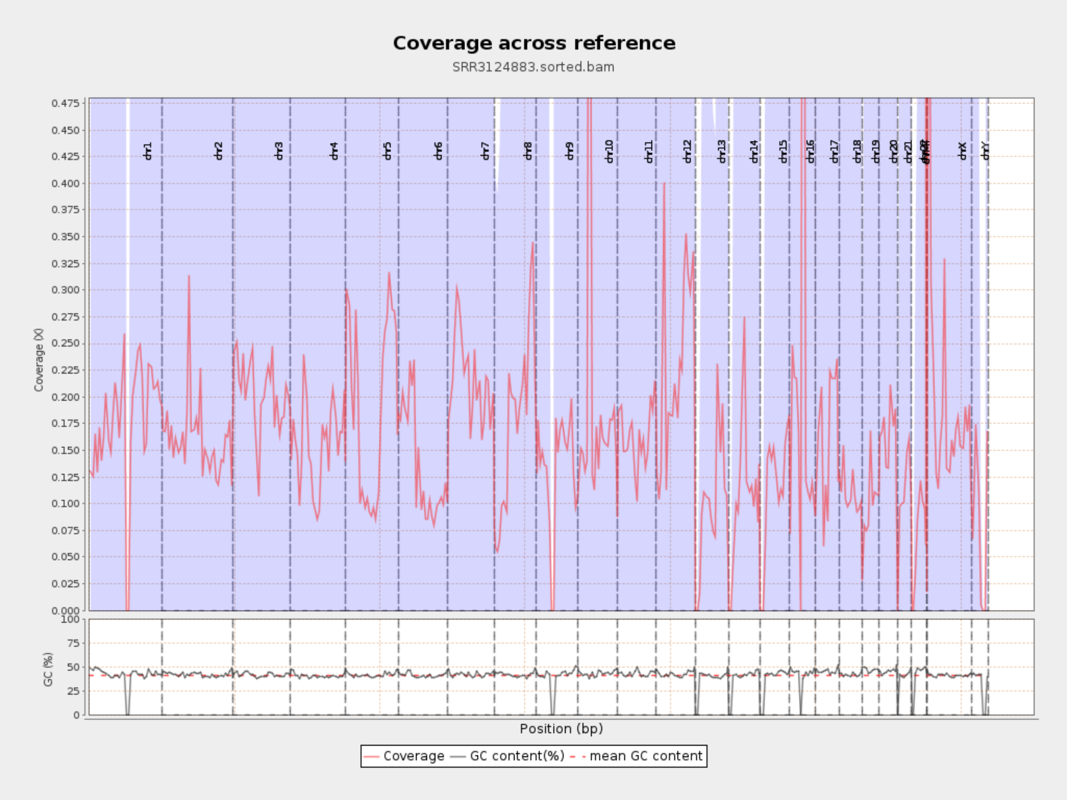
2.7. Chromosome stats

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

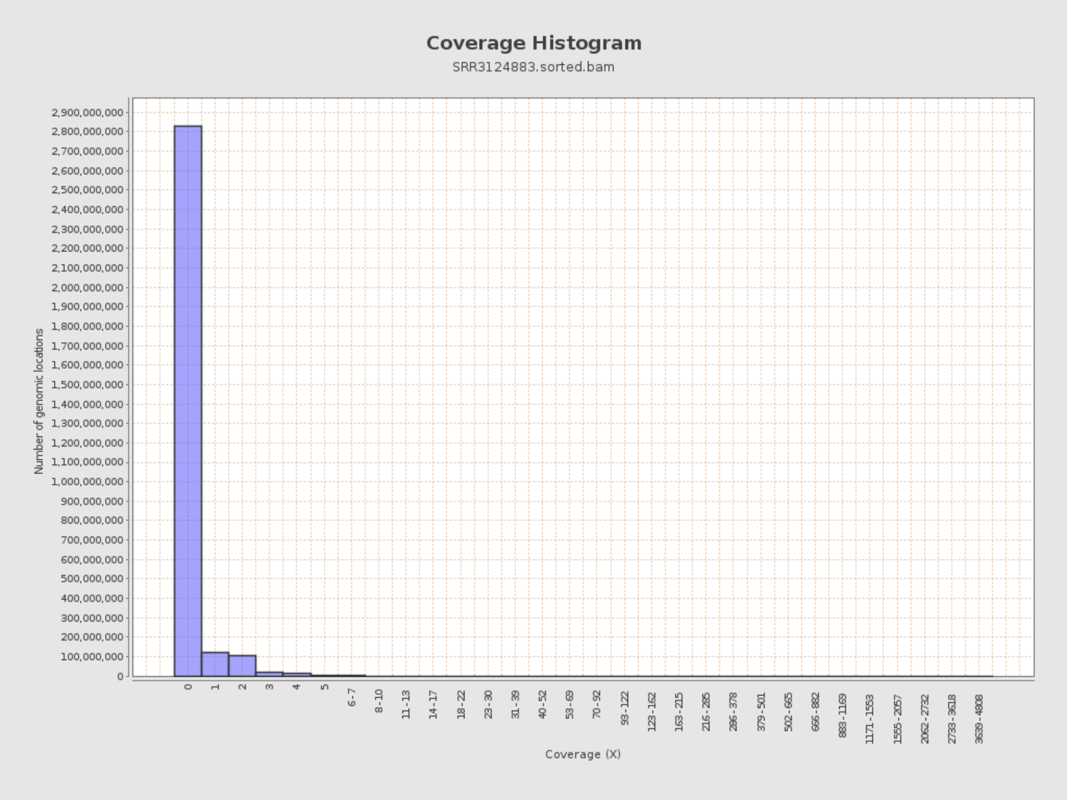
		bases	**coverage**	**deviation**
chr1	249250621	44058861	0.1768	1.169
chr2	243199373	39275156	0.1615	1.3191
chr3	198022430	40242308	0.2032	0.7776
chr4	191154276	29492099	0.1543	0.9024
chr5	180915260	34911699	0.193	0.6746
chr6	171115067	23402559	0.1368	0.7095
chr7	159138663	34622194	0.2176	1.6077
chr8	146364022	26449885	0.1807	0.6975
chr9	141213431	18777836	0.133	1.6625
chr10	135534747	27042872	0.1995	8.8275
chr11	135006516	21752151	0.1611	1.4998
chr12	133851895	30720832	0.2295	0.7473
chr13	115169878	11372941	0.0987	0.4599
chr14	107349540	11813943	0.1101	0.5008
chr15	102531392	11619960	0.1133	0.4915
chr16	90354753	20659842	0.2287	6.6099
chr17	81195210	13250526	0.1632	1.4384
chr18	78077248	8649016	0.1108	1.8902
chr19	59128983	5880328	0.0994	0.7578
chr20	63025520	10422483	0.1654	0.6606
chr21	48129895	5240766	0.1089	0.6573
chr22	51304566	3513092	0.0685	0.3946
chrMT	16571	221650	13.3758	8.4301
chrX	155270560	31756498	0.2045	1.0765

chrY	59373566	4626287	0.0779	1.3028

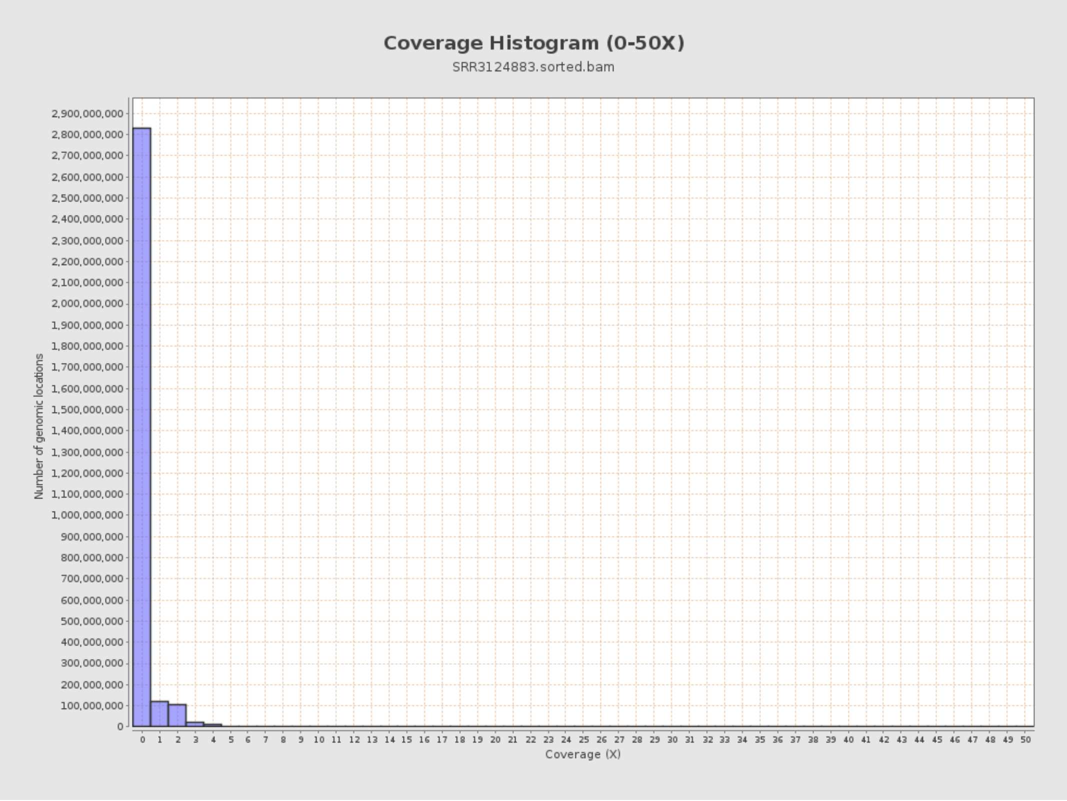
3. Results : Coverage across reference



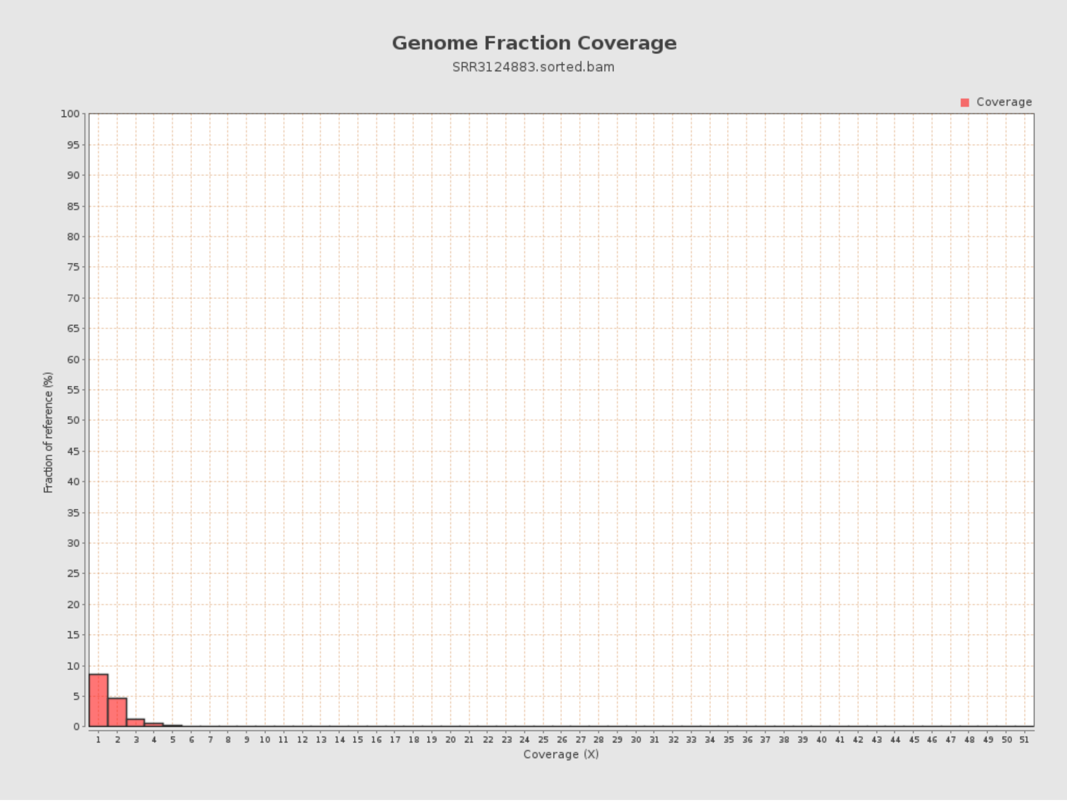
4. Results : Coverage Histogram



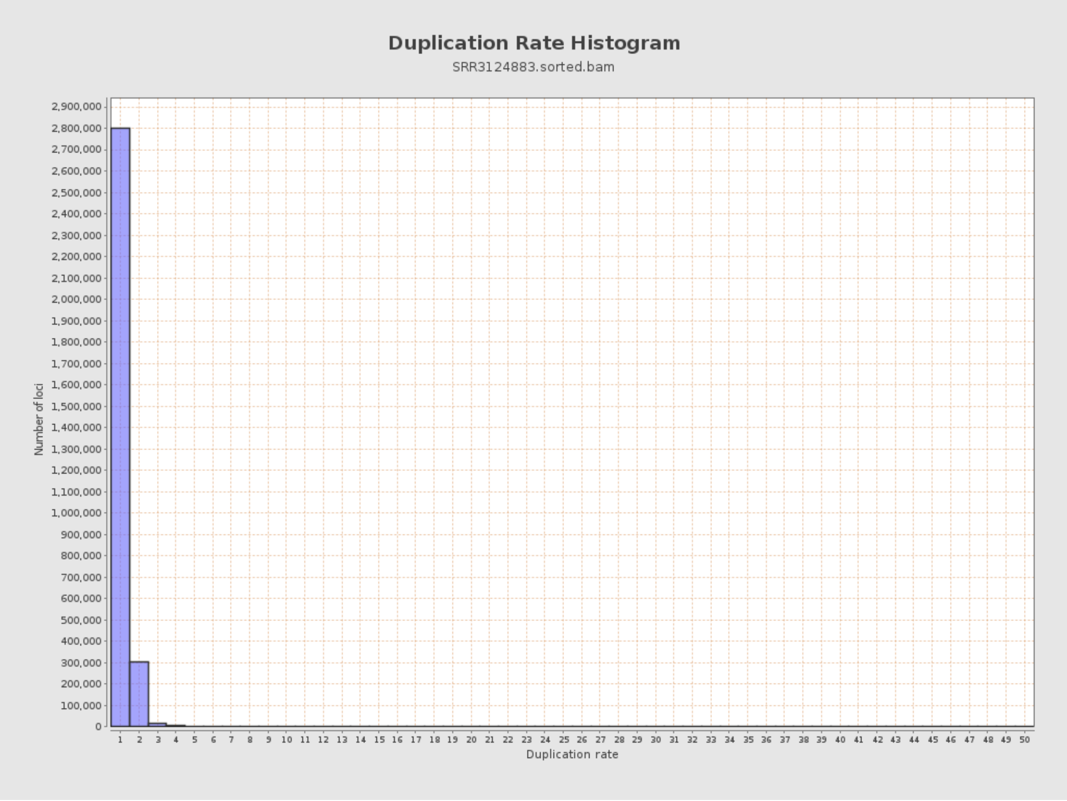
5. Results : Coverage Histogram (0-50X)



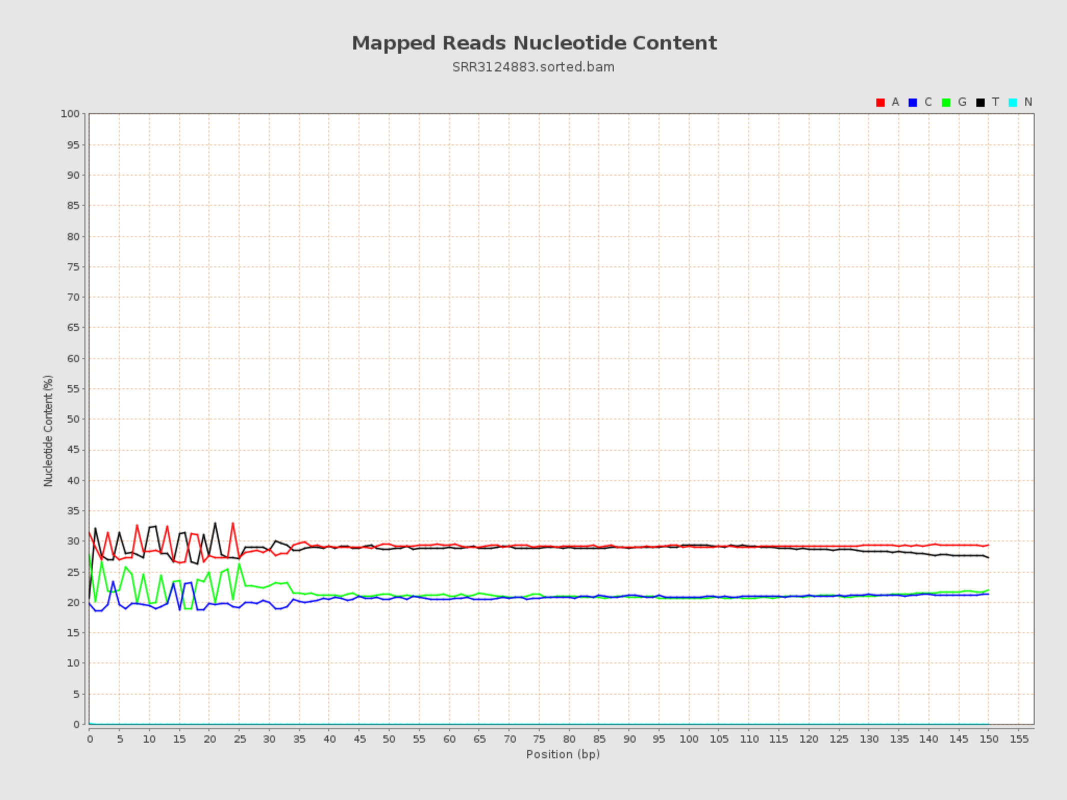
6. Results : Genome Fraction Coverage



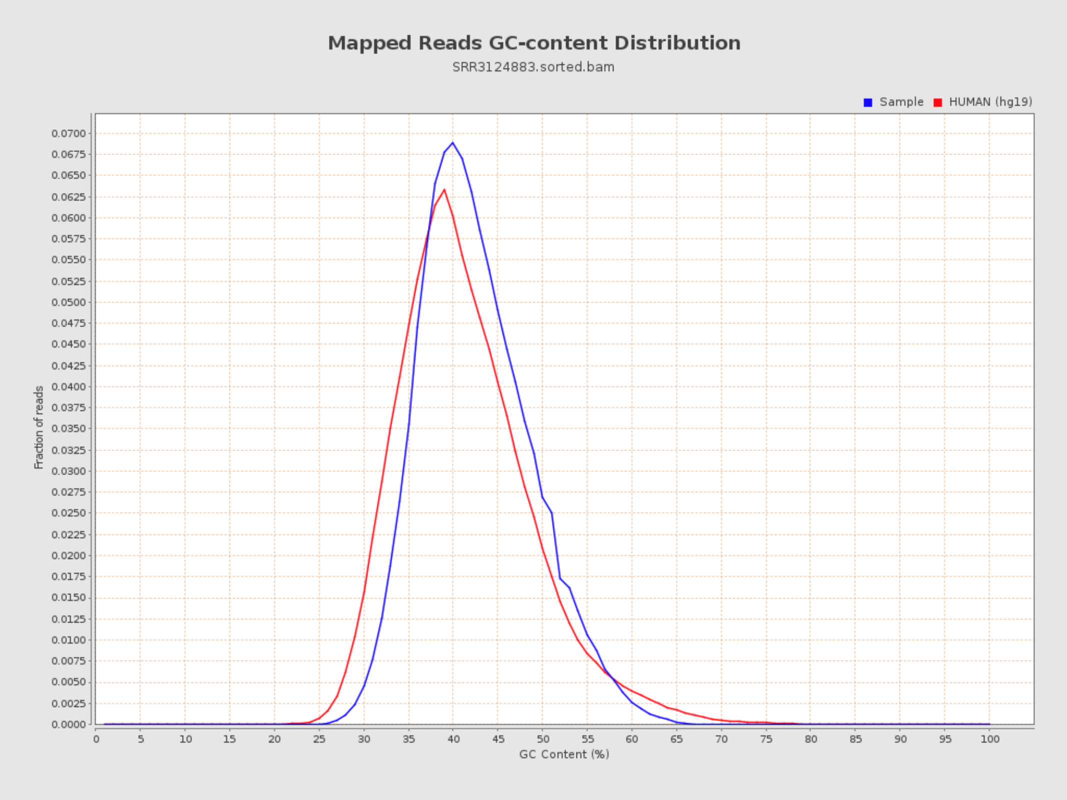
7. Results : Duplication Rate Histogram



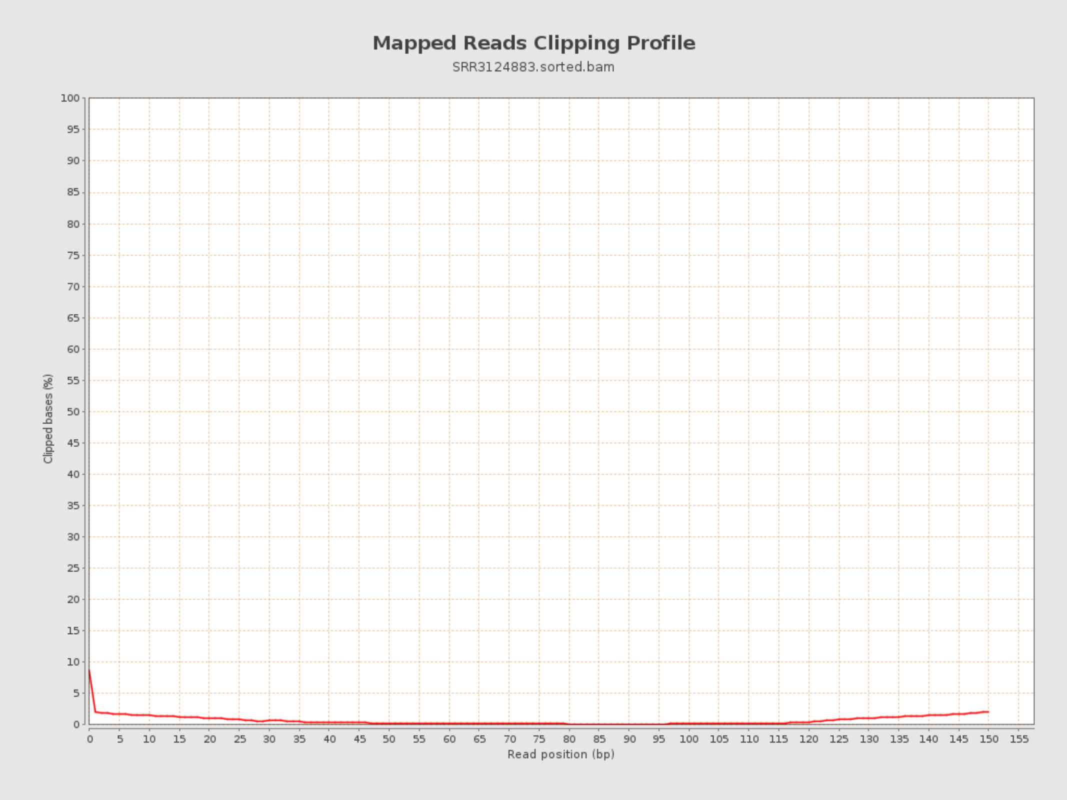
8. Results : Mapped Reads Nucleotide Content



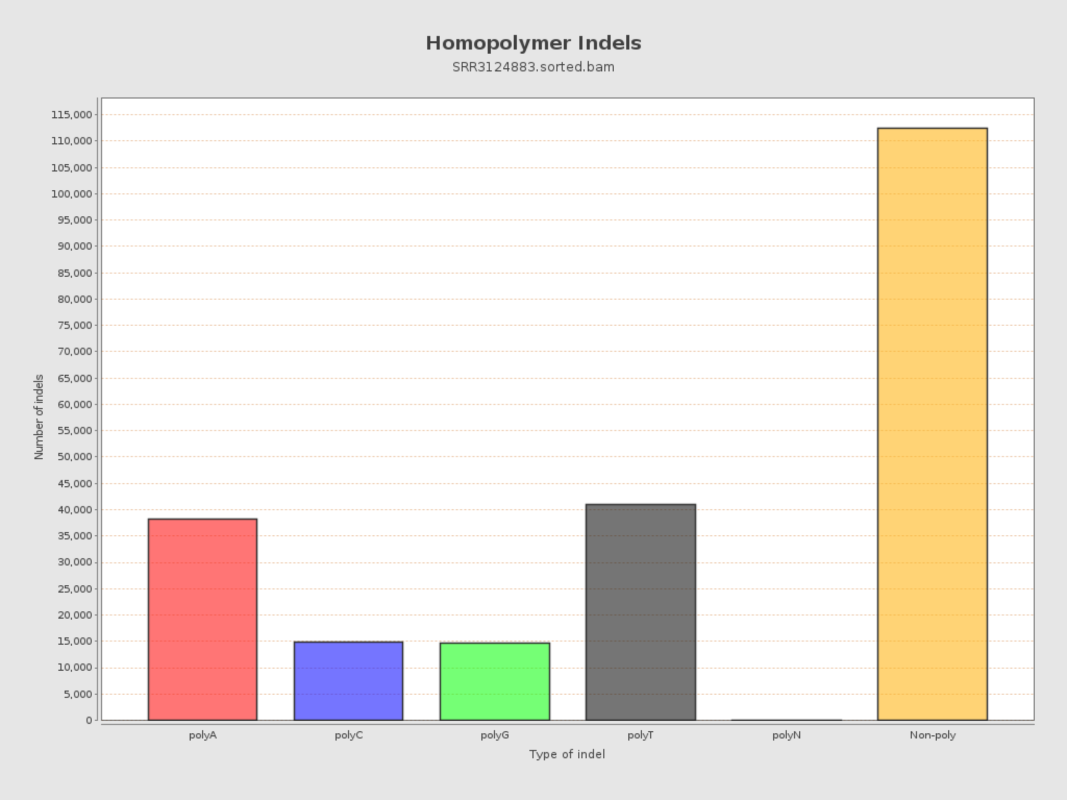
9. Results : Mapped Reads GC-content Distribution



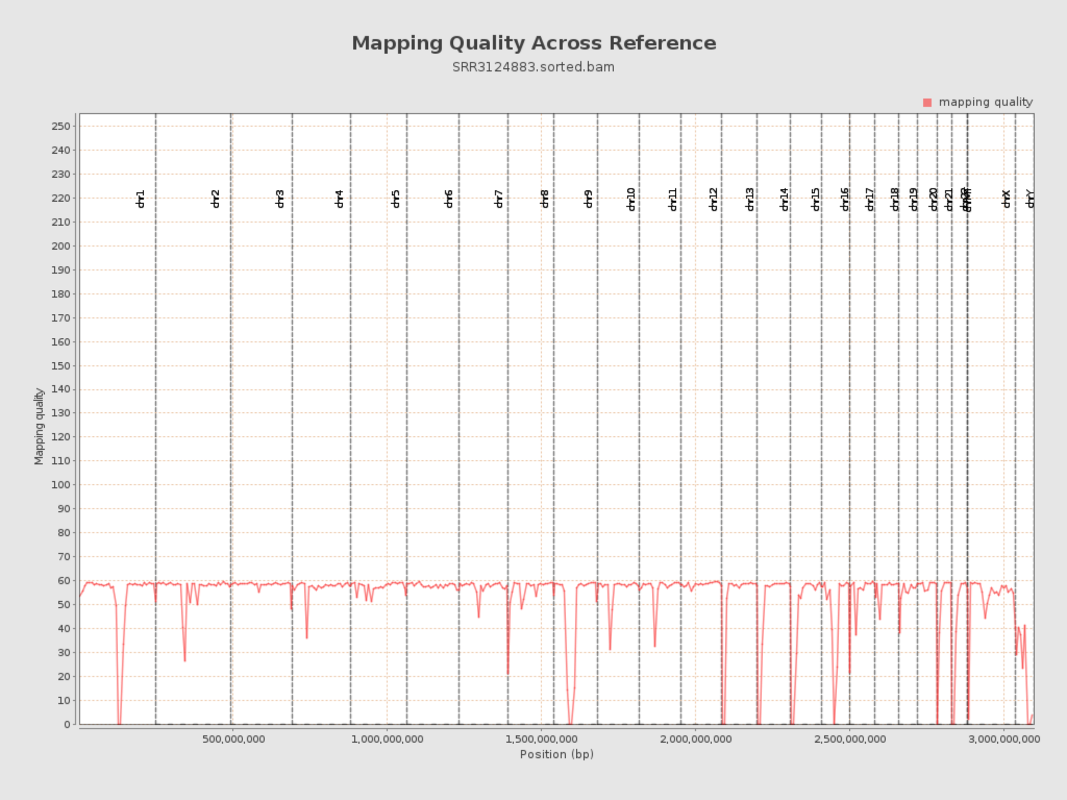
10. Results : Mapped Reads Clipping Profile



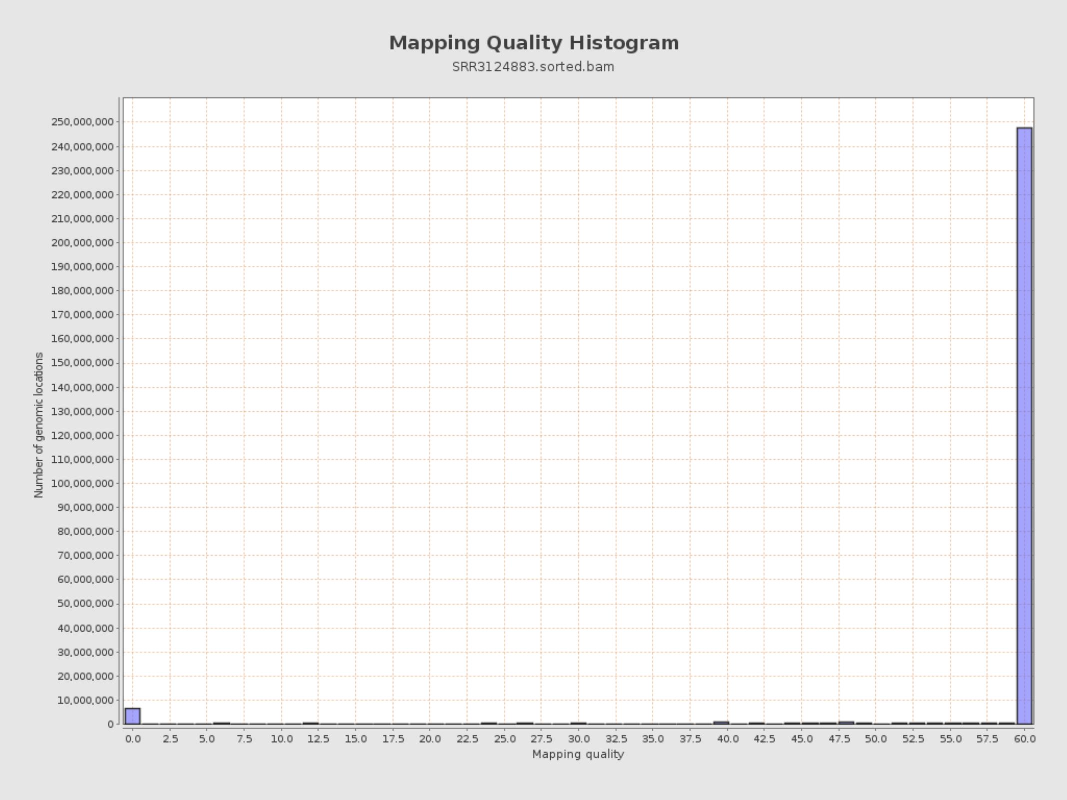
11. Results : Homopolymer Indels



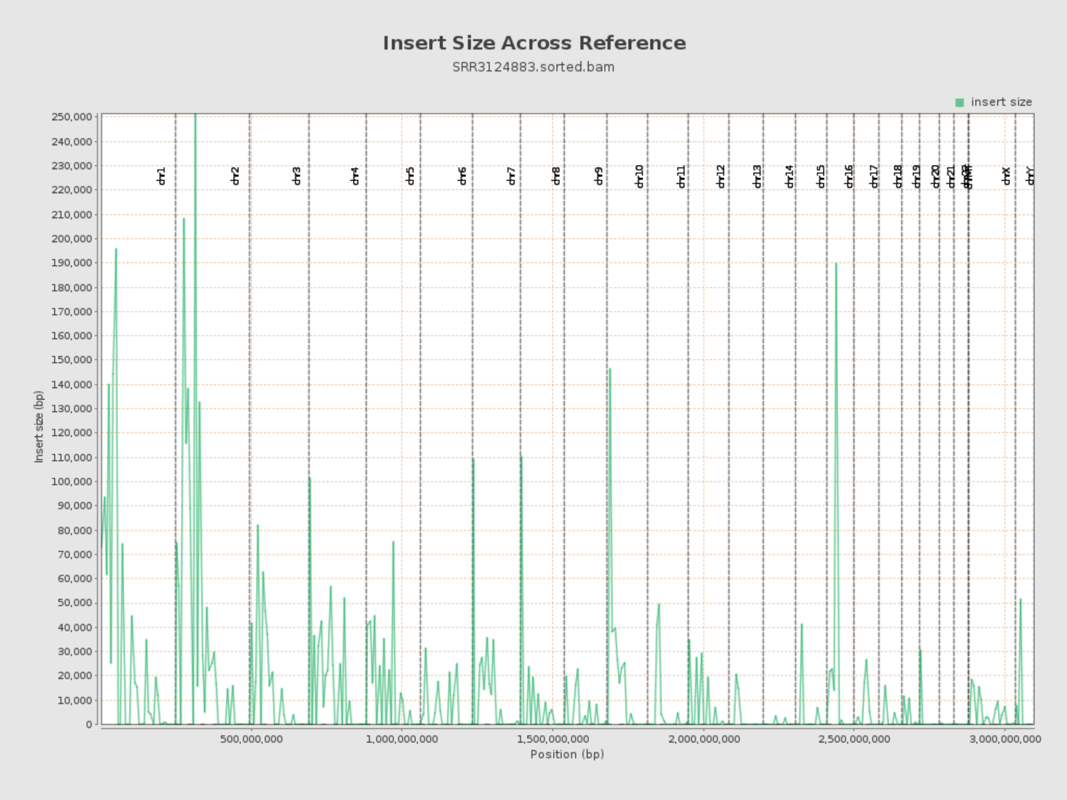
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram