Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 00:31:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124880.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_SRR3124880 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124880_1.fastq.gz SRR3124880_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 00:31:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124880.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,718,926
Mapped reads	2,694,702 / 99.11%
Unmapped reads	24,224 / 0.89%
Mapped paired reads	2,694,702 / 99.11%
Mapped reads, first in pair	1,348,564 / 49.6%
Mapped reads, second in pair	1,346,138 / 49.51%
Mapped reads, both in pair	2,688,840 / 98.89%
Mapped reads, singletons	5,862 / 0.22%
Secondary alignments	0
Supplementary alignments	26,584 / 0.98%
Read min/max/mean length	30 / 151 / 151.47
Duplicated reads (estimated)	414,445 / 15.24%
Duplication rate	14.38%
Clipped reads	1,981,606 / 72.88%

2.2. ACGT Content

Number/percentage of A's	107,303,487 / 29.48%
Number/percentage of C's	72,036,307 / 19.79%
Number/percentage of T's	108,192,417 / 29.72%
Number/percentage of G's	76,484,289 / 21.01%
Number/percentage of N's	31,776 / 0.01%

GC Percentage	40.8%

2.3. Coverage

Mean	0.1177
Standard Deviation	1.5519

2.4. Mapping Quality

Mean Mapping Quality	53.62

2.5. Insert size

Mean	46,593.78
Standard Deviation	2,047,289.16
P25/Median/P75	138 / 172 / 219

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	3,583,678
Insertions	69,762
Mapped reads with at least one insertion	2.47%
Deletions	129,504
Mapped reads with at least one deletion	4.63%
Homopolymer indels	46.05%

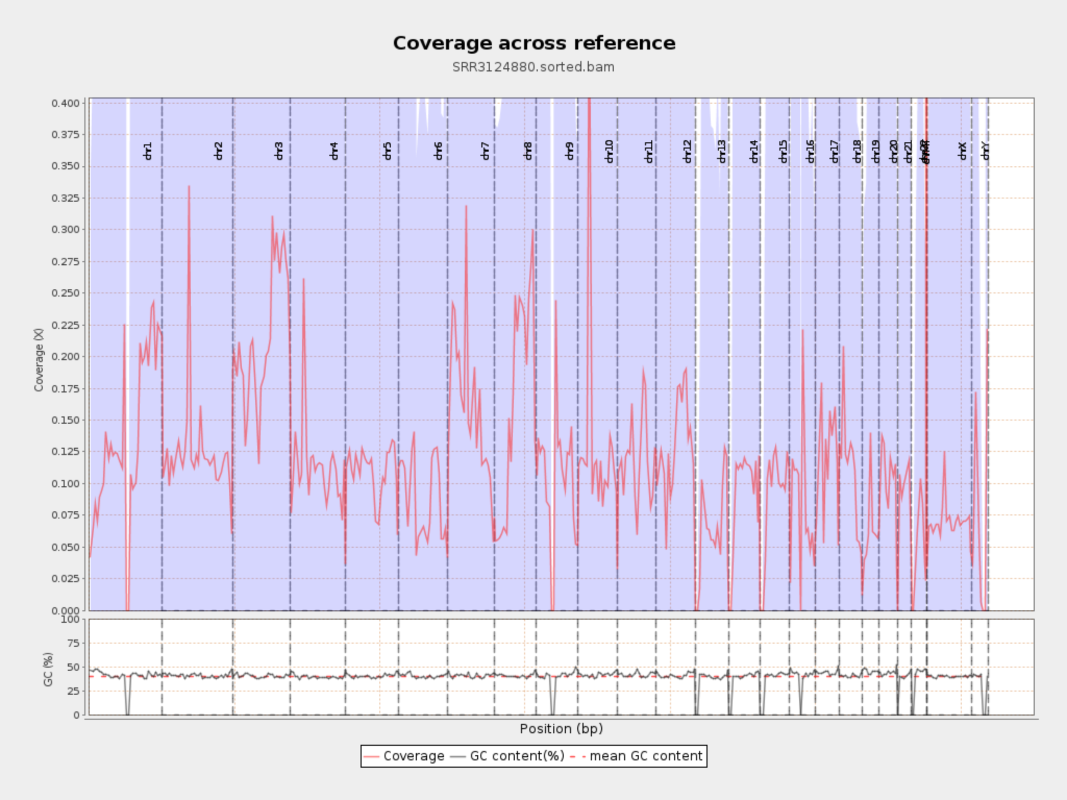
2.7. Chromosome stats

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

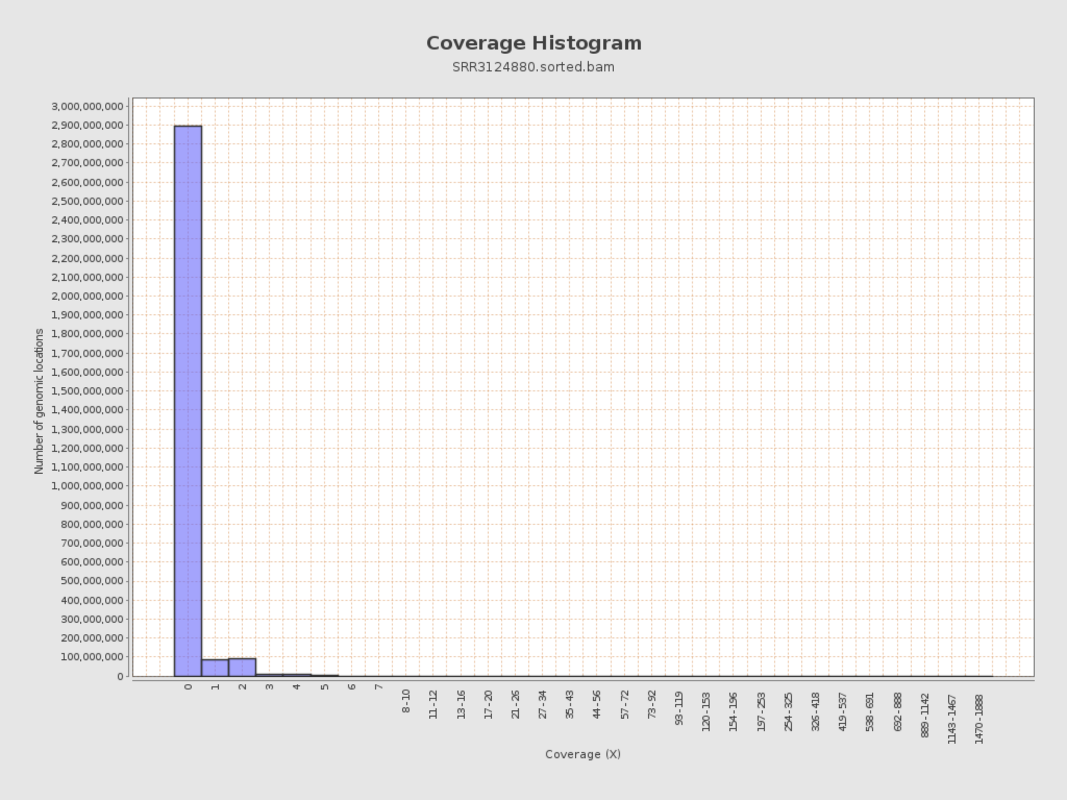
		bases	coverage	deviation
chr1	249250621	33780831	0.1355	1.9118
chr2	243199373	30342501	0.1248	1.4956
chr3	198022430	42546635	0.2149	0.6755
chr4	191154276	21641379	0.1132	0.9897
chr5	180915260	19917223	0.1101	0.4745
chr6	171115067	15105161	0.0883	0.7513
chr7	159138663	26047786	0.1637	3.2978
chr8	146364022	24062443	0.1644	0.6937
chr9	141213431	14966493	0.106	2.7873
chr10	135534747	17933203	0.1323	2.9927
chr11	135006516	15919854	0.1179	1.1733
chr12	133851895	17296126	0.1292	0.5154
chr13	115169878	7484344	0.065	0.3536
chr14	107349540	9672476	0.0901	0.4502
chr15	102531392	9055474	0.0883	0.4189
chr16	90354753	7407588	0.082	1.1896
chr17	81195210	9674458	0.1192	1.5169
chr18	78077248	8785029	0.1125	2.6241
chr19	59128983	3755273	0.0635	0.9799
chr20	63025520	6723638	0.1067	0.5439
chr21	48129895	4294589	0.0892	0.6618
chr22	51304566	2531517	0.0493	0.3172
chrMT	16571	149106	8.998	5.6329
chrX	155270560	10895201	0.0702	0.5491

chrY	59373566	4308400	0.0726	1.7946

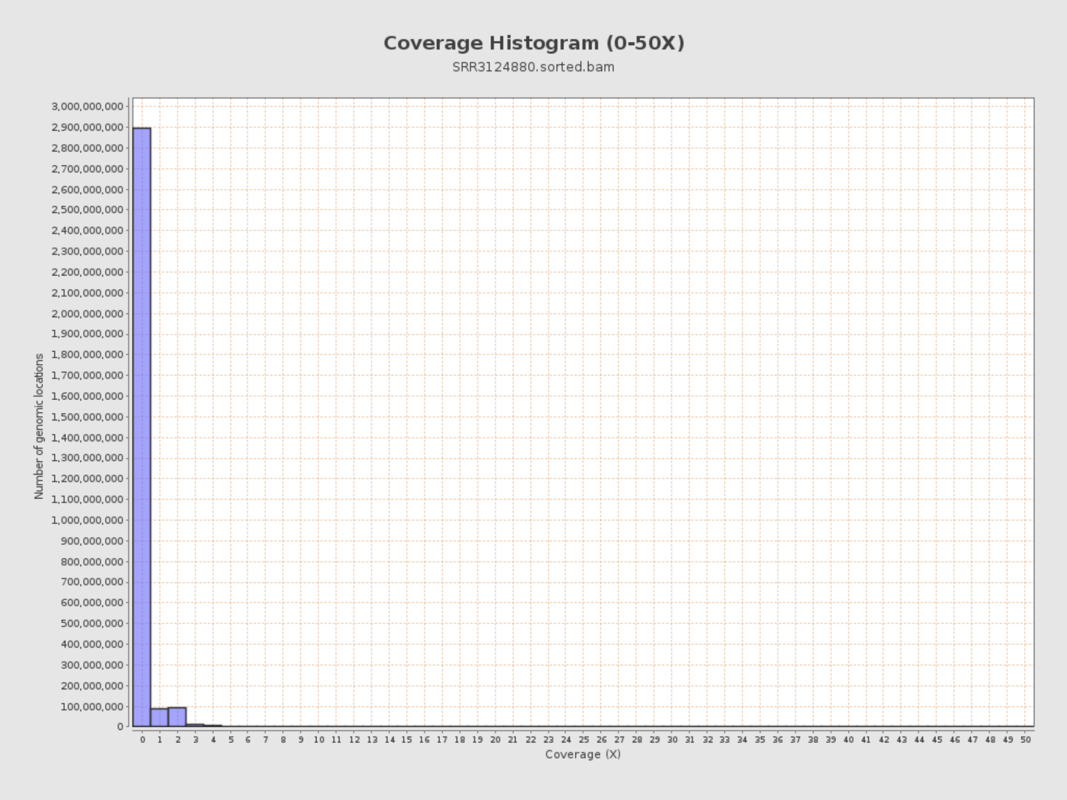
3. Results : Coverage across reference



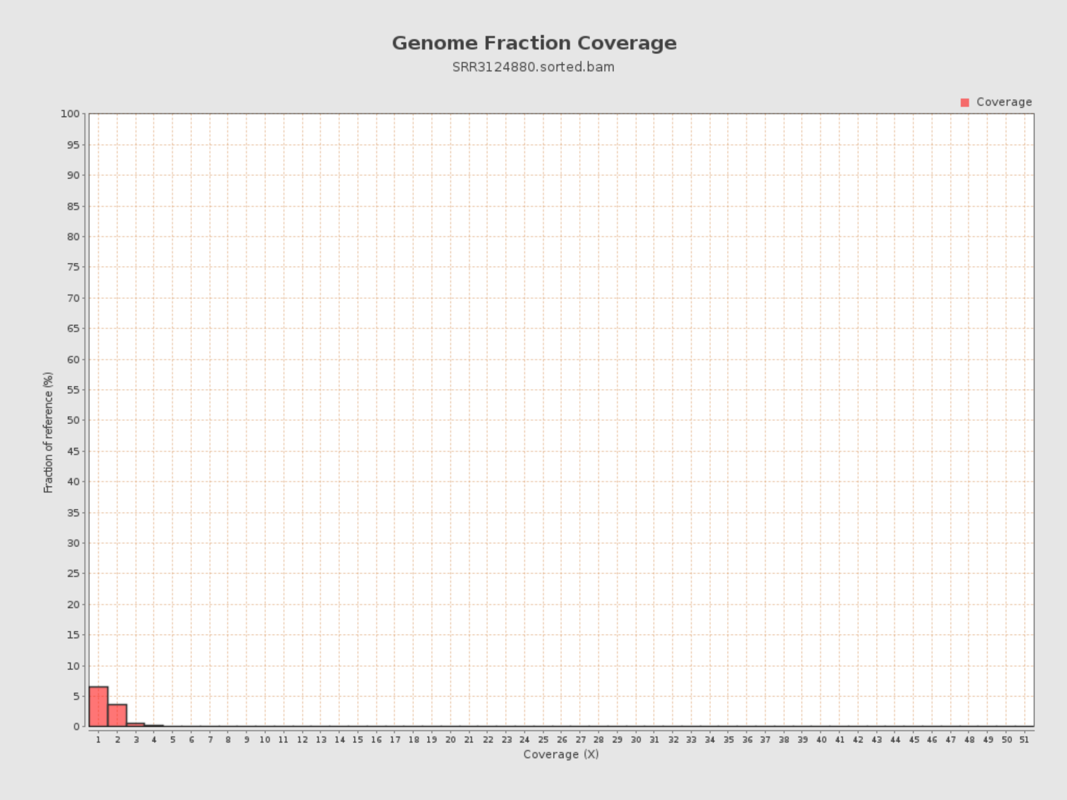
4. Results : Coverage Histogram



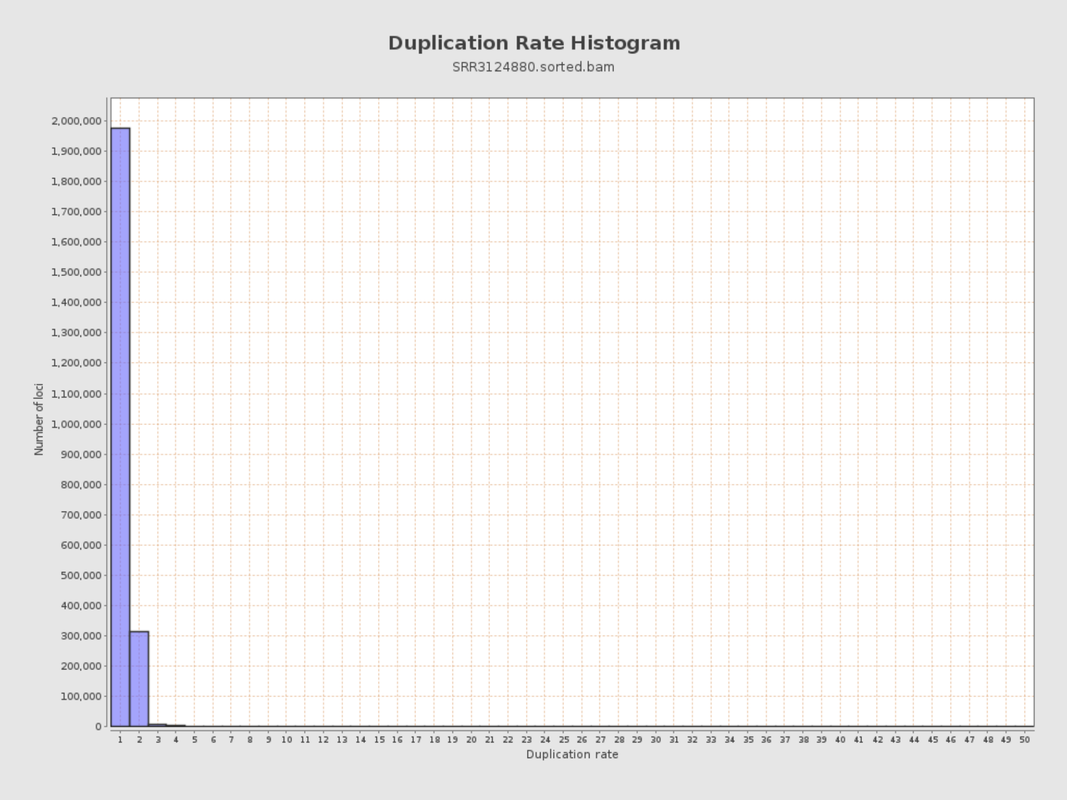
5. Results : Coverage Histogram (0-50X)



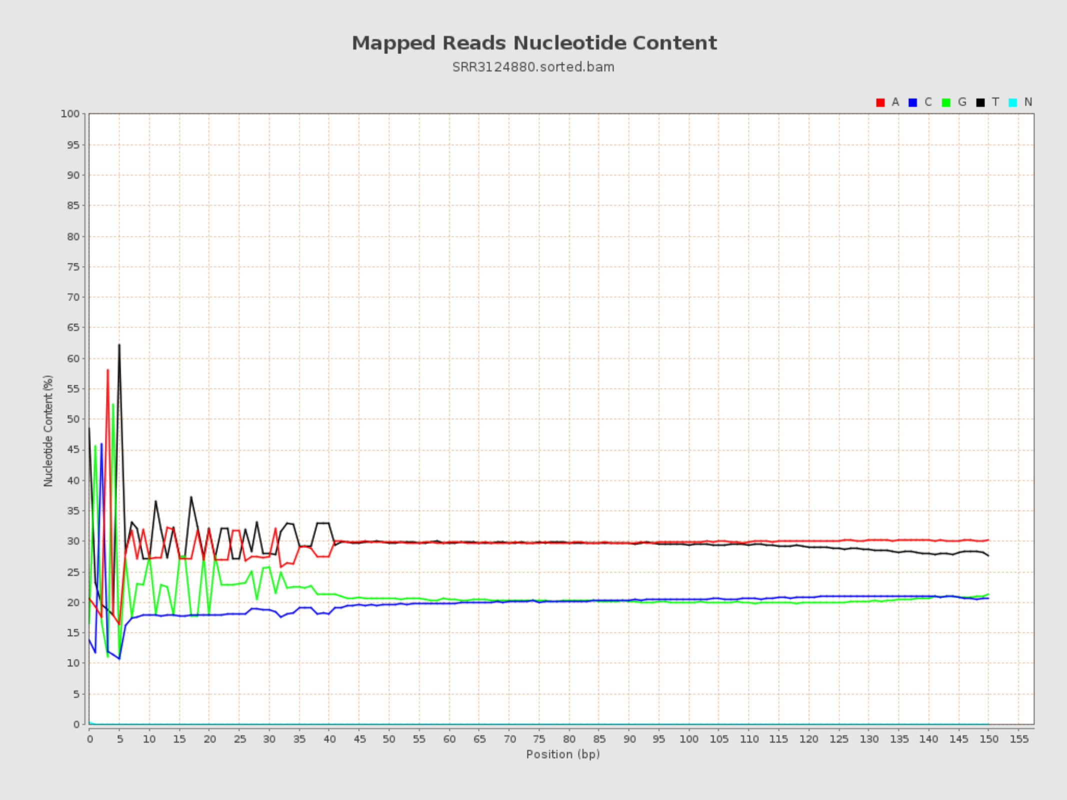
6. Results : Genome Fraction Coverage



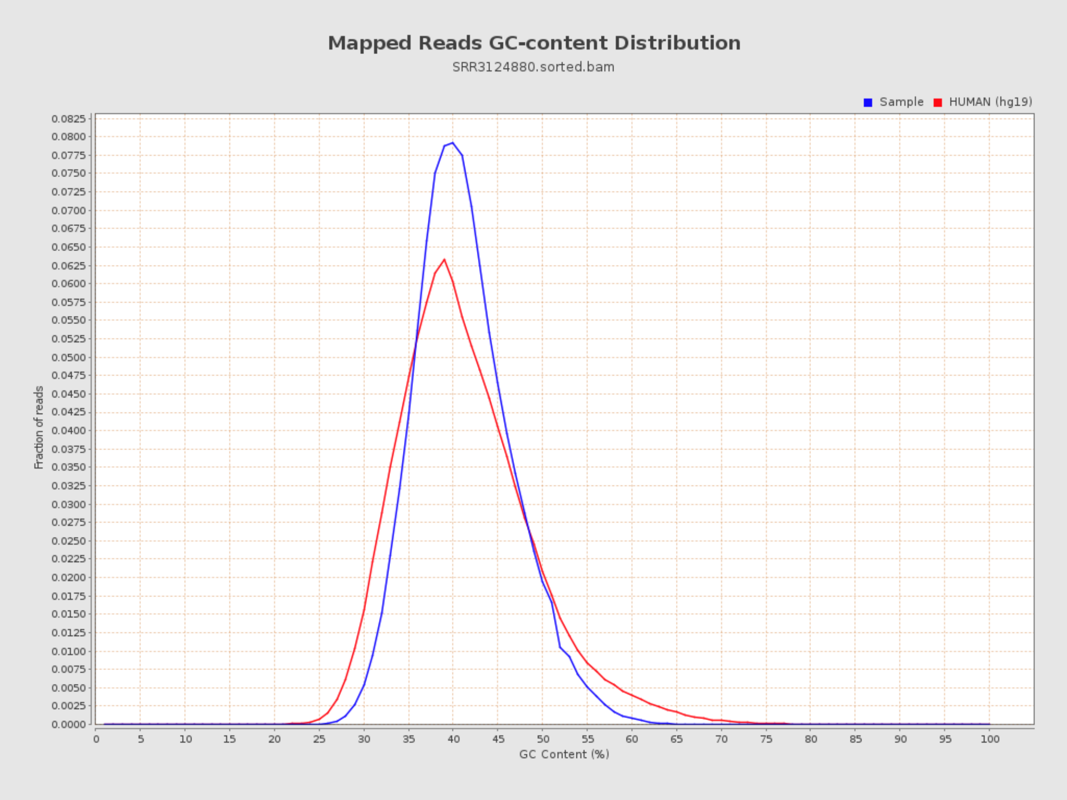
7. Results : Duplication Rate Histogram



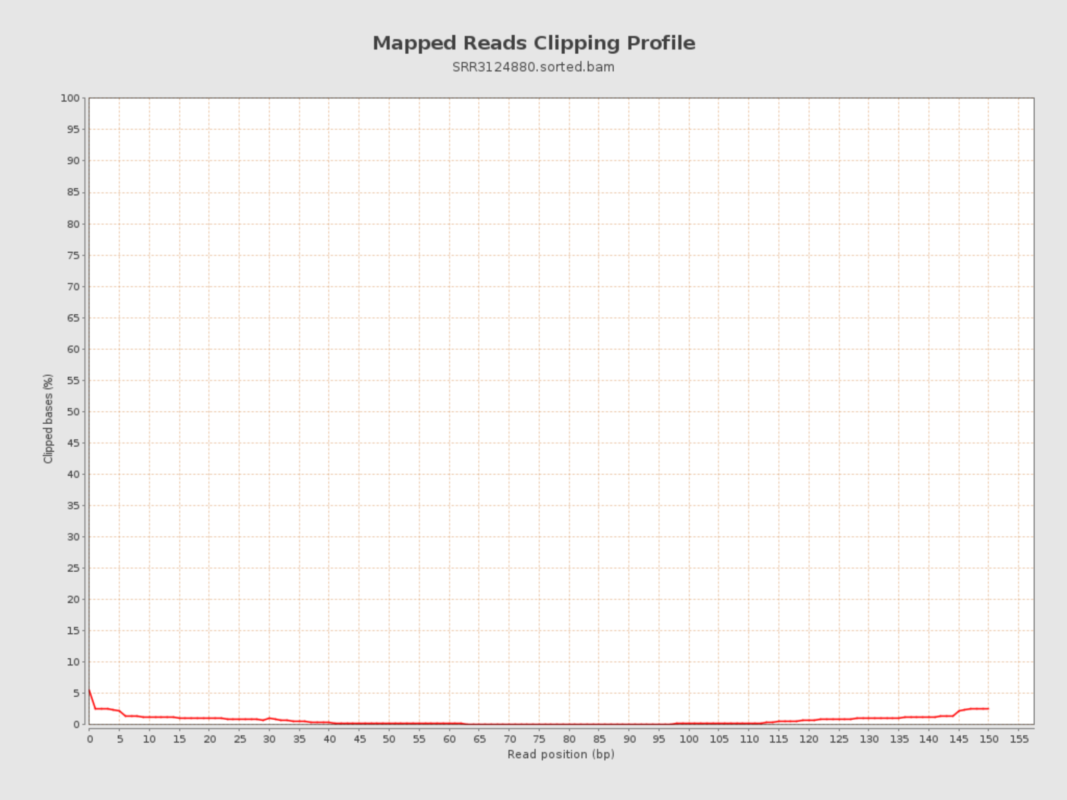
8. Results : Mapped Reads Nucleotide Content



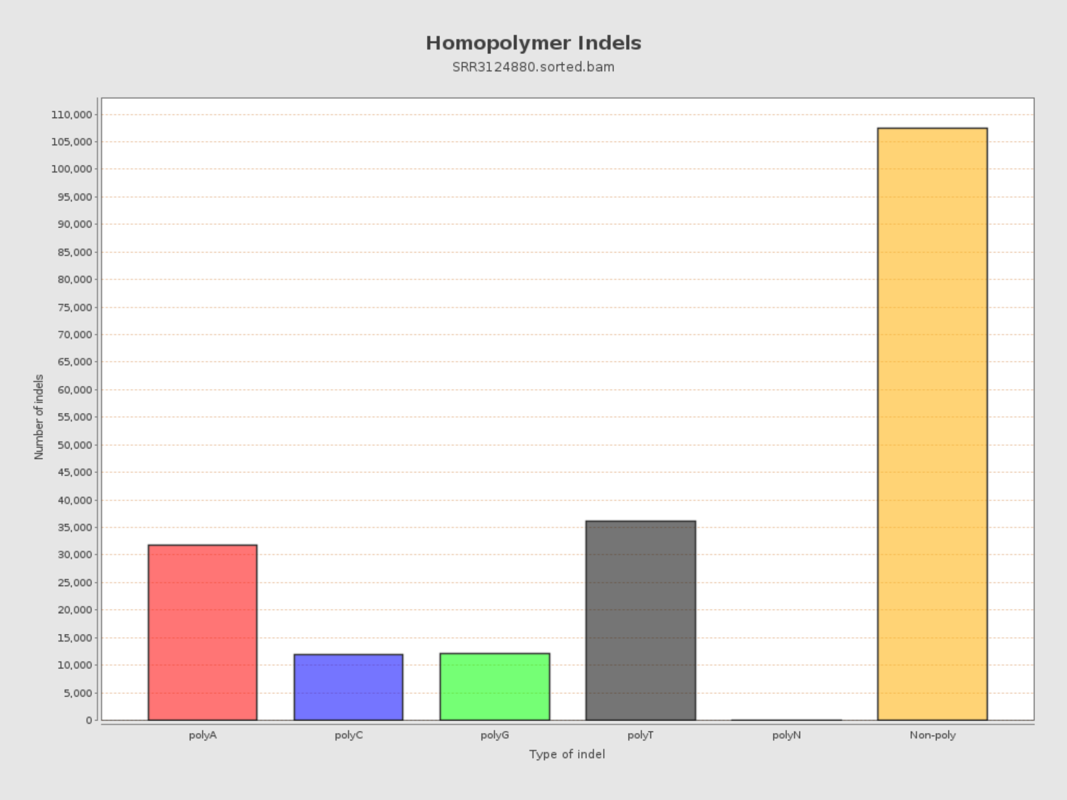
9. Results : Mapped Reads GC-content Distribution



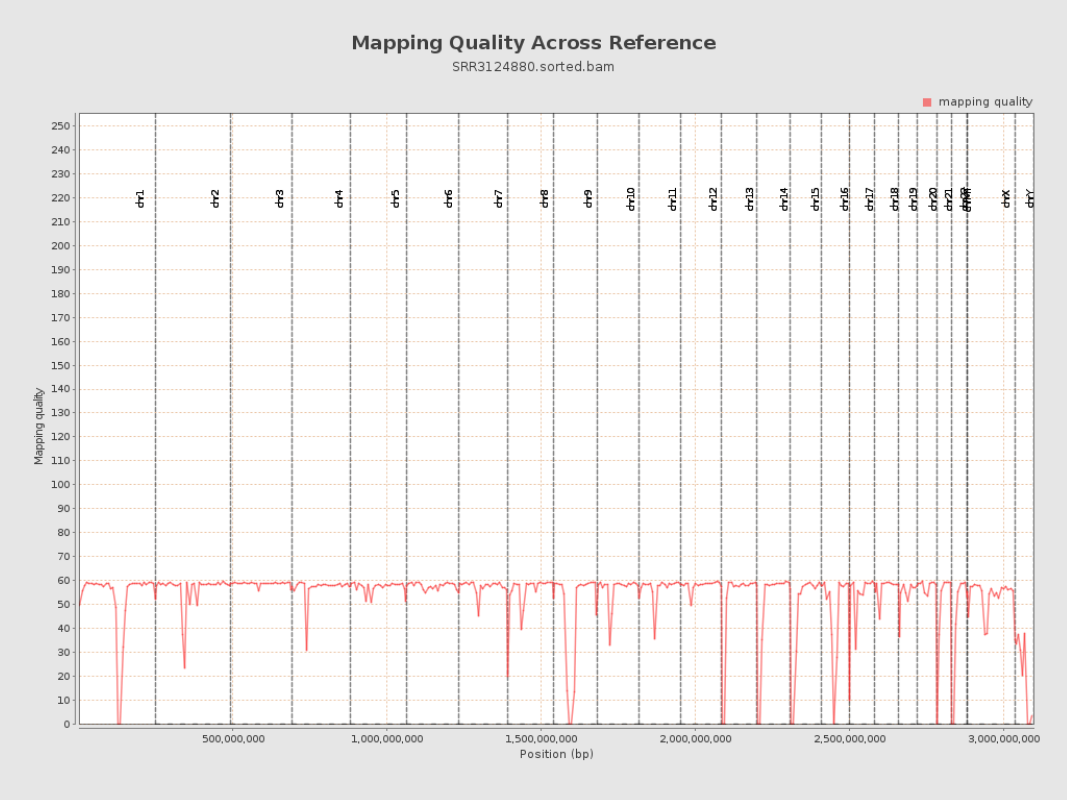
10. Results : Mapped Reads Clipping Profile



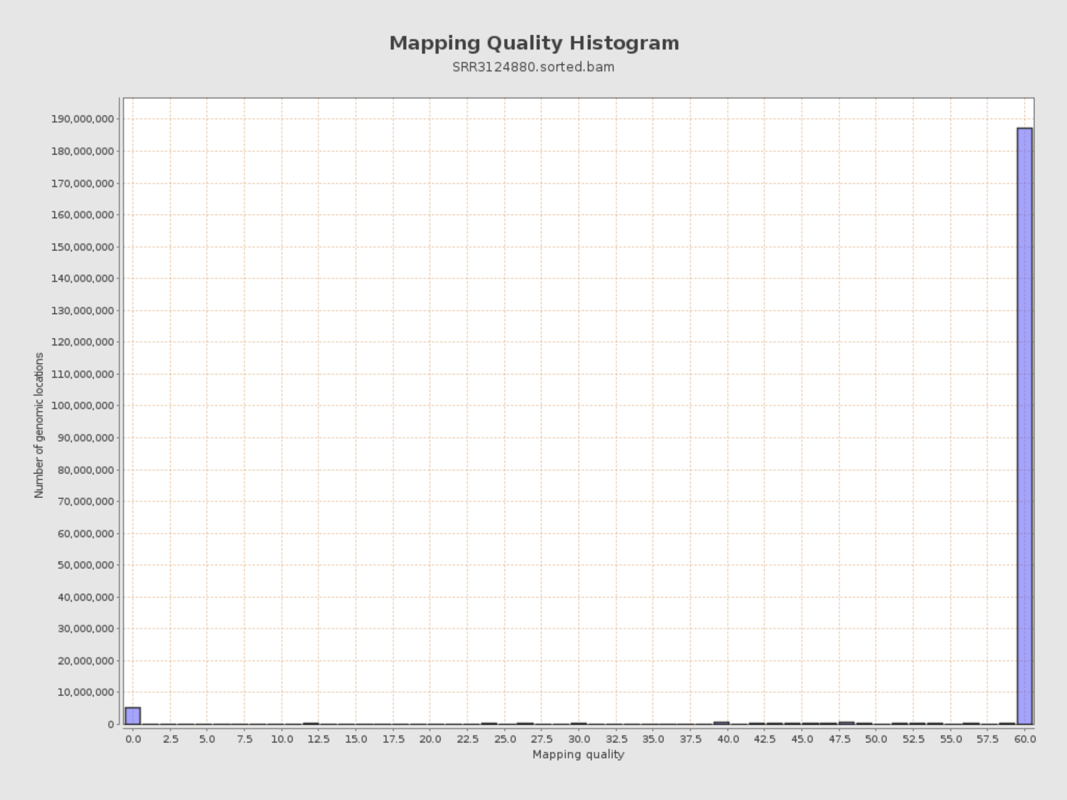
11. Results : Homopolymer Indels



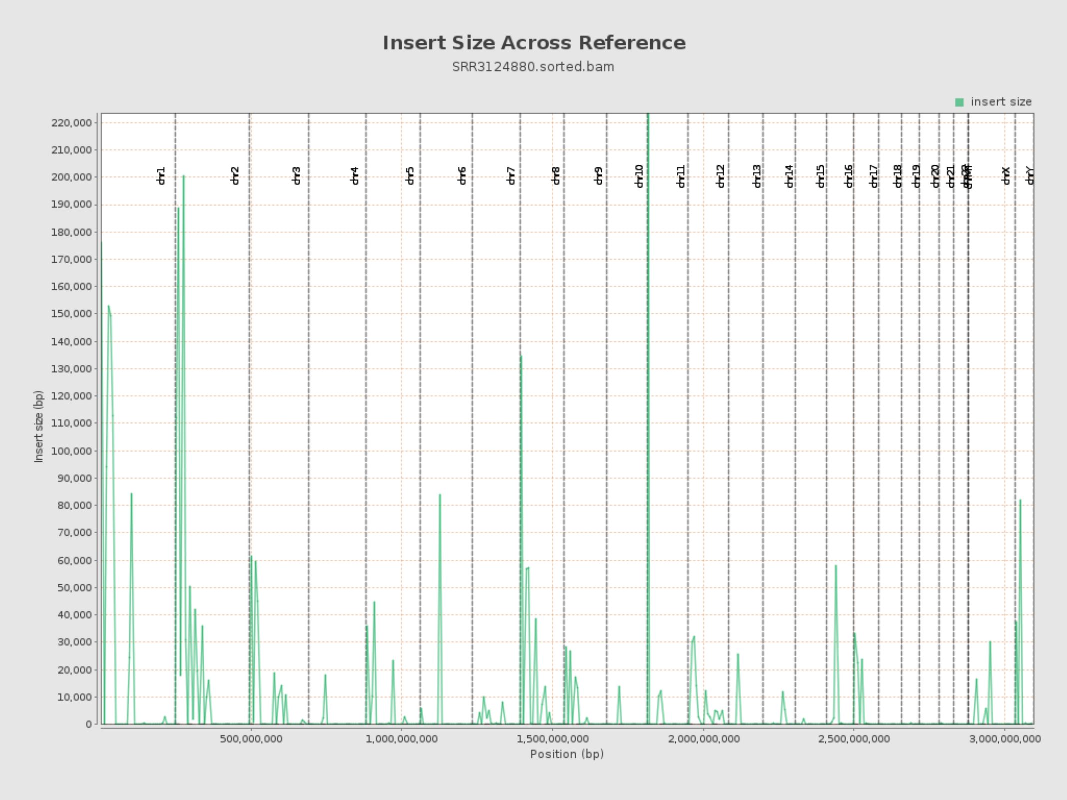
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram