Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 03:06:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124902.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_SRR3124902 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124902_1.fastq.gz SRR3124902_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 03:06:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124902.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,314,148
Mapped reads	5,191,544 / 97.69%
Unmapped reads	122,604 / 2.31%
Mapped paired reads	5,191,544 / 97.69%
Mapped reads, first in pair	2,597,461 / 48.88%
Mapped reads, second in pair	2,594,083 / 48.81%
Mapped reads, both in pair	5,172,680 / 97.34%
Mapped reads, singletons	18,864 / 0.35%
Secondary alignments	0
Supplementary alignments	18,066 / 0.34%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	334,582 / 6.3%
Duplication rate	4.33%
Clipped reads	2,072,589 / 39%

2.2. ACGT Content

Number/percentage of A's	134,337,725 / 28.52%
Number/percentage of C's	91,219,138 / 19.37%
Number/percentage of T's	139,157,909 / 29.55%
Number/percentage of G's	106,269,088 / 22.56%
Number/percentage of N's	6,692 / 0%

GC Percentage	41.93%

2.3. Coverage

Mean	0.1522
Standard Deviation	1.3483

2.4. Mapping Quality

Mean Mapping Quality	53.41

2.5. Insert size

Mean	40,794.9
Standard Deviation	1,924,631.57
P25/Median/P75	147 / 192 / 260

2.6. Mismatches and indels

General error rate	0.74%
Mismatches	3,382,897
Insertions	53,725
Mapped reads with at least one insertion	1.01%
Deletions	162,886
Mapped reads with at least one deletion	3.08%
Homopolymer indels	48.7%

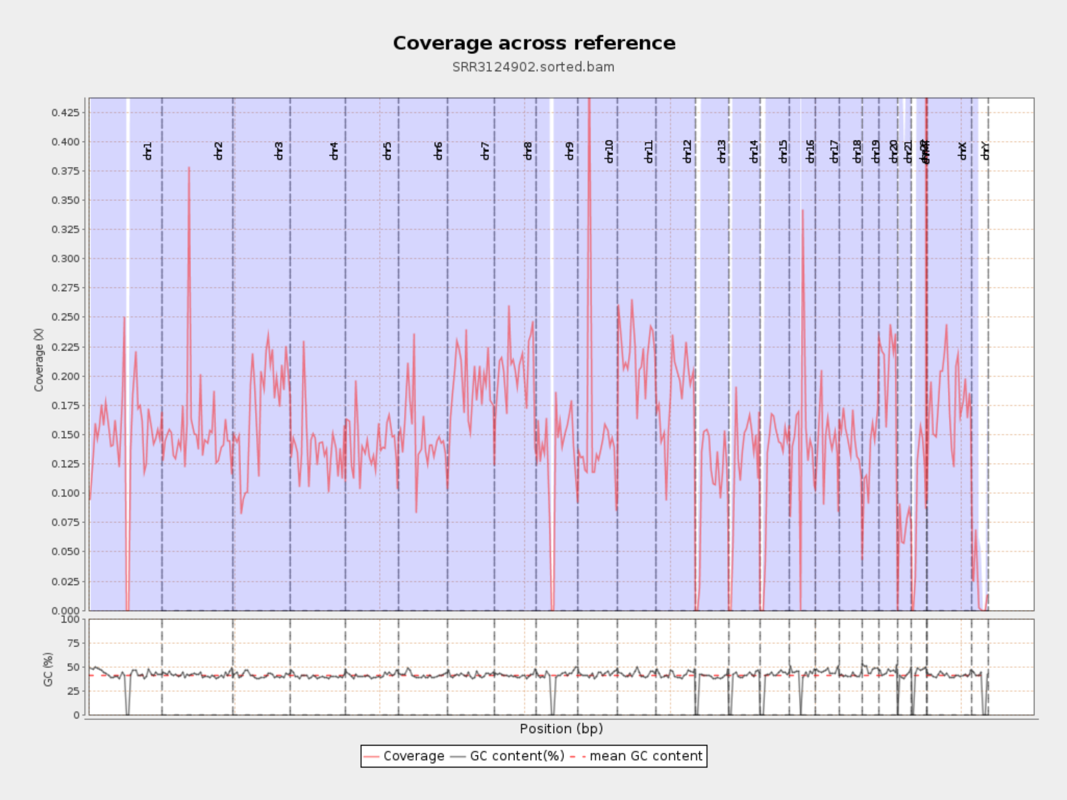
2.7. Chromosome stats

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

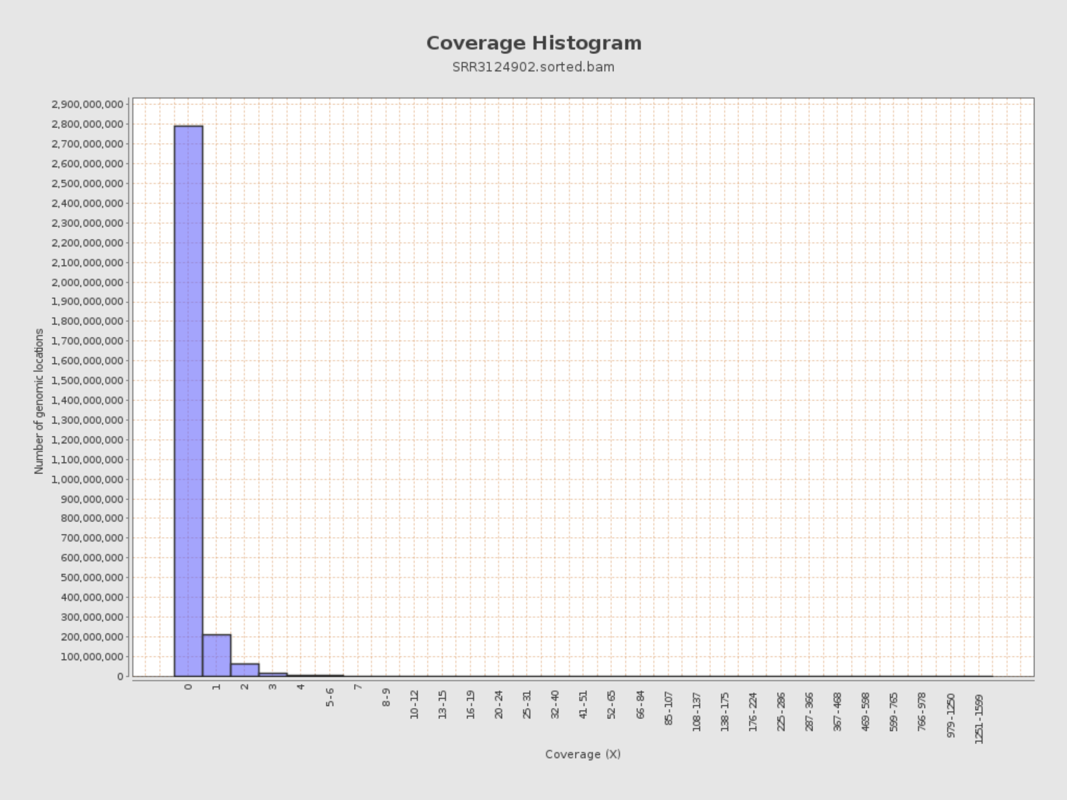
		bases	coverage	deviation
chr1	249250621	36723692	0.1473	1.6238
chr2	243199373	37589877	0.1546	1.6017
chr3	198022430	34412572	0.1738	0.5974
chr4	191154276	26340141	0.1378	0.8049
chr5	180915260	25616498	0.1416	0.5567
chr6	171115067	25472860	0.1489	1.072
chr7	159138663	30502158	0.1917	1.8012
chr8	146364022	29948757	0.2046	0.8781
chr9	141213431	18445559	0.1306	1.8159
chr10	135534747	20732475	0.153	2.9721
chr11	135006516	29211386	0.2164	1.8553
chr12	133851895	24599347	0.1838	0.653
chr13	115169878	12383471	0.1075	0.4562
chr14	107349540	12919364	0.1203	0.5574
chr15	102531392	12357952	0.1205	0.5112
chr16	90354753	13123804	0.1452	1.6169
chr17	81195210	11518242	0.1419	1.5778
chr18	78077248	11485566	0.1471	1.8327
chr19	59128983	7905359	0.1337	0.9583
chr20	63025520	13209919	0.2096	0.7649
chr21	48129895	3252108	0.0676	0.4863
chr22	51304566	4697810	0.0916	0.4718
chrMT	16571	163149	9.8455	6.1172
chrX	155270560	27660367	0.1781	0.9149

chrY	59373566	993931	0.0167	0.9212

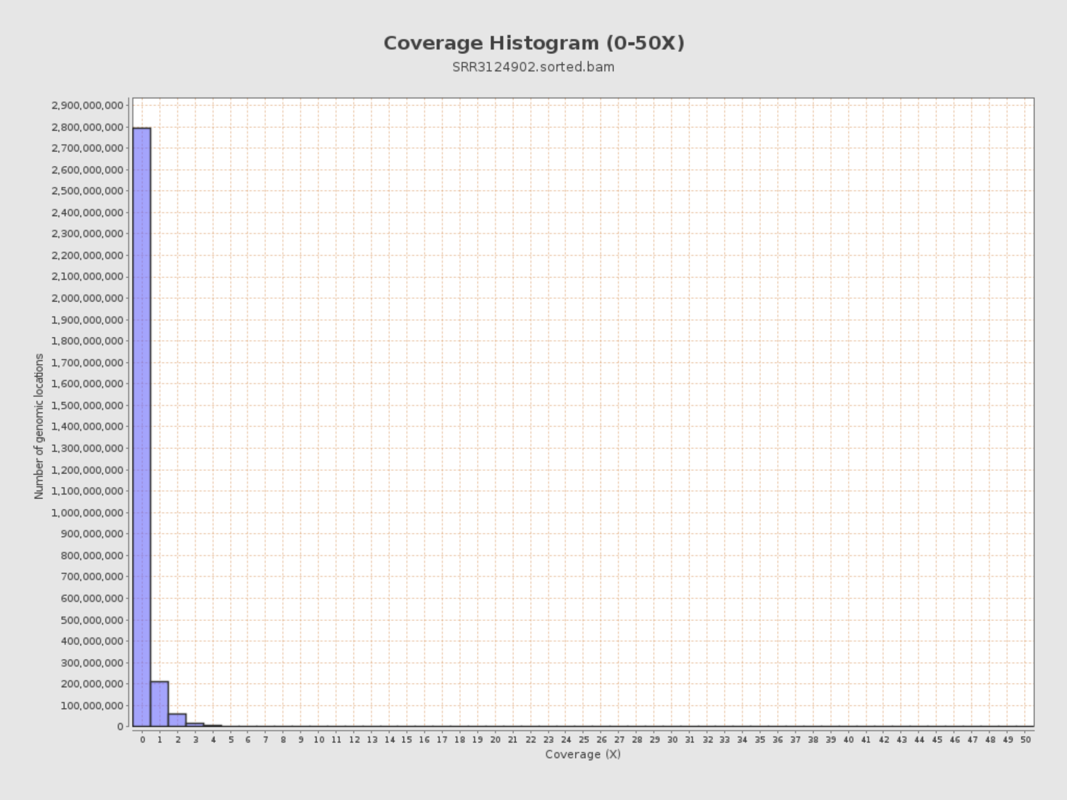
3. Results : Coverage across reference



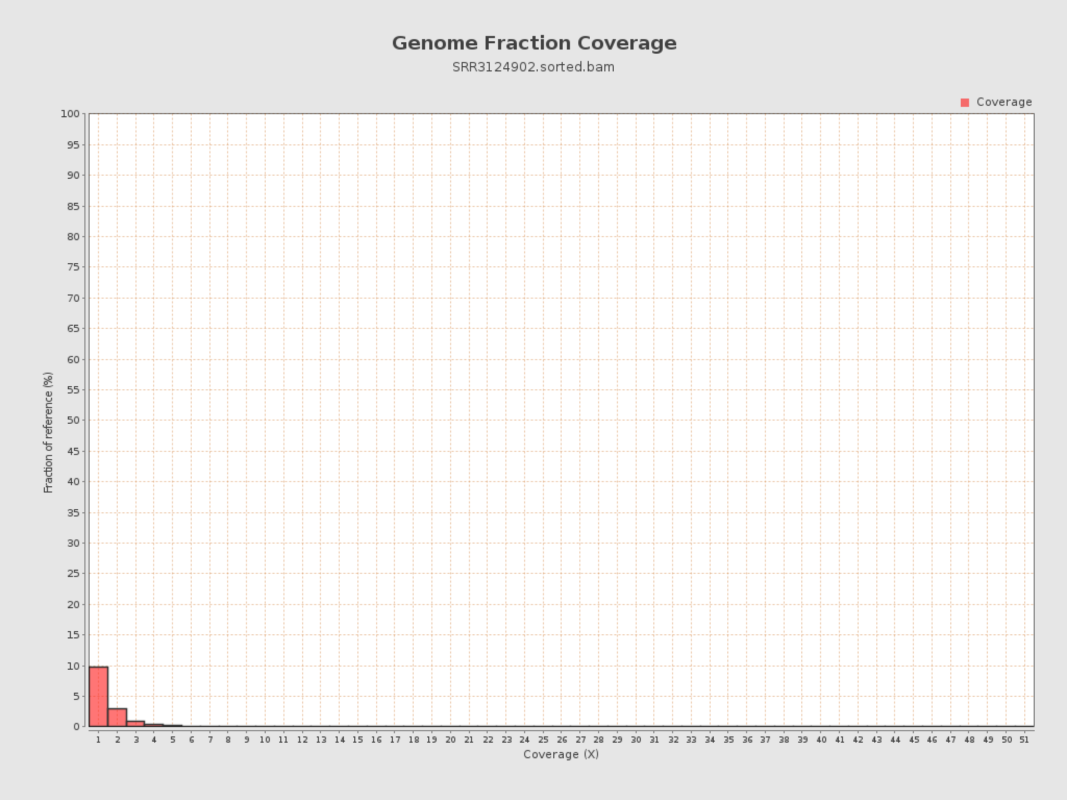
4. Results : Coverage Histogram



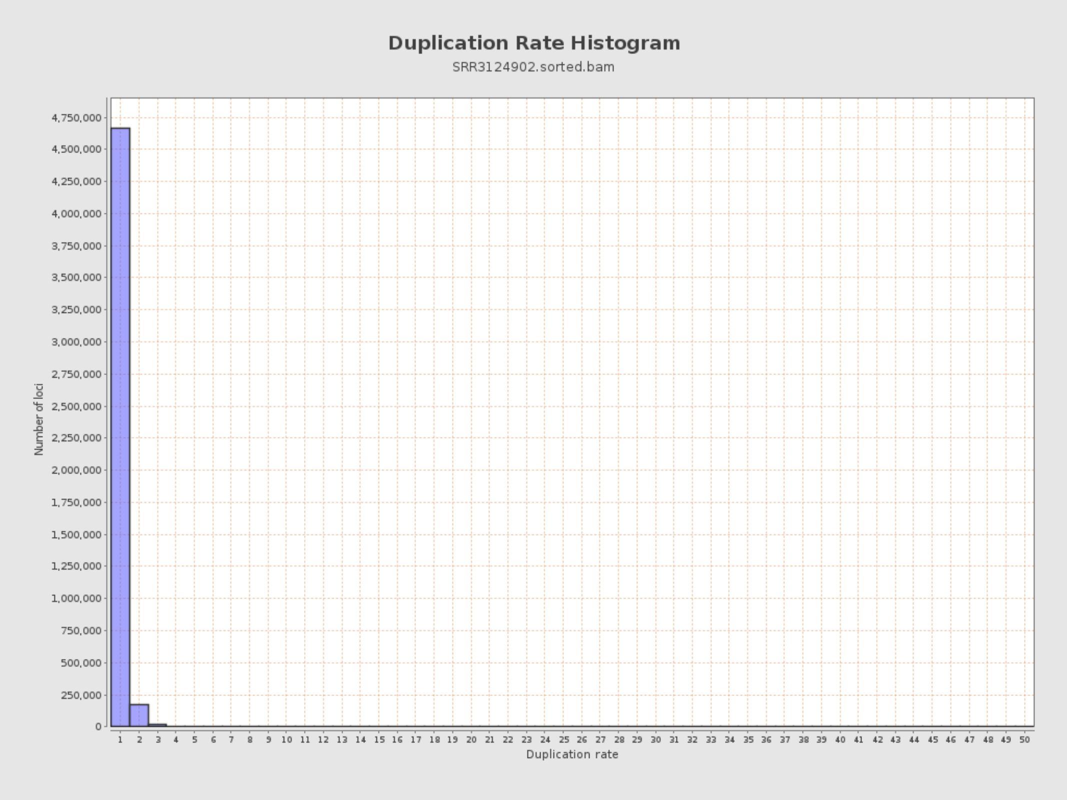
5. Results : Coverage Histogram (0-50X)



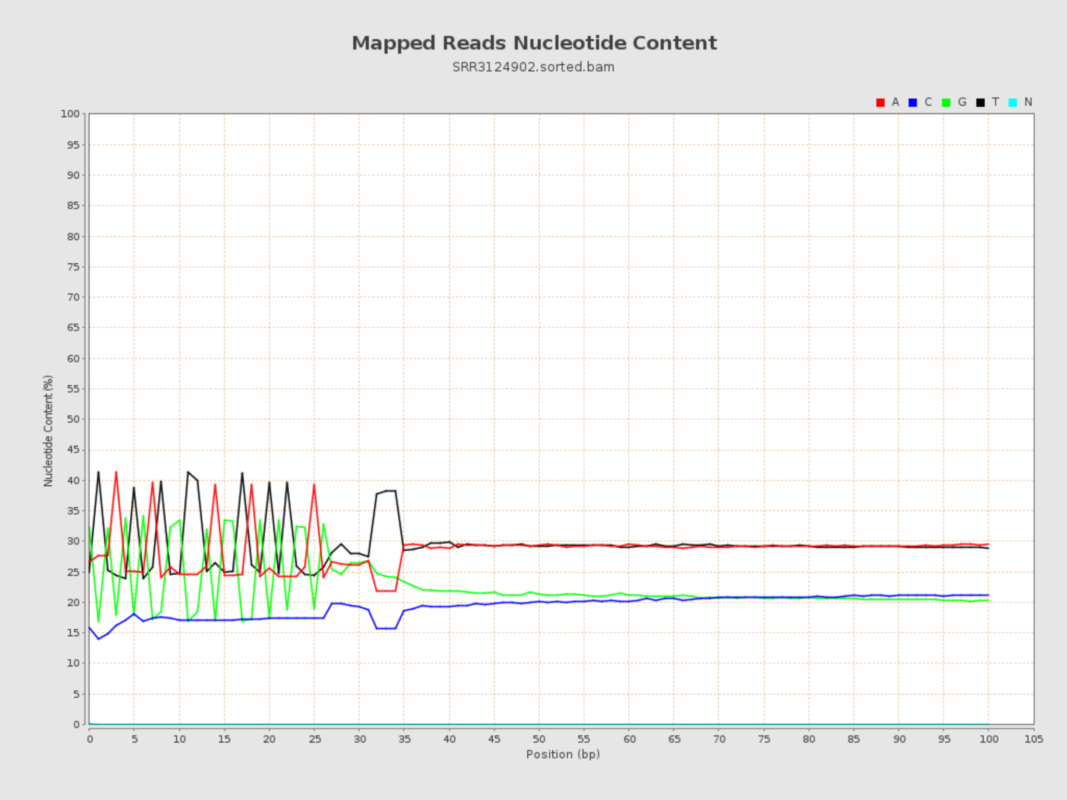
6. Results : Genome Fraction Coverage



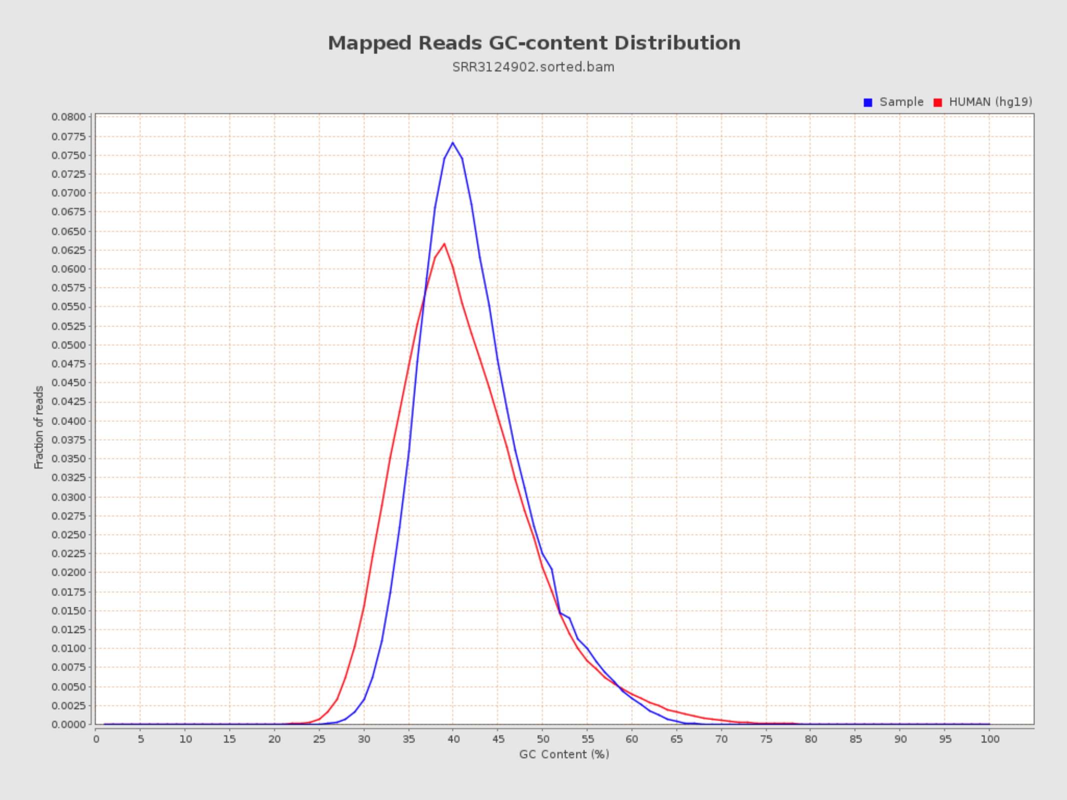
7. Results : Duplication Rate Histogram



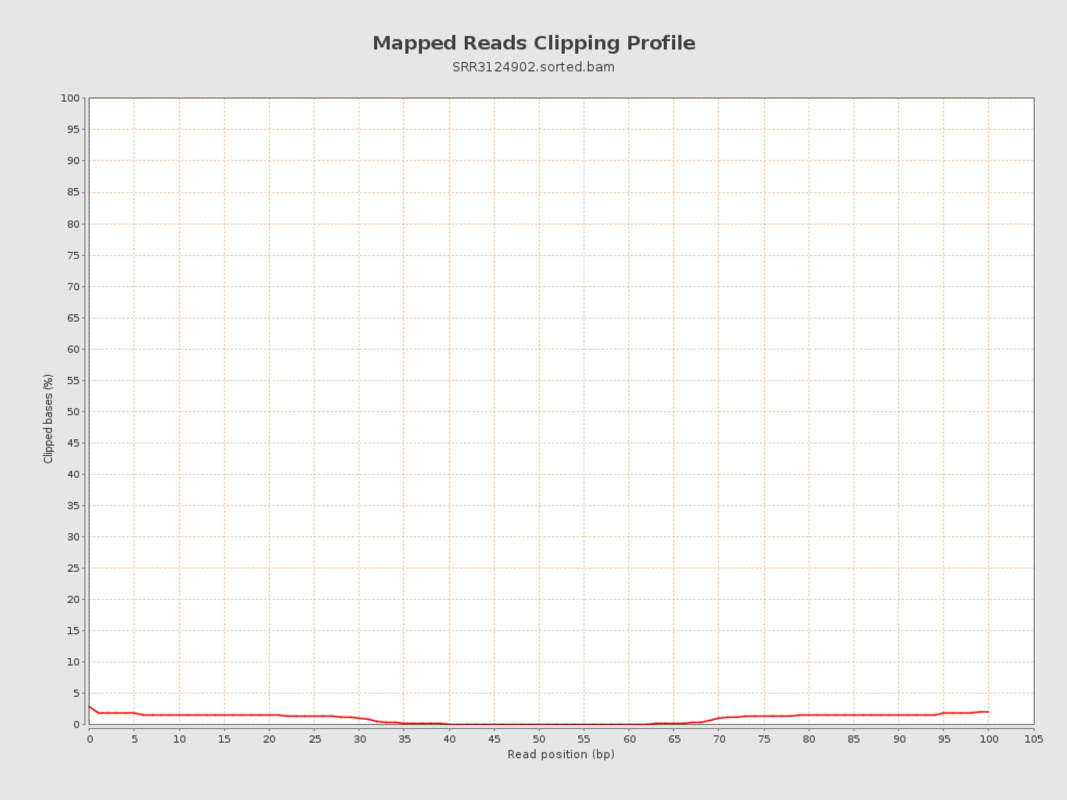
8. Results : Mapped Reads Nucleotide Content



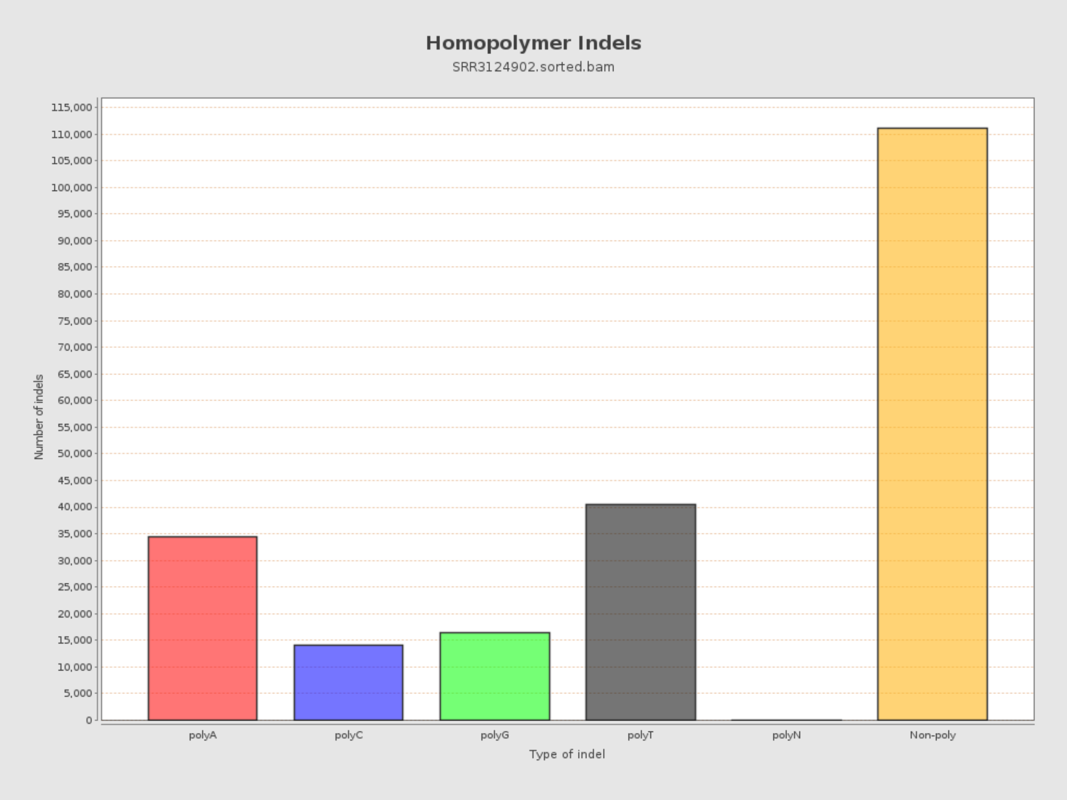
9. Results : Mapped Reads GC-content Distribution



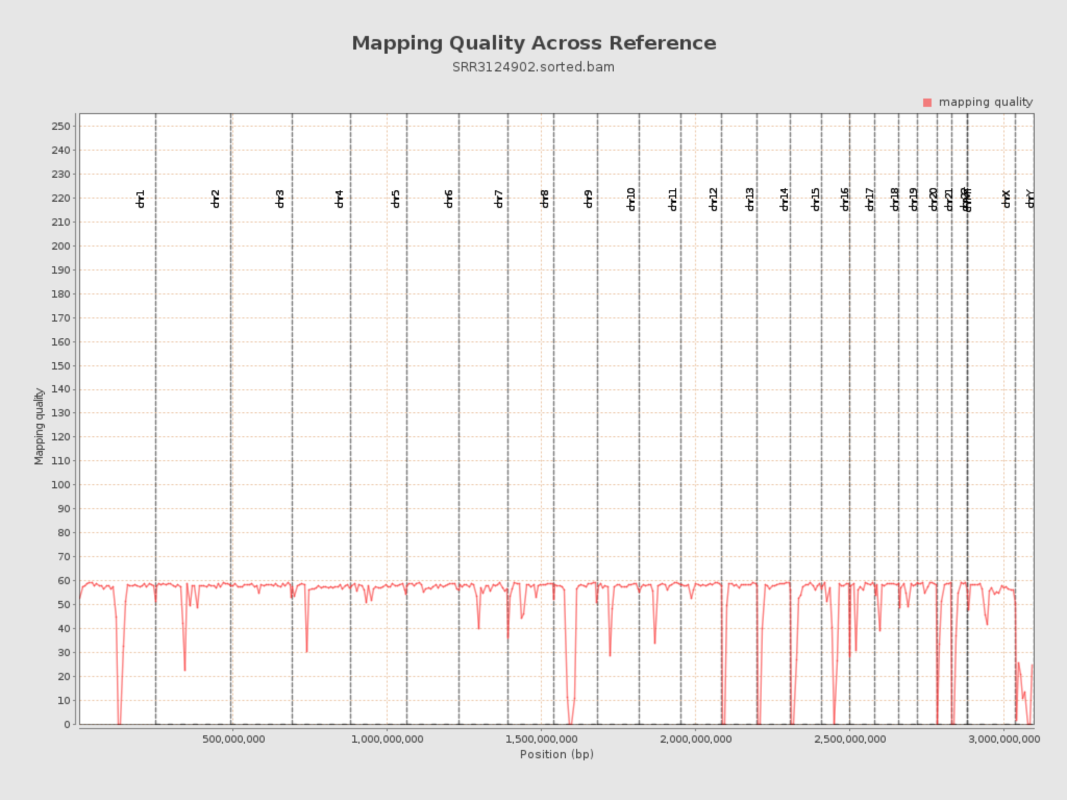
10. Results : Mapped Reads Clipping Profile



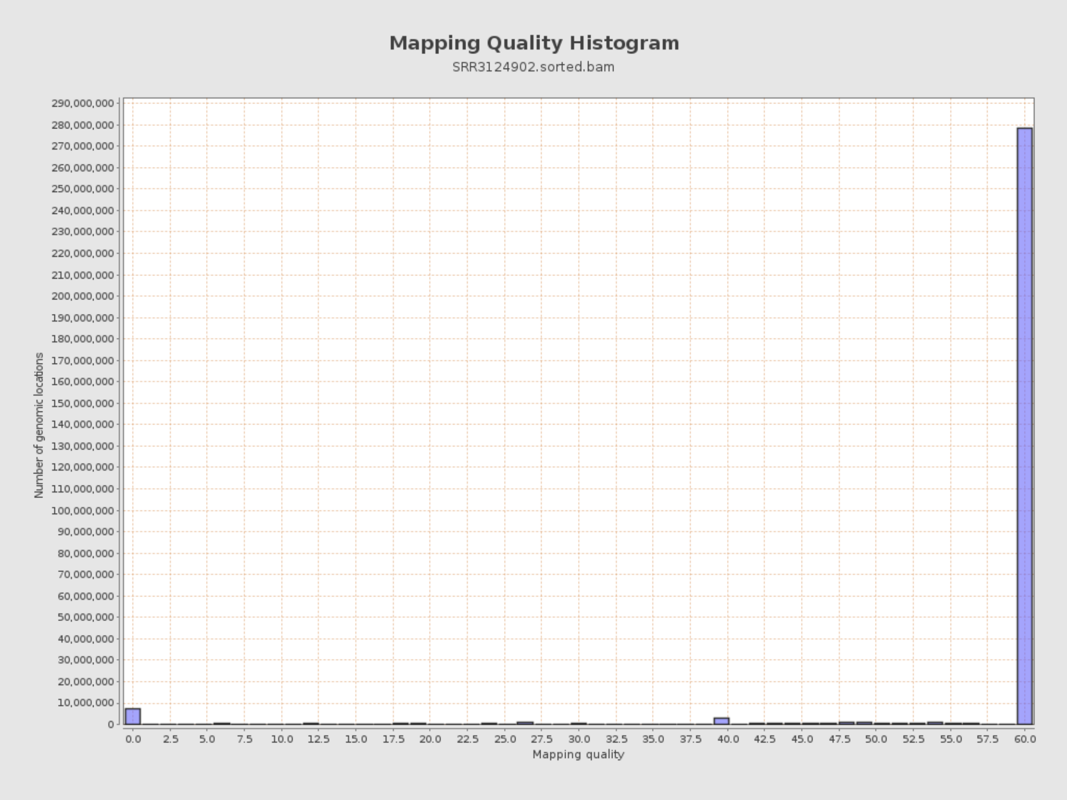
11. Results : Homopolymer Indels



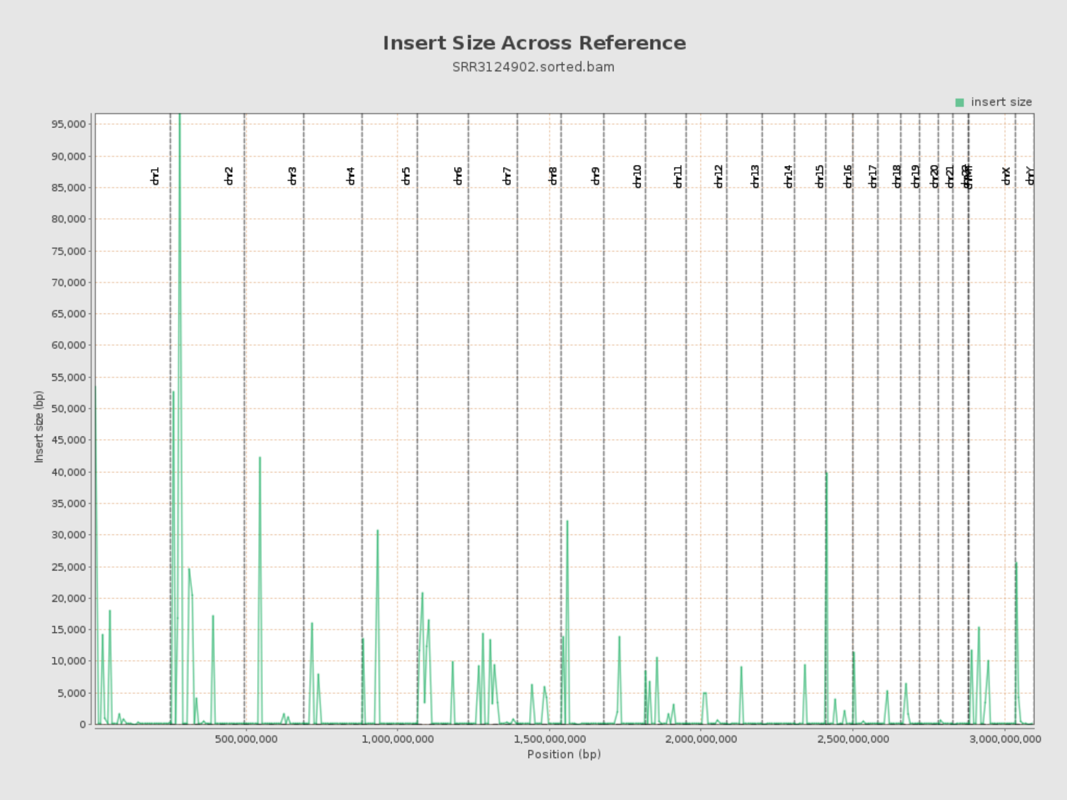
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram