Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 02:59:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124901.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_SRR3124901 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124901_1.fastq.gz SRR3124901_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 02:59:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124901.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,221,068
Mapped reads	5,160,244 / 98.84%
Unmapped reads	60,824 / 1.16%
Mapped paired reads	5,160,244 / 98.84%
Mapped reads, first in pair	2,581,223 / 49.44%
Mapped reads, second in pair	2,579,021 / 49.4%
Mapped reads, both in pair	5,144,548 / 98.53%
Mapped reads, singletons	15,696 / 0.3%
Secondary alignments	0
Supplementary alignments	21,549 / 0.41%
Read min/max/mean length	30 / 101 / 101.16
Duplicated reads (estimated)	301,694 / 5.78%
Duplication rate	3.99%
Clipped reads	2,164,587 / 41.46%

2.2. ACGT Content

Number/percentage of A's	131,358,799 / 28.13%
Number/percentage of C's	92,216,927 / 19.75%
Number/percentage of T's	136,093,801 / 29.14%
Number/percentage of G's	107,312,058 / 22.98%
Number/percentage of N's	6,766 / 0%

GC Percentage	42.73%

2.3. Coverage

Mean	0.1509
Standard Deviation	1.2342

2.4. Mapping Quality

Mean Mapping Quality	53.58

2.5. Insert size

Mean	50,322.78
Standard Deviation	2,153,178.49
P25/Median/P75	143 / 185 / 249

2.6. Mismatches and indels

General error rate	0.72%
Mismatches	3,244,270
Insertions	60,135
Mapped reads with at least one insertion	1.13%
Deletions	146,233
Mapped reads with at least one deletion	2.78%
Homopolymer indels	46.77%

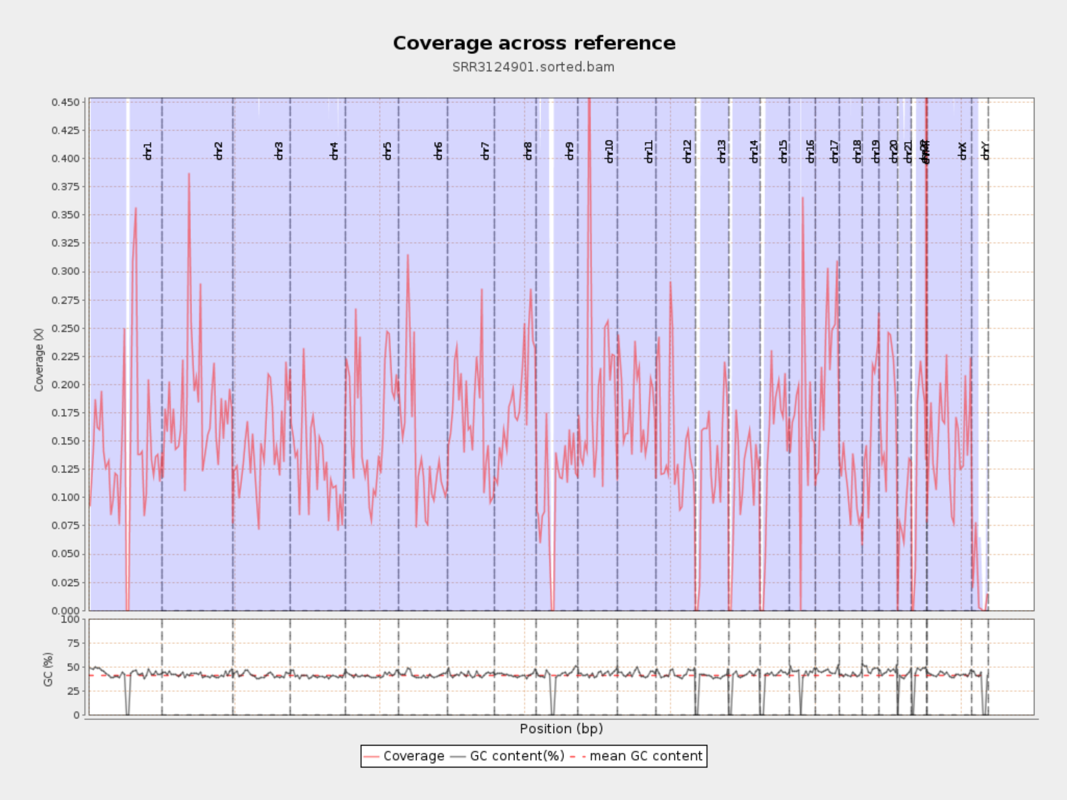
2.7. Chromosome stats

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

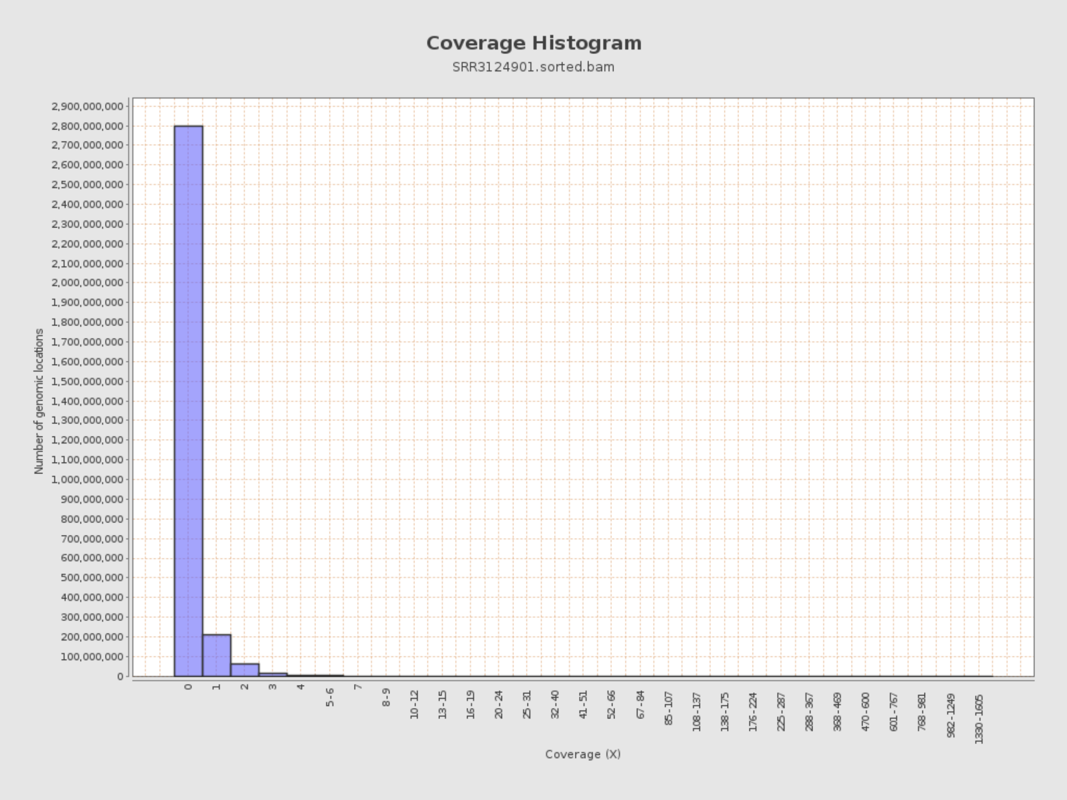
		bases	coverage	deviation
chr1	249250621	35253644	0.1414	1.3133
chr2	243199373	44194913	0.1817	1.6323
chr3	198022430	28754650	0.1452	0.5748
chr4	191154276	24638923	0.1289	0.8386
chr5	180915260	30563643	0.1689	0.635
chr6	171115067	24509410	0.1432	0.8739
chr7	159138663	27419636	0.1723	1.5381
chr8	146364022	27103588	0.1852	0.7199
chr9	141213431	14687647	0.104	1.3297
chr10	135534747	26630387	0.1965	3.0467
chr11	135006516	24057864	0.1782	0.9204
chr12	133851895	20354241	0.1521	0.6416
chr13	115169878	14493663	0.1258	0.5066
chr14	107349540	11818990	0.1101	0.5706
chr15	102531392	14652118	0.1429	0.5707
chr16	90354753	15266836	0.169	1.8198
chr17	81195210	17795013	0.2192	1.4466
chr18	78077248	8654724	0.1108	1.6172
chr19	59128983	9763473	0.1651	0.9514
chr20	63025520	11313836	0.1795	0.8008
chr21	48129895	4137837	0.086	0.5346
chr22	51304566	6659207	0.1298	0.5833
chrMT	16571	300890	18.1576	10.4072
chrX	155270560	23096816	0.1488	0.8334

chrY	59373566	1112273	0.0187	1.2274

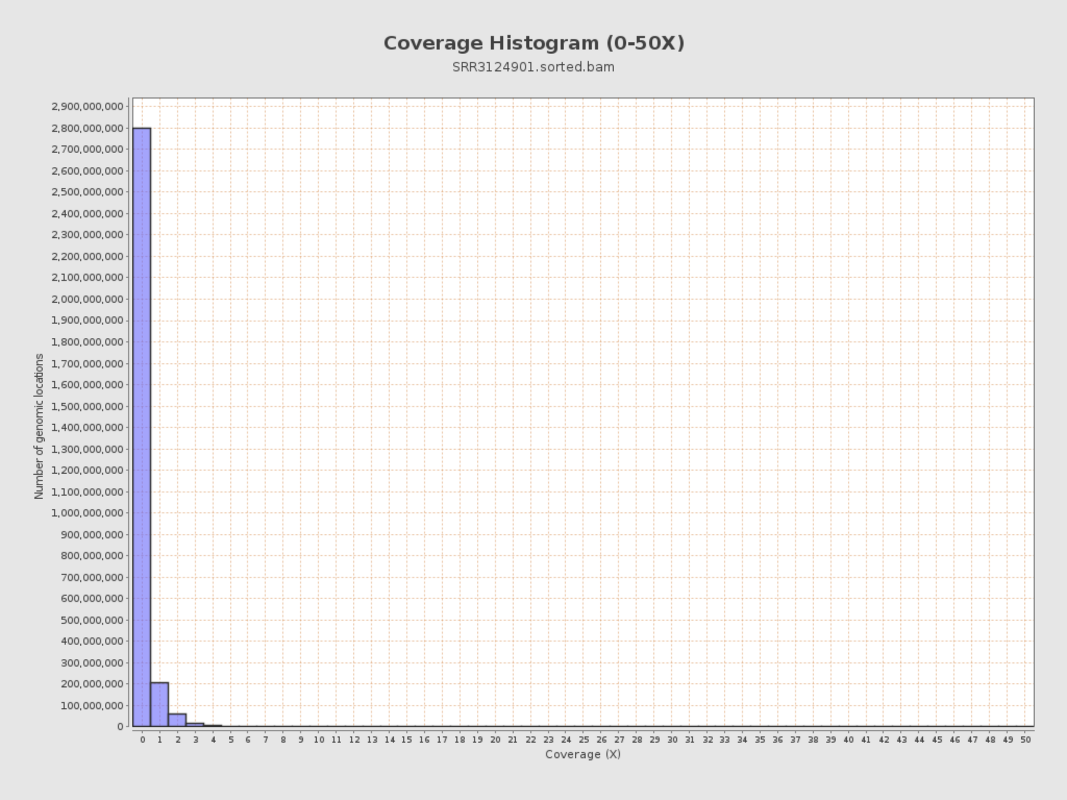
3. Results : Coverage across reference



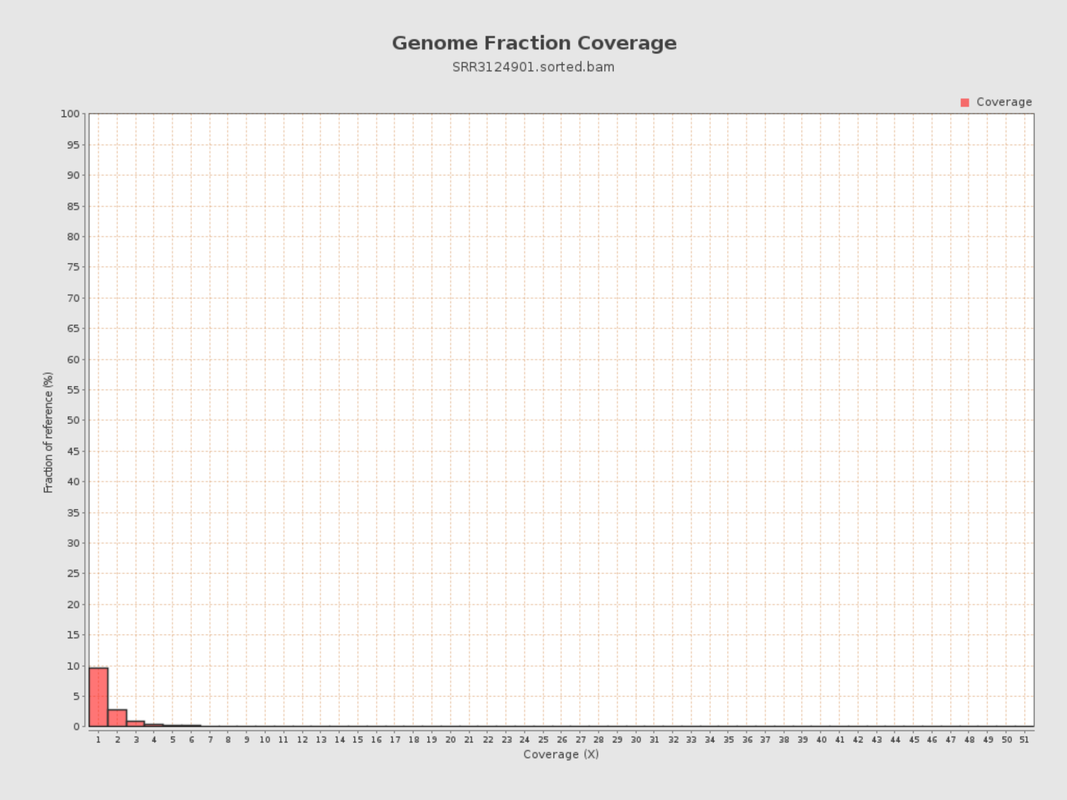
4. Results : Coverage Histogram



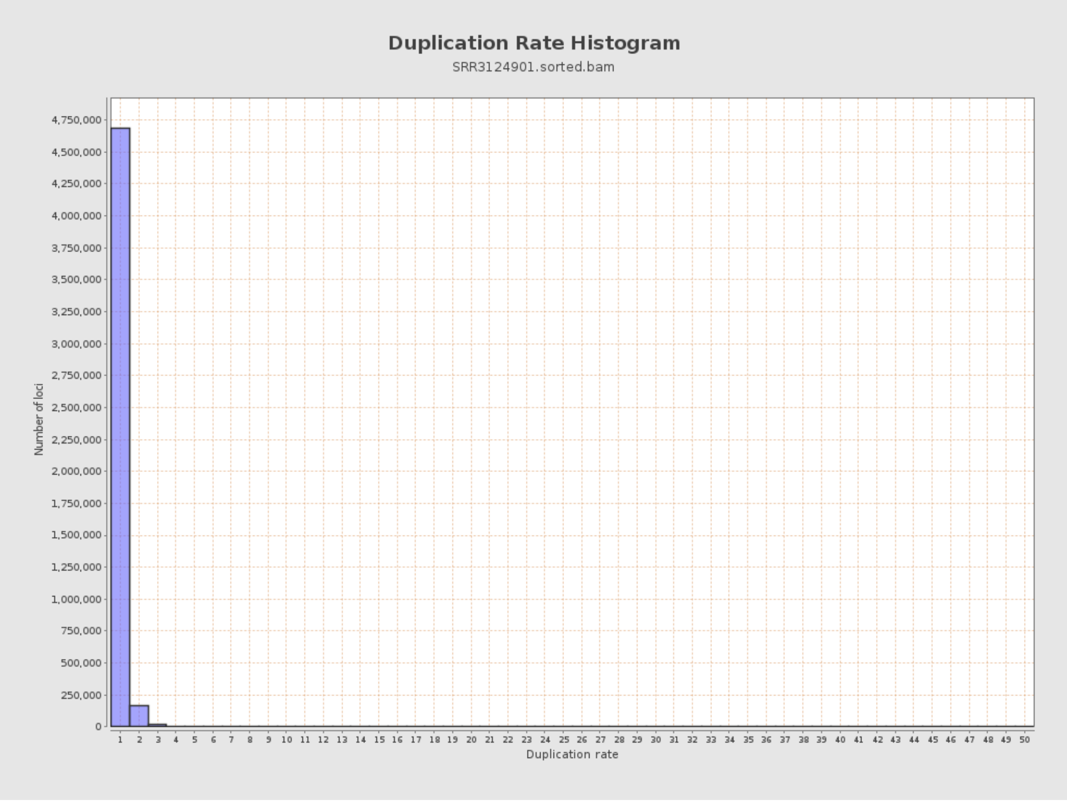
5. Results : Coverage Histogram (0-50X)



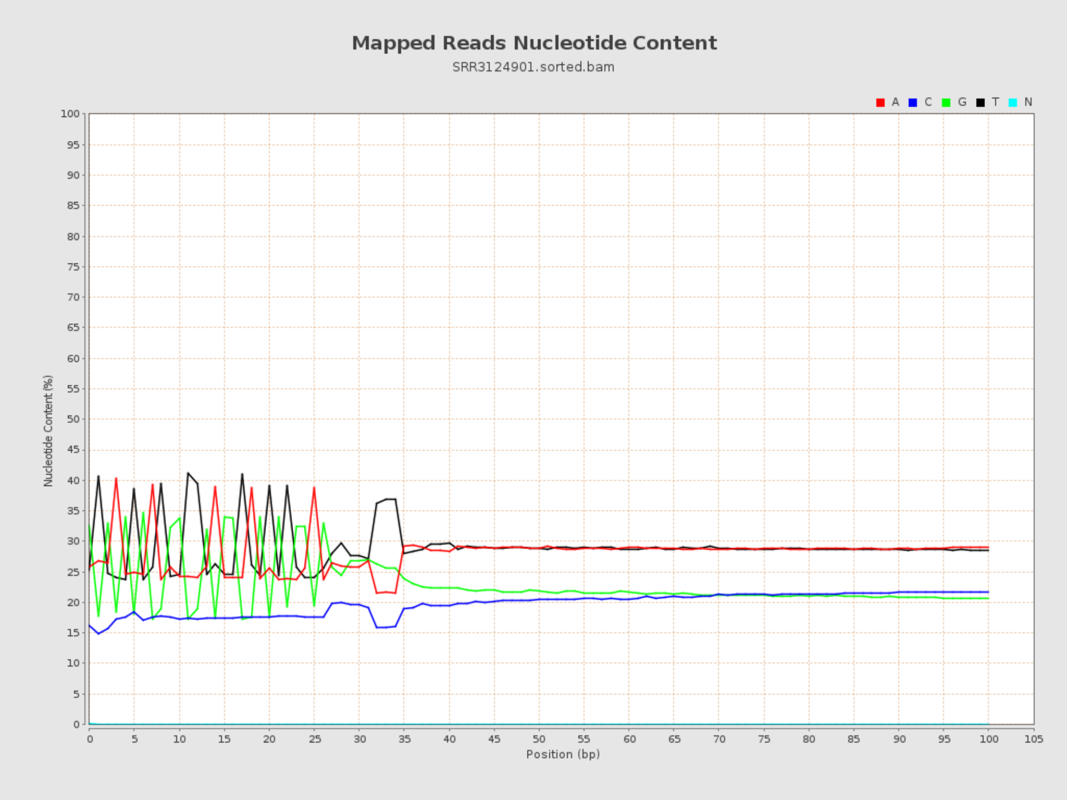
6. Results : Genome Fraction Coverage



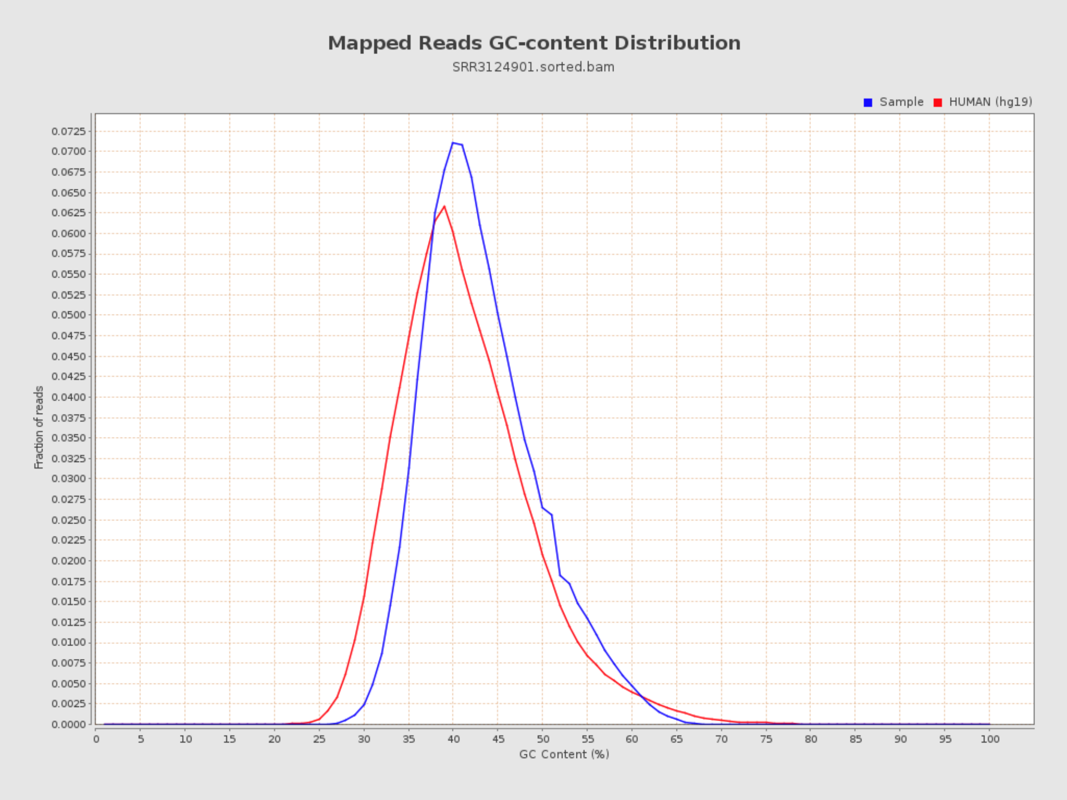
7. Results : Duplication Rate Histogram



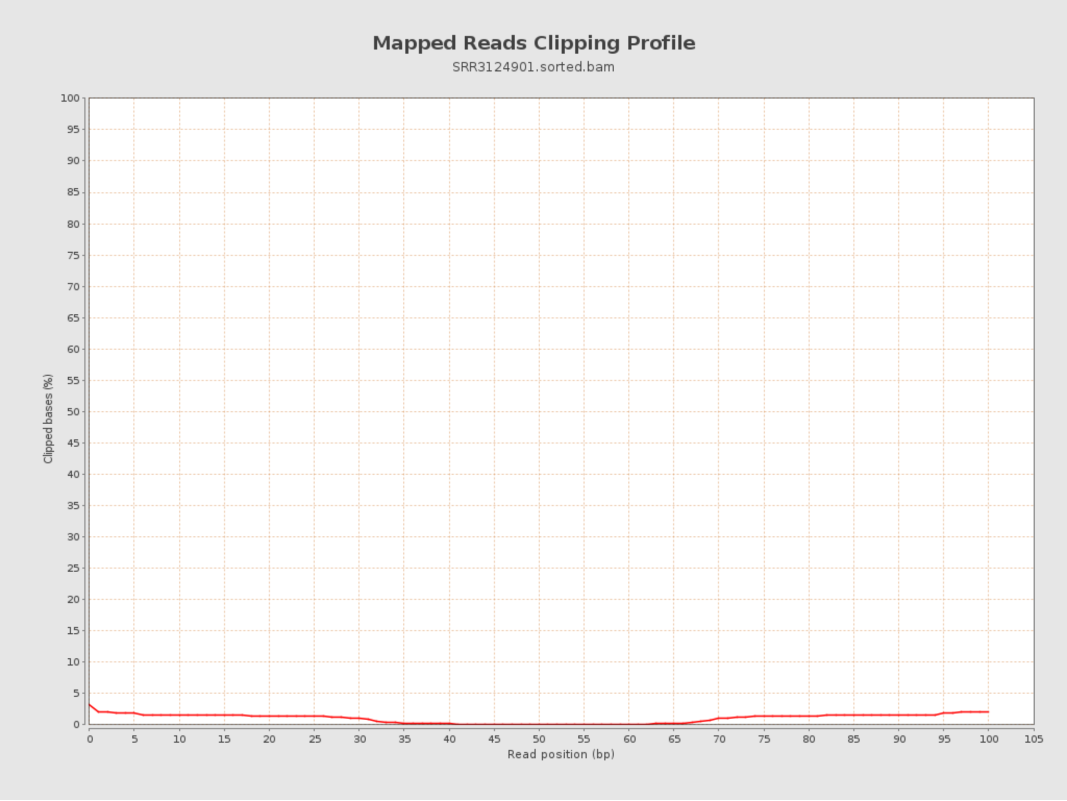
8. Results : Mapped Reads Nucleotide Content



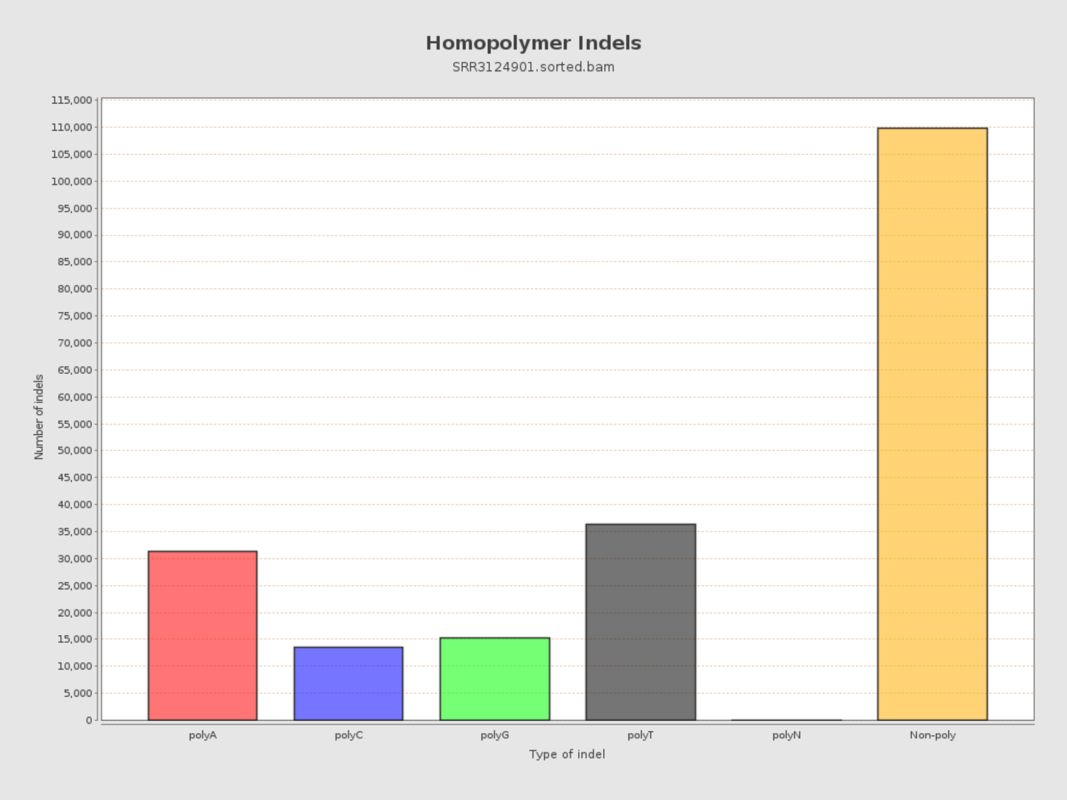
9. Results : Mapped Reads GC-content Distribution



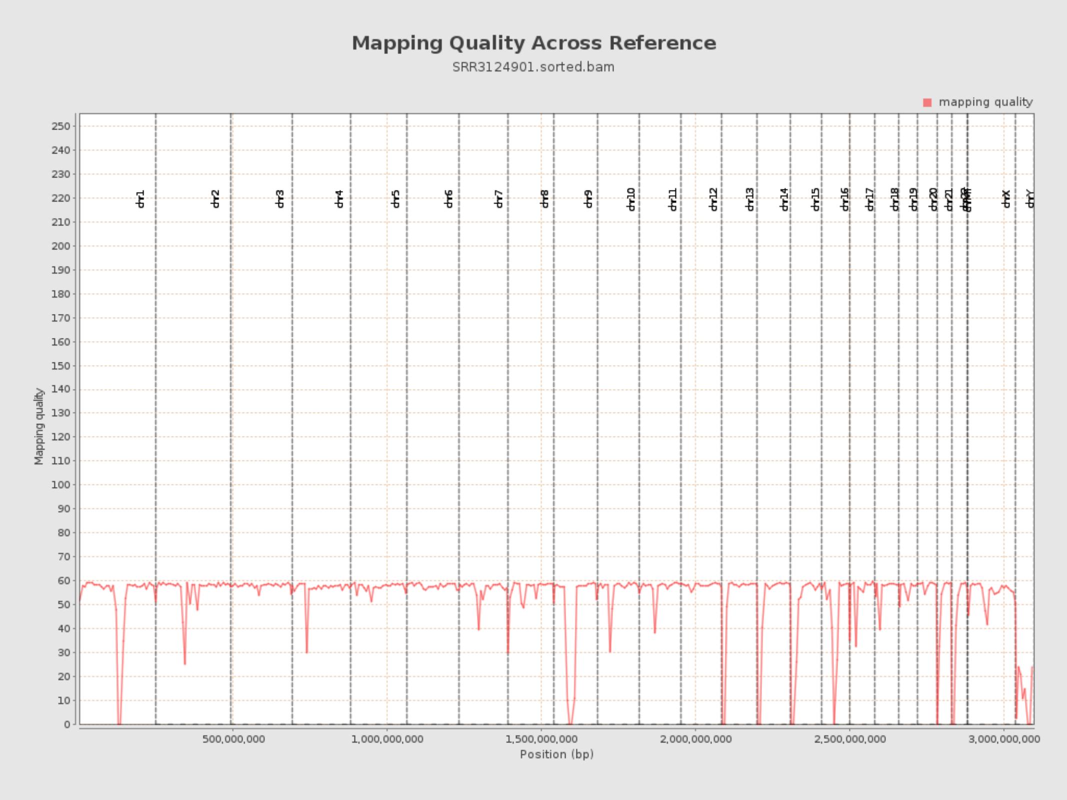
10. Results : Mapped Reads Clipping Profile



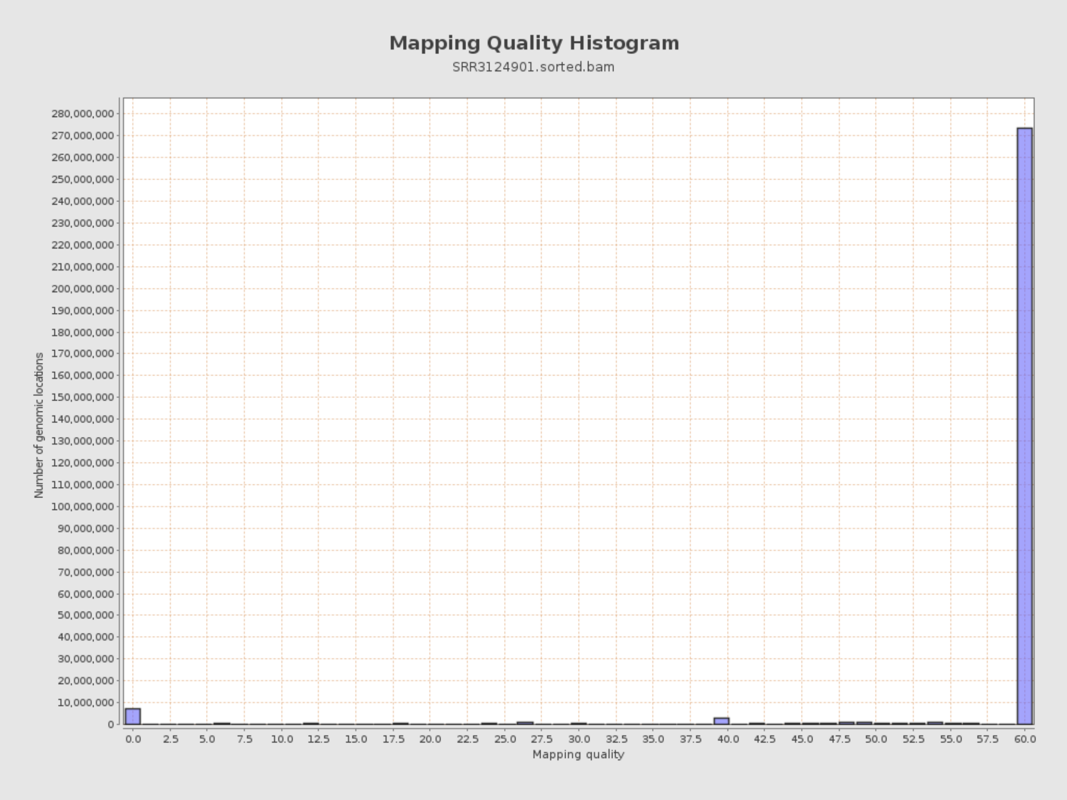
11. Results : Homopolymer Indels



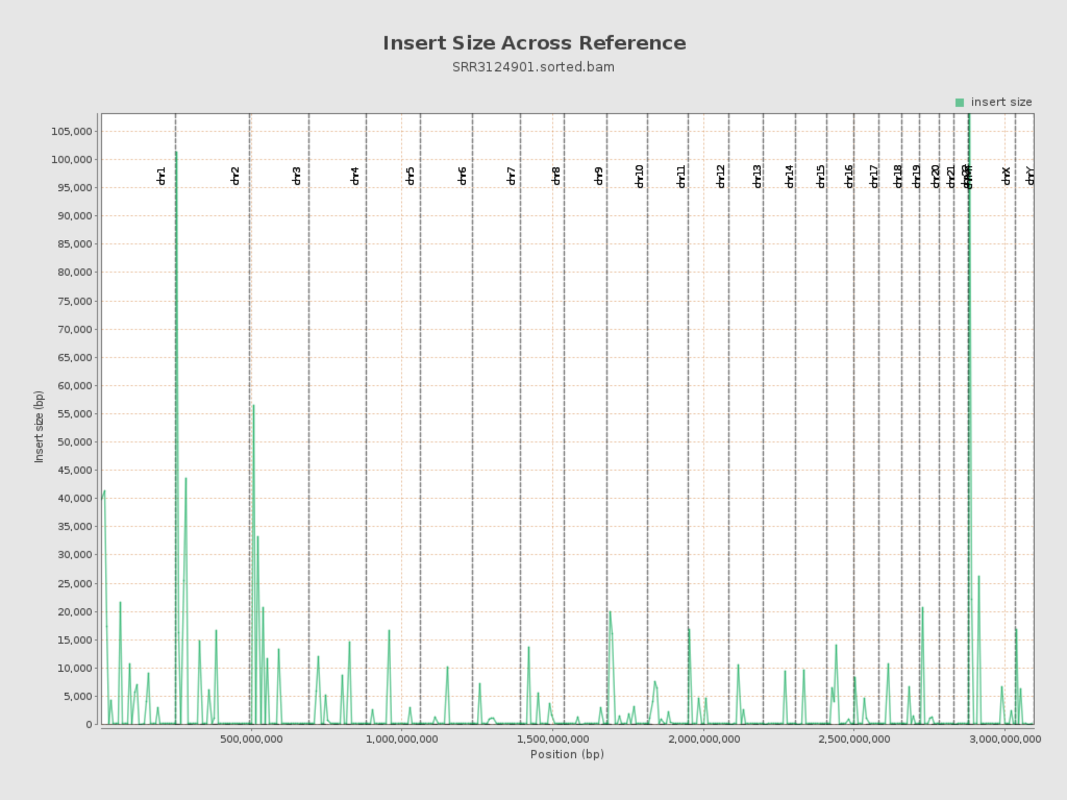
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram