Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 09:05:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124949.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_SRR3124949 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124949_1.fastq.gz SRR3124949_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 09:05:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124949.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,113,326
Mapped reads	6,955,990 / 97.79%
Unmapped reads	157,336 / 2.21%
Mapped paired reads	6,955,990 / 97.79%
Mapped reads, first in pair	3,512,095 / 49.37%
Mapped reads, second in pair	3,443,895 / 48.41%
Mapped reads, both in pair	6,867,056 / 96.54%
Mapped reads, singletons	88,934 / 1.25%
Secondary alignments	0
Supplementary alignments	6,625 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	453,058 / 6.37%
Duplication rate	4.69%
Clipped reads	3,122,738 / 43.9%

2.2. ACGT Content

Number/percentage of A's	119,314,645 / 27.44%
Number/percentage of C's	78,564,603 / 18.07%
Number/percentage of T's	129,628,731 / 29.82%
Number/percentage of G's	107,242,994 / 24.67%
Number/percentage of N's	3,280 / 0%

GC Percentage	42.74%

2.3. Coverage

Mean	0.1405
Standard Deviation	1.006

2.4. Mapping Quality

Mean Mapping Quality	51.84

2.5. Insert size

Mean	25,284.07
Standard Deviation	1,514,760
P25/Median/P75	140 / 187 / 259

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	2,766,127
Insertions	42,585
Mapped reads with at least one insertion	0.61%
Deletions	120,253
Mapped reads with at least one deletion	1.71%
Homopolymer indels	48.45%

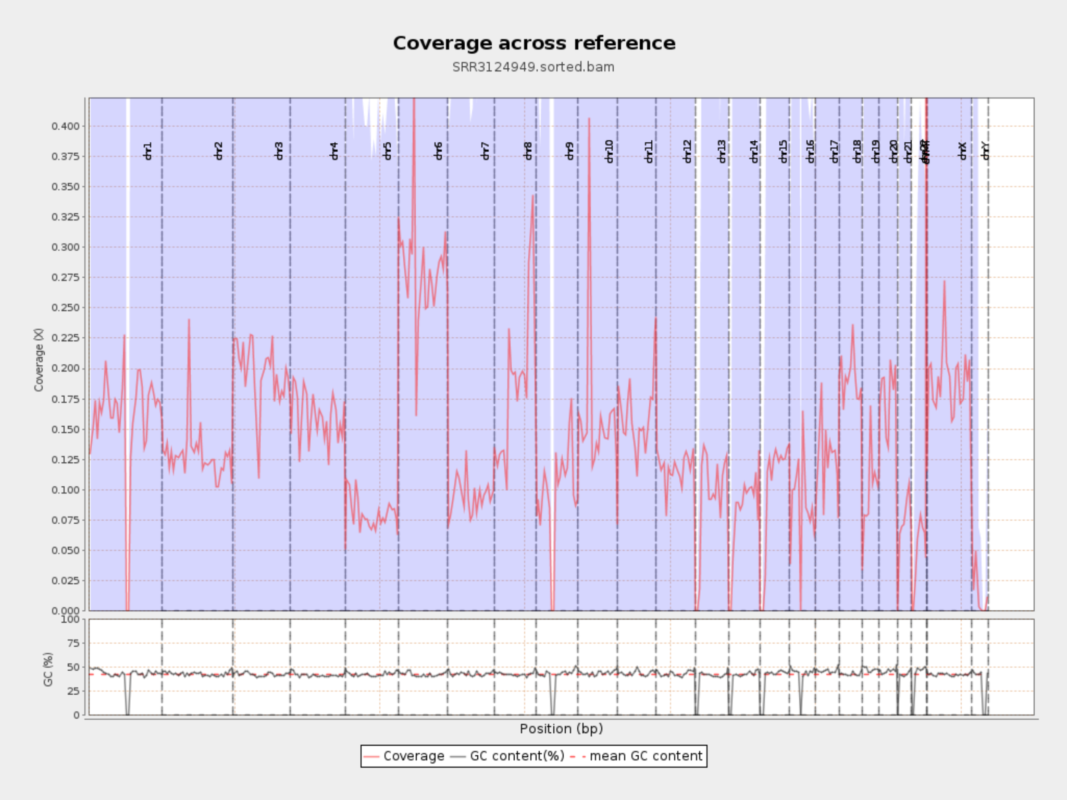
2.7. Chromosome stats

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

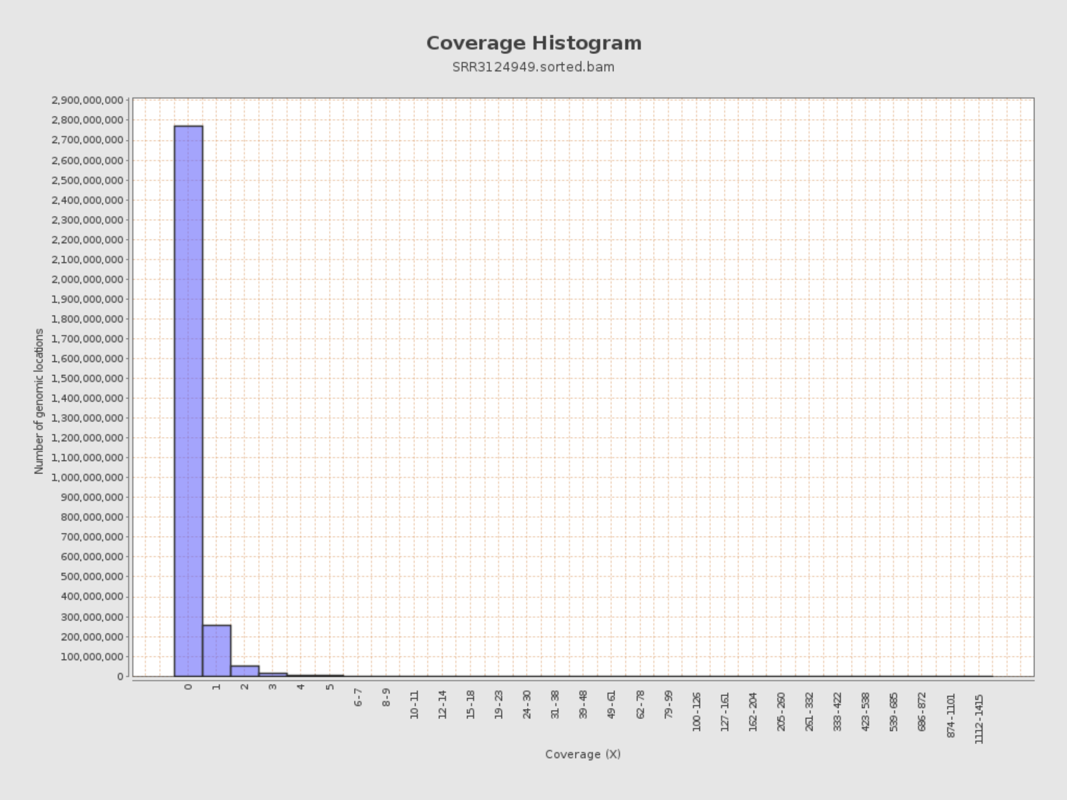
		bases	coverage	deviation
chr1	249250621	39624633	0.159	1.0513
chr2	243199373	31450534	0.1293	0.9472
chr3	198022430	38712809	0.1955	0.5638
chr4	191154276	30577479	0.16	0.5913
chr5	180915260	14562239	0.0805	0.3462
chr6	171115067	48468627	0.2833	2.021
chr7	159138663	15126999	0.0951	0.9816
chr8	146364022	28117790	0.1921	0.6932
chr9	141213431	13894490	0.0984	0.8682
chr10	135534747	21851866	0.1612	2.1707
chr11	135006516	21371531	0.1583	1.0499
chr12	133851895	15682262	0.1172	0.4253
chr13	115169878	10471793	0.0909	0.3592
chr14	107349540	8514834	0.0793	0.4215
chr15	102531392	10232812	0.0998	0.4245
chr16	90354753	7882324	0.0872	0.7984
chr17	81195210	10144537	0.1249	1.3532
chr18	78077248	15093696	0.1933	1.2823
chr19	59128983	5960639	0.1008	1.0526
chr20	63025520	10977559	0.1742	0.5407
chr21	48129895	3460838	0.0719	0.4015
chr22	51304566	2392780	0.0466	0.2565
chrMT	16571	54179	3.2695	2.8913
chrX	155270560	29464125	0.1898	0.9423

chrY	59373566	836665	0.0141	0.5383

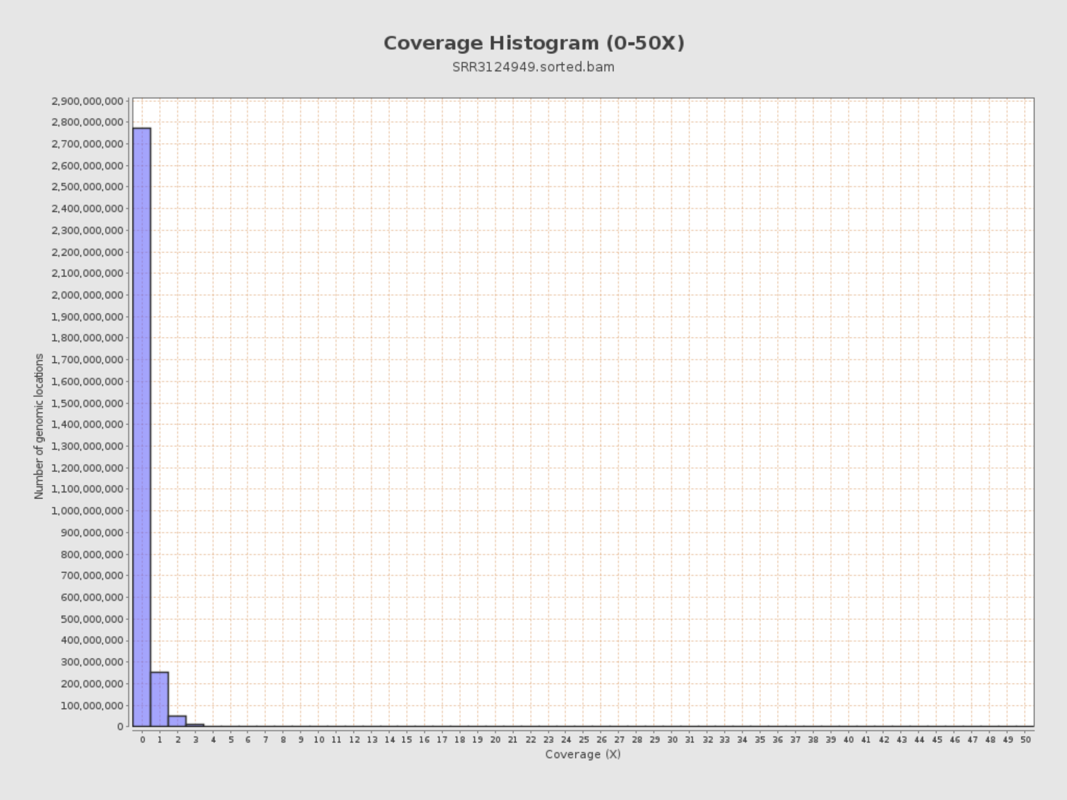
3. Results : Coverage across reference



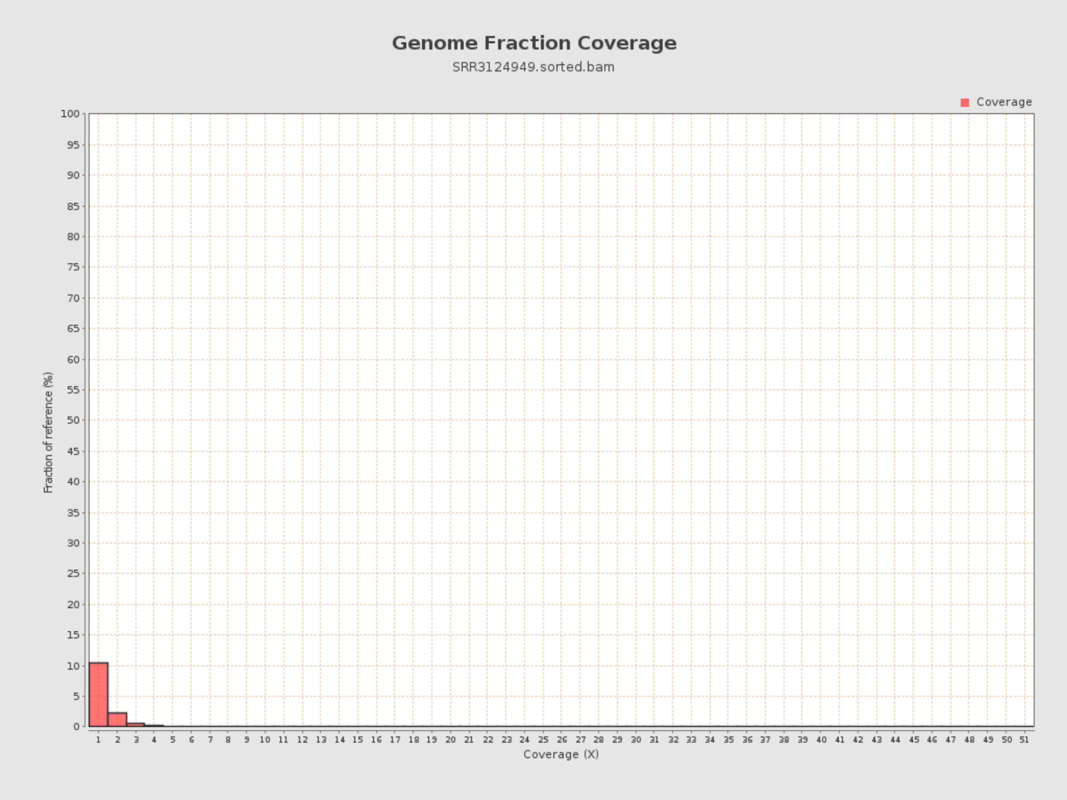
4. Results : Coverage Histogram



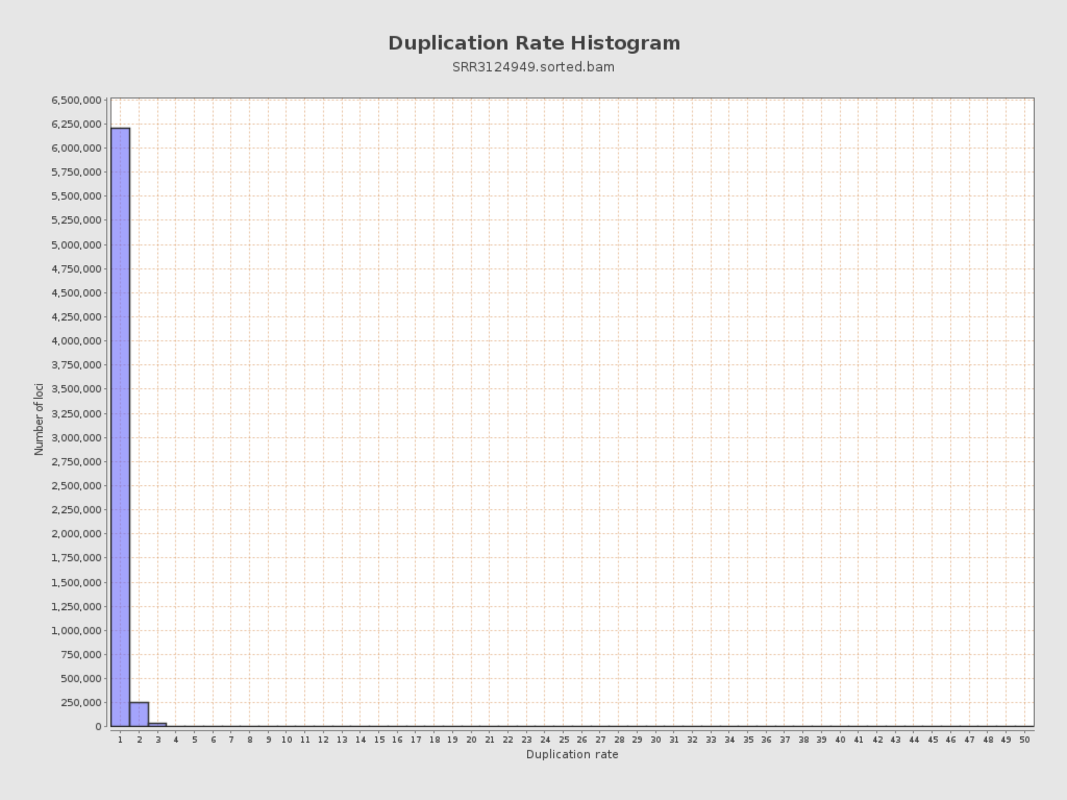
5. Results : Coverage Histogram (0-50X)



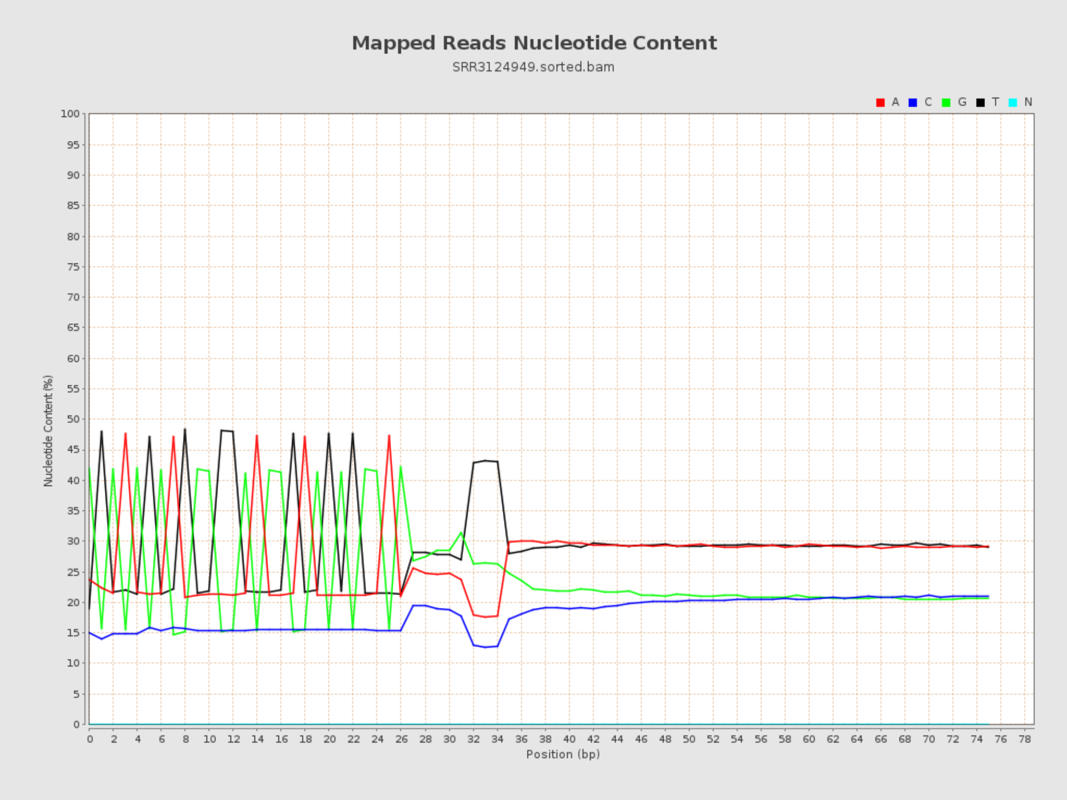
6. Results : Genome Fraction Coverage



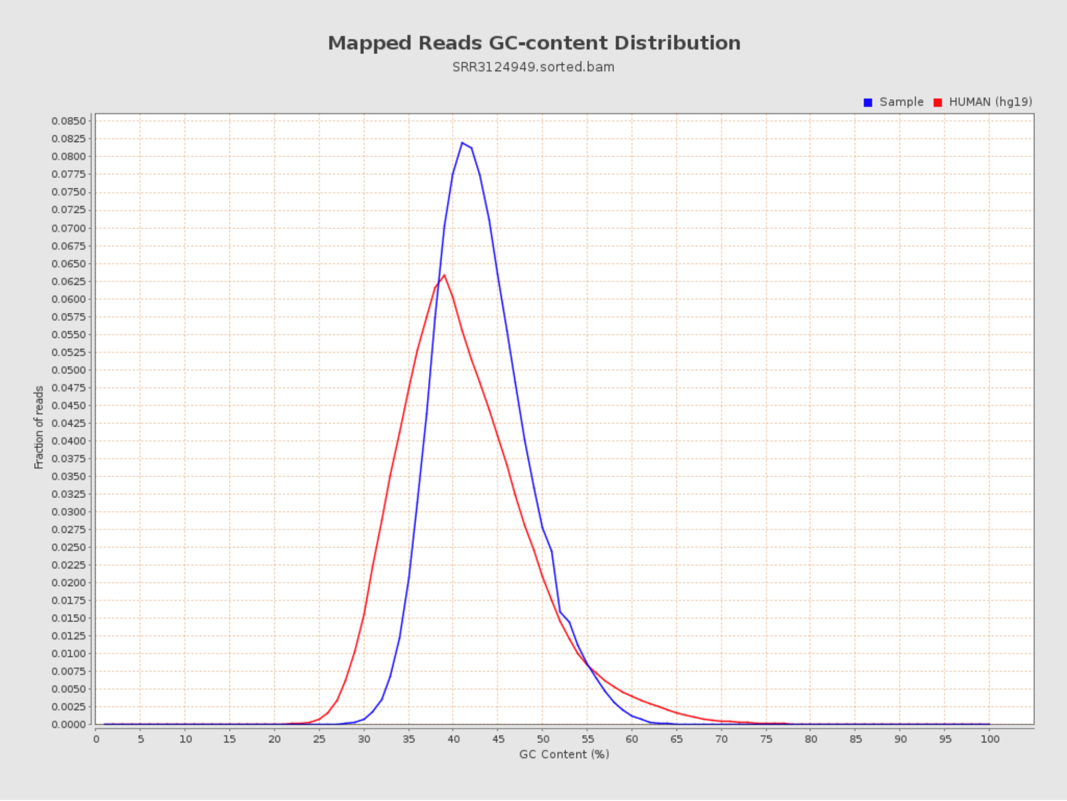
7. Results : Duplication Rate Histogram



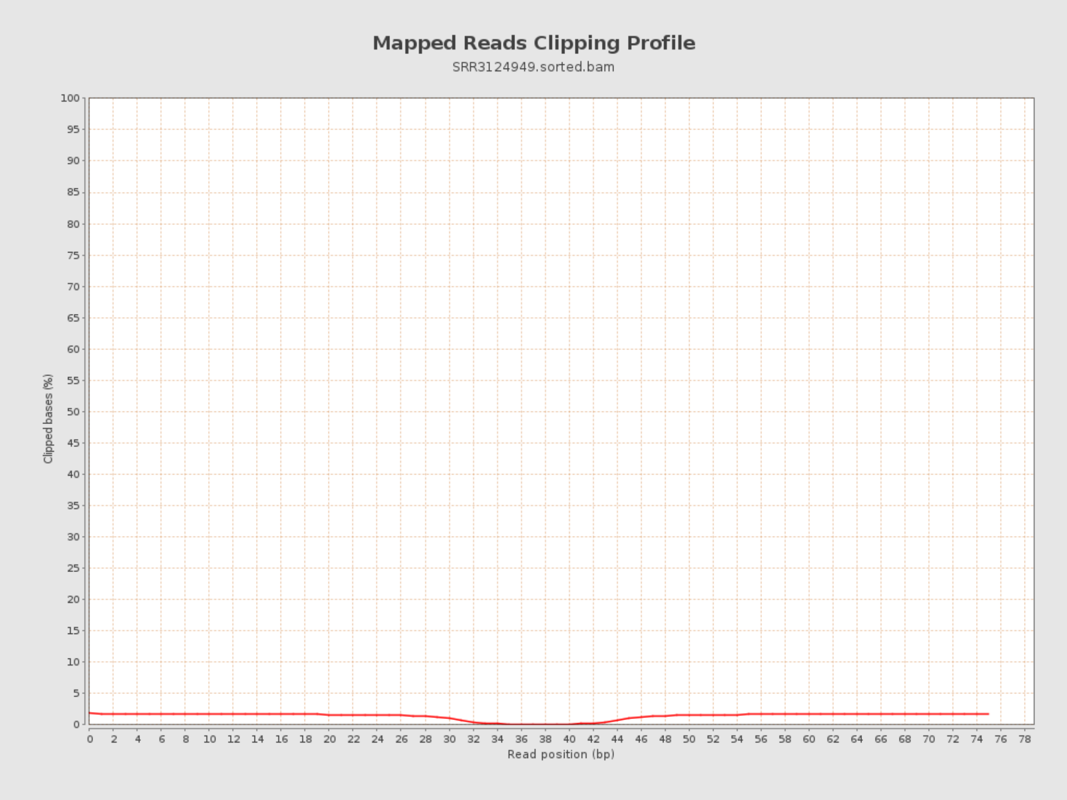
8. Results : Mapped Reads Nucleotide Content



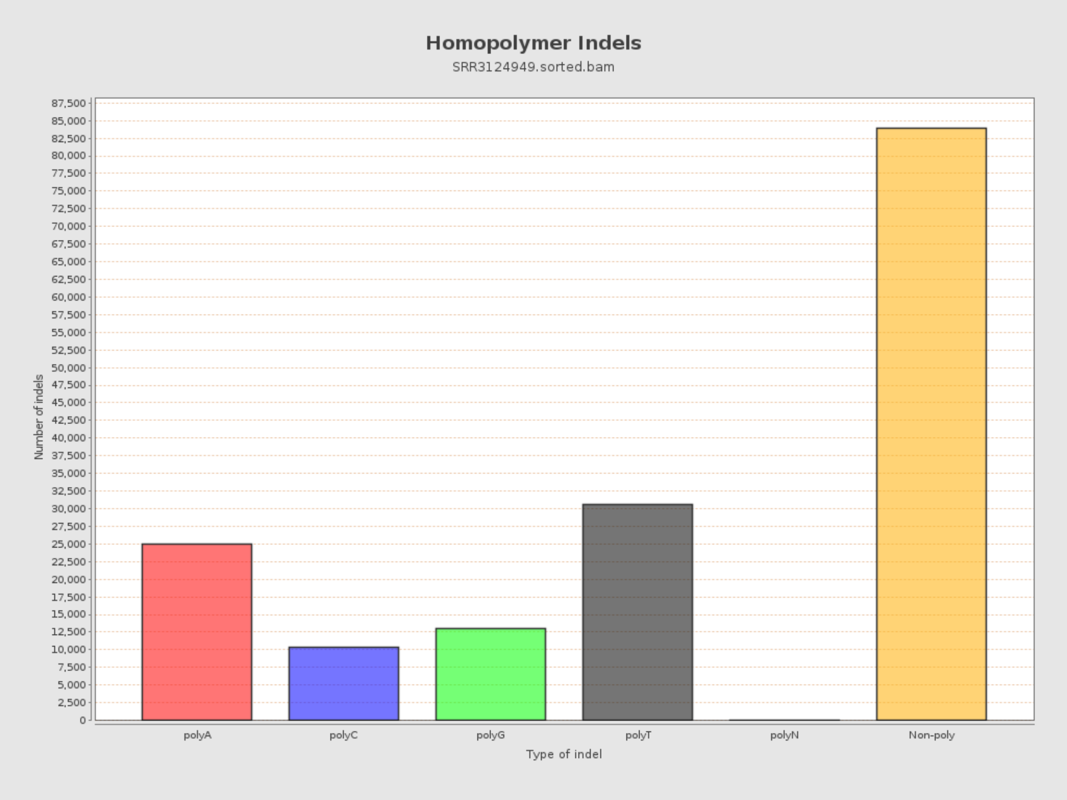
9. Results : Mapped Reads GC-content Distribution



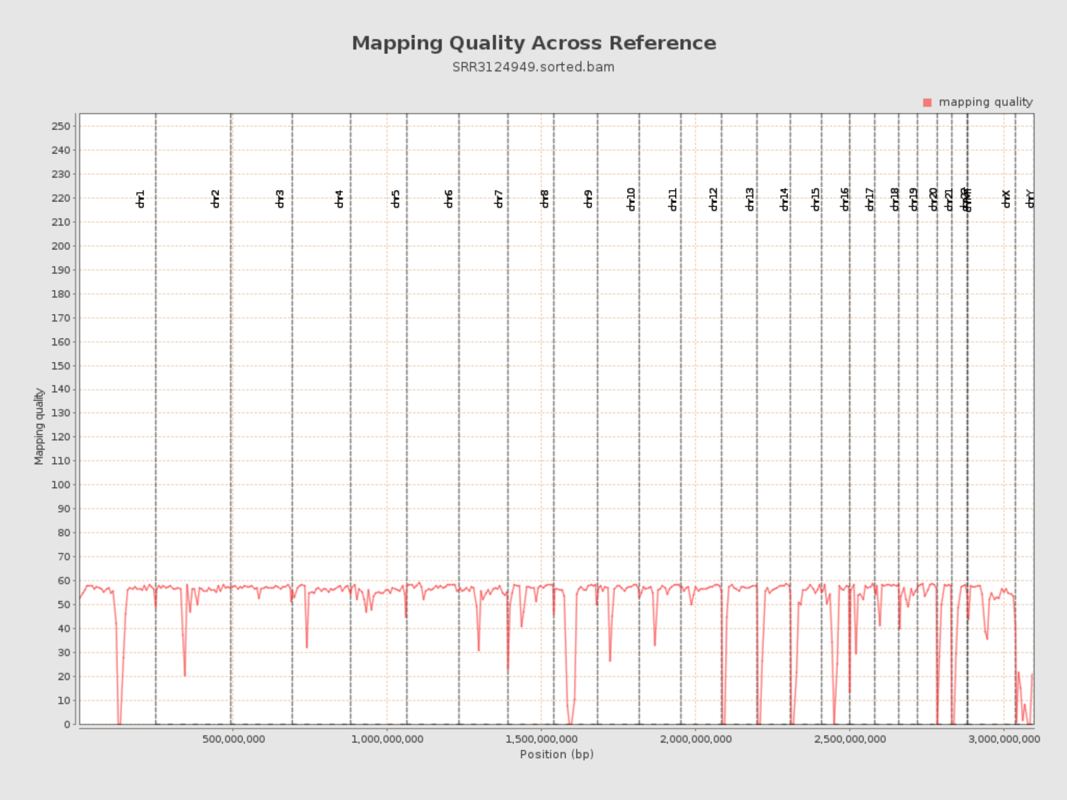
10. Results : Mapped Reads Clipping Profile



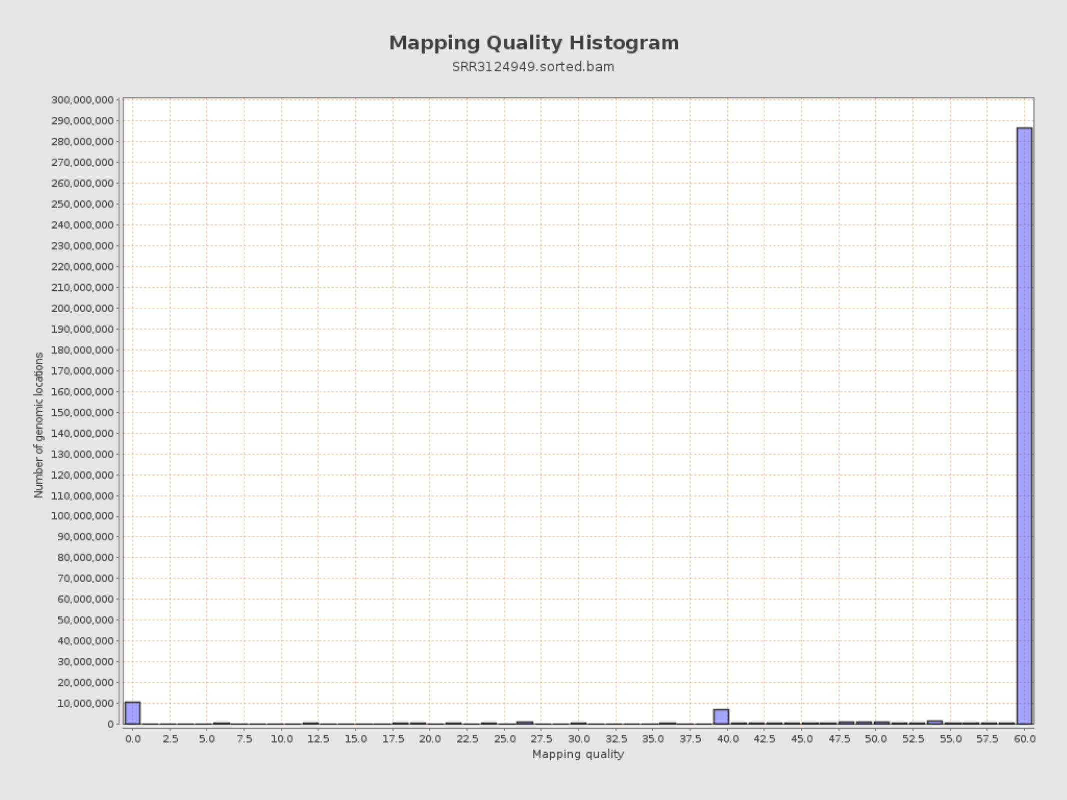
11. Results : Homopolymer Indels



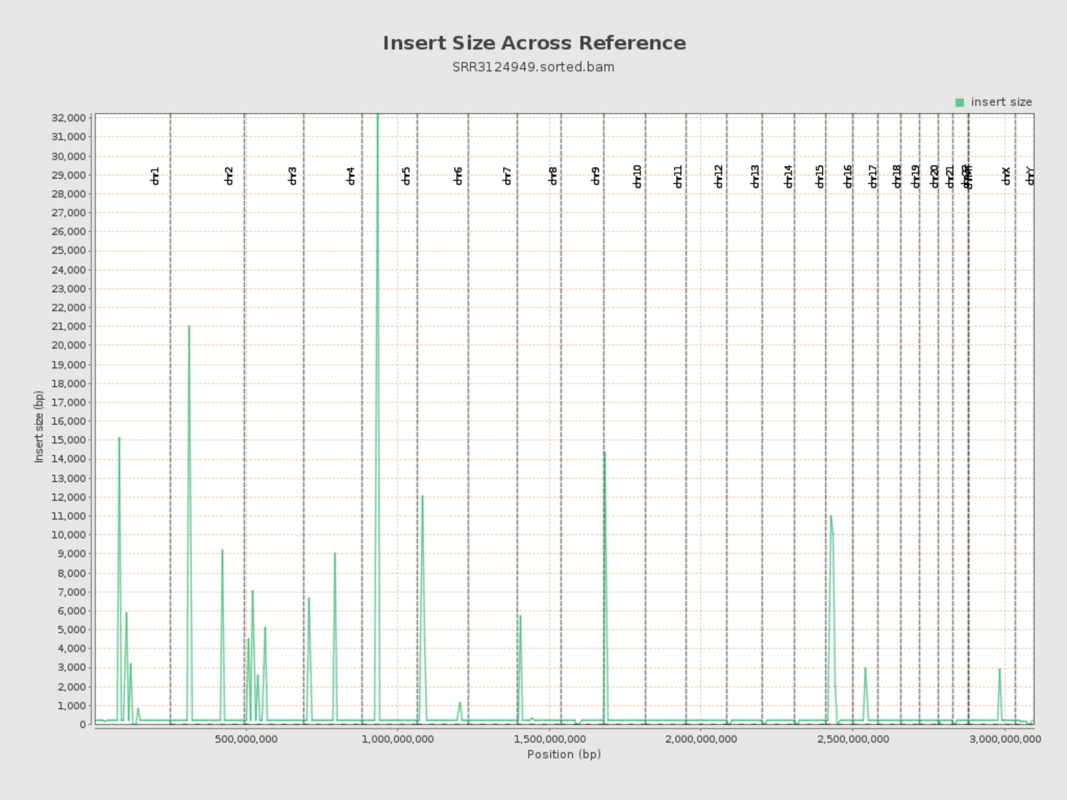
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram