Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 03:56:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124909.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_SRR3124909 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124909_1.fastq.gz SRR3124909_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 03:56:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124909.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,610,214
Mapped reads	4,510,879 / 97.85%
Unmapped reads	99,335 / 2.15%
Mapped paired reads	4,510,879 / 97.85%
Mapped reads, first in pair	2,260,932 / 49.04%
Mapped reads, second in pair	2,249,947 / 48.8%
Mapped reads, both in pair	4,478,762 / 97.15%
Mapped reads, singletons	32,117 / 0.7%
Secondary alignments	0
Supplementary alignments	37,631 / 0.82%
Read min/max/mean length	30 / 101 / 101.32
Duplicated reads (estimated)	519,029 / 11.26%
Duplication rate	7.22%
Clipped reads	2,119,789 / 45.98%

2.2. ACGT Content

Number/percentage of A's	109,631,830 / 27.97%
Number/percentage of C's	74,161,966 / 18.92%
Number/percentage of T's	115,896,794 / 29.57%
Number/percentage of G's	92,275,337 / 23.54%
Number/percentage of N's	5,499 / 0%

GC Percentage	42.46%

2.3. Coverage

Mean	0.1267
Standard Deviation	1.5731

2.4. Mapping Quality

Mean Mapping Quality	52.42

2.5. Insert size

Mean	62,111.62
Standard Deviation	2,286,992.56
P25/Median/P75	150 / 203 / 284

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	3,361,446
Insertions	70,932
Mapped reads with at least one insertion	1.5%
Deletions	150,552
Mapped reads with at least one deletion	3.25%
Homopolymer indels	44.72%

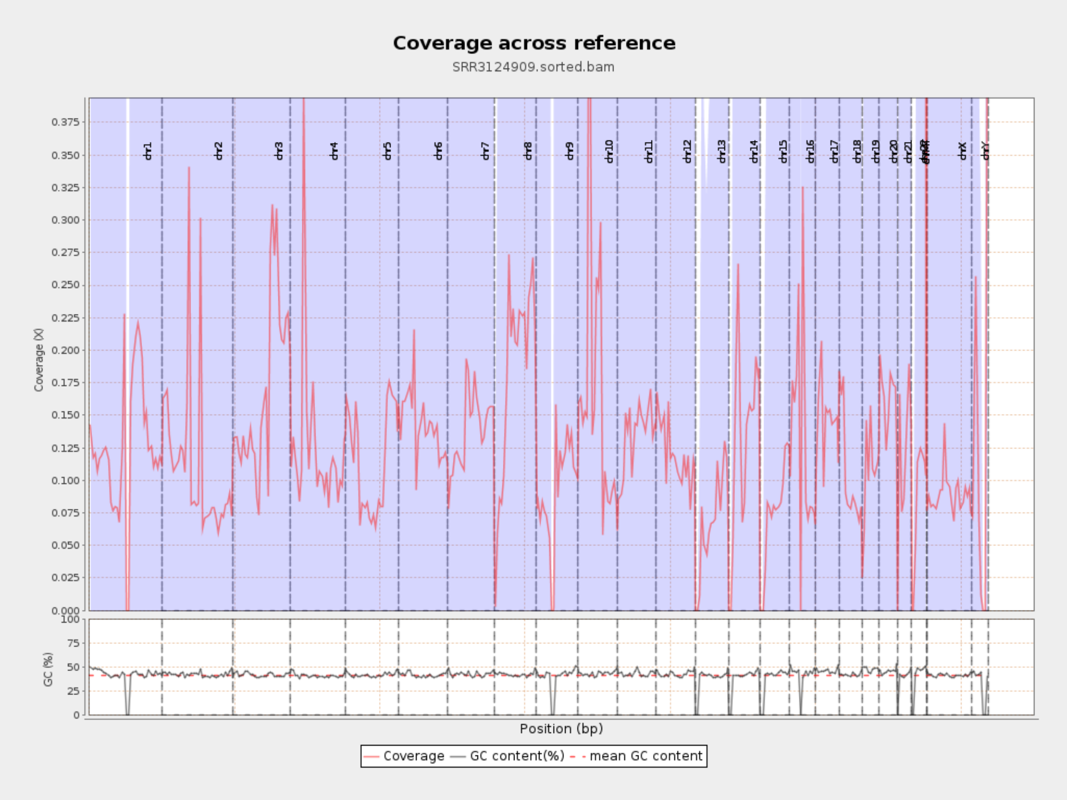
2.7. Chromosome stats

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

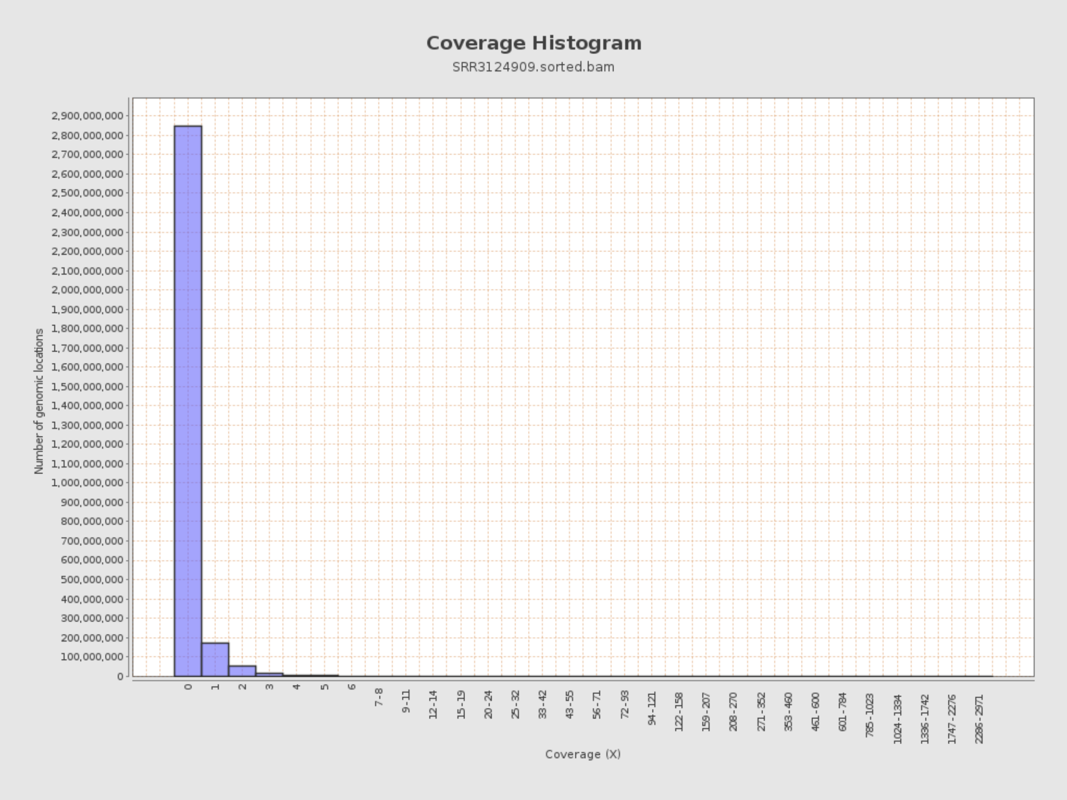
		bases	coverage	deviation
chr1	249250621	31261057	0.1254	1.3487
chr2	243199373	27492108	0.113	2.9424
chr3	198022430	33473659	0.169	0.5996
chr4	191154276	23688540	0.1239	1.4097
chr5	180915260	20790071	0.1149	0.5708
chr6	171115067	24472314	0.143	1.0588
chr7	159138663	22302487	0.1401	1.1648
chr8	146364022	26789272	0.183	0.7914
chr9	141213431	13062496	0.0925	1.5458
chr10	135534747	23190724	0.1711	3.427
chr11	135006516	18060690	0.1338	0.766
chr12	133851895	16206346	0.1211	0.4993
chr13	115169878	7864016	0.0683	0.3712
chr14	107349540	14101233	0.1314	0.6114
chr15	102531392	7621131	0.0743	0.3812
chr16	90354753	11982163	0.1326	2.2663
chr17	81195210	11857993	0.146	1.0944
chr18	78077248	8095287	0.1037	1.6068
chr19	59128983	6456524	0.1092	0.9812
chr20	63025520	10337426	0.164	0.7309
chr21	48129895	5857035	0.1217	1.1067
chr22	51304566	4235464	0.0826	0.5388
chrMT	16571	1610954	97.2153	59.1833
chrX	155270560	13928906	0.0897	0.6198

chrY	59373566	7524972	0.1267	3.615

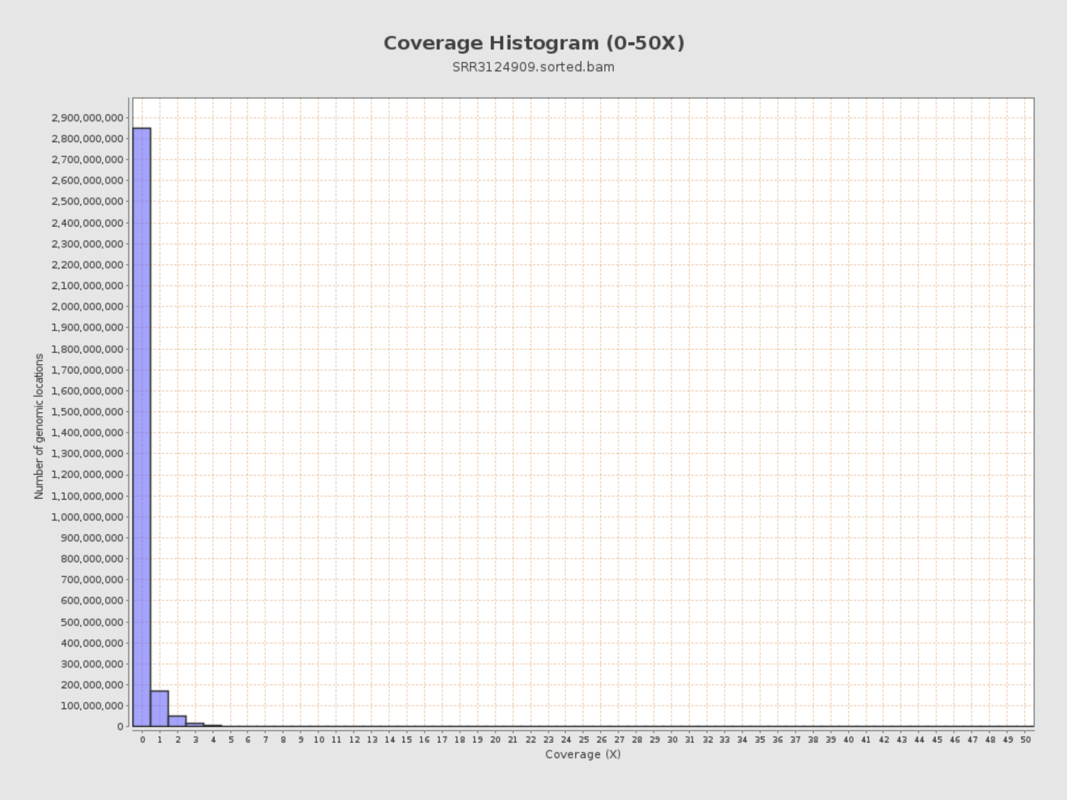
3. Results : Coverage across reference



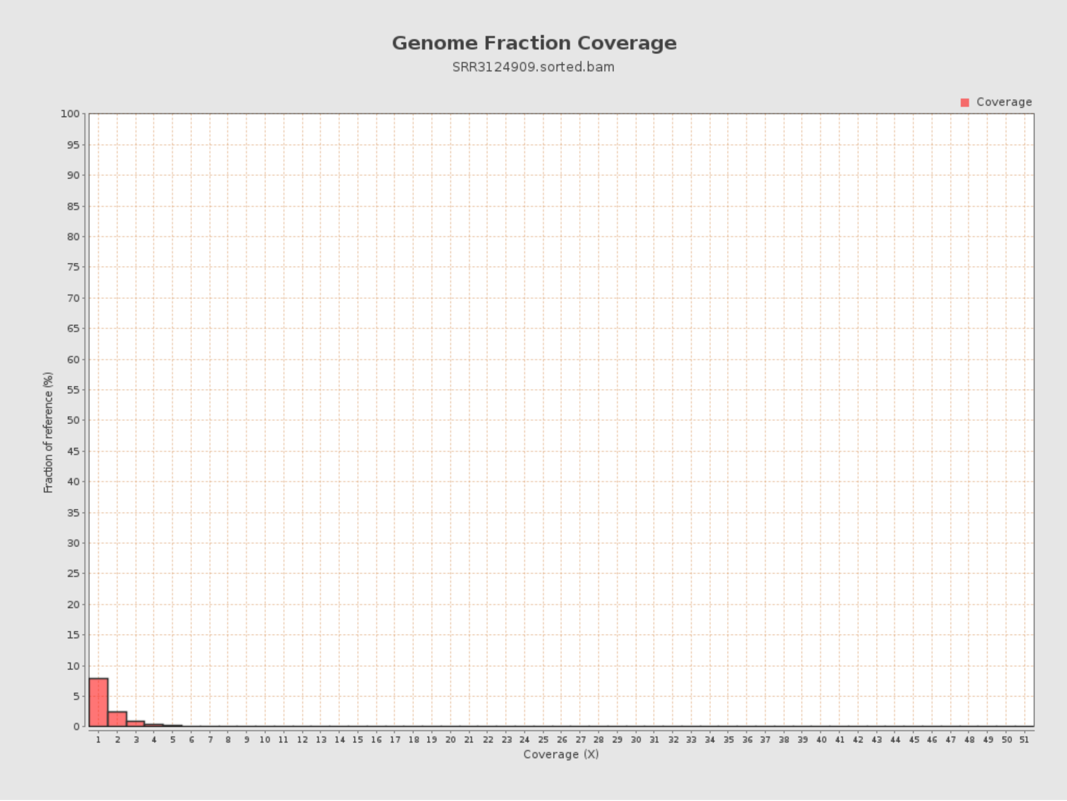
4. Results : Coverage Histogram



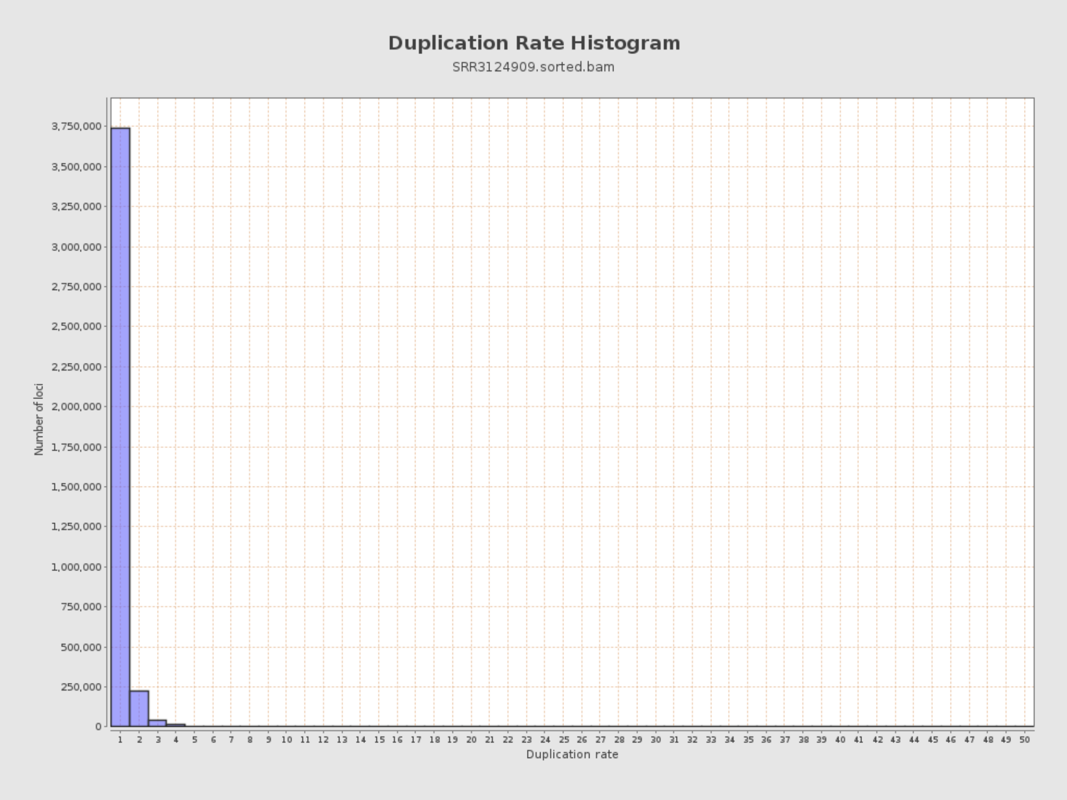
5. Results : Coverage Histogram (0-50X)



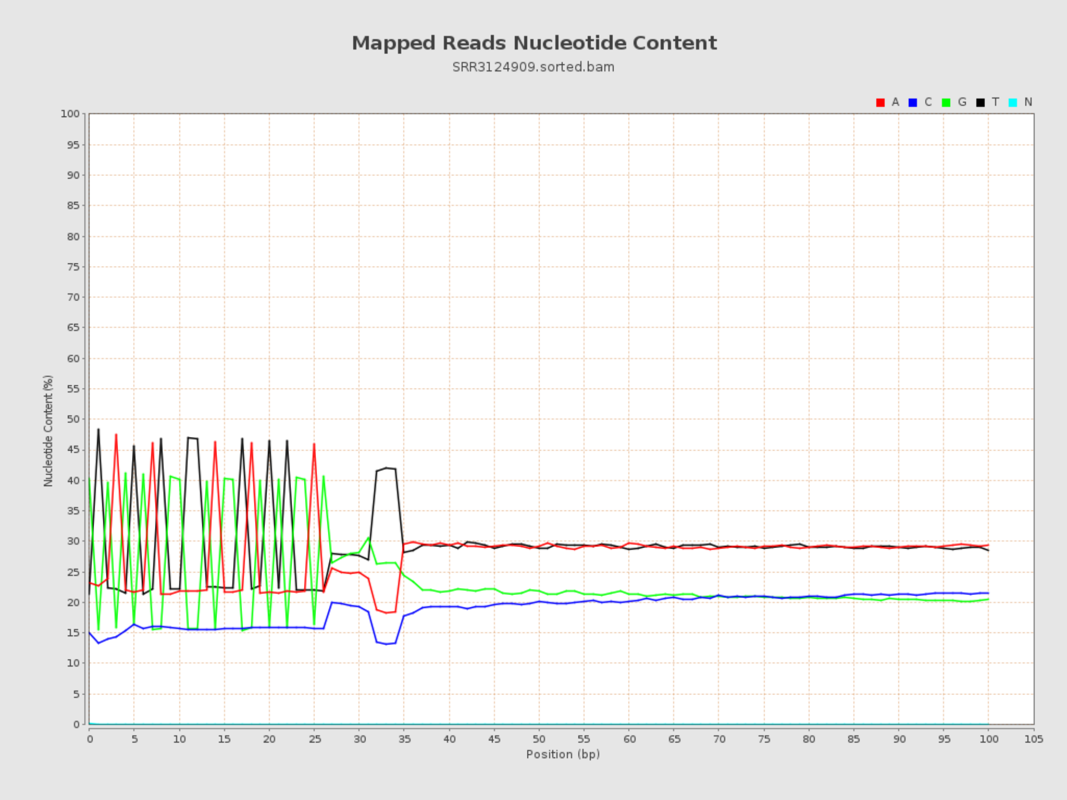
6. Results : Genome Fraction Coverage



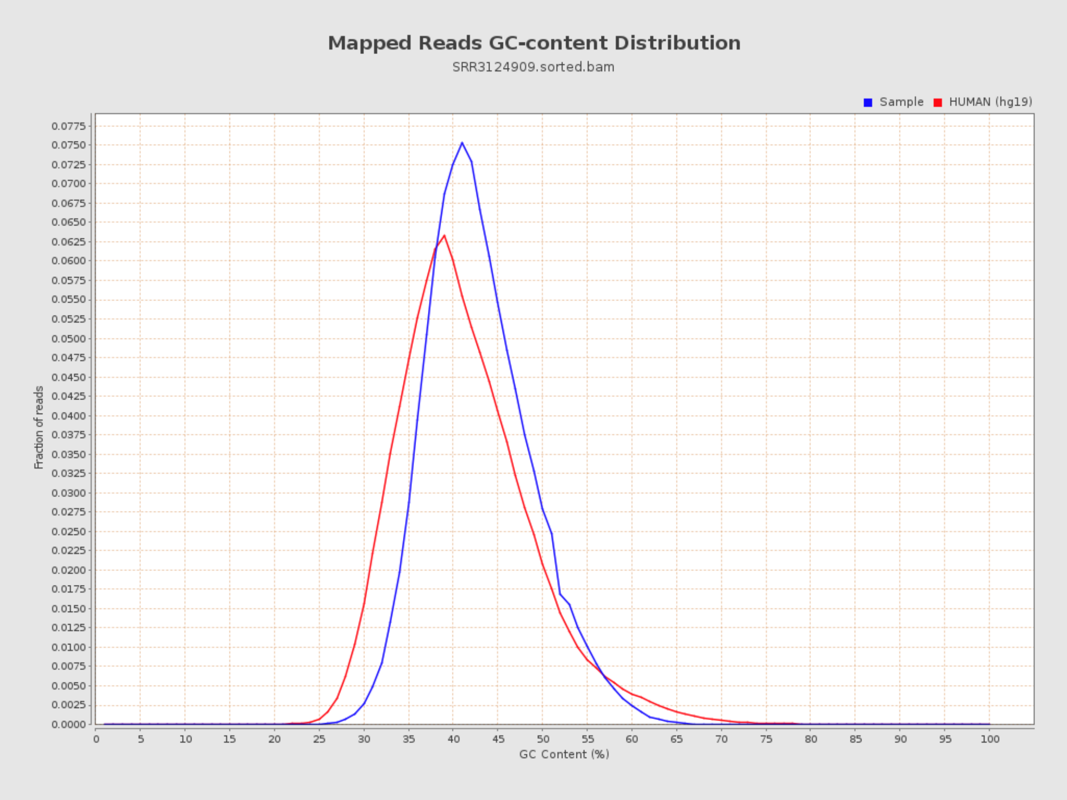
7. Results : Duplication Rate Histogram



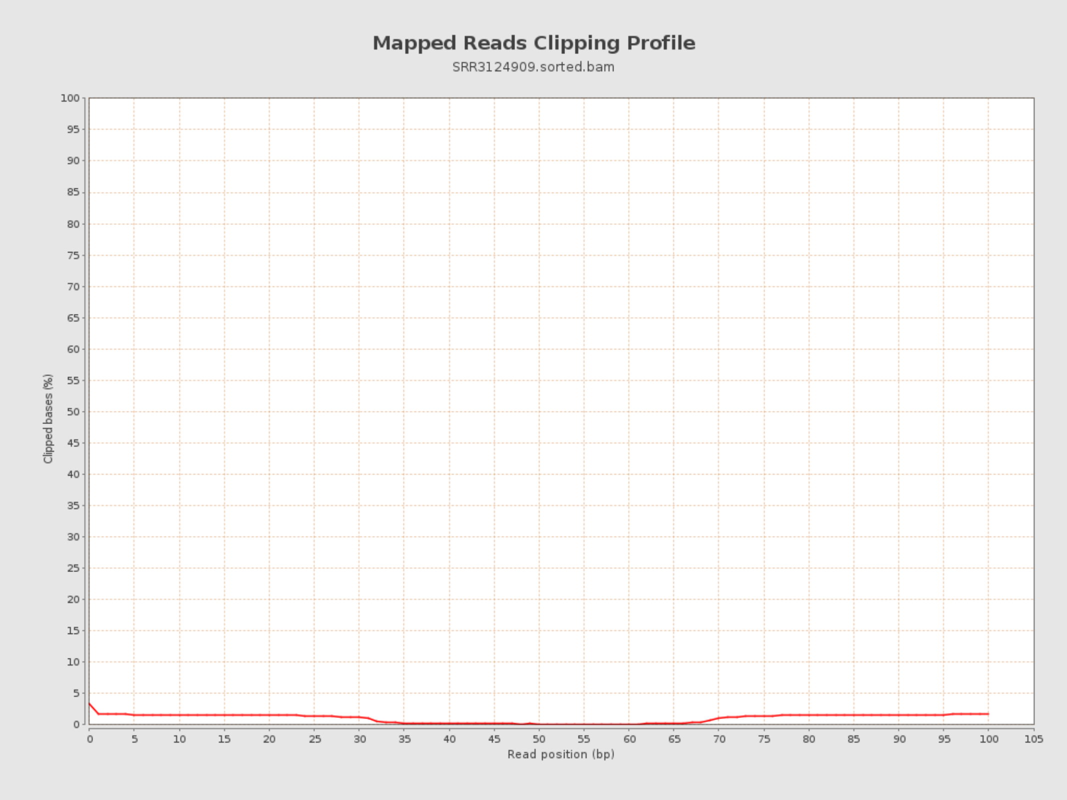
8. Results : Mapped Reads Nucleotide Content



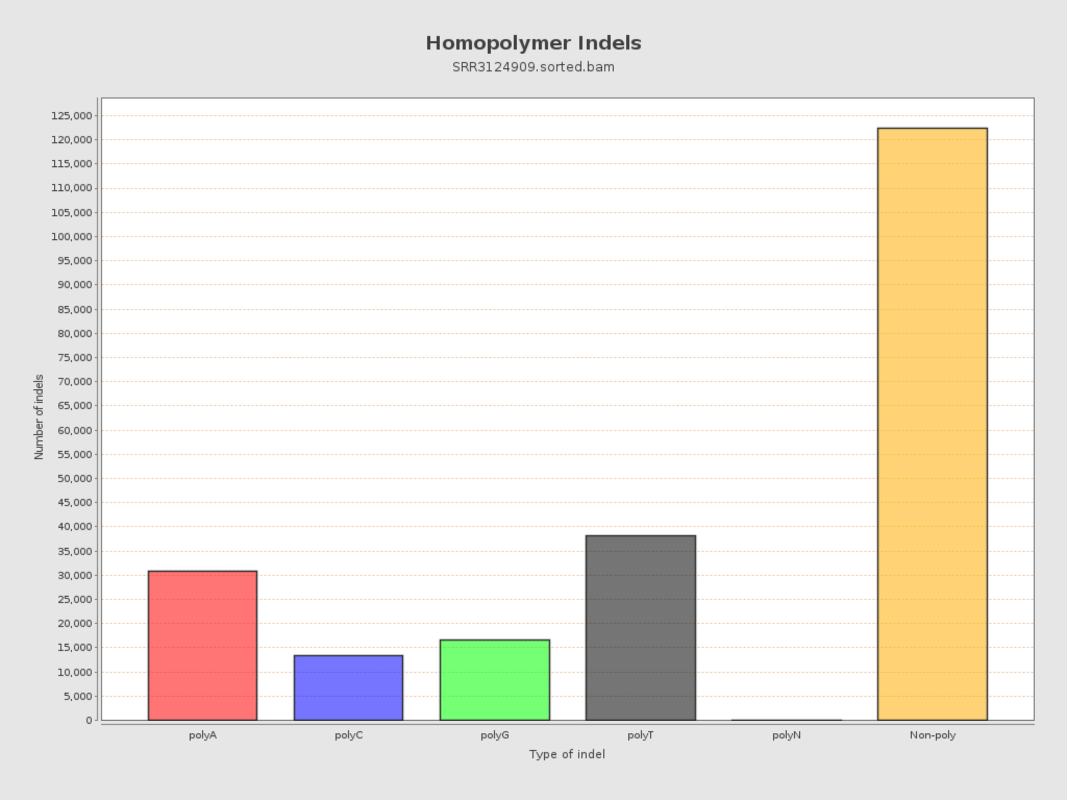
9. Results : Mapped Reads GC-content Distribution



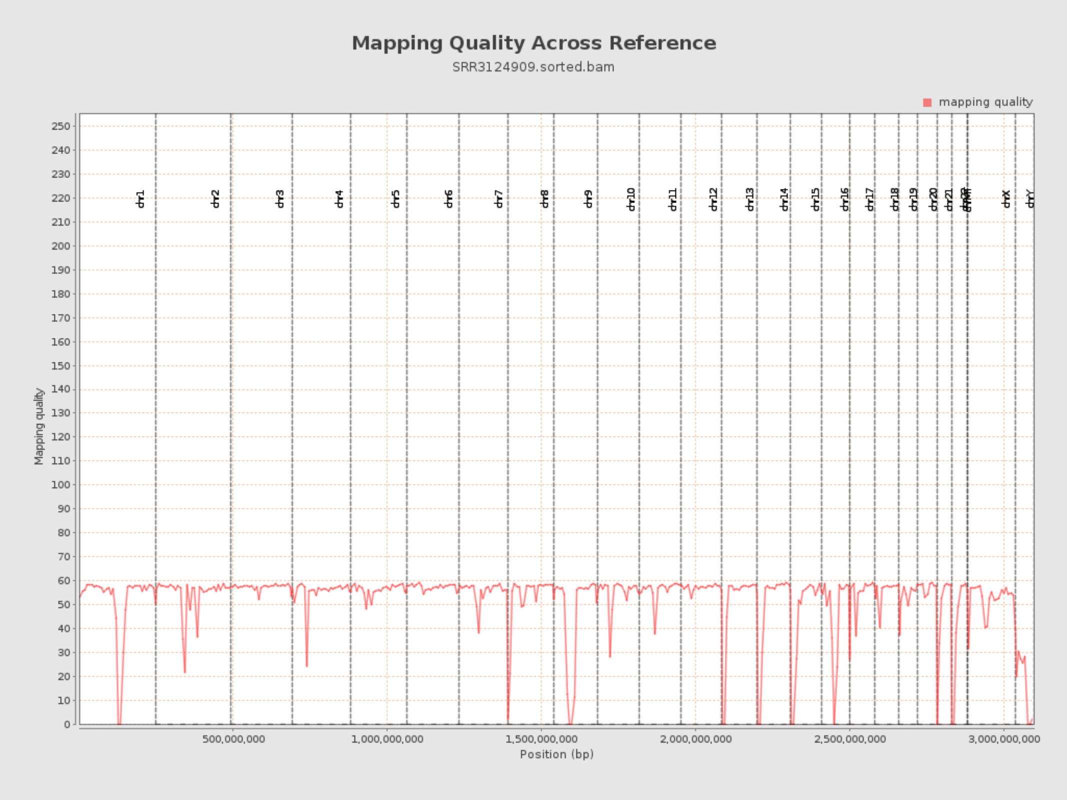
10. Results : Mapped Reads Clipping Profile



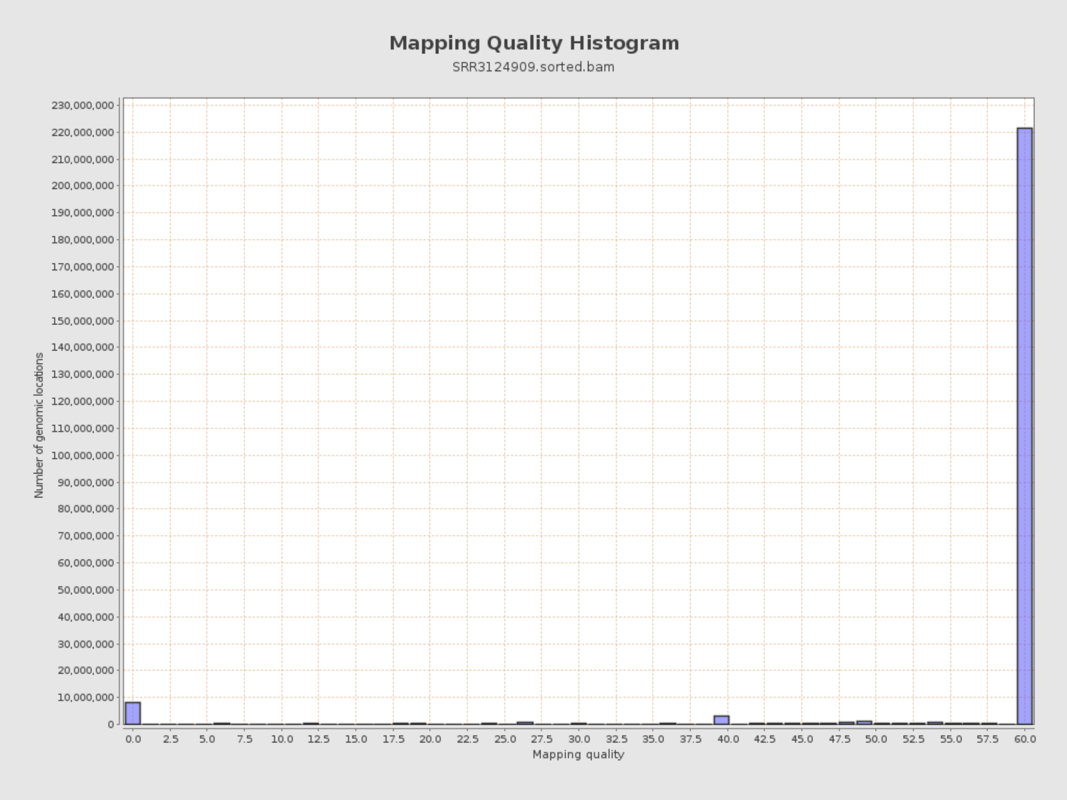
11. Results : Homopolymer Indels



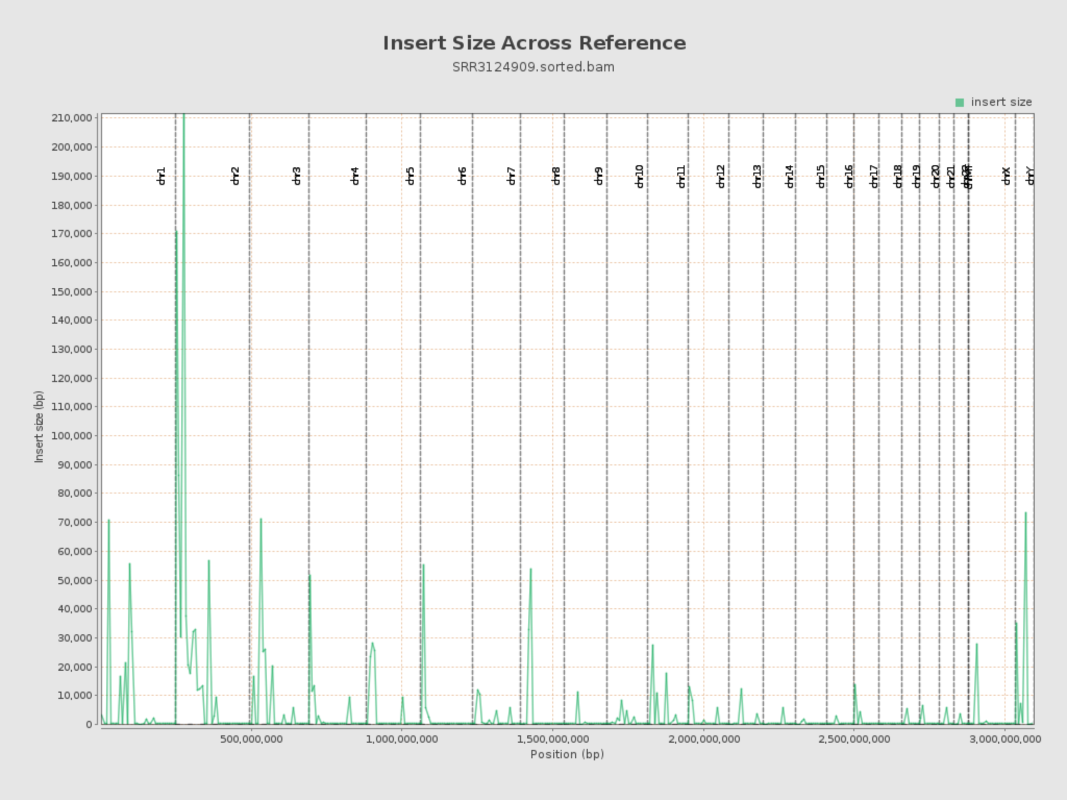
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram