Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 11:58:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124973.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_SRR3124973 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124973_1.fastq.gz SRR3124973_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 11:58:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124973.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,115,768
Mapped reads	2,933,348 / 94.15%
Unmapped reads	182,420 / 5.85%
Mapped paired reads	2,933,348 / 94.15%
Mapped reads, first in pair	1,498,424 / 48.09%
Mapped reads, second in pair	1,434,924 / 46.05%
Mapped reads, both in pair	2,843,180 / 91.25%
Mapped reads, singletons	90,168 / 2.89%
Secondary alignments	0
Supplementary alignments	9,182 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	308,856 / 9.91%
Duplication rate	7.06%
Clipped reads	1,514,413 / 48.6%

2.2. ACGT Content

Number/percentage of A's	49,496,520 / 27.69%
Number/percentage of C's	31,710,746 / 17.74%
Number/percentage of T's	53,332,264 / 29.84%
Number/percentage of G's	44,191,762 / 24.73%
Number/percentage of N's	0 / 0%

GC Percentage	42.47%

2.3. Coverage

Mean	0.0578
Standard Deviation	0.7951

2.4. Mapping Quality

Mean Mapping Quality	51.73

2.5. Insert size

Mean	60,871.45
Standard Deviation	2,250,777.34
P25/Median/P75	127 / 170 / 231

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	1,589,738
Insertions	27,136
Mapped reads with at least one insertion	0.91%
Deletions	68,468
Mapped reads with at least one deletion	2.3%
Homopolymer indels	44.76%

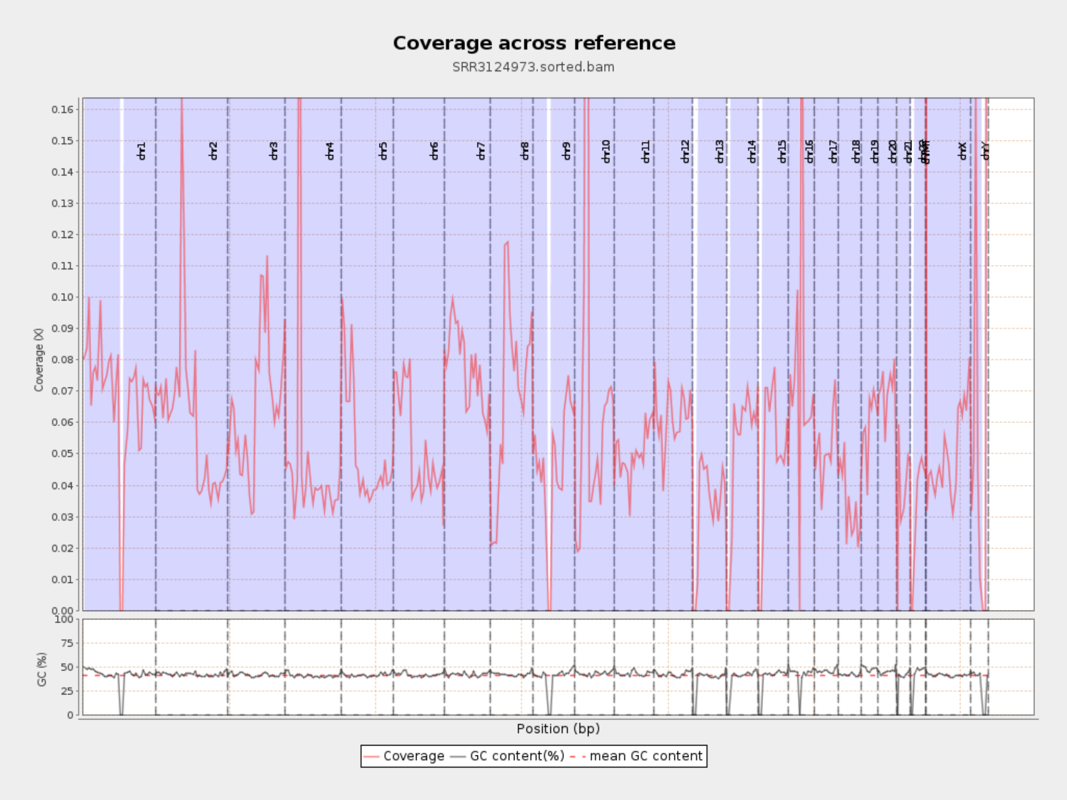
2.7. Chromosome stats

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

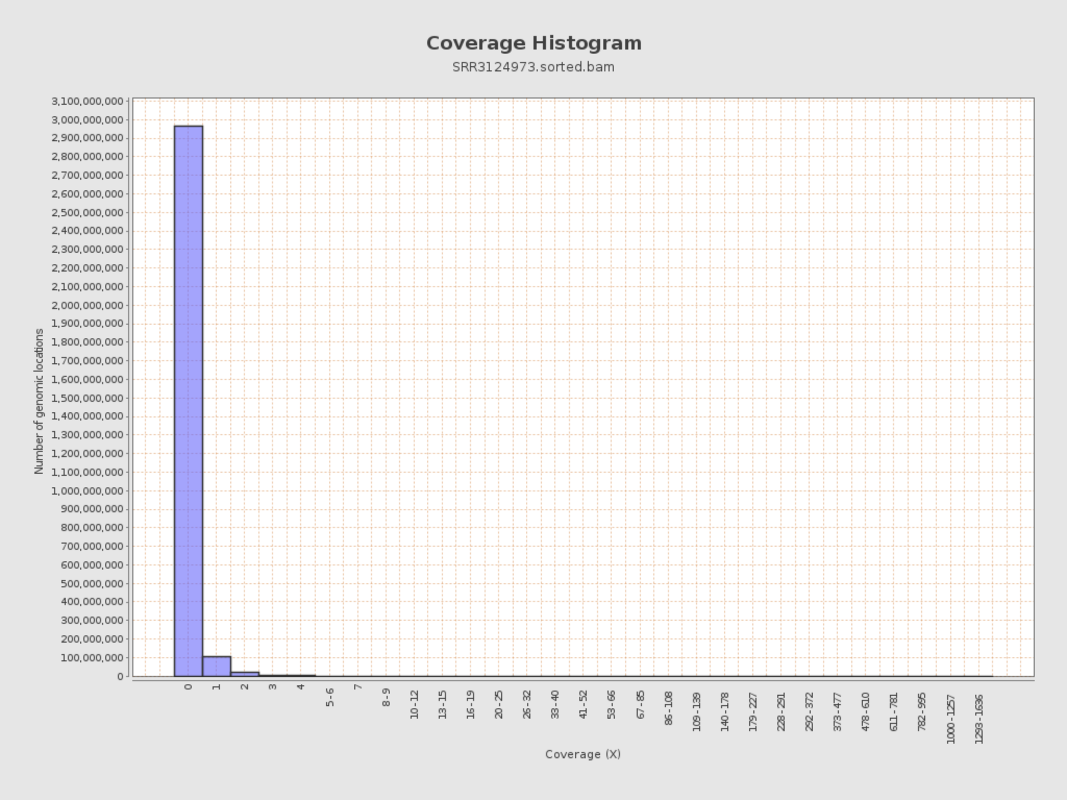
		bases	coverage	deviation
chr1	249250621	16899235	0.0678	0.3962
chr2	243199373	14924361	0.0614	1.0109
chr3	198022430	12974893	0.0655	0.3491
chr4	191154276	9513675	0.0498	1.1224
chr5	180915260	9311856	0.0515	0.2919
chr6	171115067	8986750	0.0525	0.329
chr7	159138663	12434726	0.0781	0.4949
chr8	146364022	10136329	0.0693	0.355
chr9	141213431	6588746	0.0467	0.395
chr10	135534747	9585291	0.0707	2.3843
chr11	135006516	6766592	0.0501	0.3093
chr12	133851895	8337953	0.0623	0.315
chr13	115169878	3839771	0.0333	0.2252
chr14	107349540	5556769	0.0518	0.3019
chr15	102531392	5049348	0.0492	0.2799
chr16	90354753	7129578	0.0789	1.3541
chr17	81195210	4240085	0.0522	0.3767
chr18	78077248	2663164	0.0341	0.4389
chr19	59128983	3497732	0.0592	0.3644
chr20	63025520	4429959	0.0703	0.4628
chr21	48129895	1861548	0.0387	0.5581
chr22	51304566	1629855	0.0318	0.2445
chrMT	16571	7651	0.4617	0.7282
chrX	155270560	7787344	0.0502	0.3018

chrY	59373566	4692505	0.079	1.9433

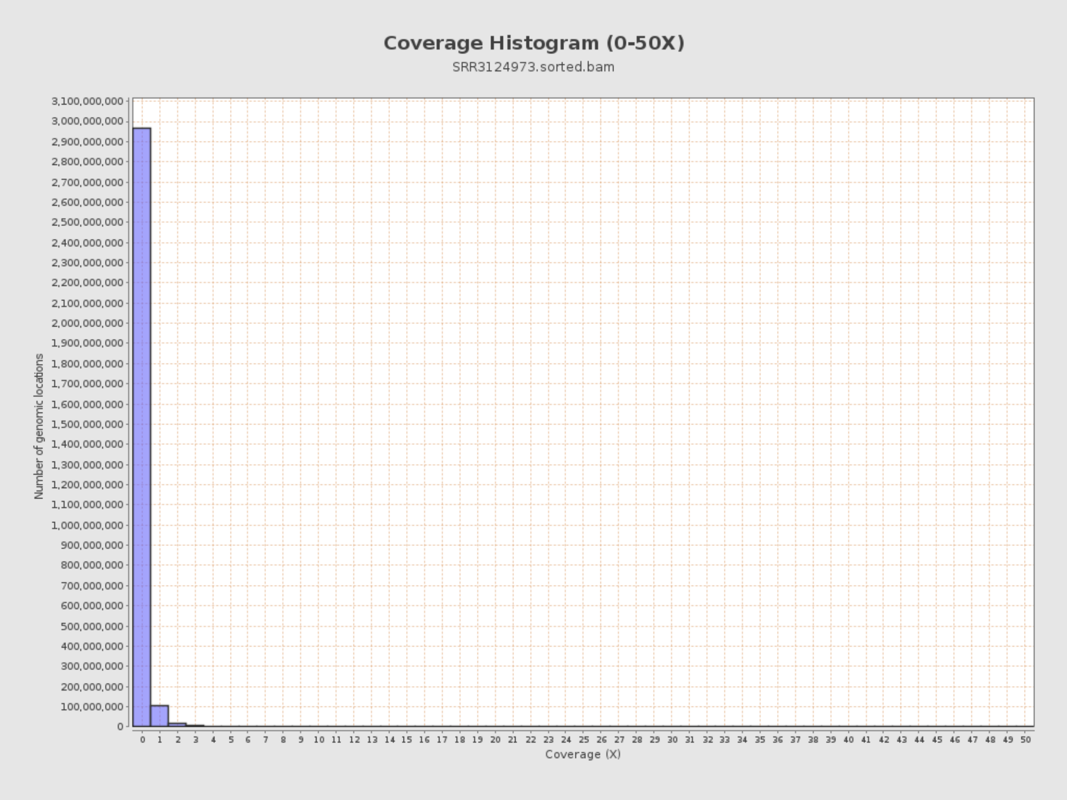
3. Results : Coverage across reference



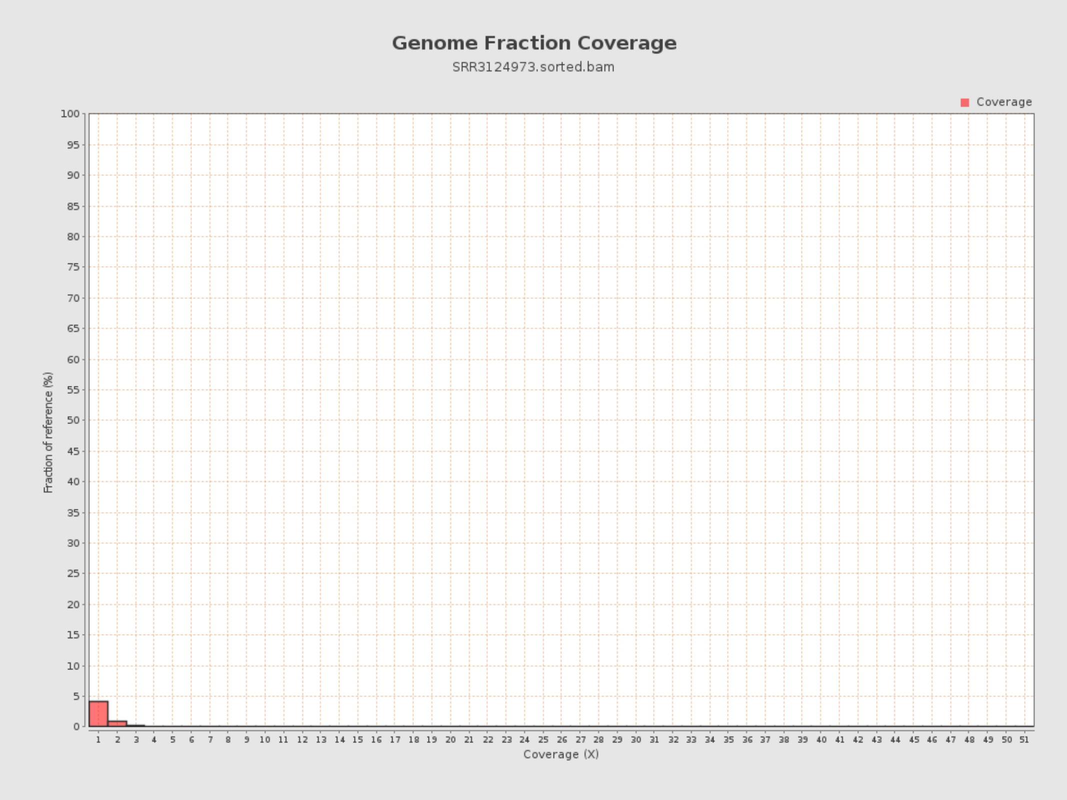
4. Results : Coverage Histogram



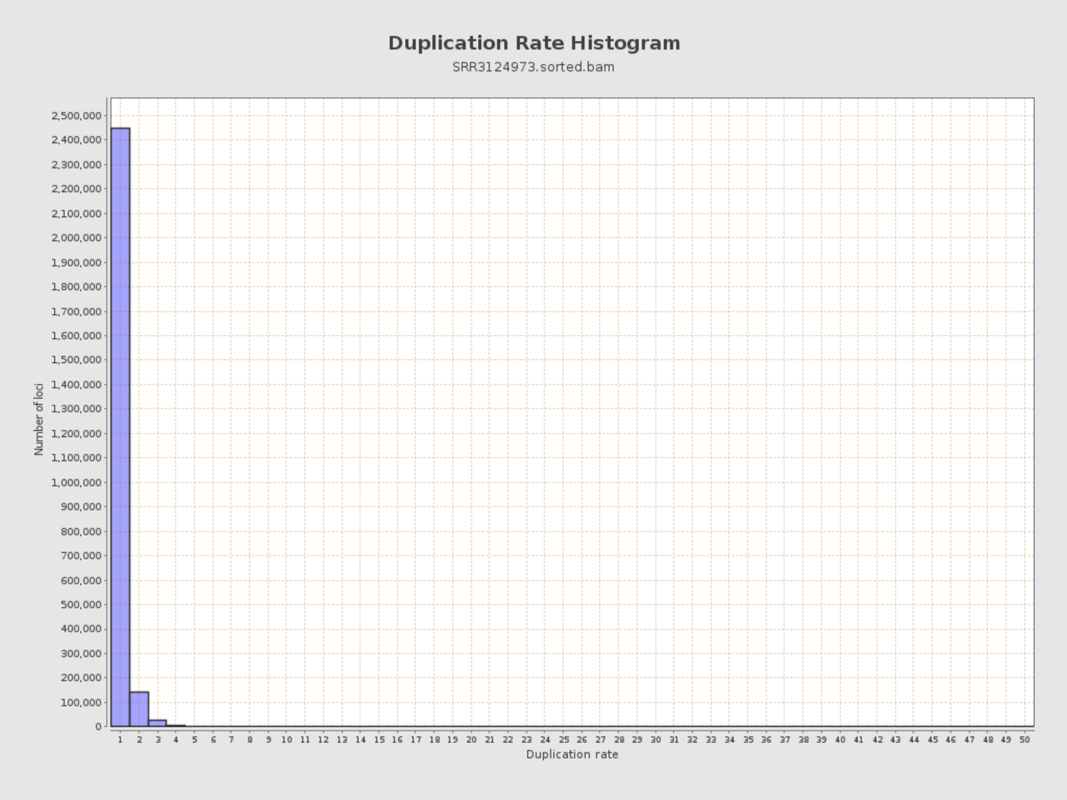
5. Results : Coverage Histogram (0-50X)



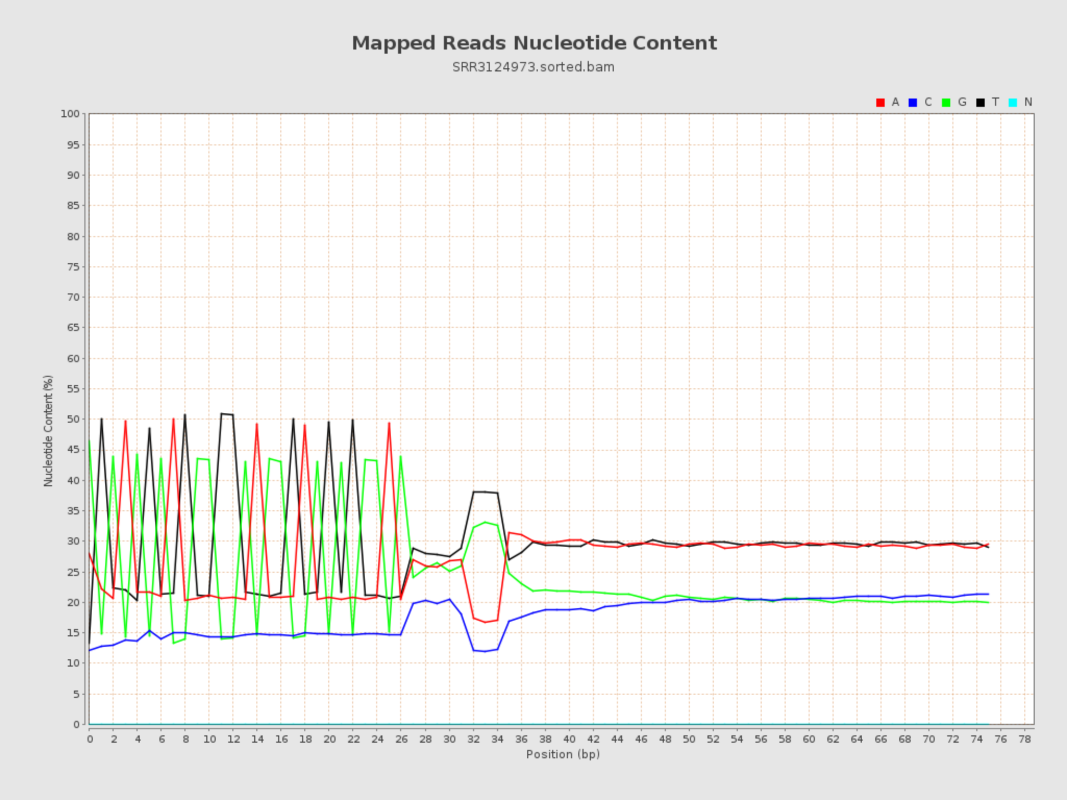
6. Results : Genome Fraction Coverage



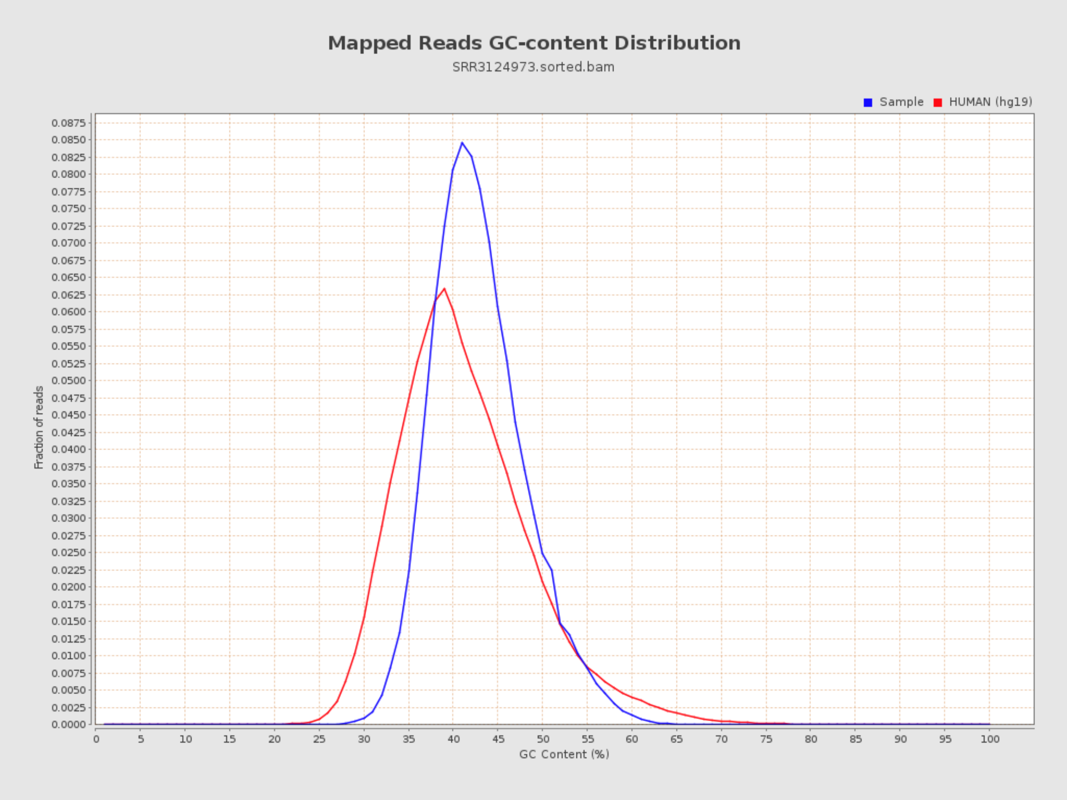
7. Results : Duplication Rate Histogram



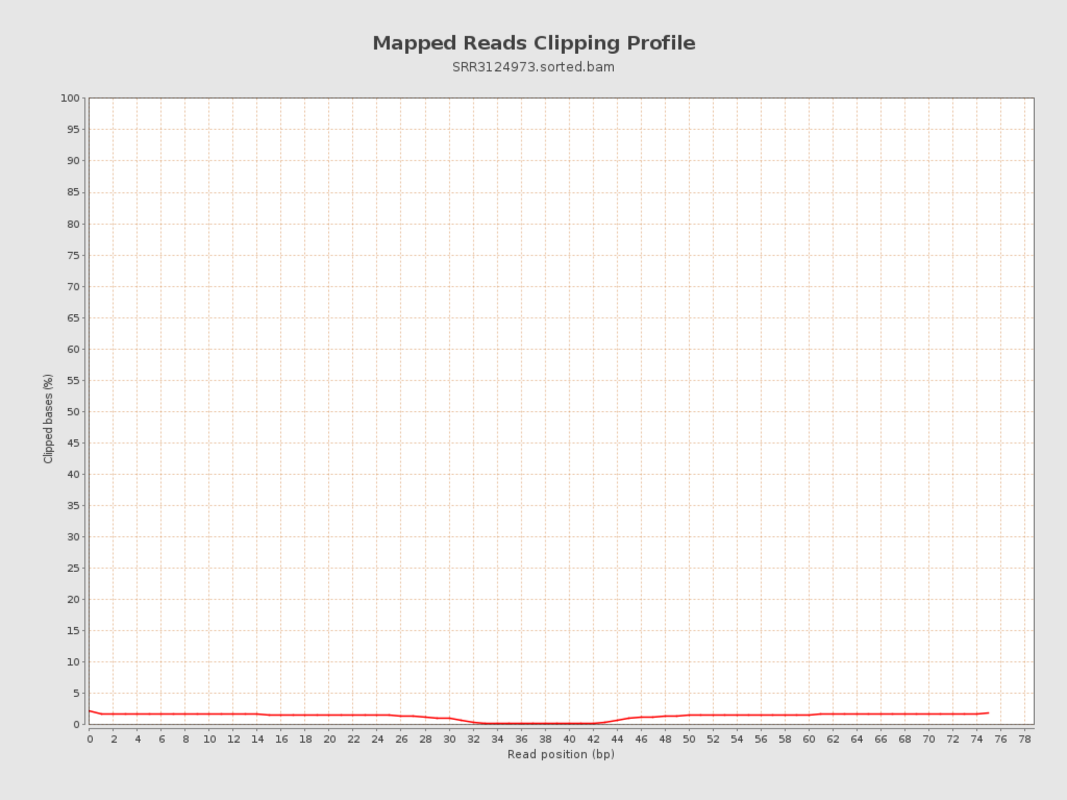
8. Results : Mapped Reads Nucleotide Content



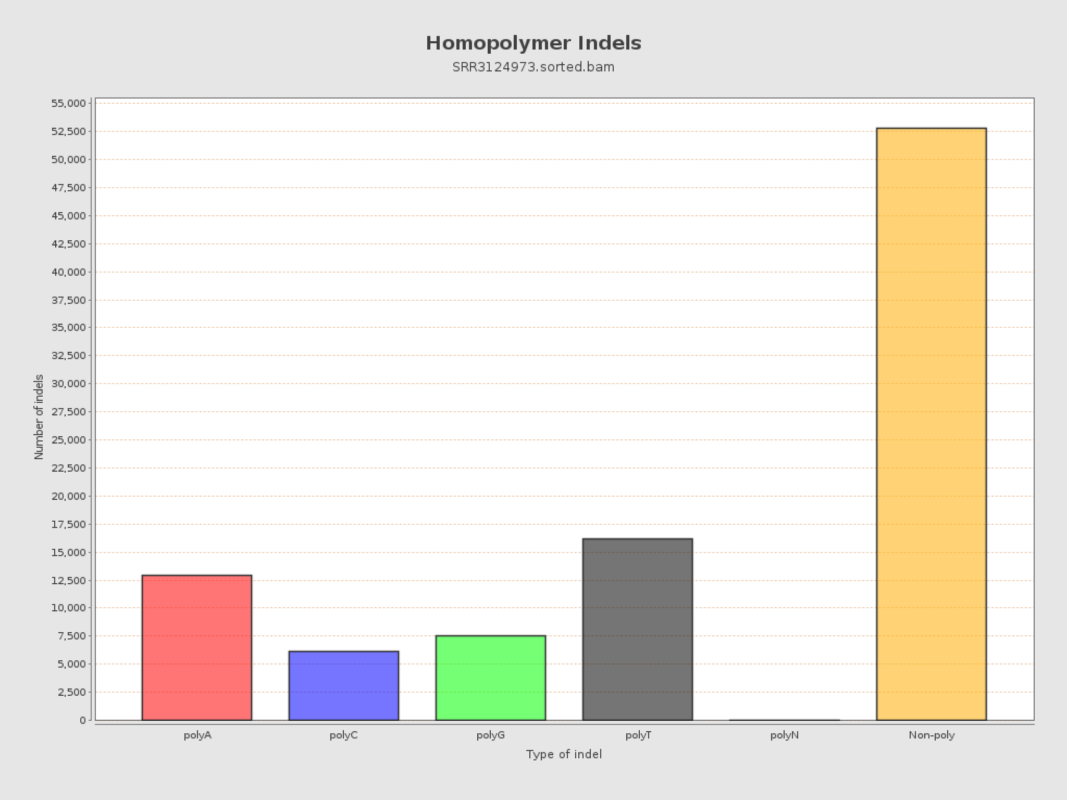
9. Results : Mapped Reads GC-content Distribution



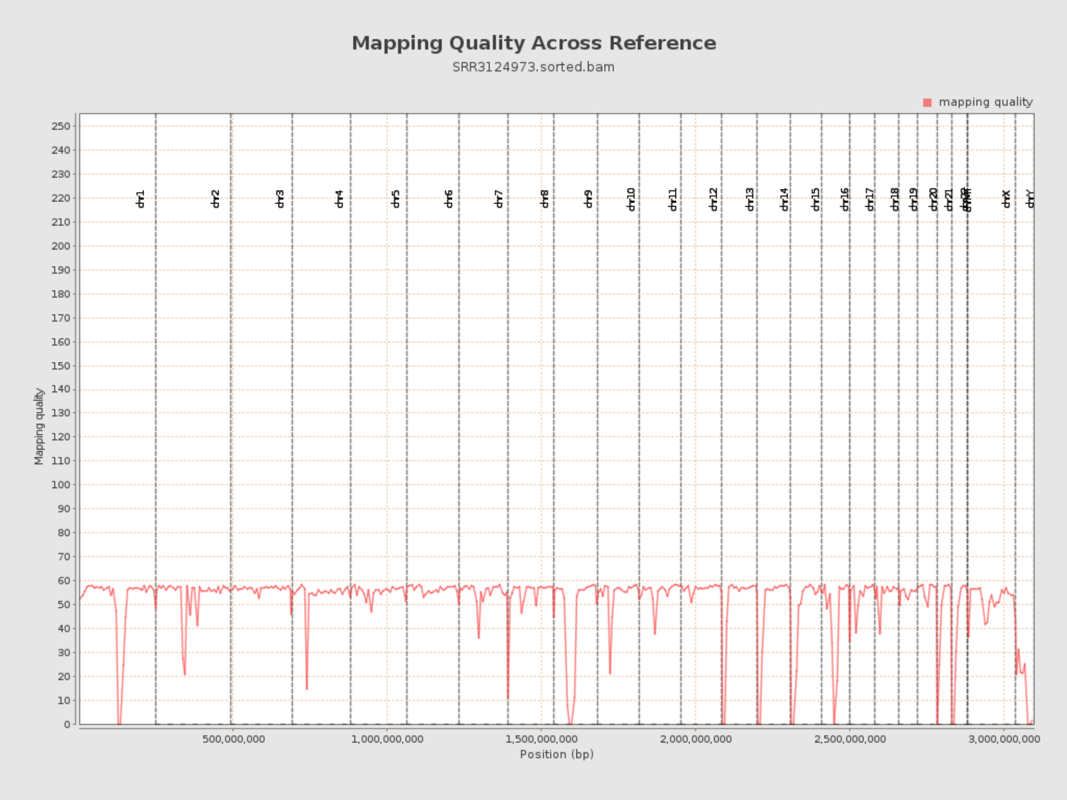
10. Results : Mapped Reads Clipping Profile



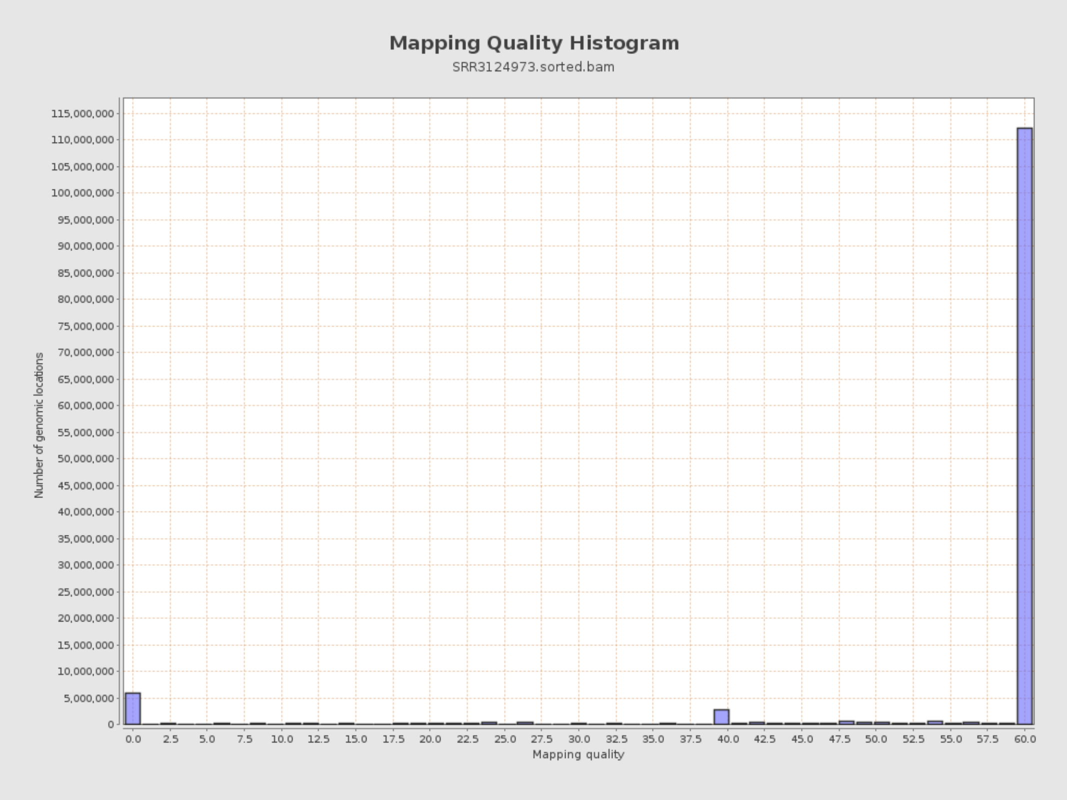
11. Results : Homopolymer Indels



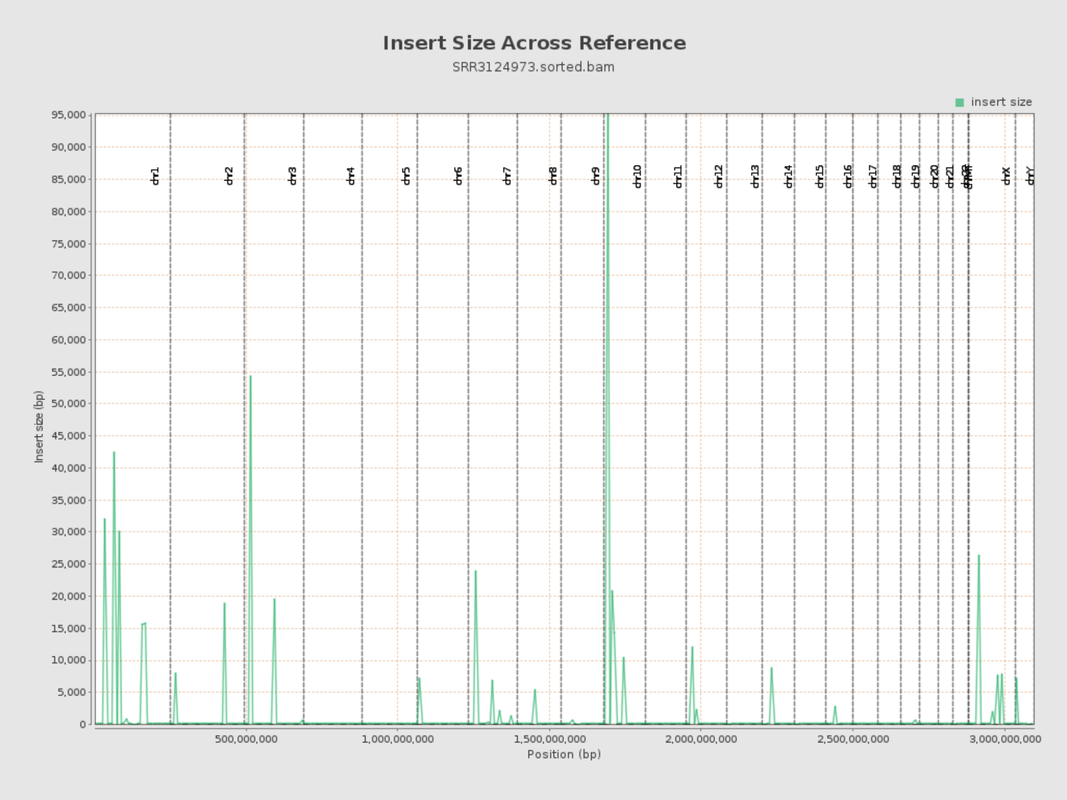
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram