Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:06:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472440.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_SRR3472440 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472440_1.fastq.gz SRR3472440_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:06:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472440.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,254,074
Mapped reads	19,103,987 / 99.22%
Unmapped reads	150,087 / 0.78%
Mapped paired reads	19,103,987 / 99.22%
Mapped reads, first in pair	9,580,002 / 49.76%
Mapped reads, second in pair	9,523,985 / 49.46%
Mapped reads, both in pair	19,014,808 / 98.76%
Mapped reads, singletons	89,179 / 0.46%
Secondary alignments	0
Supplementary alignments	77,168 / 0.4%
Read min/max/mean length	30 / 100 / 99.41
Duplicated reads (estimated)	12,336,736 / 64.07%
Duplication rate	47.64%
Clipped reads	1,304,633 / 6.78%

2.2. ACGT Content

Number/percentage of A's	512,821,068 / 27.35%
Number/percentage of C's	425,823,524 / 22.71%
Number/percentage of T's	513,663,285 / 27.4%
Number/percentage of G's	422,470,796 / 22.53%
Number/percentage of N's	236,418 / 0.01%

GC Percentage	45.24%

2.3. Coverage

Mean	0.6058
Standard Deviation	19.3737

2.4. Mapping Quality

Mean Mapping Quality	54.72

2.5. Insert size

Mean	18,573.11
Standard Deviation	1,343,603.79
P25/Median/P75	154 / 213 / 286

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	9,892,220
Insertions	117,673
Mapped reads with at least one insertion	0.61%
Deletions	89,581
Mapped reads with at least one deletion	0.46%
Homopolymer indels	45.43%

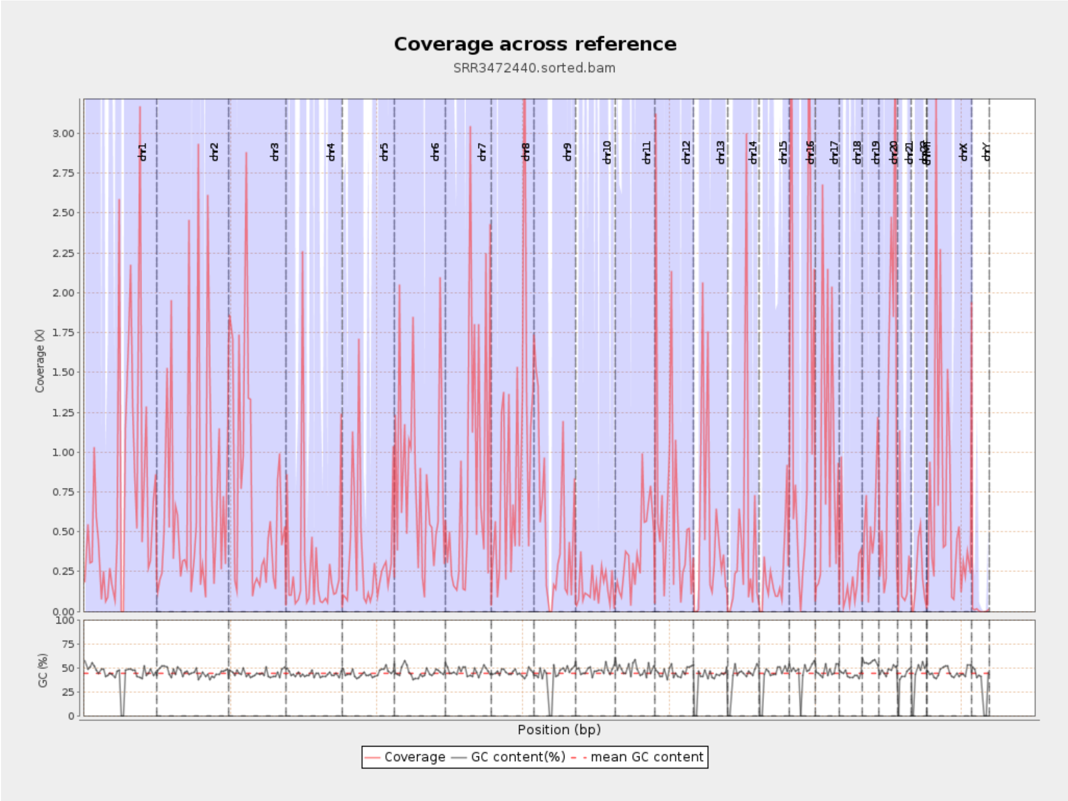
2.7. Chromosome stats

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

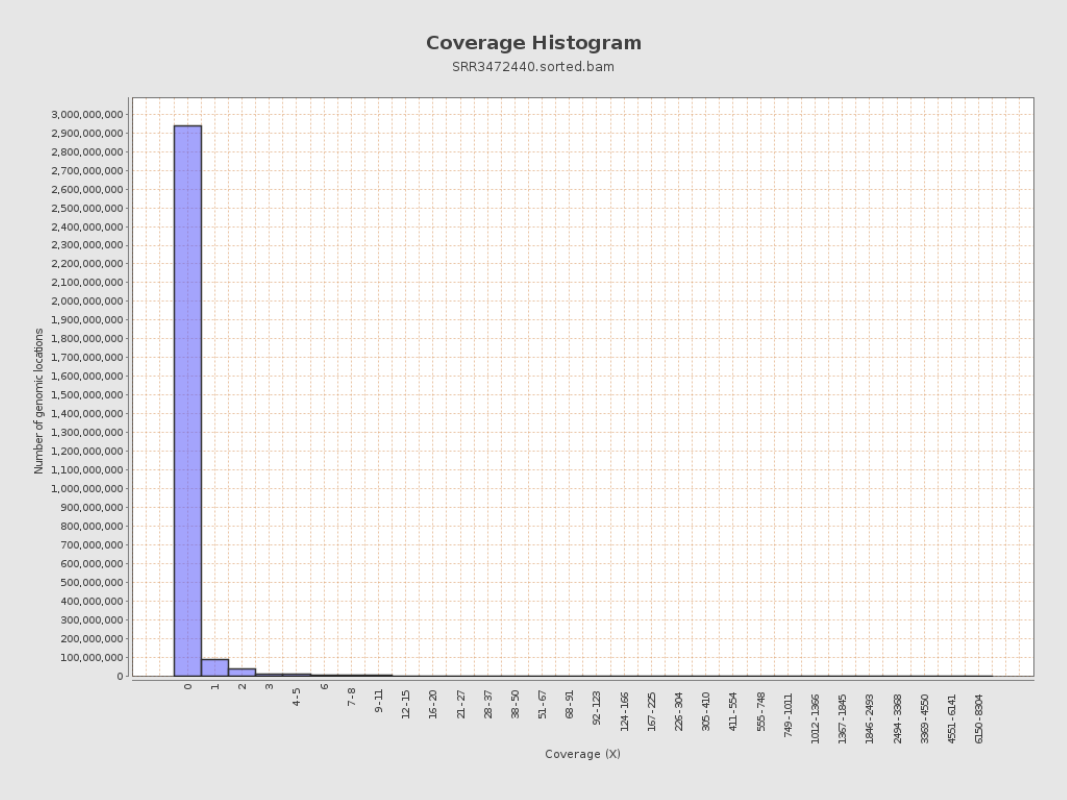
		bases	coverage	deviation
chr1	249250621	178404325	0.7158	20.6562
chr2	243199373	180231979	0.7411	23.7516
chr3	198022430	148333826	0.7491	18.2508
chr4	191154276	57633797	0.3015	14.7221
chr5	180915260	64528552	0.3567	12.0724
chr6	171115067	139259081	0.8138	18.088
chr7	159138663	137384241	0.8633	30.0368
chr8	146364022	138871635	0.9488	23.1798
chr9	141213431	72320052	0.5121	15.389
chr10	135534747	20302370	0.1498	5.8861
chr11	135006516	51055364	0.3782	13.483
chr12	133851895	94277364	0.7043	17.4561
chr13	115169878	59083286	0.513	15.739
chr14	107349540	46954599	0.4374	19.217
chr15	102531392	23237117	0.2266	7.4525
chr16	90354753	115832195	1.282	31.8011
chr17	81195210	78068685	0.9615	24.9601
chr18	78077248	17958022	0.23	8.3008
chr19	59128983	32396301	0.5479	15.8053
chr20	63025520	83534065	1.3254	39.765
chr21	48129895	14283450	0.2968	18.4766
chr22	51304566	11182700	0.218	5.9402
chrMT	16571	2860	0.1726	0.538
chrX	155270560	109706605	0.7066	17.7278

chrY	59373566	390420	0.0066	0.5002

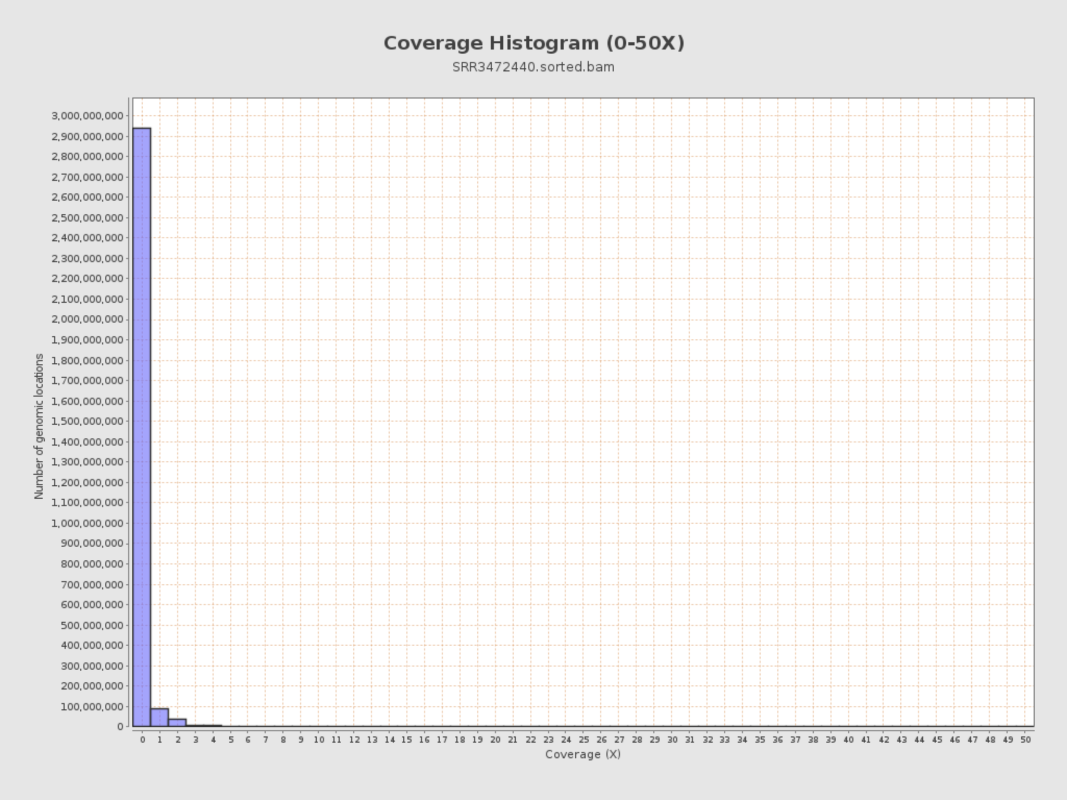
3. Results : Coverage across reference



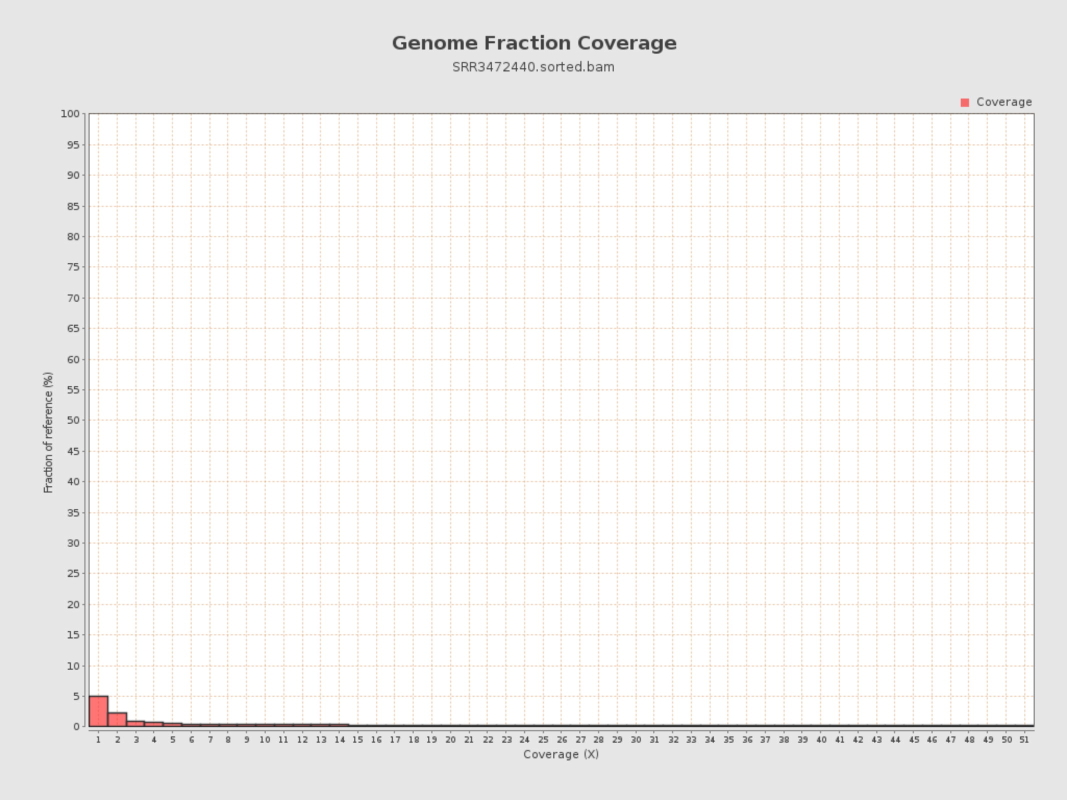
4. Results : Coverage Histogram



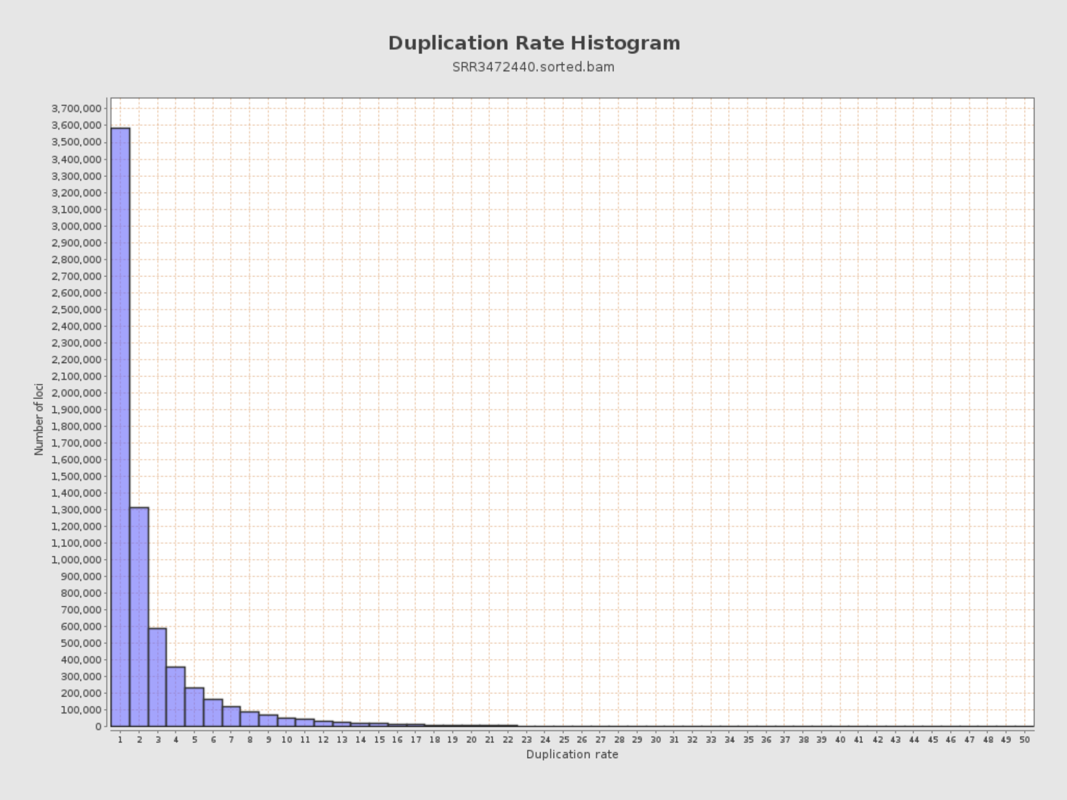
5. Results : Coverage Histogram (0-50X)



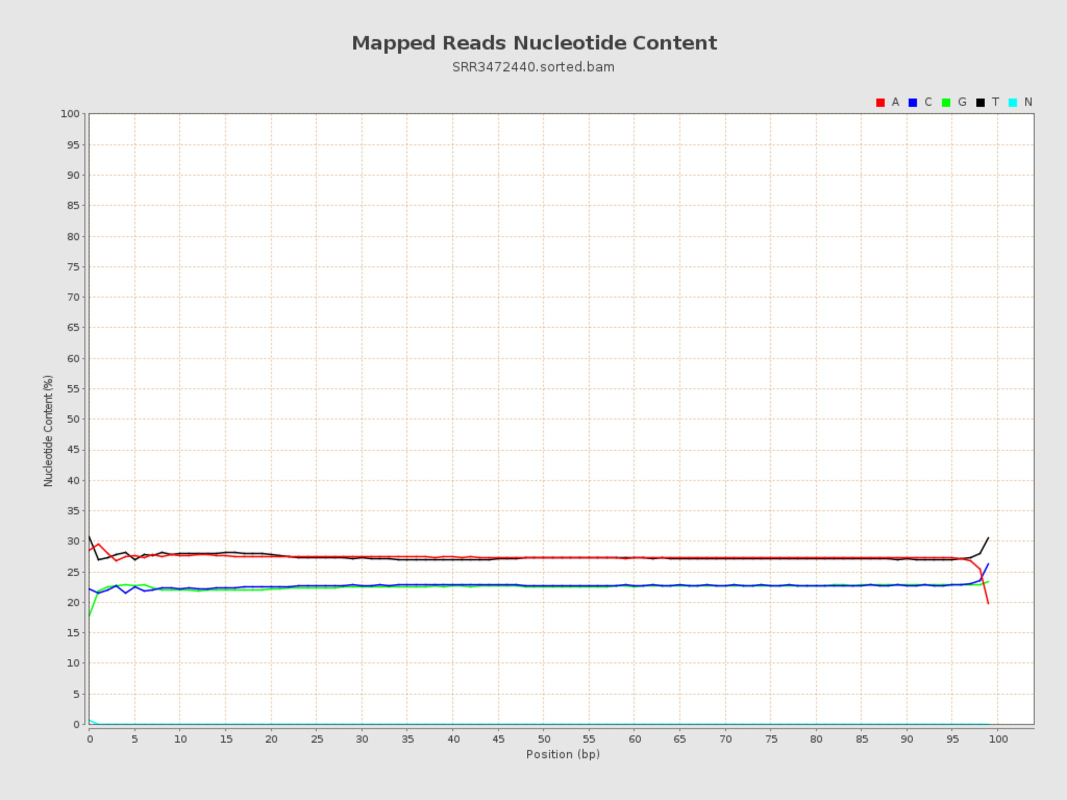
6. Results : Genome Fraction Coverage



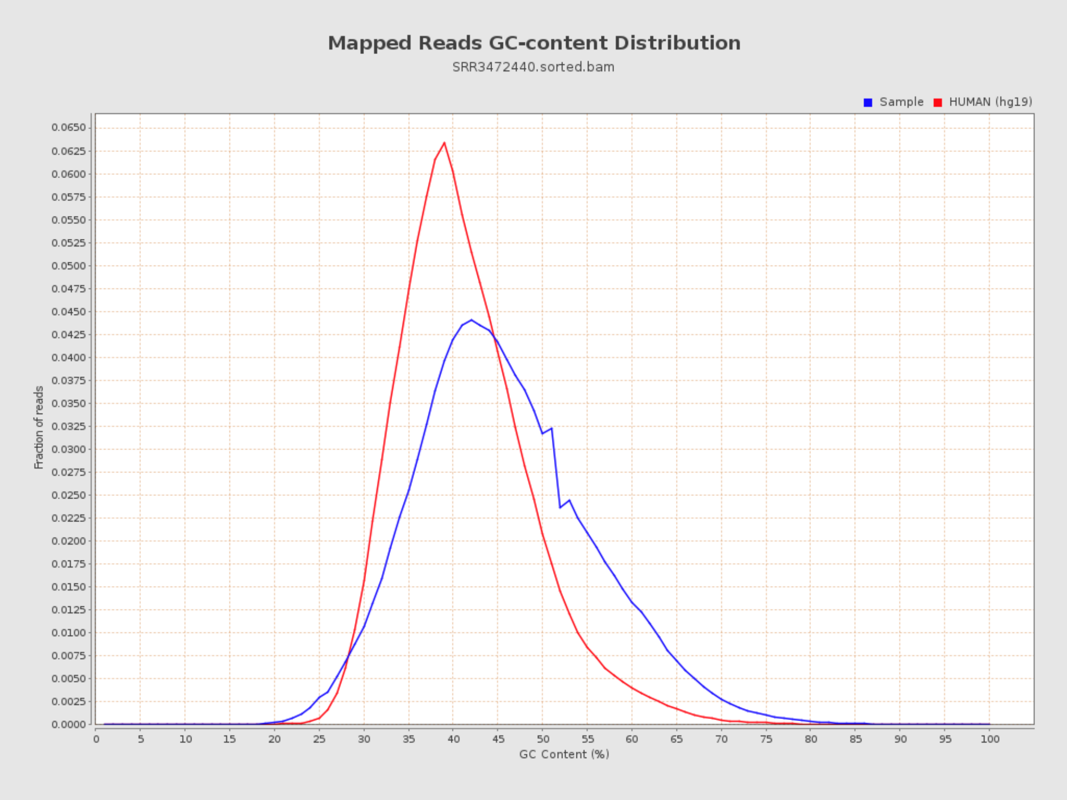
7. Results : Duplication Rate Histogram



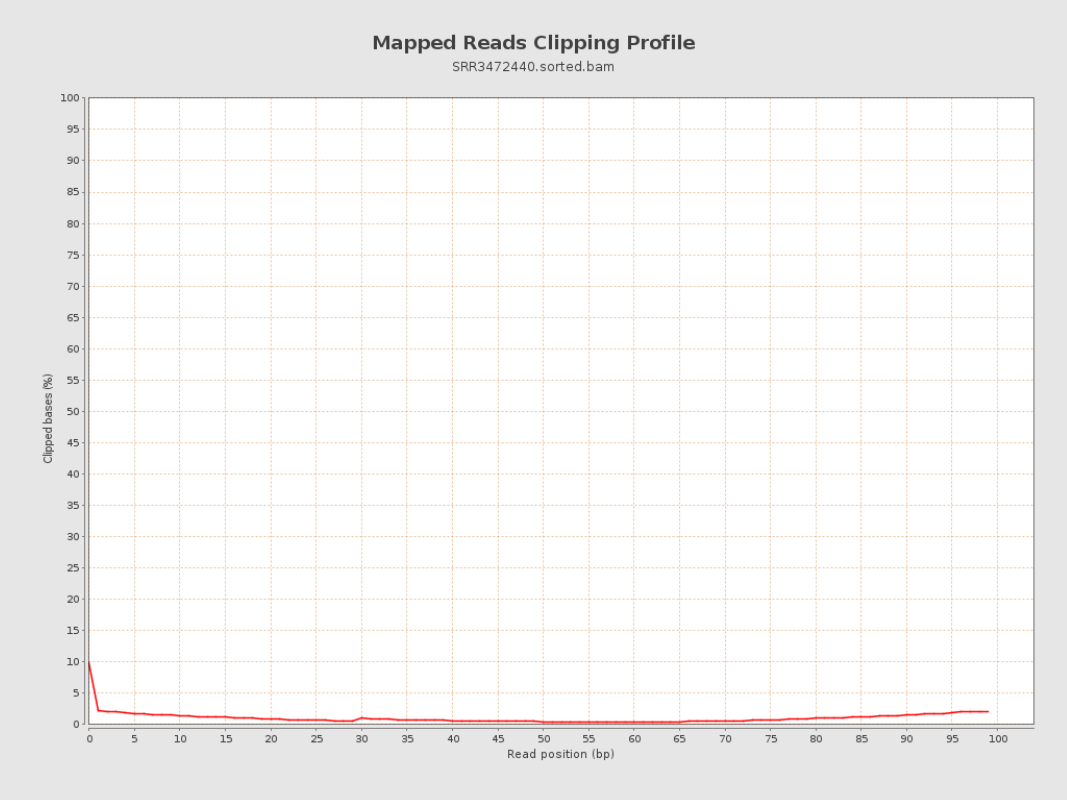
8. Results : Mapped Reads Nucleotide Content



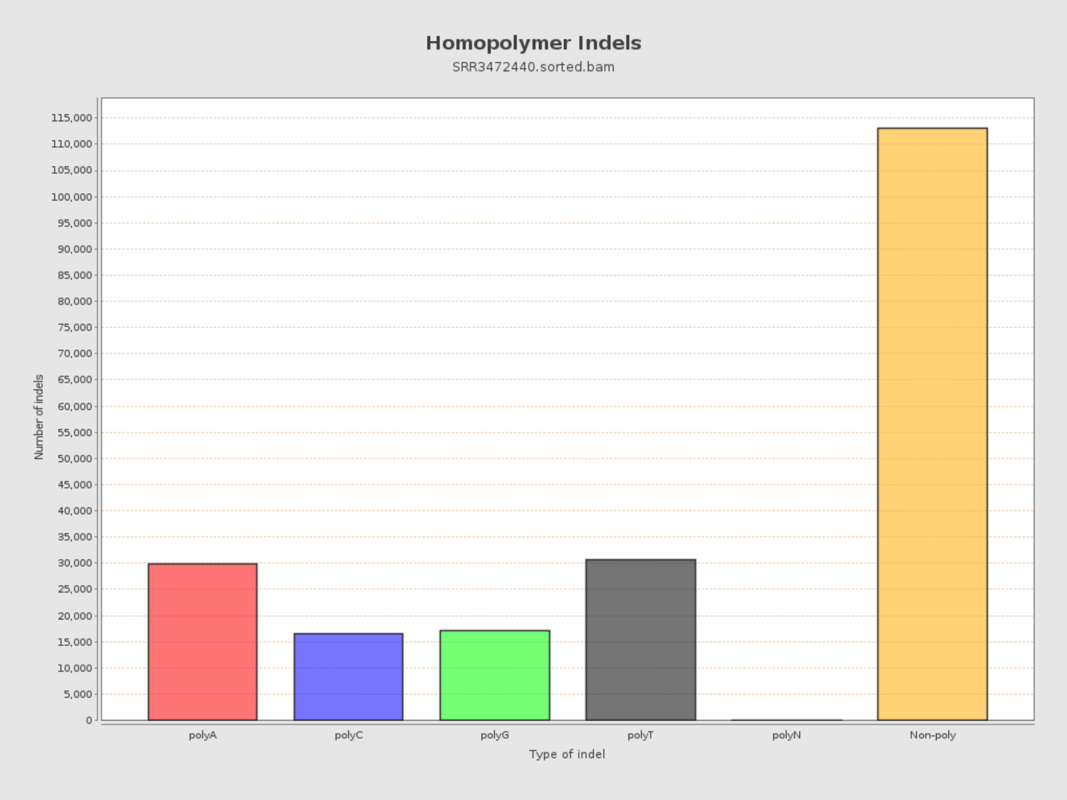
9. Results : Mapped Reads GC-content Distribution



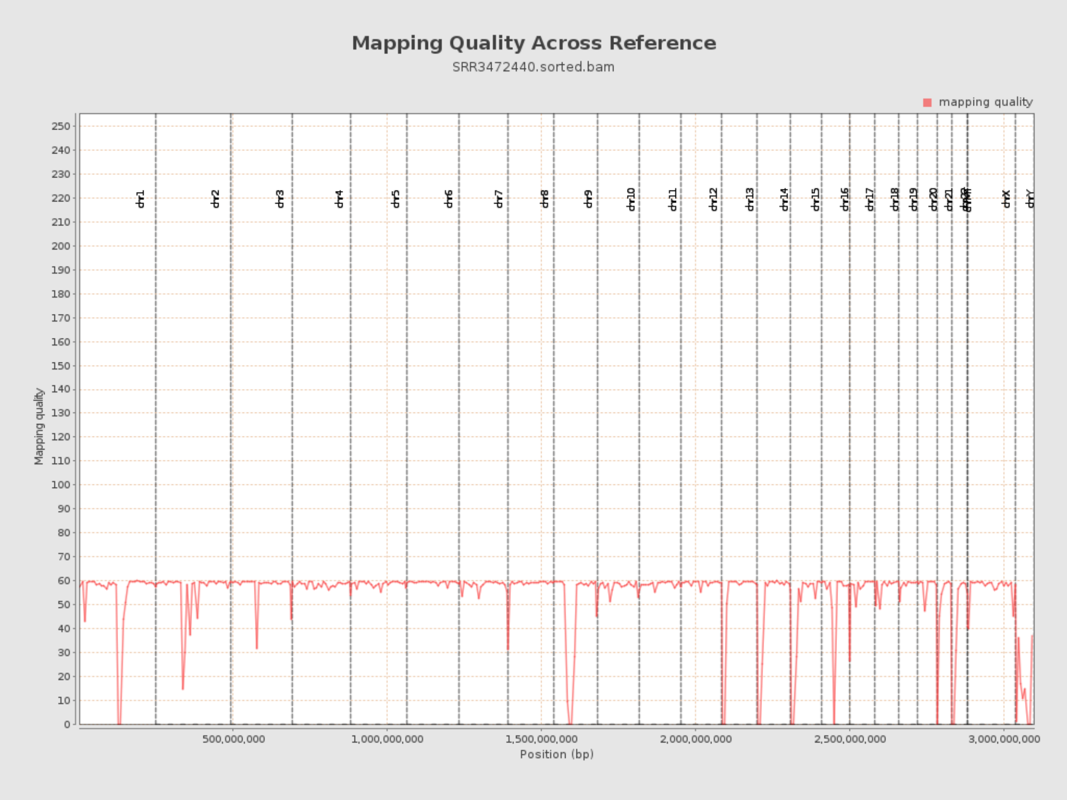
10. Results : Mapped Reads Clipping Profile



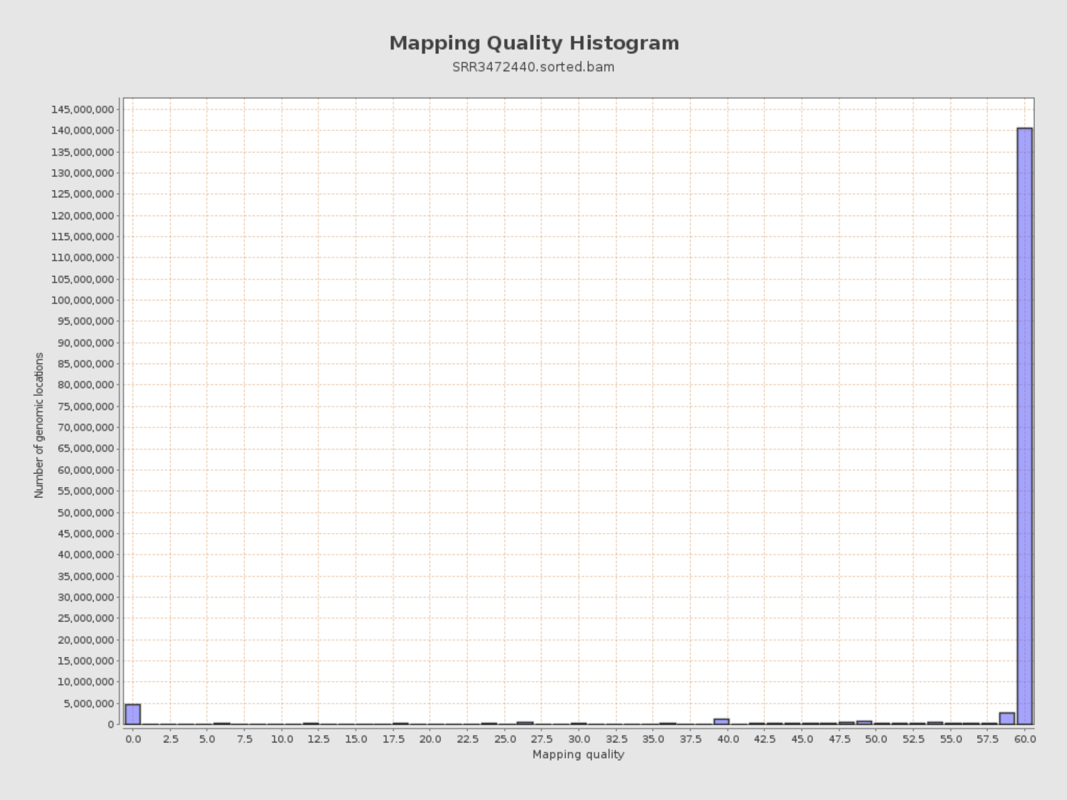
11. Results : Homopolymer Indels



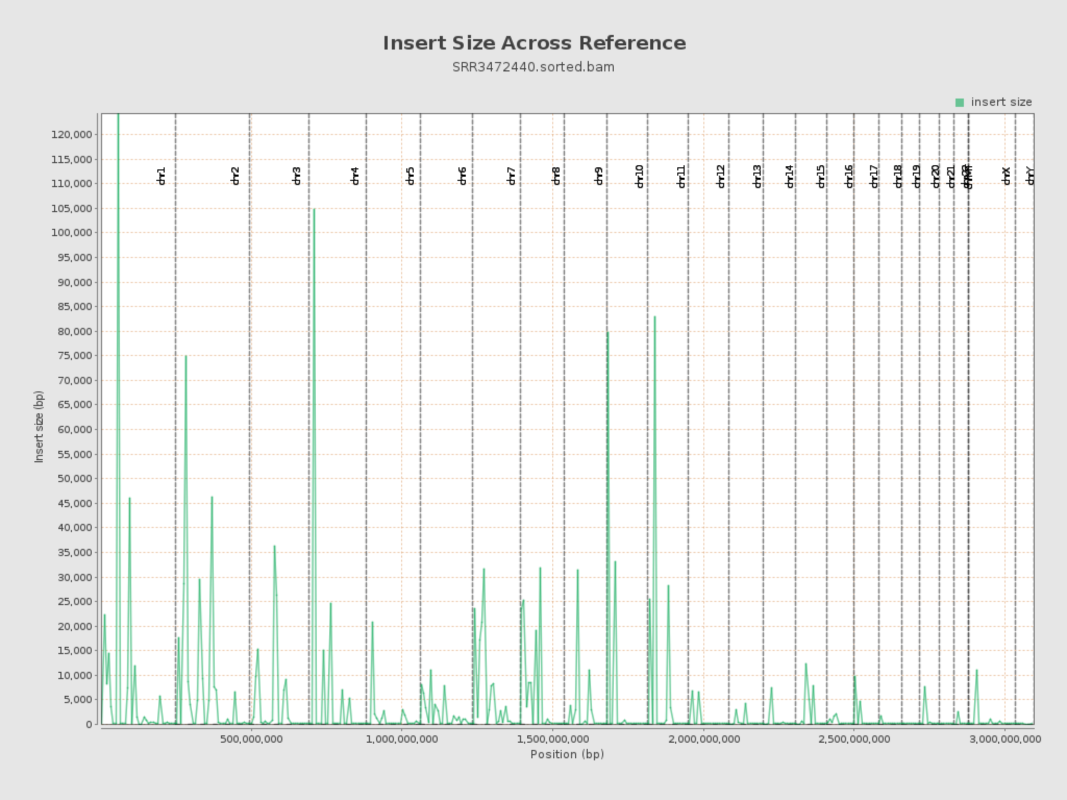
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram