Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:08:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472534.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_SRR3472534 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472534_1.fastq.gz SRR3472534_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:08:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472534.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,648,668
Mapped reads	20,387,537 / 98.74%
Unmapped reads	261,131 / 1.26%
Mapped paired reads	20,387,537 / 98.74%
Mapped reads, first in pair	10,228,466 / 49.54%
Mapped reads, second in pair	10,159,071 / 49.2%
Mapped reads, both in pair	20,254,894 / 98.09%
Mapped reads, singletons	132,643 / 0.64%
Secondary alignments	0
Supplementary alignments	69,141 / 0.33%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	13,179,533 / 63.83%
Duplication rate	46.45%
Clipped reads	1,535,939 / 7.44%

2.2. ACGT Content

Number/percentage of A's	558,789,799 / 27.82%
Number/percentage of C's	448,098,369 / 22.31%
Number/percentage of T's	556,239,077 / 27.69%
Number/percentage of G's	445,181,695 / 22.16%
Number/percentage of N's	309,421 / 0.02%

GC Percentage	44.47%

2.3. Coverage

Mean	0.6489
Standard Deviation	22.3566

2.4. Mapping Quality

Mean Mapping Quality	54.89

2.5. Insert size

Mean	22,393.48
Standard Deviation	1,447,911.57
P25/Median/P75	175 / 242 / 327

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	12,322,190
Insertions	110,342
Mapped reads with at least one insertion	0.54%
Deletions	103,301
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.13%

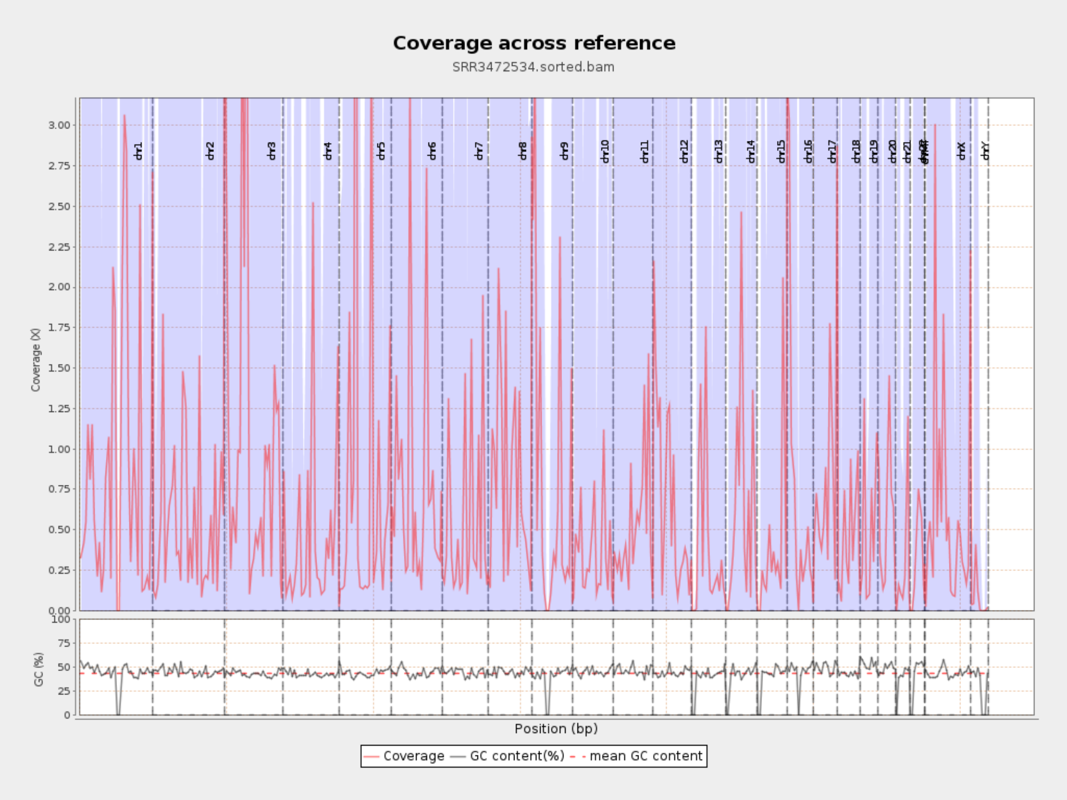
2.7. Chromosome stats

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

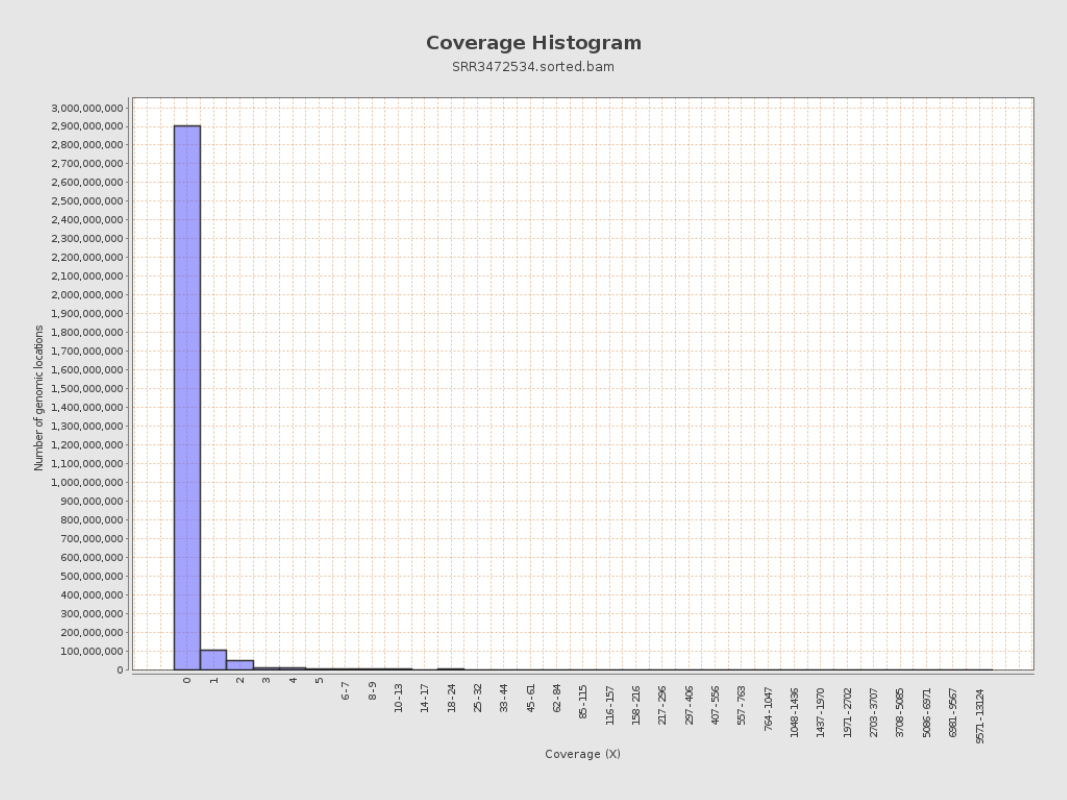
		bases	coverage	deviation
chr1	249250621	216766662	0.8697	30.8288
chr2	243199373	133803509	0.5502	23.5627
chr3	198022430	226980540	1.1462	26.743
chr4	191154276	85418617	0.4469	16.9086
chr5	180915260	157213043	0.869	37.6973
chr6	171115067	130704887	0.7638	23.0803
chr7	159138663	87265389	0.5484	18.6804
chr8	146364022	117768522	0.8046	23.2791
chr9	141213431	116474208	0.8248	22.1546
chr10	135534747	49352724	0.3641	13.8979
chr11	135006516	72906120	0.54	15.8876
chr12	133851895	94223570	0.7039	20.381
chr13	115169878	46582712	0.4045	16.398
chr14	107349540	66367710	0.6182	22.4519
chr15	102531392	40794089	0.3979	11.852
chr16	90354753	69444775	0.7686	22.049
chr17	81195210	62979206	0.7757	16.8983
chr18	78077248	34835222	0.4462	13.7376
chr19	59128983	30730637	0.5197	15.9161
chr20	63025520	38512732	0.6111	15.7621
chr21	48129895	13991628	0.2907	16.1531
chr22	51304566	16254080	0.3168	9.0472
chrMT	16571	4822	0.291	0.7847
chrX	155270560	94653162	0.6096	22.7587

chrY	59373566	4846538	0.0816	5.064

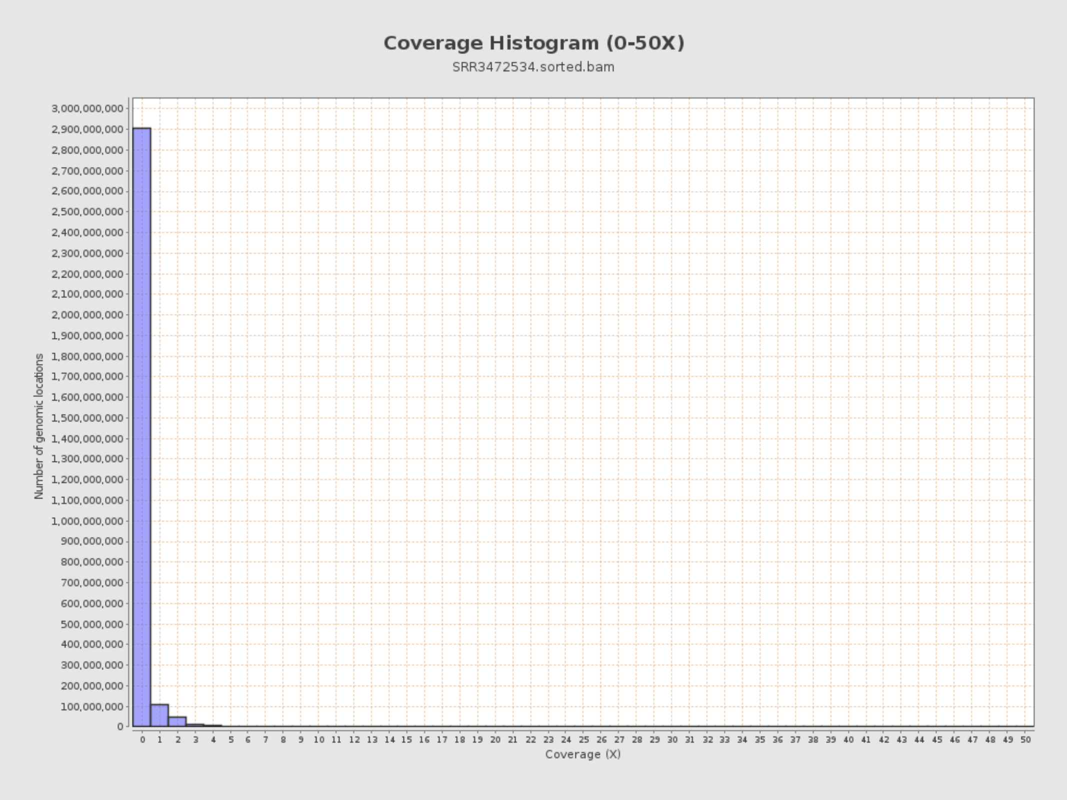
3. Results : Coverage across reference



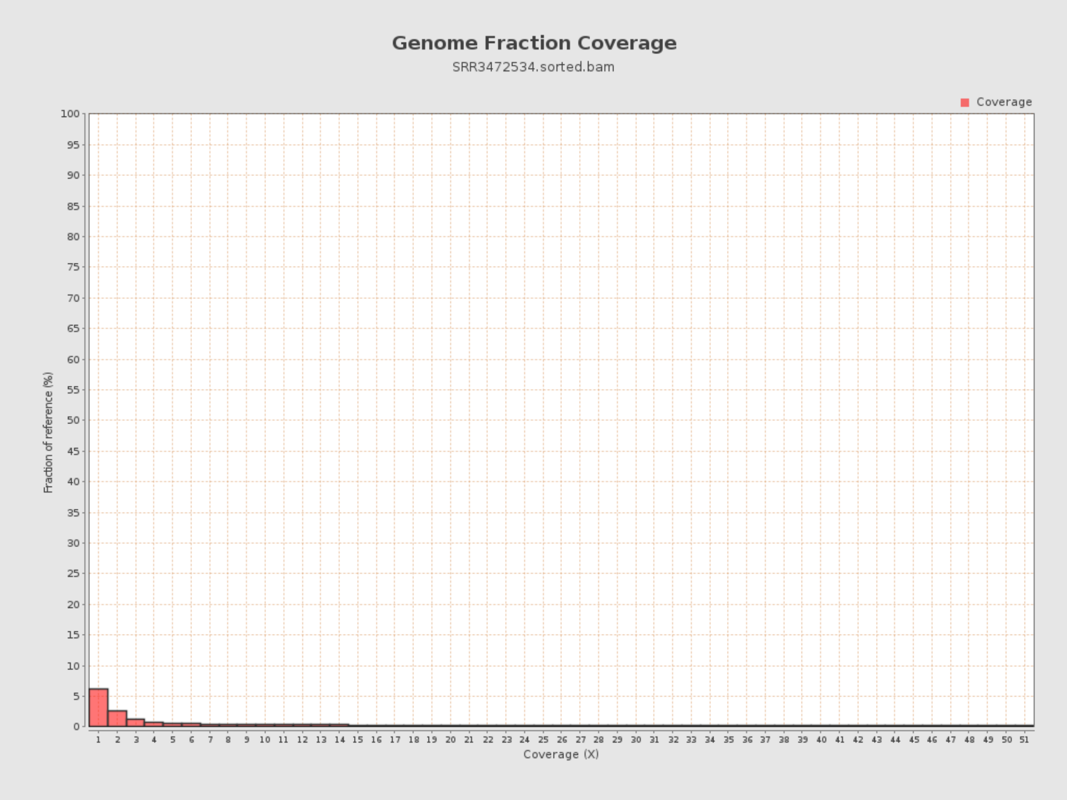
4. Results : Coverage Histogram



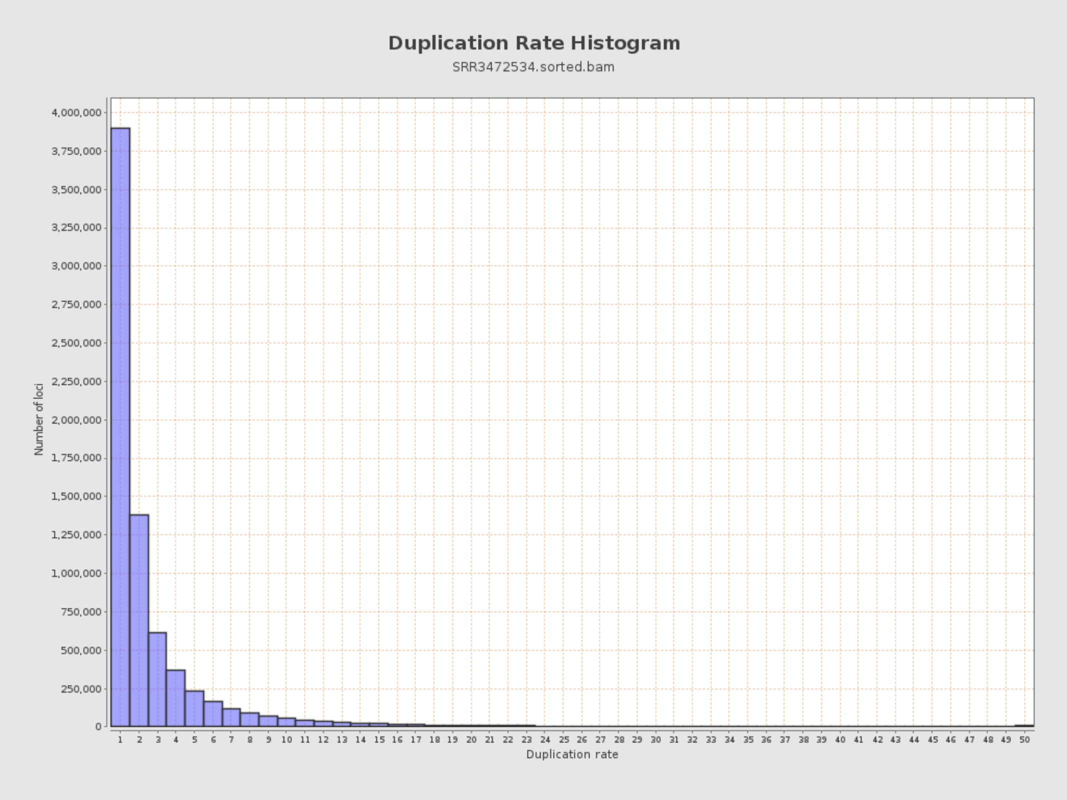
5. Results : Coverage Histogram (0-50X)



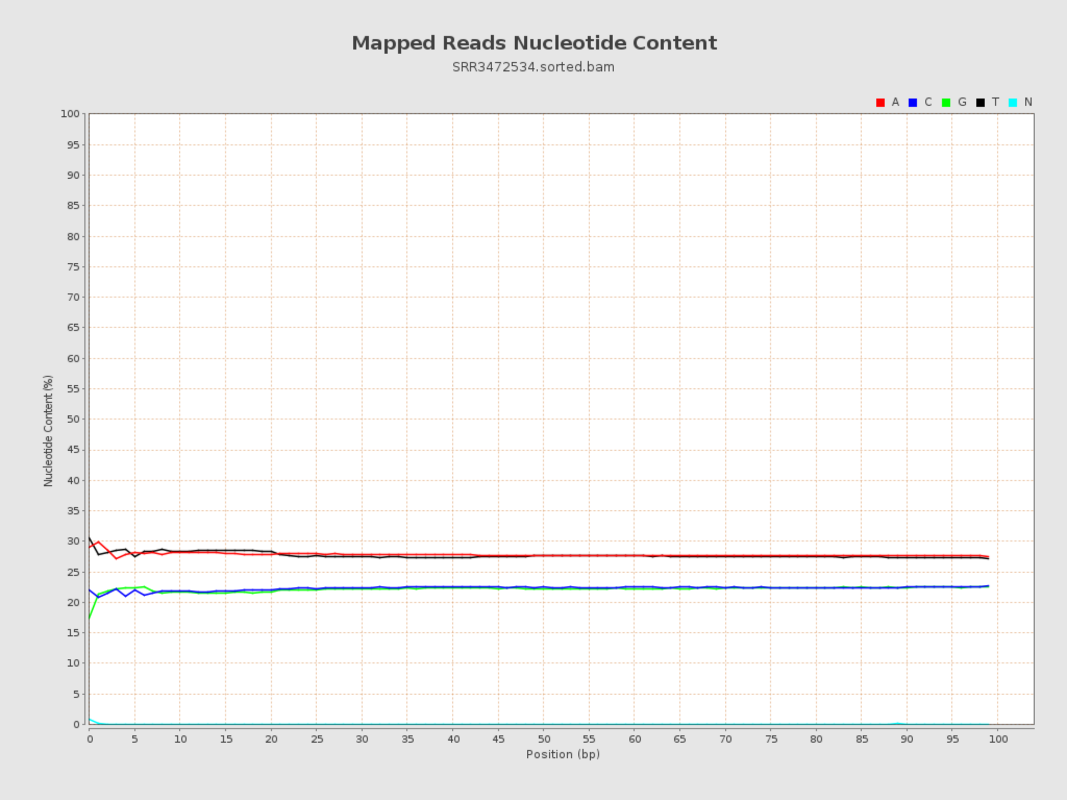
6. Results : Genome Fraction Coverage



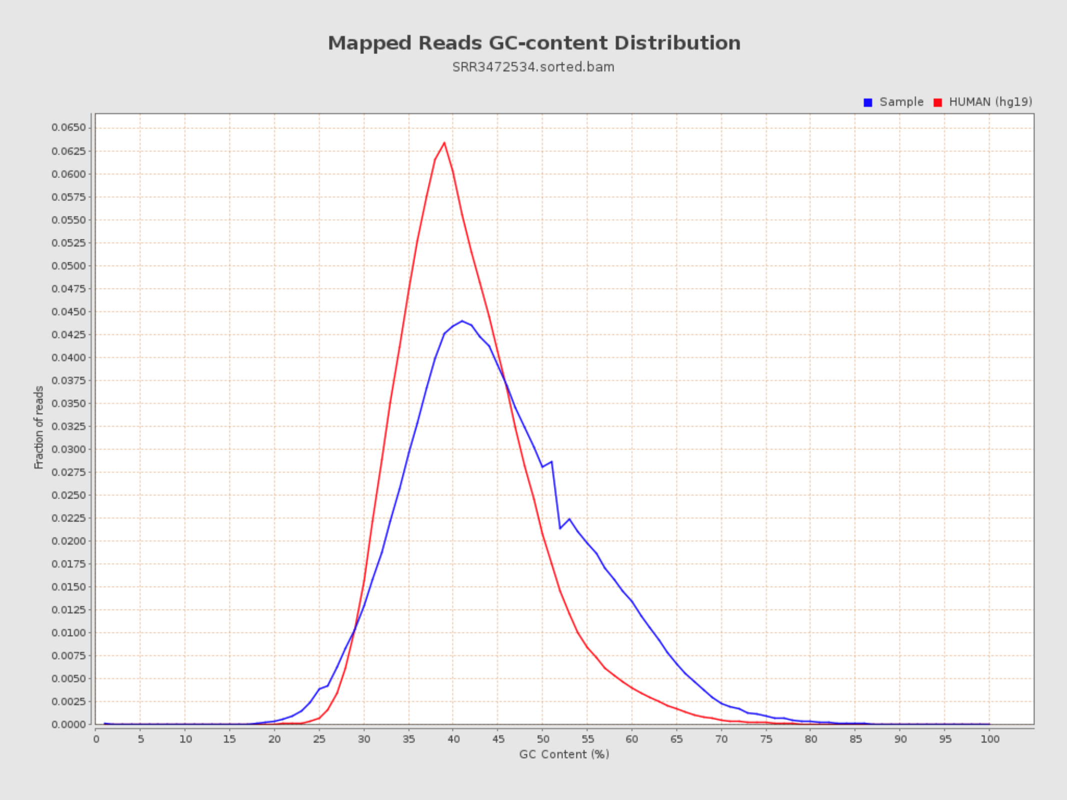
7. Results : Duplication Rate Histogram



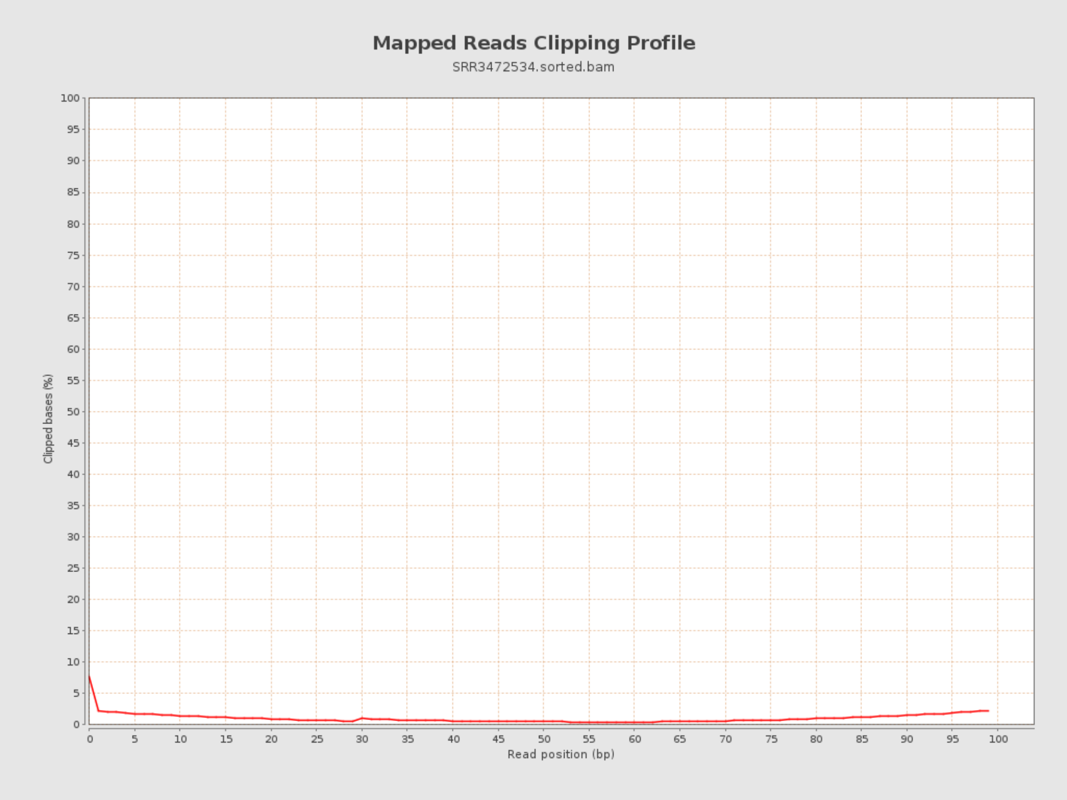
8. Results : Mapped Reads Nucleotide Content



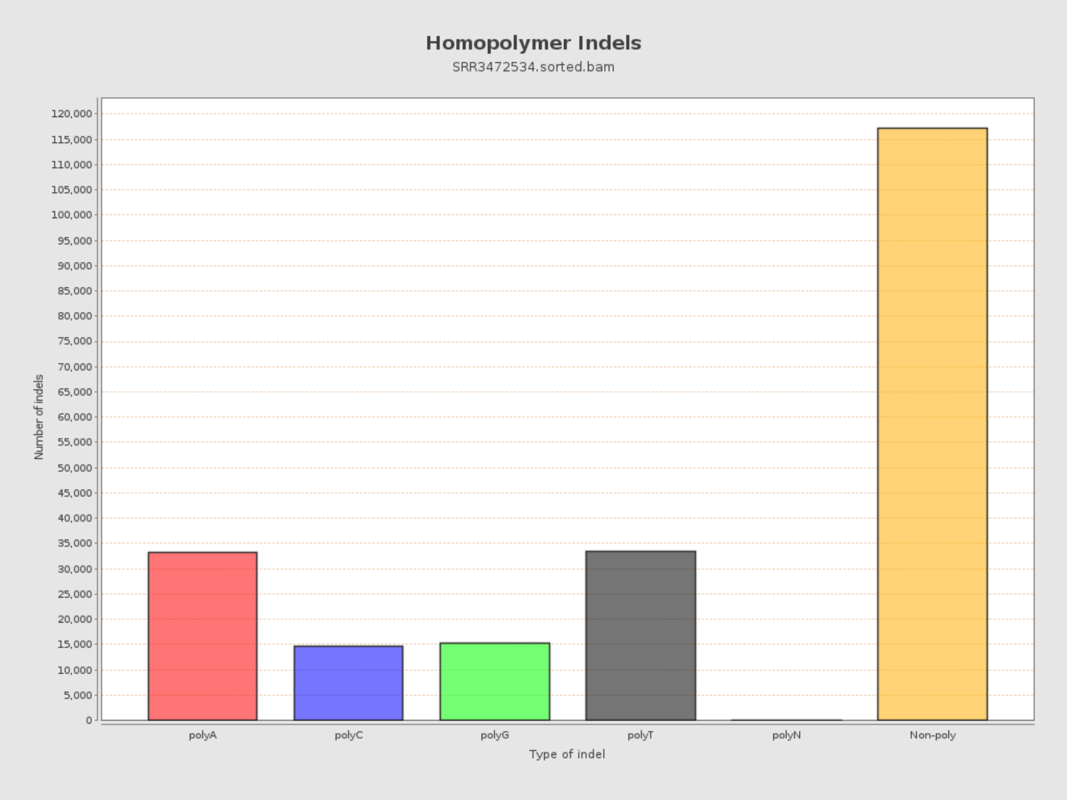
9. Results : Mapped Reads GC-content Distribution



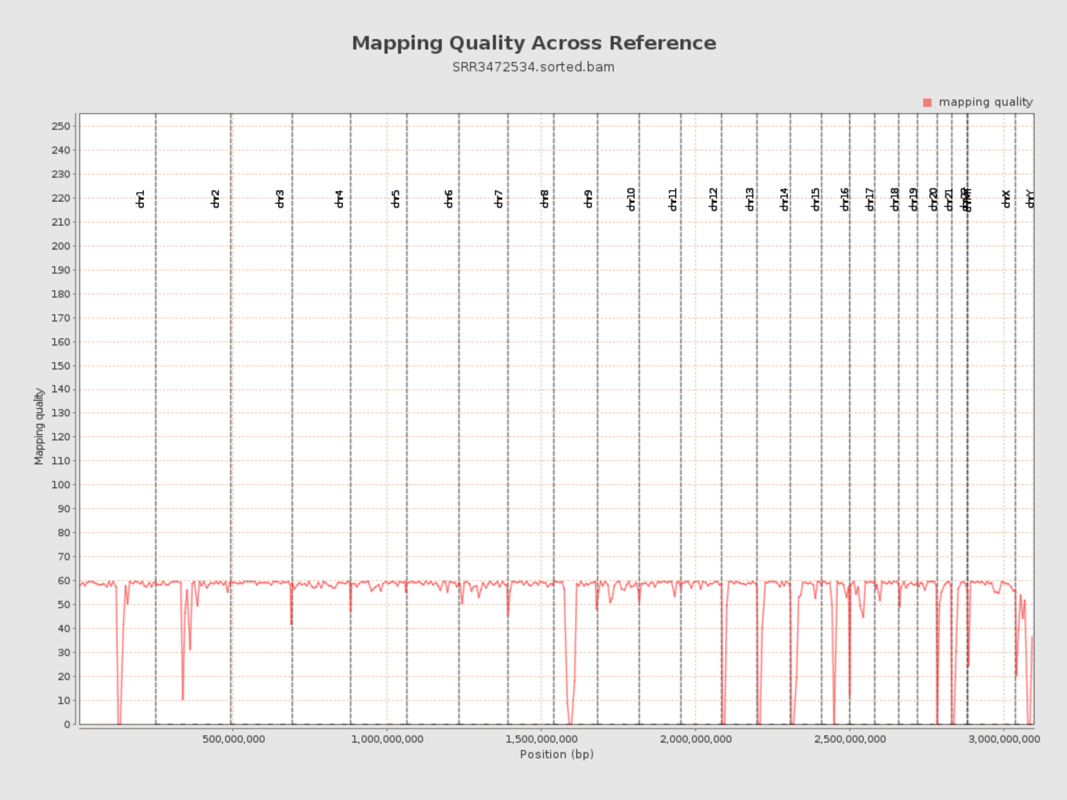
10. Results : Mapped Reads Clipping Profile



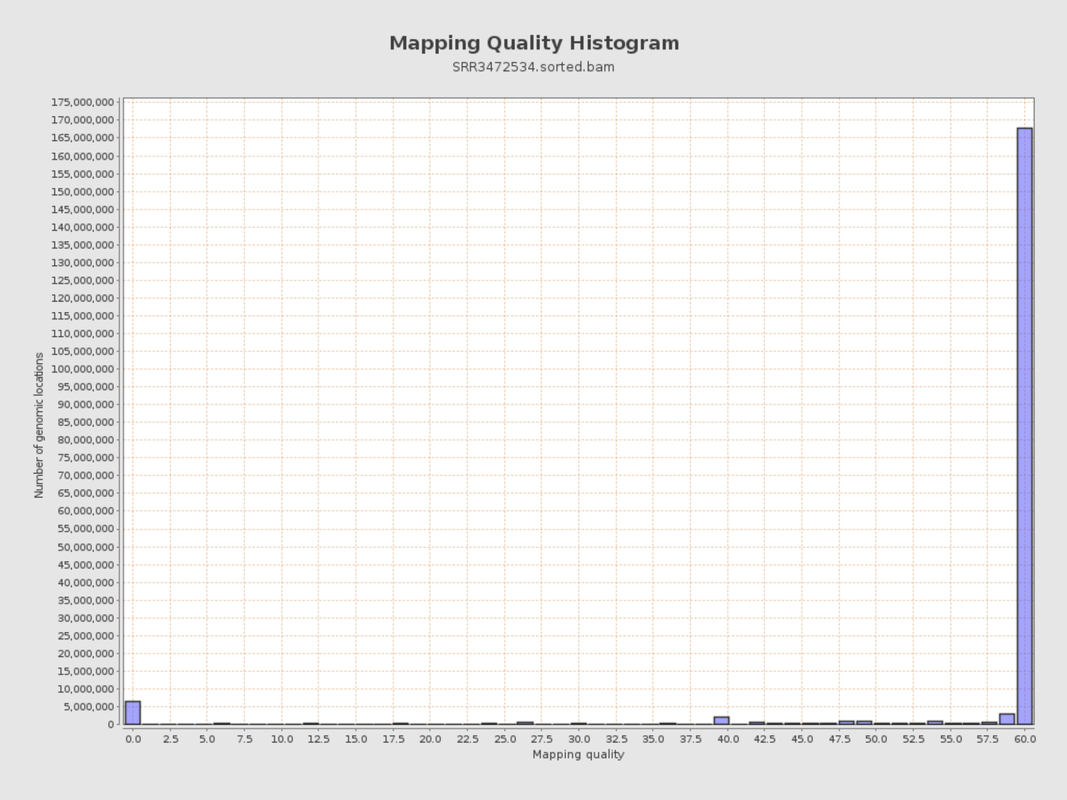
11. Results : Homopolymer Indels



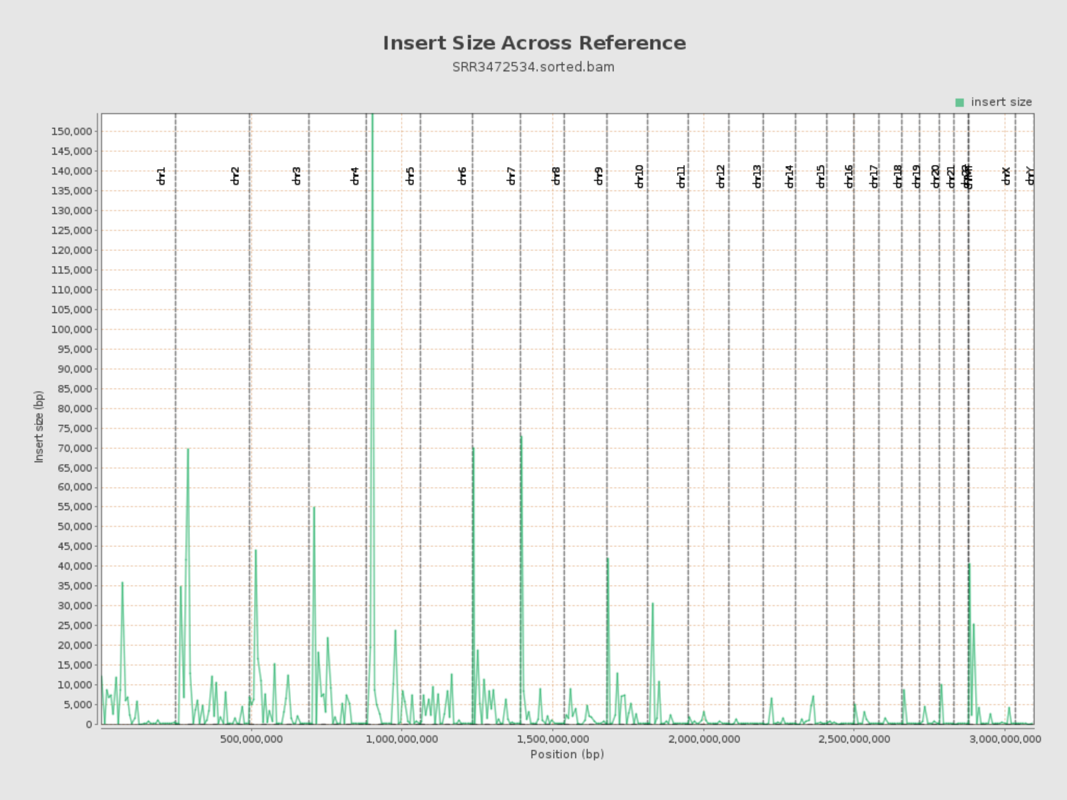
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram