Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:50:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472409.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_SRR3472409 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472409_1.fastq.gz SRR3472409_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:50:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472409.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,376,138
Mapped reads	18,205,789 / 99.07%
Unmapped reads	170,349 / 0.93%
Mapped paired reads	18,205,789 / 99.07%
Mapped reads, first in pair	9,127,879 / 49.67%
Mapped reads, second in pair	9,077,910 / 49.4%
Mapped reads, both in pair	18,096,556 / 98.48%
Mapped reads, singletons	109,233 / 0.59%
Secondary alignments	0
Supplementary alignments	112,364 / 0.61%
Read min/max/mean length	30 / 100 / 99.44
Duplicated reads (estimated)	11,159,190 / 60.73%
Duplication rate	45.91%
Clipped reads	1,502,922 / 8.18%

2.2. ACGT Content

Number/percentage of A's	492,737,640 / 27.66%
Number/percentage of C's	399,692,253 / 22.44%
Number/percentage of T's	488,610,831 / 27.43%
Number/percentage of G's	400,006,779 / 22.46%
Number/percentage of N's	224,289 / 0.01%

GC Percentage	44.89%

2.3. Coverage

Mean	0.5755
Standard Deviation	16.9409

2.4. Mapping Quality

Mean Mapping Quality	54.88

2.5. Insert size

Mean	119,390.9
Standard Deviation	3,425,788.59
P25/Median/P75	154 / 217 / 294

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	9,992,496
Insertions	114,764
Mapped reads with at least one insertion	0.62%
Deletions	97,732
Mapped reads with at least one deletion	0.53%
Homopolymer indels	45.77%

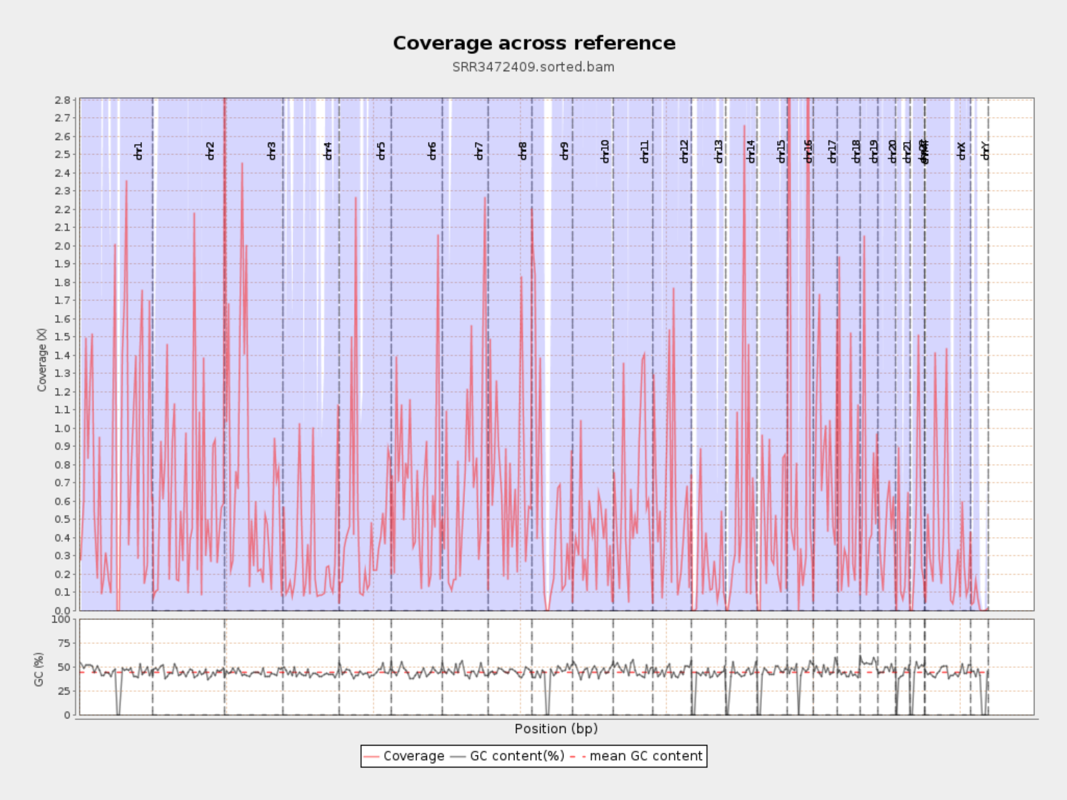
2.7. Chromosome stats

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

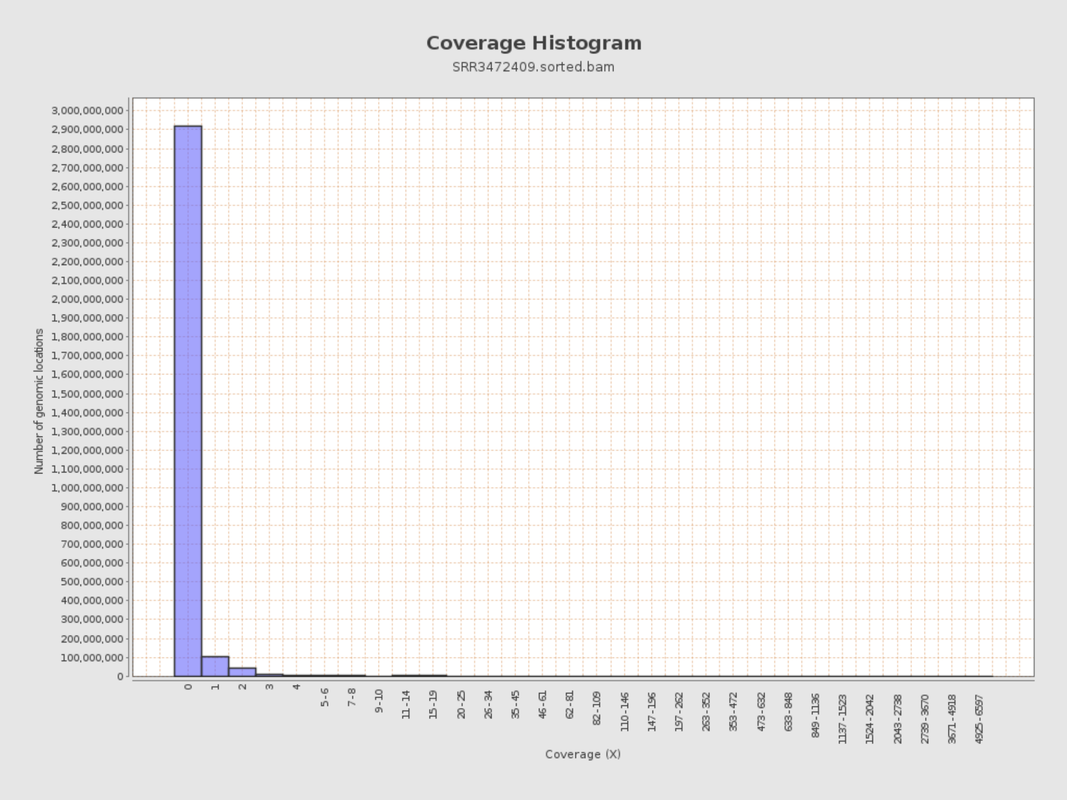
		bases	coverage	deviation
chr1	249250621	208753299	0.8375	20.7172
chr2	243199373	146312850	0.6016	17.8868
chr3	198022430	150483039	0.7599	17.176
chr4	191154276	54278362	0.284	8.9411
chr5	180915260	86994083	0.4809	12.6075
chr6	171115067	112579318	0.6579	14.7953
chr7	159138663	115277750	0.7244	24.4738
chr8	146364022	109786989	0.7501	18.7772
chr9	141213431	78821687	0.5582	13.2788
chr10	135534747	52945953	0.3906	15.4155
chr11	135006516	83300717	0.617	19.5428
chr12	133851895	82444115	0.6159	16.8776
chr13	115169878	27234122	0.2365	7.1322
chr14	107349540	59286837	0.5523	23.8059
chr15	102531392	44273161	0.4318	13.4243
chr16	90354753	84783729	0.9383	24.7833
chr17	81195210	68970156	0.8494	19.7326
chr18	78077248	48889692	0.6262	22.4802
chr19	59128983	39163497	0.6623	14.6456
chr20	63025520	28183983	0.4472	10.5587
chr21	48129895	14839157	0.3083	13.9199
chr22	51304566	21266722	0.4145	14.9105
chrMT	16571	2626	0.1585	0.5857
chrX	155270560	60210245	0.3878	10.6358

chrY	59373566	2421092	0.0408	1.6214

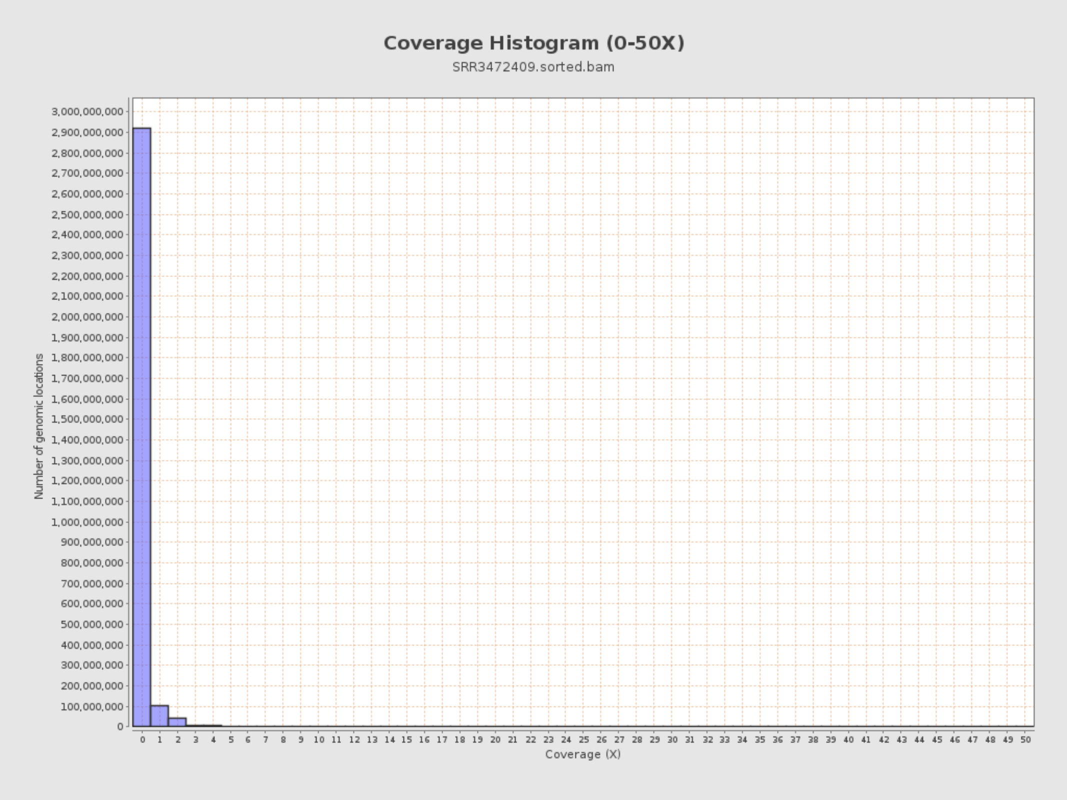
3. Results : Coverage across reference



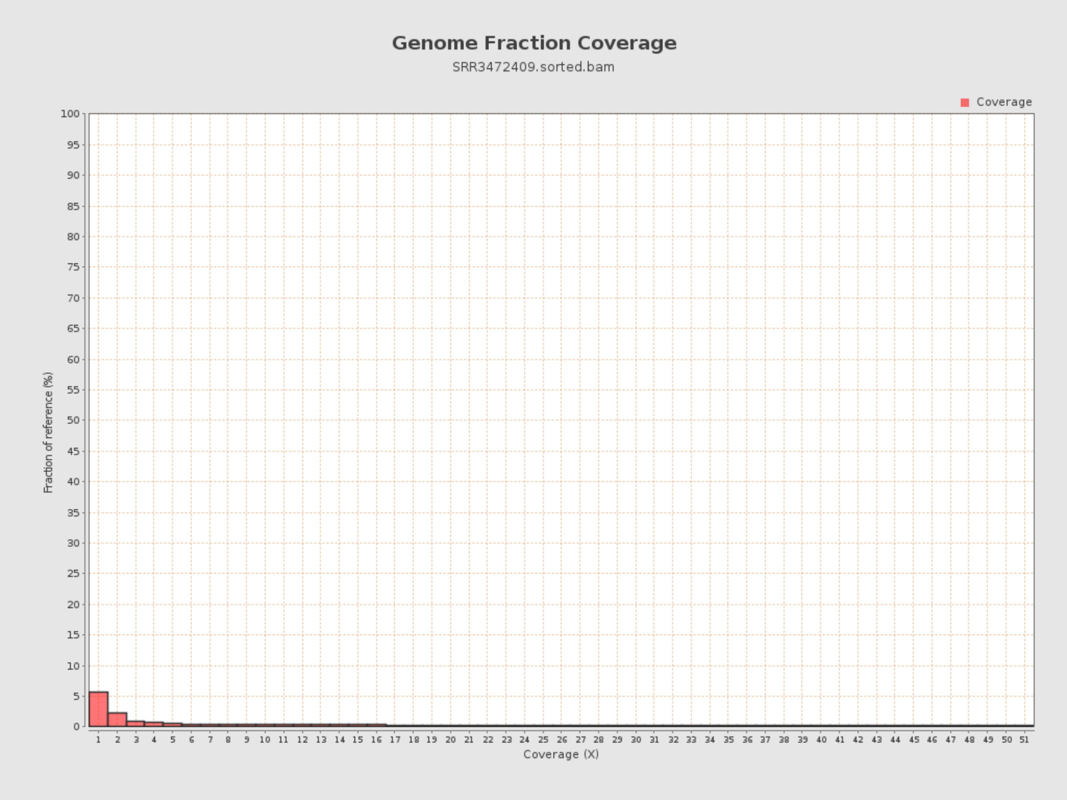
4. Results : Coverage Histogram



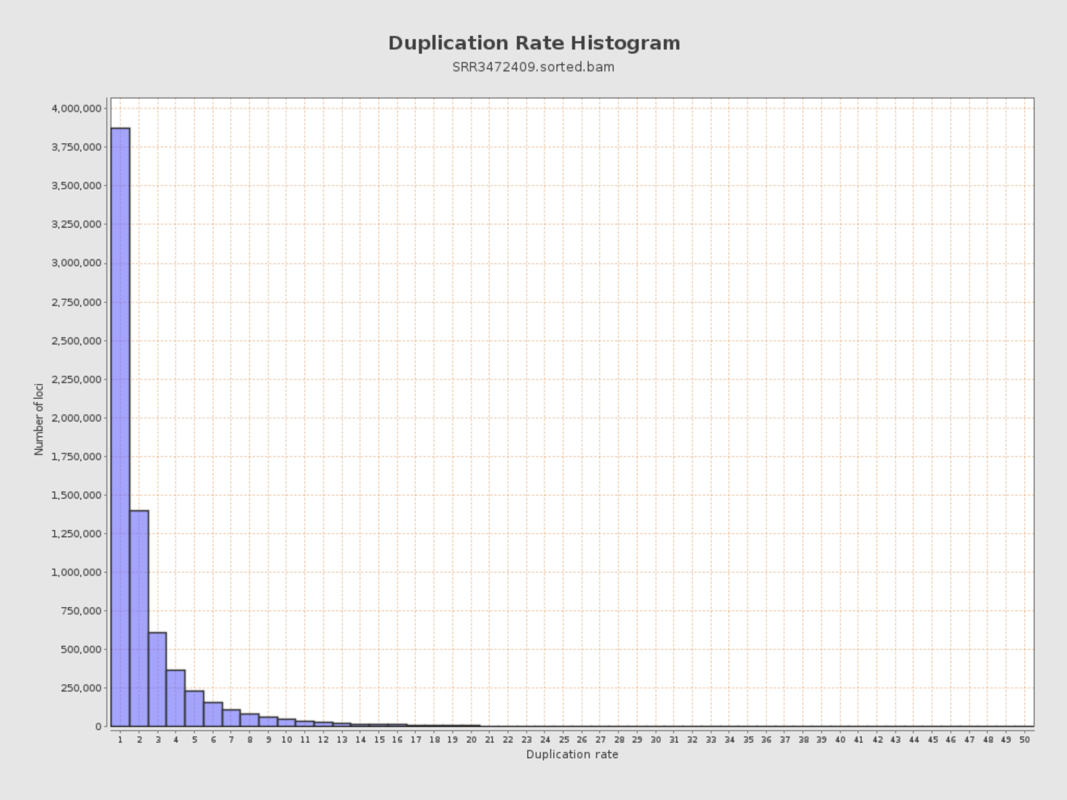
5. Results : Coverage Histogram (0-50X)



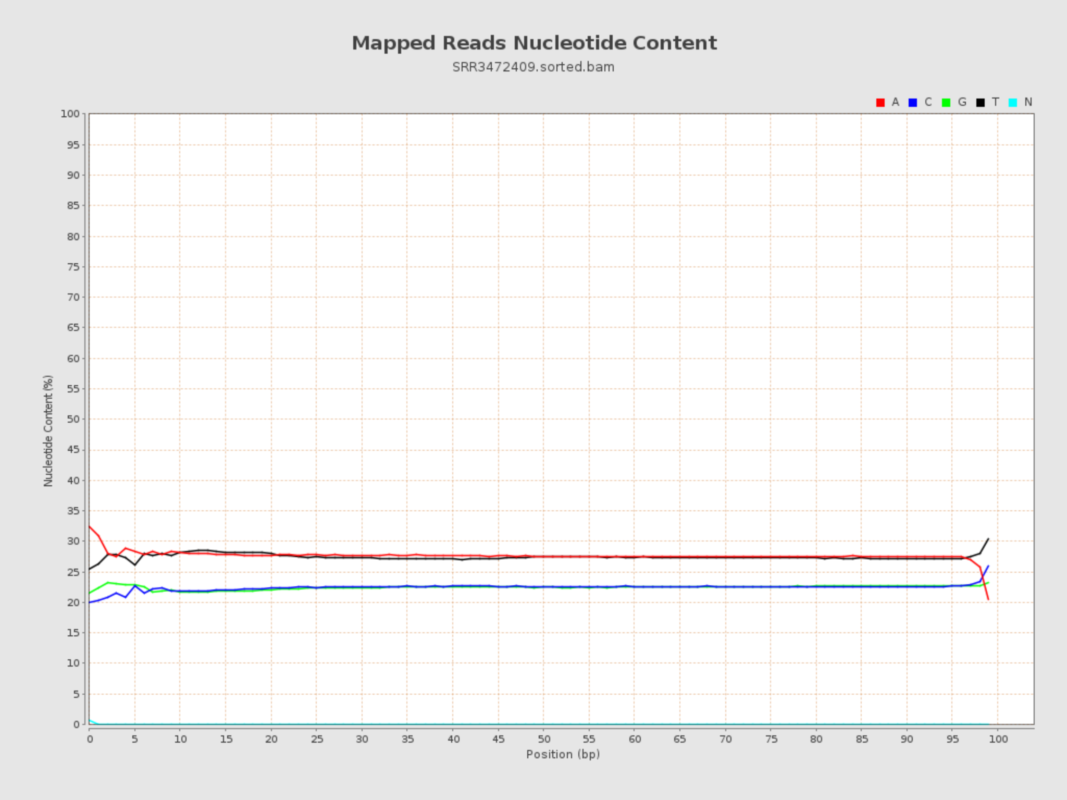
6. Results : Genome Fraction Coverage



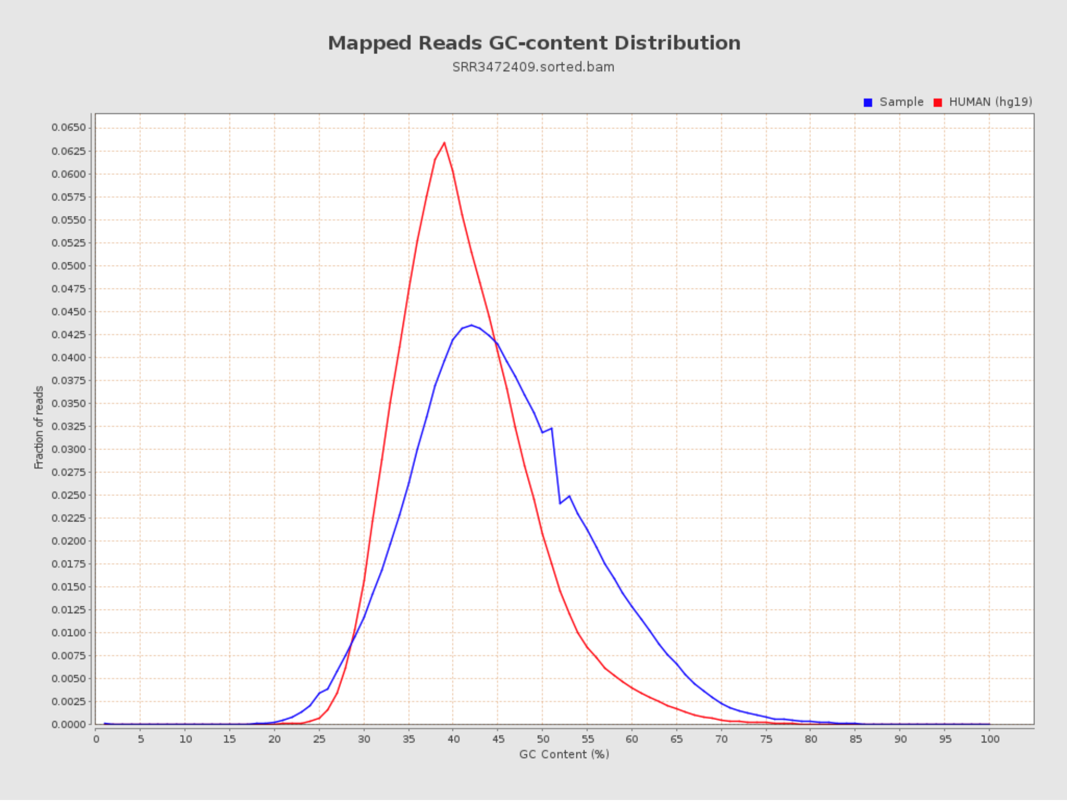
7. Results : Duplication Rate Histogram



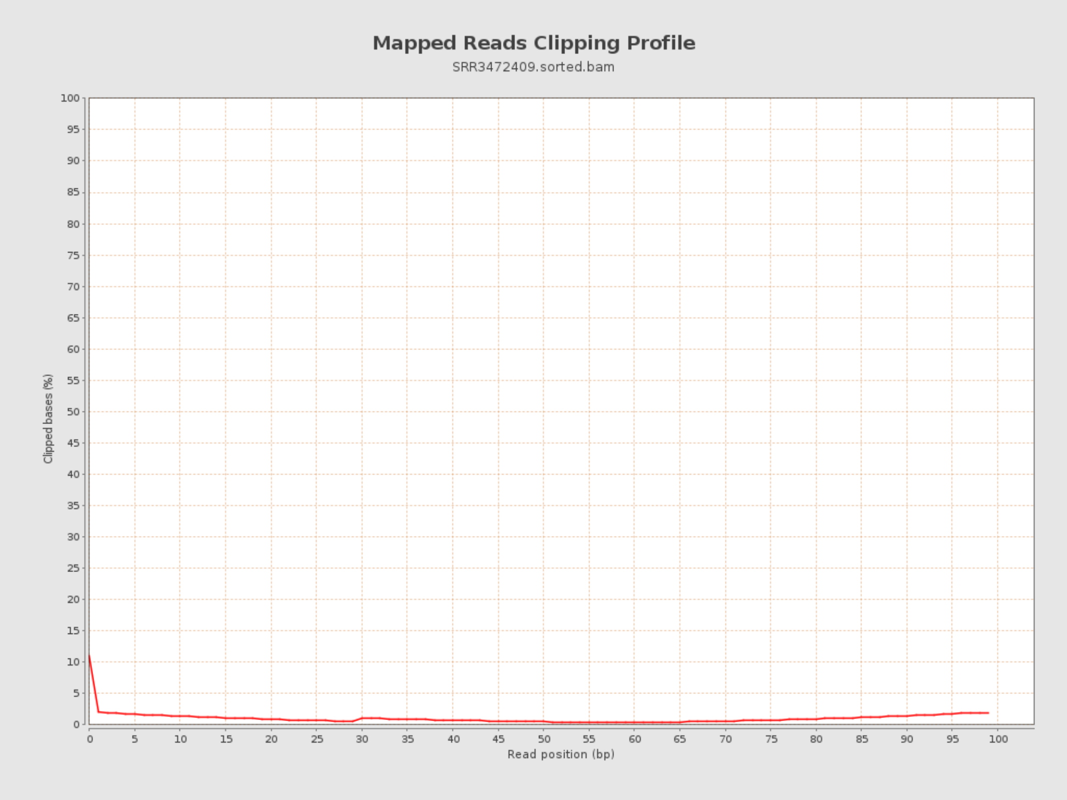
8. Results : Mapped Reads Nucleotide Content



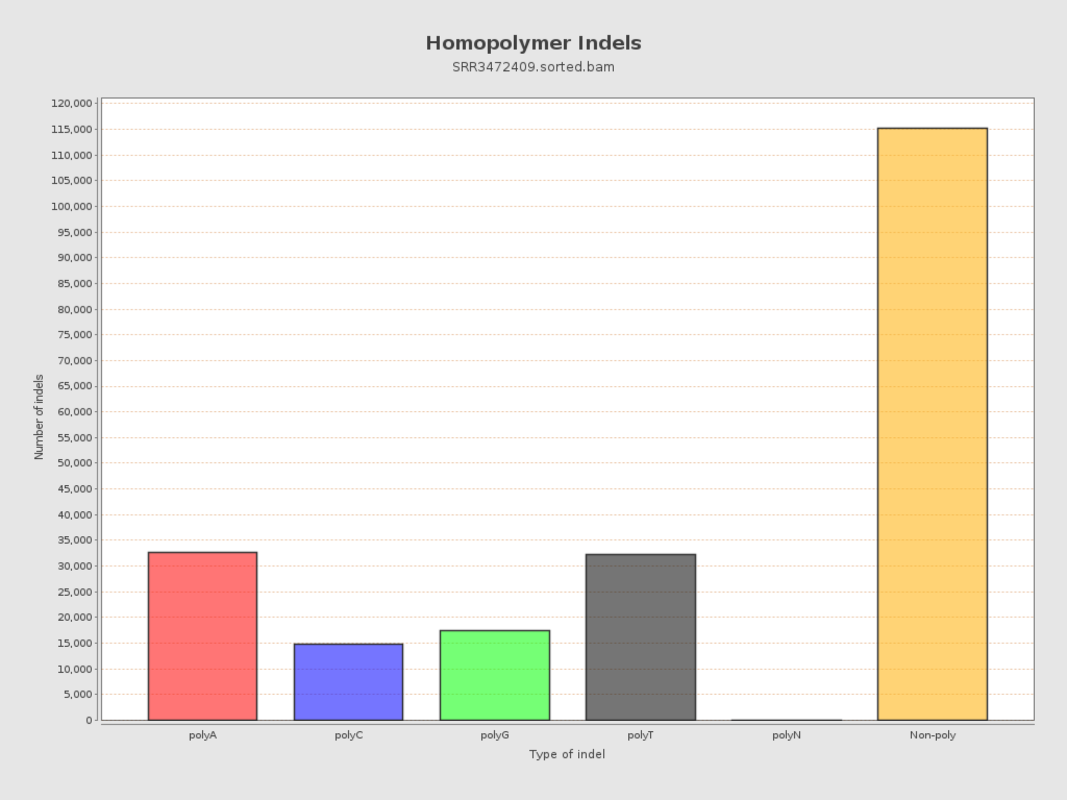
9. Results : Mapped Reads GC-content Distribution



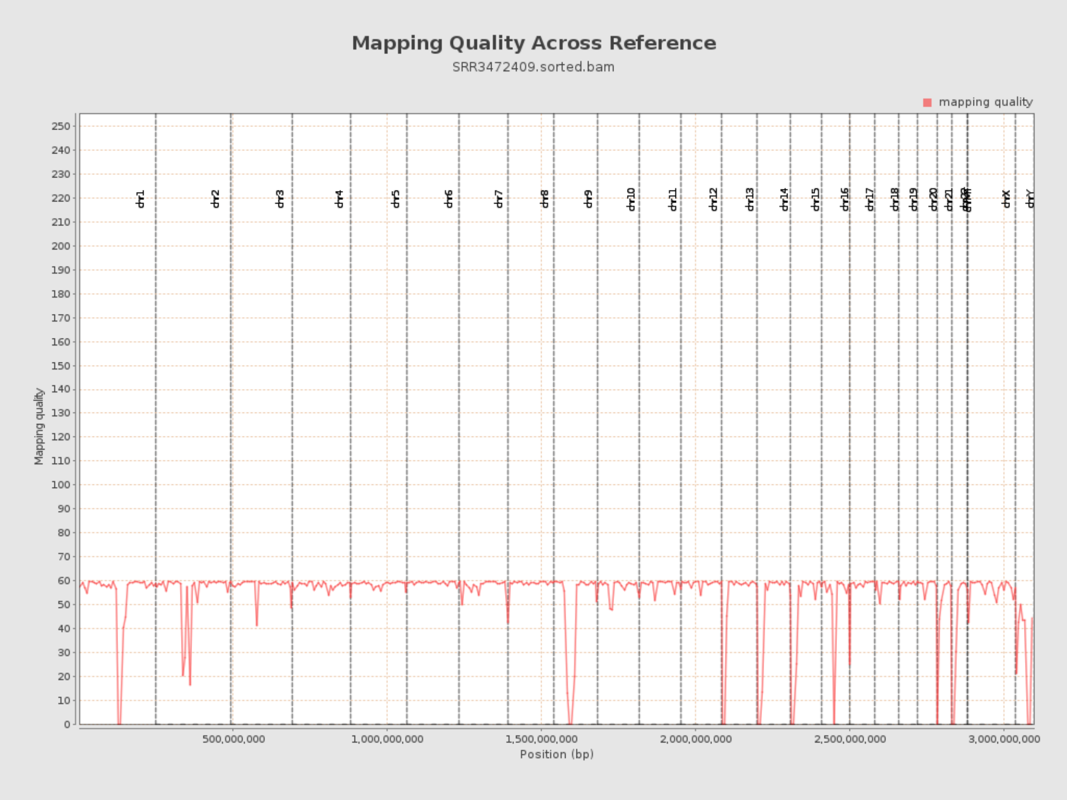
10. Results : Mapped Reads Clipping Profile



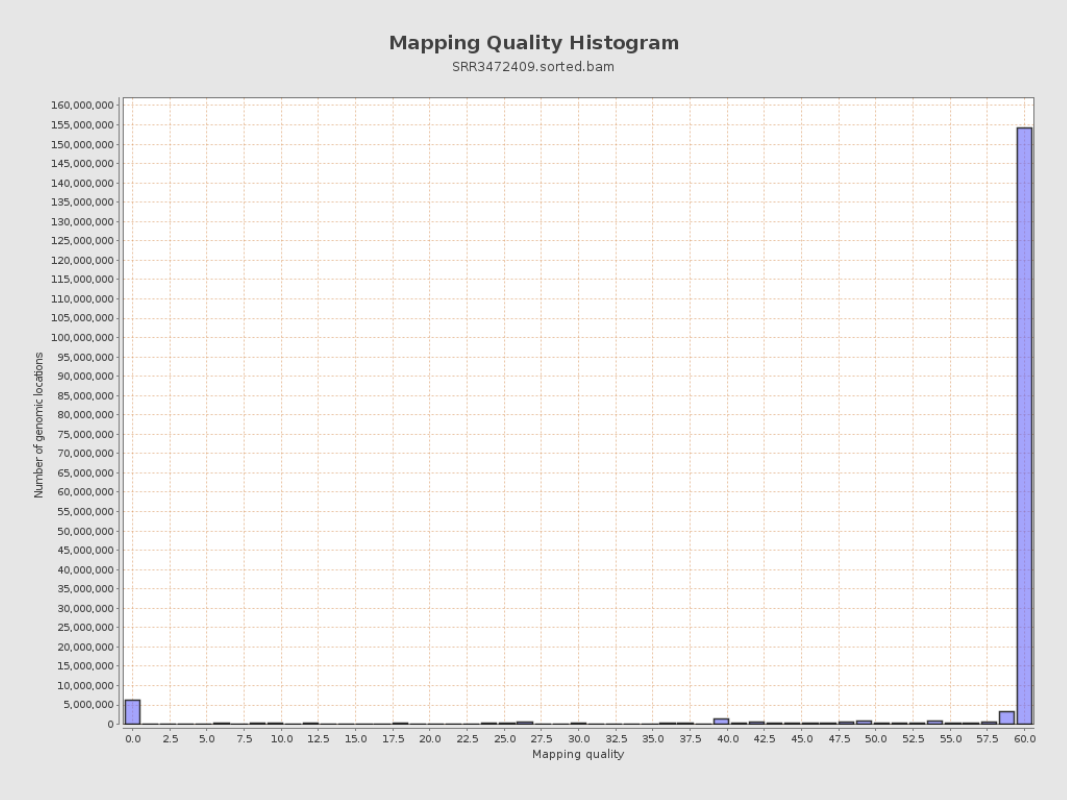
11. Results : Homopolymer Indels



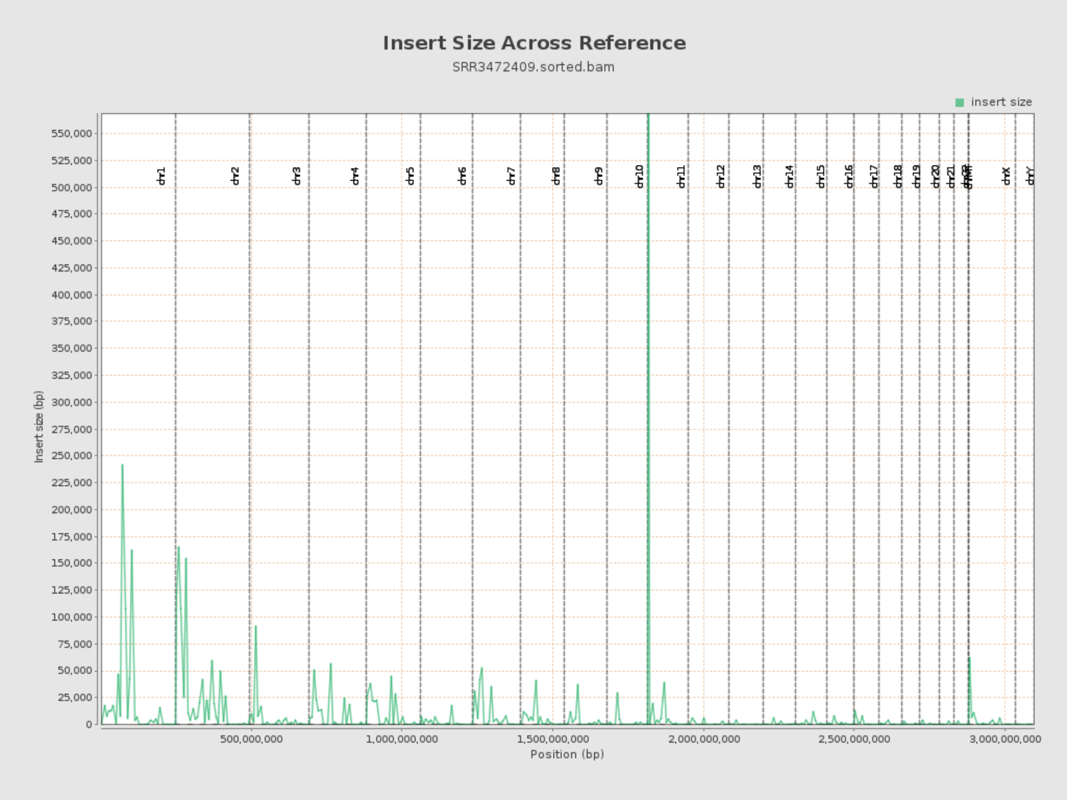
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram