Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 06:51:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472600.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_SRR3472600 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472600_1.fastq.gz SRR3472600_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 06:50:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472600.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,580,196
Mapped reads	7,860,822 / 91.62%
Unmapped reads	719,374 / 8.38%
Mapped paired reads	7,860,822 / 91.62%
Mapped reads, first in pair	3,966,655 / 46.23%
Mapped reads, second in pair	3,894,167 / 45.39%
Mapped reads, both in pair	7,679,798 / 89.51%
Mapped reads, singletons	181,024 / 2.11%
Secondary alignments	0
Supplementary alignments	258,555 / 3.01%
Read min/max/mean length	30 / 100 / 101.17
Duplicated reads (estimated)	1,215,223 / 14.16%
Duplication rate	13.48%
Clipped reads	6,033,311 / 70.32%

2.2. ACGT Content

Number/percentage of A's	164,309,434 / 25.76%
Number/percentage of C's	128,392,502 / 20.13%
Number/percentage of T's	189,056,178 / 29.64%
Number/percentage of G's	155,628,275 / 24.4%
Number/percentage of N's	402,128 / 0.06%

GC Percentage	44.53%

2.3. Coverage

Mean	0.2061
Standard Deviation	2.0207

2.4. Mapping Quality

Mean Mapping Quality	50.47

2.5. Insert size

Mean	240,774.84
Standard Deviation	4,698,867.5
P25/Median/P75	89 / 125 / 171

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	7,349,404
Insertions	59,850
Mapped reads with at least one insertion	0.75%
Deletions	143,070
Mapped reads with at least one deletion	1.78%
Homopolymer indels	42.39%

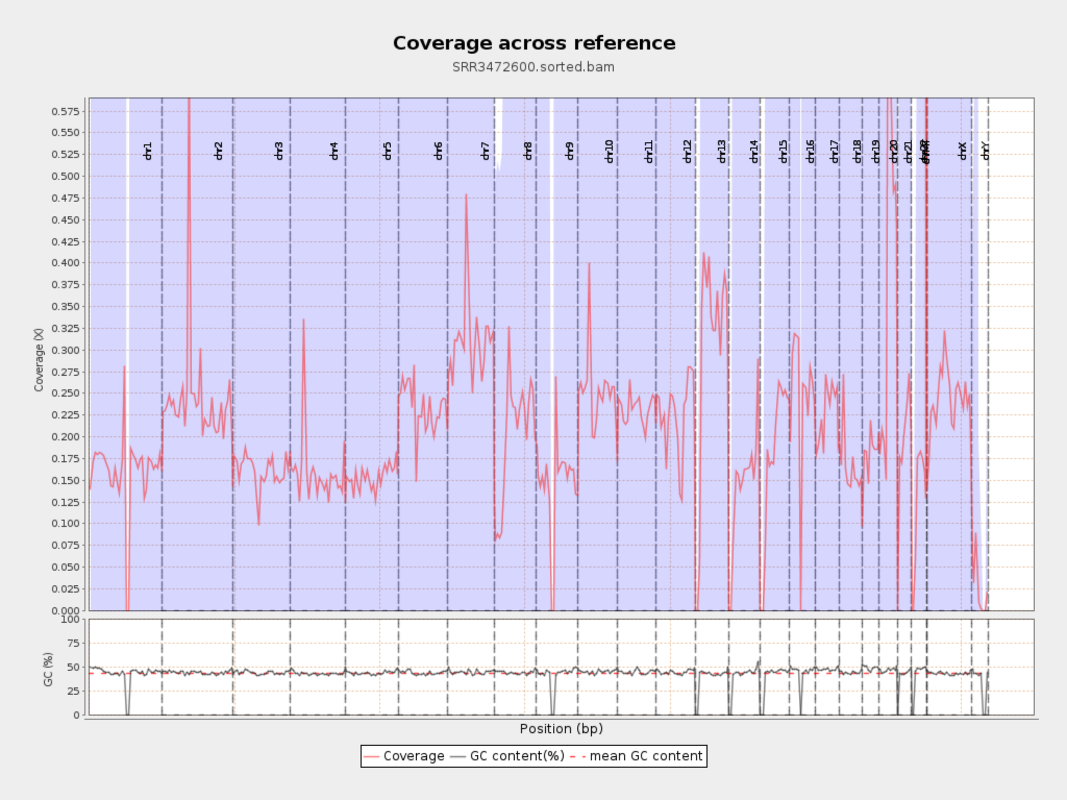
2.7. Chromosome stats

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

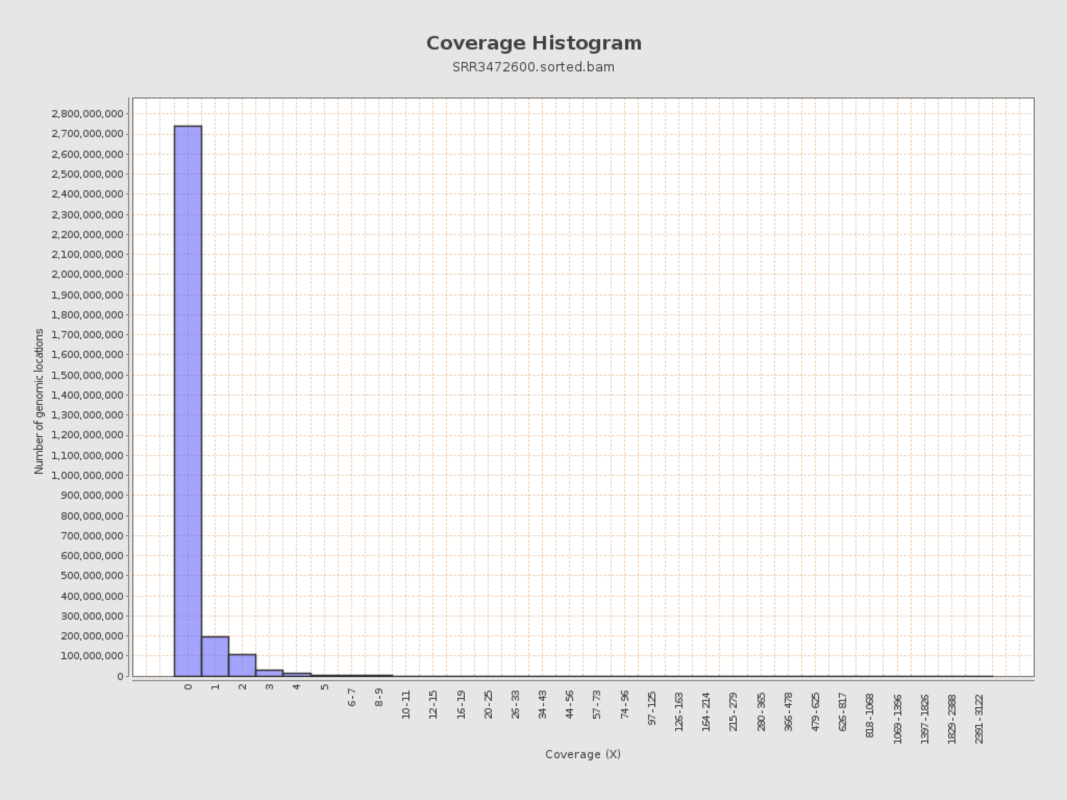
		bases	coverage	deviation
chr1	249250621	39600728	0.1589	2.2958
chr2	243199373	59846835	0.2461	3.216
chr3	198022430	31760422	0.1604	0.5904
chr4	191154276	30346084	0.1588	1.0595
chr5	180915260	27764287	0.1535	0.5997
chr6	171115067	40112547	0.2344	1.0765
chr7	159138663	49958038	0.3139	3.2422
chr8	146364022	29493007	0.2015	1.6486
chr9	141213431	20422795	0.1446	1.9904
chr10	135534747	34347614	0.2534	1.921
chr11	135006516	31148319	0.2307	1.7381
chr12	133851895	29989493	0.224	0.7294
chr13	115169878	34319580	0.298	0.8702
chr14	107349540	15437069	0.1438	5.2148
chr15	102531392	18106900	0.1766	0.6414
chr16	90354753	22505110	0.2491	1.1234
chr17	81195210	18538564	0.2283	1.3291
chr18	78077248	13162617	0.1686	3.1449
chr19	59128983	10729196	0.1815	1.6772
chr20	63025520	25528199	0.405	1.4008
chr21	48129895	9235953	0.1919	0.851
chr22	51304566	6083608	0.1186	0.5131
chrMT	16571	433756	26.1756	16.1151
chrX	155270560	37677166	0.2427	1.0408

chrY	59373566	1509904	0.0254	0.845

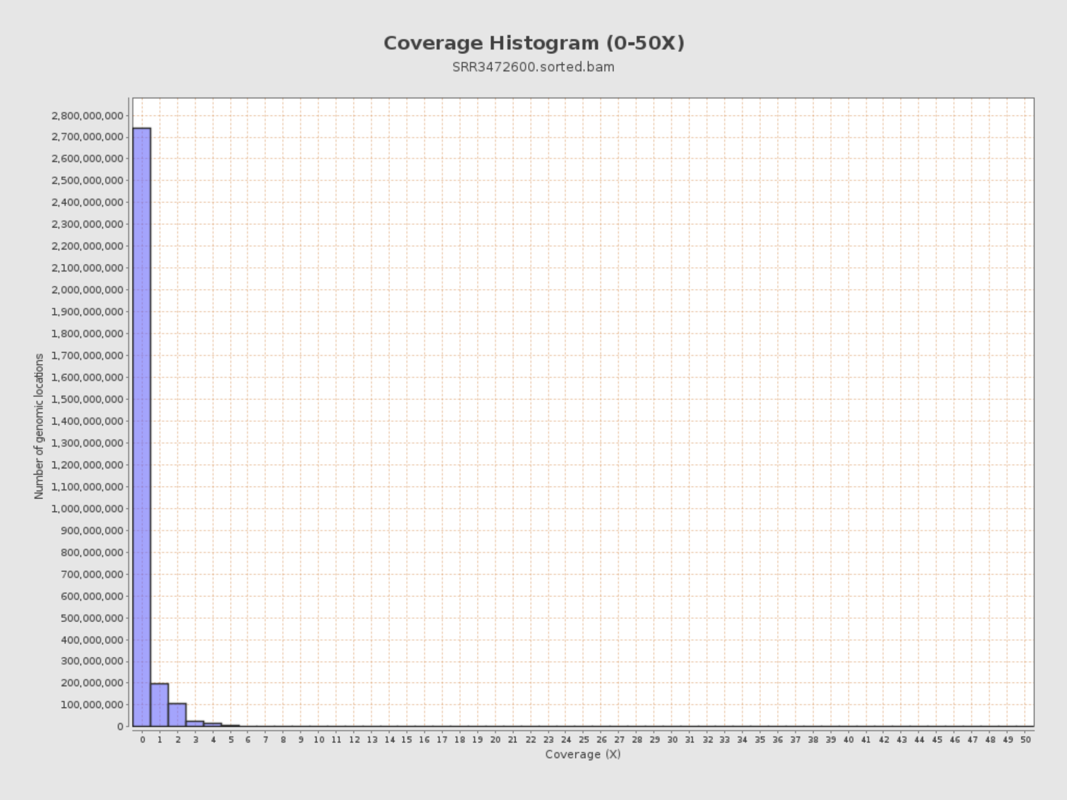
3. Results : Coverage across reference



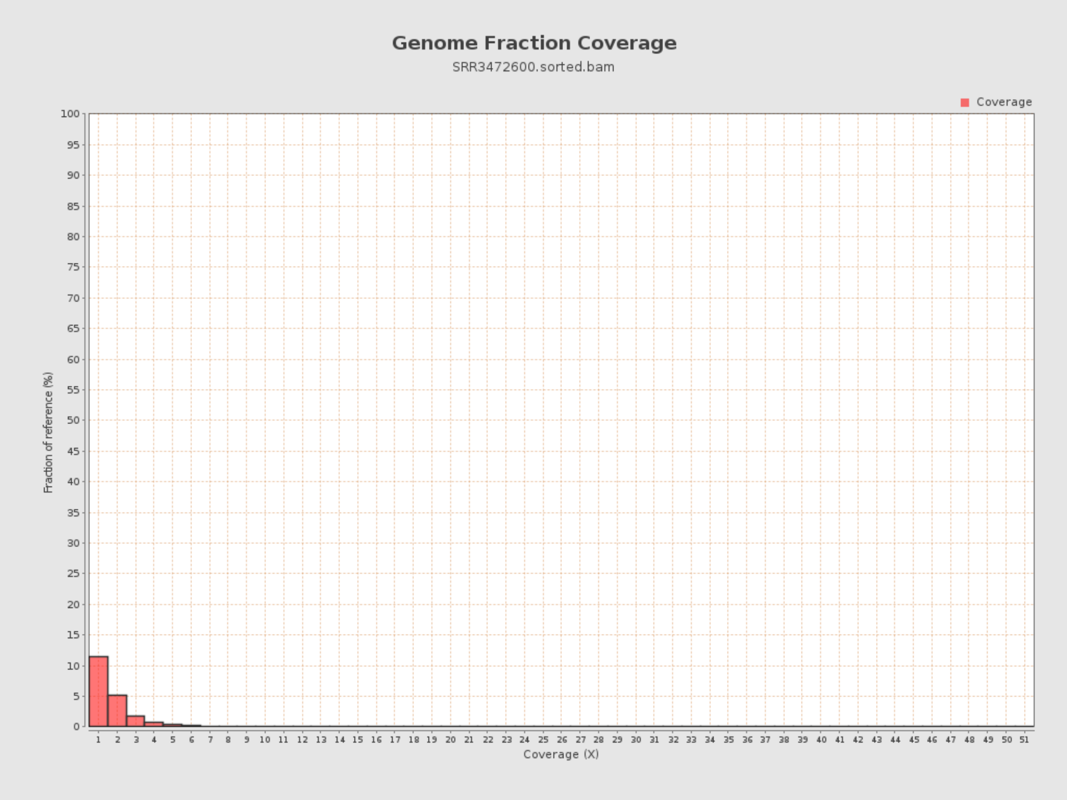
4. Results : Coverage Histogram



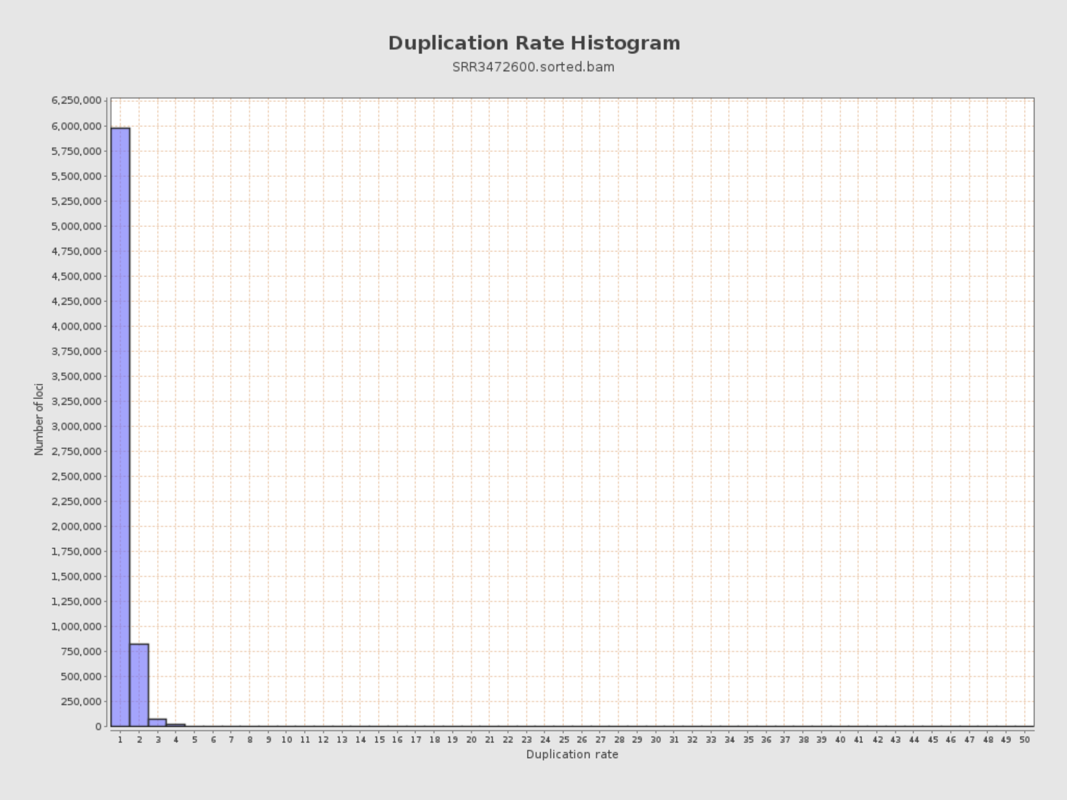
5. Results : Coverage Histogram (0-50X)



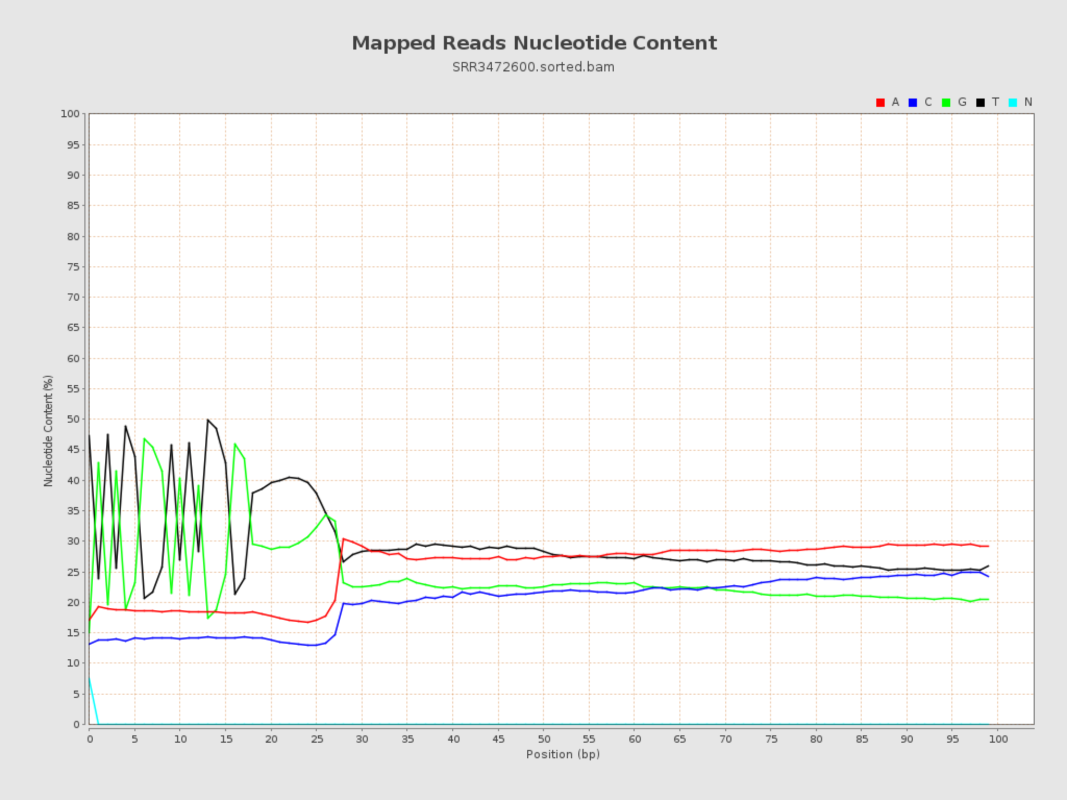
6. Results : Genome Fraction Coverage



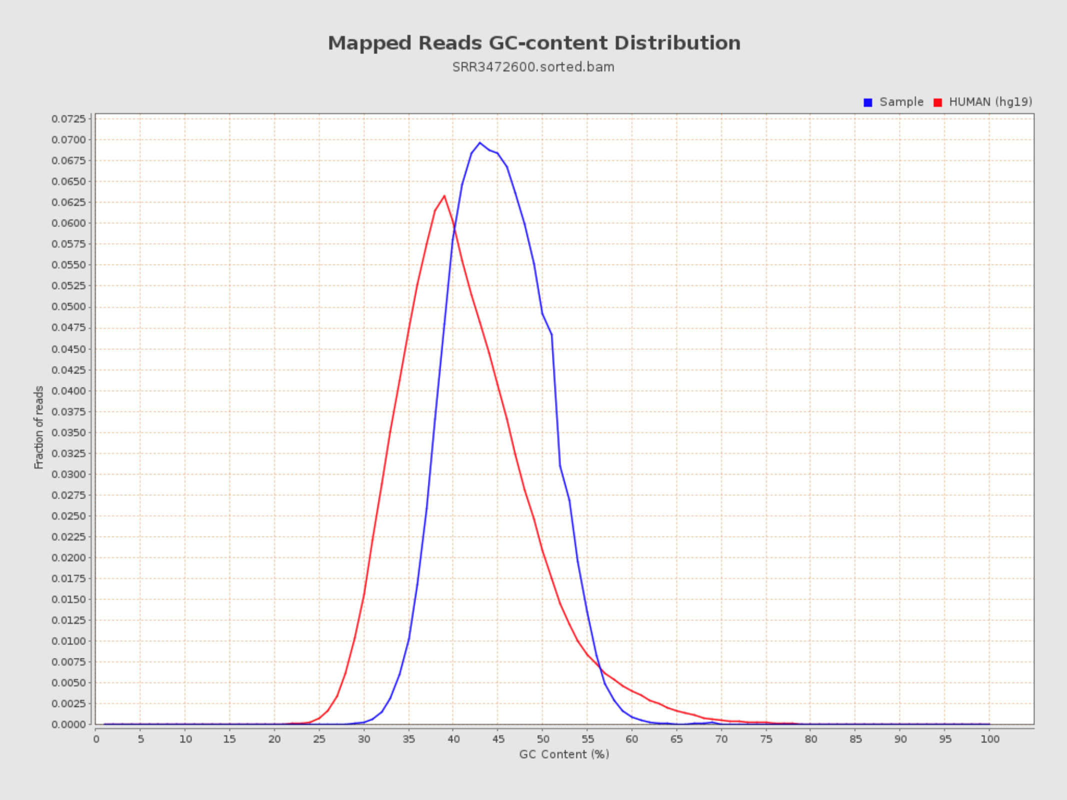
7. Results : Duplication Rate Histogram



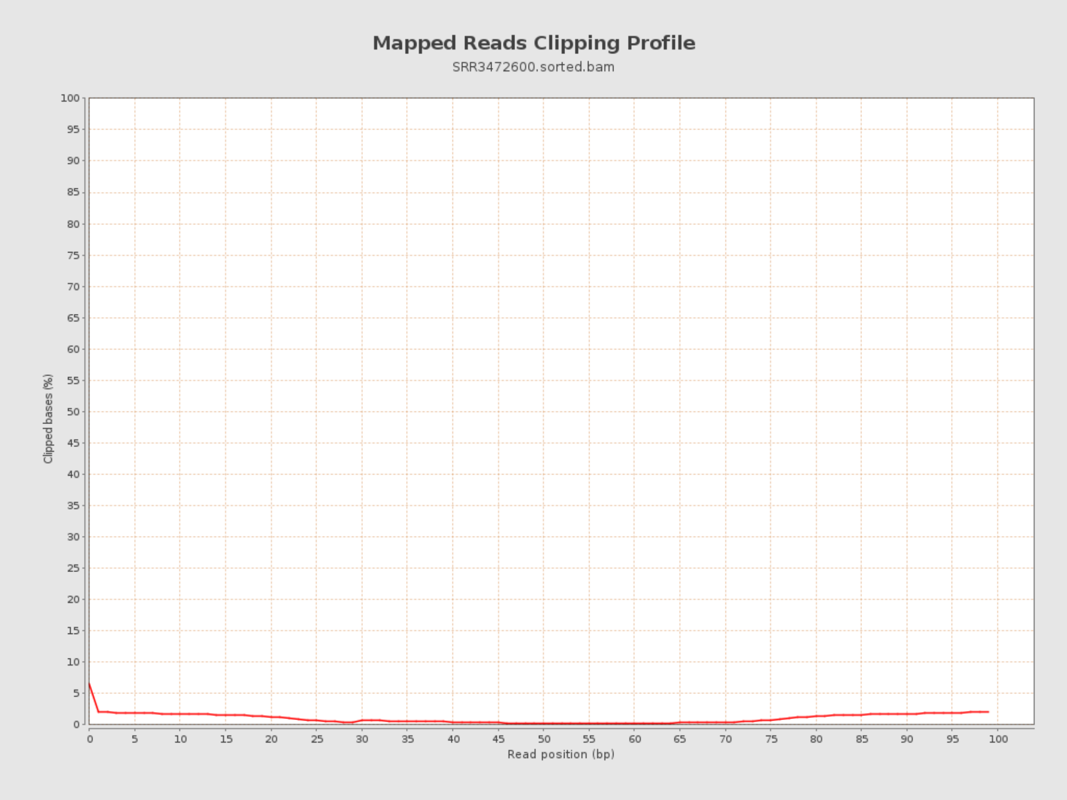
8. Results : Mapped Reads Nucleotide Content



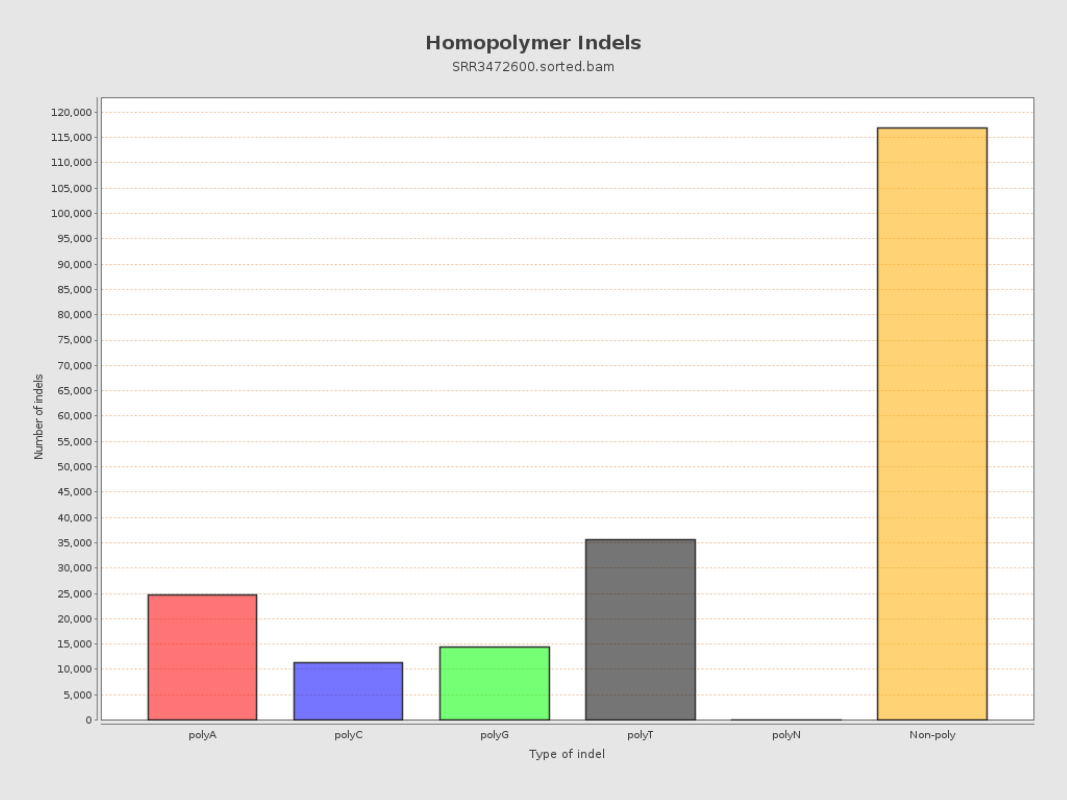
9. Results : Mapped Reads GC-content Distribution



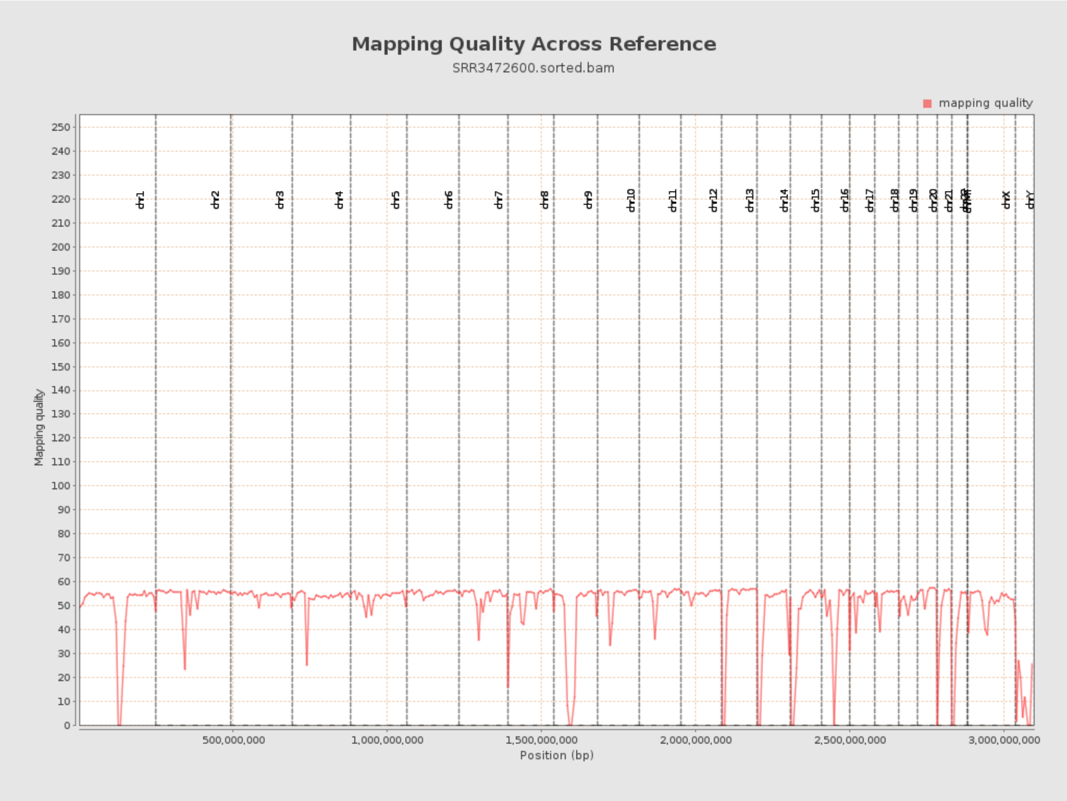
10. Results : Mapped Reads Clipping Profile



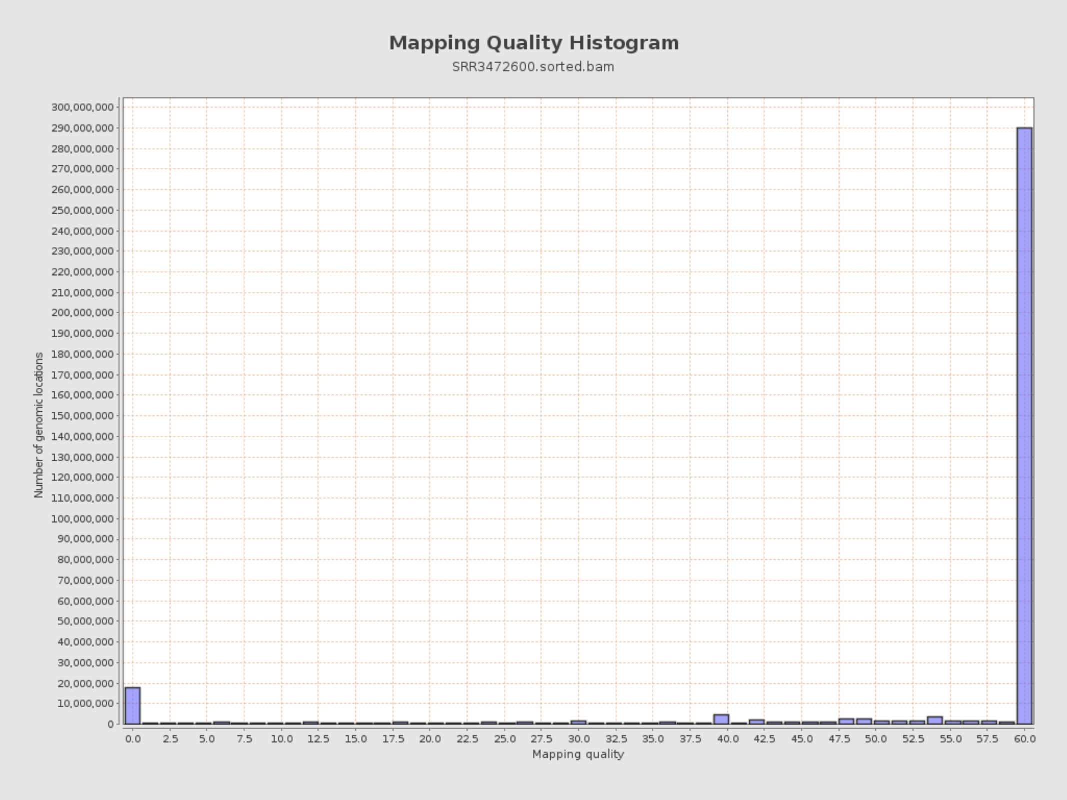
11. Results : Homopolymer Indels



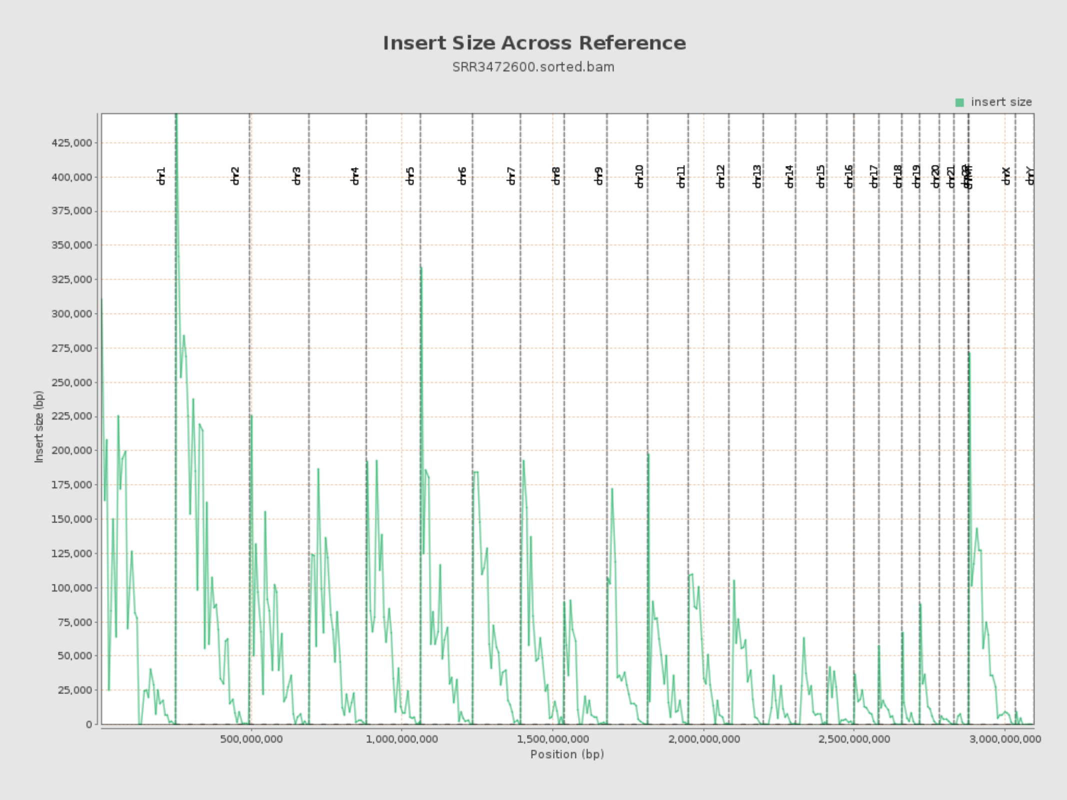
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram