Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 04:35:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472590.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_SRR3472590 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472590_1.fastq.gz SRR3472590_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 04:35:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472590.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,397,244
Mapped reads	8,632,775 / 91.86%
Unmapped reads	764,469 / 8.14%
Mapped paired reads	8,632,775 / 91.86%
Mapped reads, first in pair	4,359,950 / 46.4%
Mapped reads, second in pair	4,272,825 / 45.47%
Mapped reads, both in pair	8,419,890 / 89.6%
Mapped reads, singletons	212,885 / 2.27%
Secondary alignments	0
Supplementary alignments	286,456 / 3.05%
Read min/max/mean length	30 / 100 / 101.19
Duplicated reads (estimated)	1,273,342 / 13.55%
Duplication rate	12.55%
Clipped reads	6,604,895 / 70.29%

2.2. ACGT Content

Number/percentage of A's	184,913,695 / 26.27%
Number/percentage of C's	136,828,238 / 19.44%
Number/percentage of T's	213,676,560 / 30.36%
Number/percentage of G's	167,931,306 / 23.86%
Number/percentage of N's	441,433 / 0.06%

GC Percentage	43.3%

2.3. Coverage

Mean	0.2274
Standard Deviation	2.1053

2.4. Mapping Quality

Mean Mapping Quality	50.56

2.5. Insert size

Mean	242,863.77
Standard Deviation	4,692,751.86
P25/Median/P75	94 / 135 / 187

2.6. Mismatches and indels

General error rate	1.2%
Mismatches	8,341,248
Insertions	66,830
Mapped reads with at least one insertion	0.76%
Deletions	164,077
Mapped reads with at least one deletion	1.86%
Homopolymer indels	43.34%

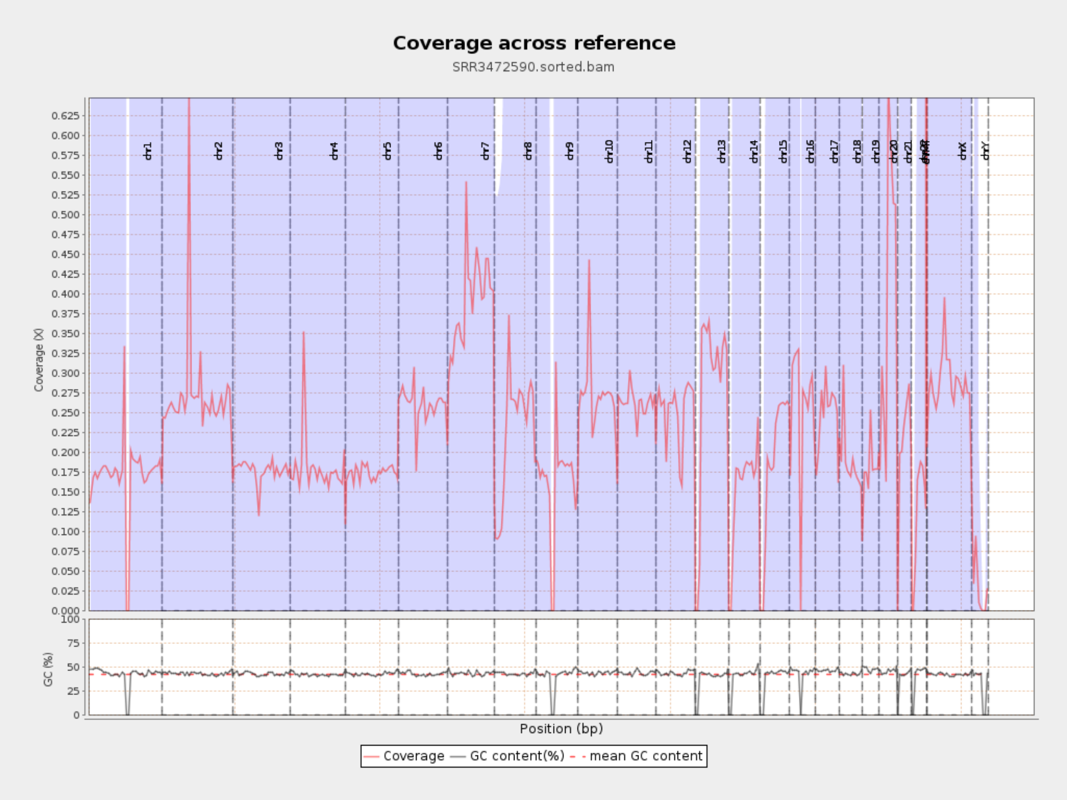
2.7. Chromosome stats

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

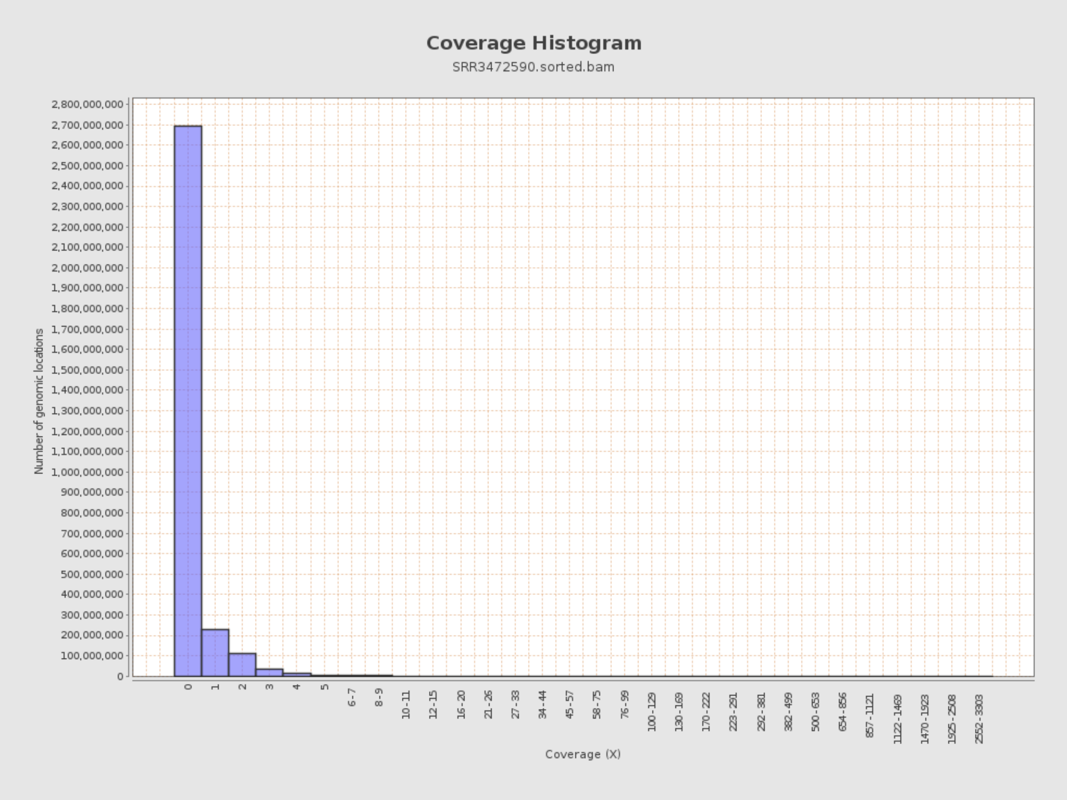
		bases	coverage	deviation
chr1	249250621	42505037	0.1705	2.9553
chr2	243199373	66650181	0.2741	3.1684
chr3	198022430	35002420	0.1768	0.6121
chr4	191154276	34462189	0.1803	1.1013
chr5	180915260	31501328	0.1741	0.6422
chr6	171115067	44576909	0.2605	1.2035
chr7	159138663	62656256	0.3937	3.8335
chr8	146364022	33075364	0.226	1.8215
chr9	141213431	22947337	0.1625	2.3834
chr10	135534747	37049063	0.2734	2.1937
chr11	135006516	35255686	0.2611	2.0667
chr12	133851895	33640579	0.2513	0.7631
chr13	115169878	31831388	0.2764	0.8029
chr14	107349540	16496397	0.1537	3.5026
chr15	102531392	19007715	0.1854	0.6444
chr16	90354753	23300573	0.2579	1.1351
chr17	81195210	20060536	0.2471	1.8602
chr18	78077248	14920468	0.1911	3.6697
chr19	59128983	10676108	0.1806	2.0117
chr20	63025520	25430140	0.4035	1.1831
chr21	48129895	10184165	0.2116	0.8699
chr22	51304566	6084633	0.1186	0.5055
chrMT	16571	267966	16.1708	10.1036
chrX	155270560	44752027	0.2882	1.1805

chrY	59373566	1760820	0.0297	0.8616

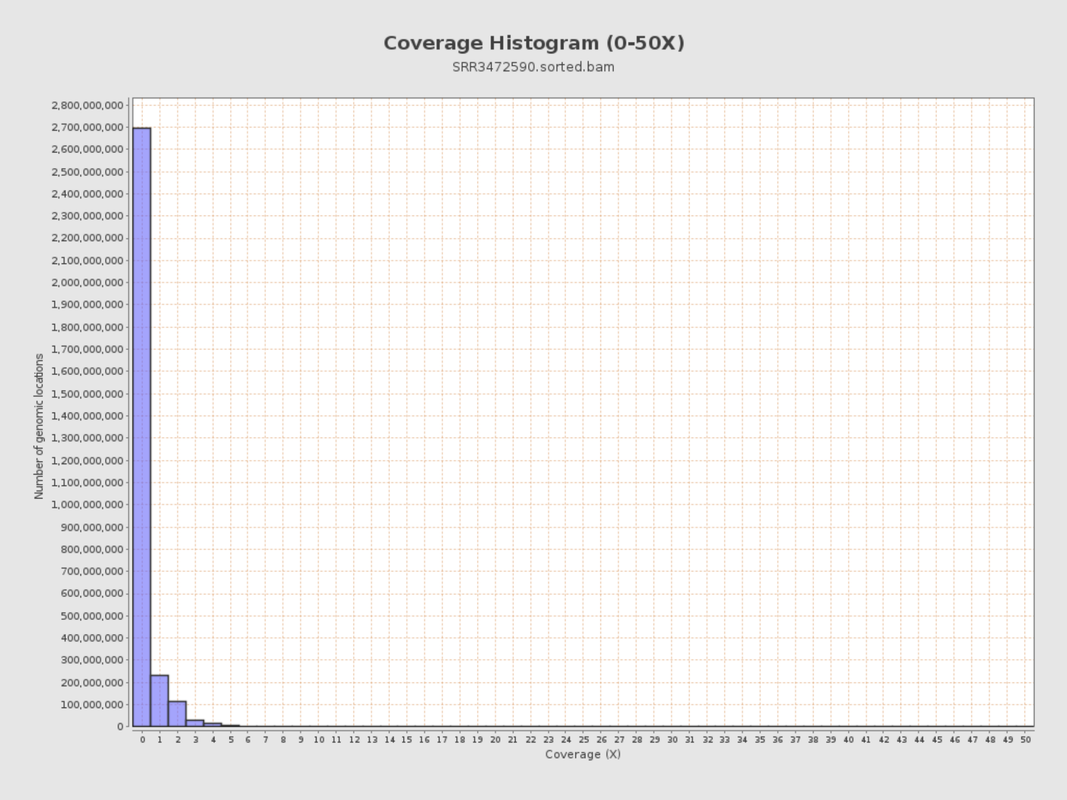
3. Results : Coverage across reference



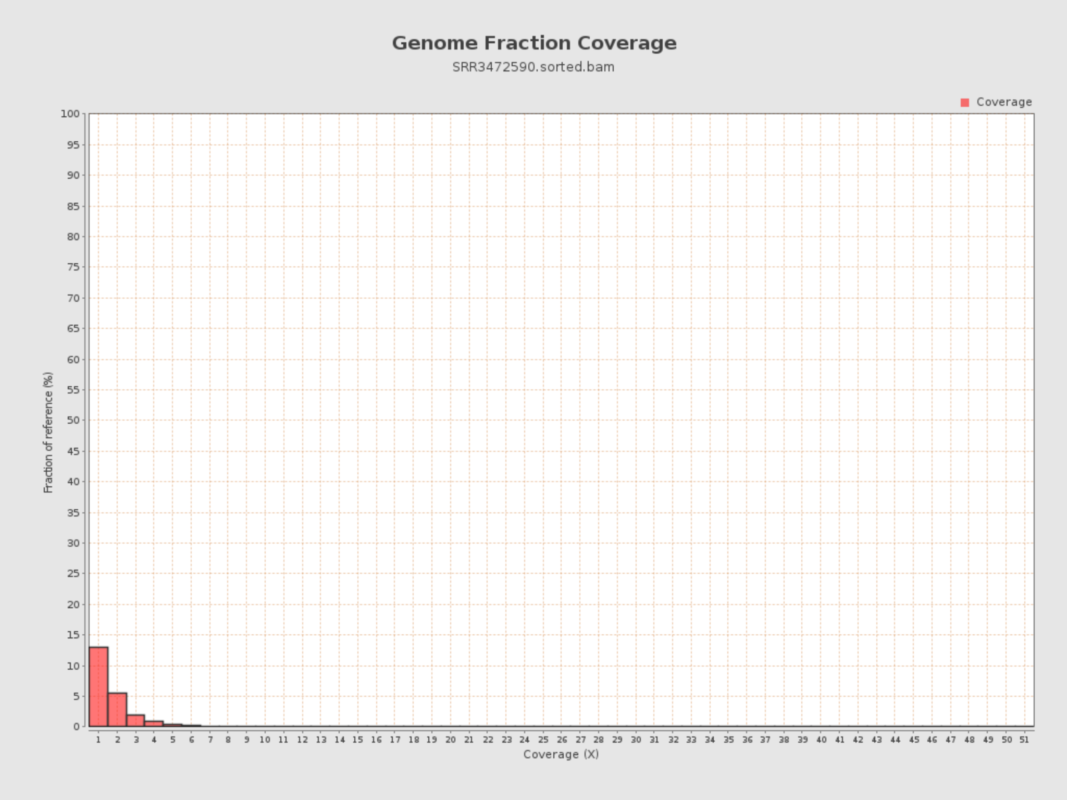
4. Results : Coverage Histogram



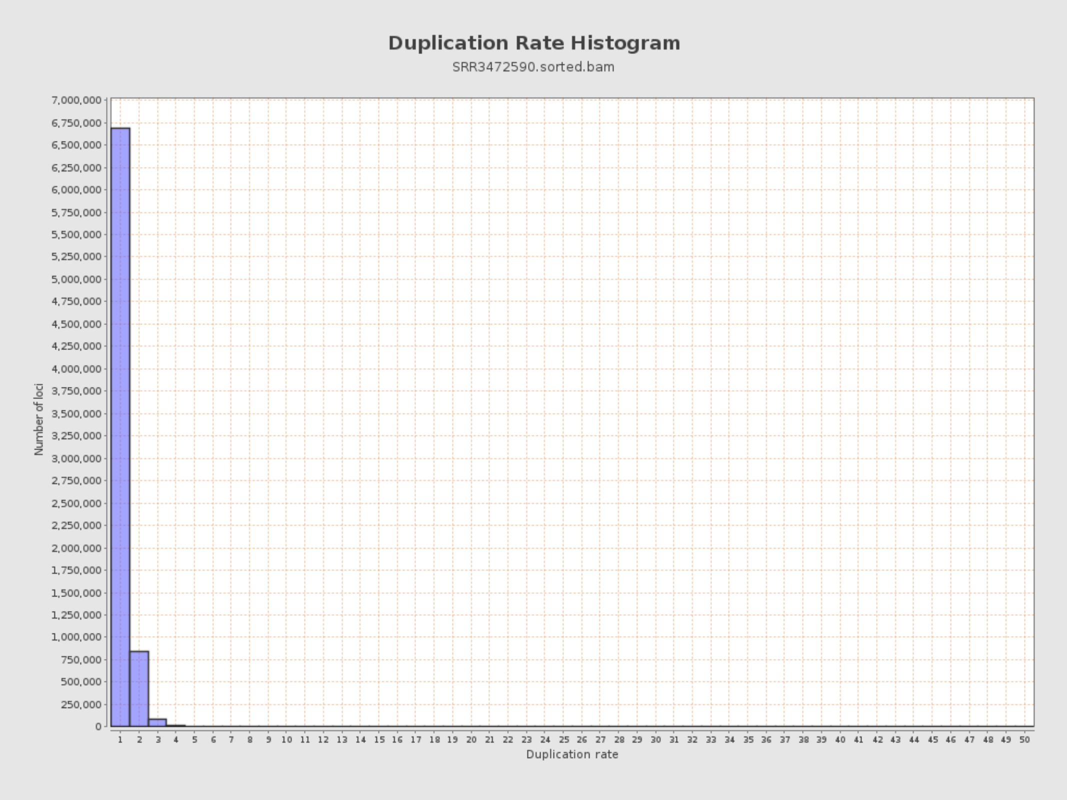
5. Results : Coverage Histogram (0-50X)



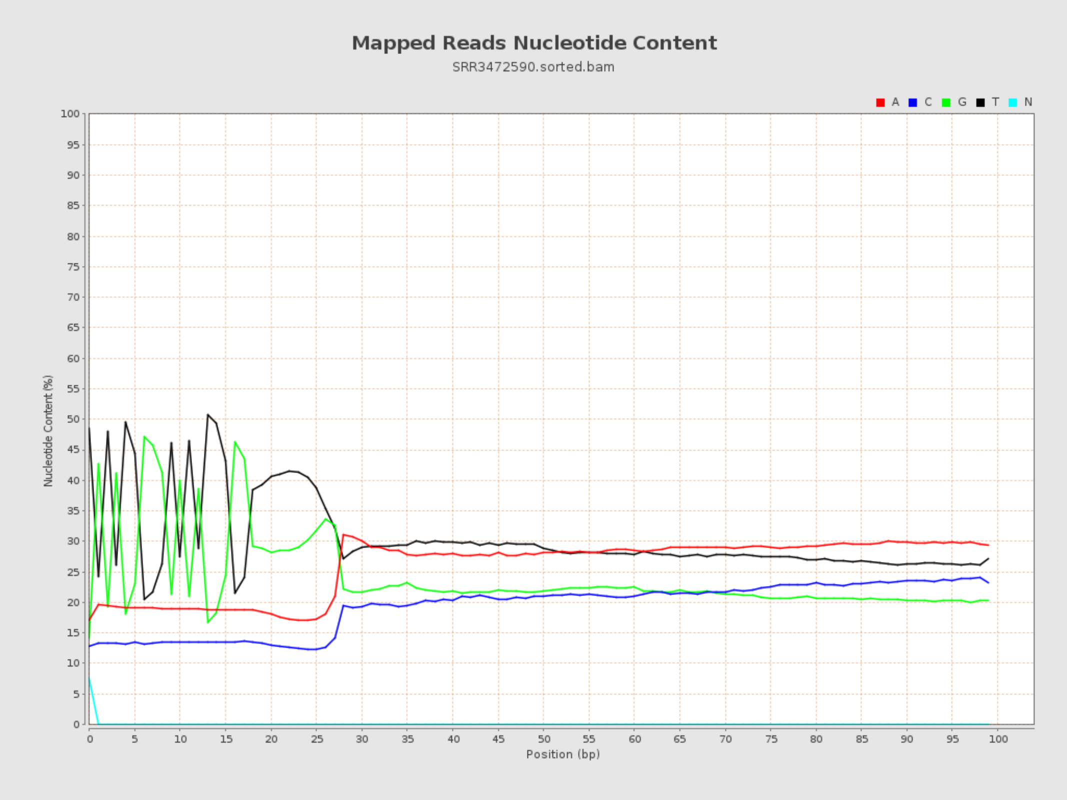
6. Results : Genome Fraction Coverage



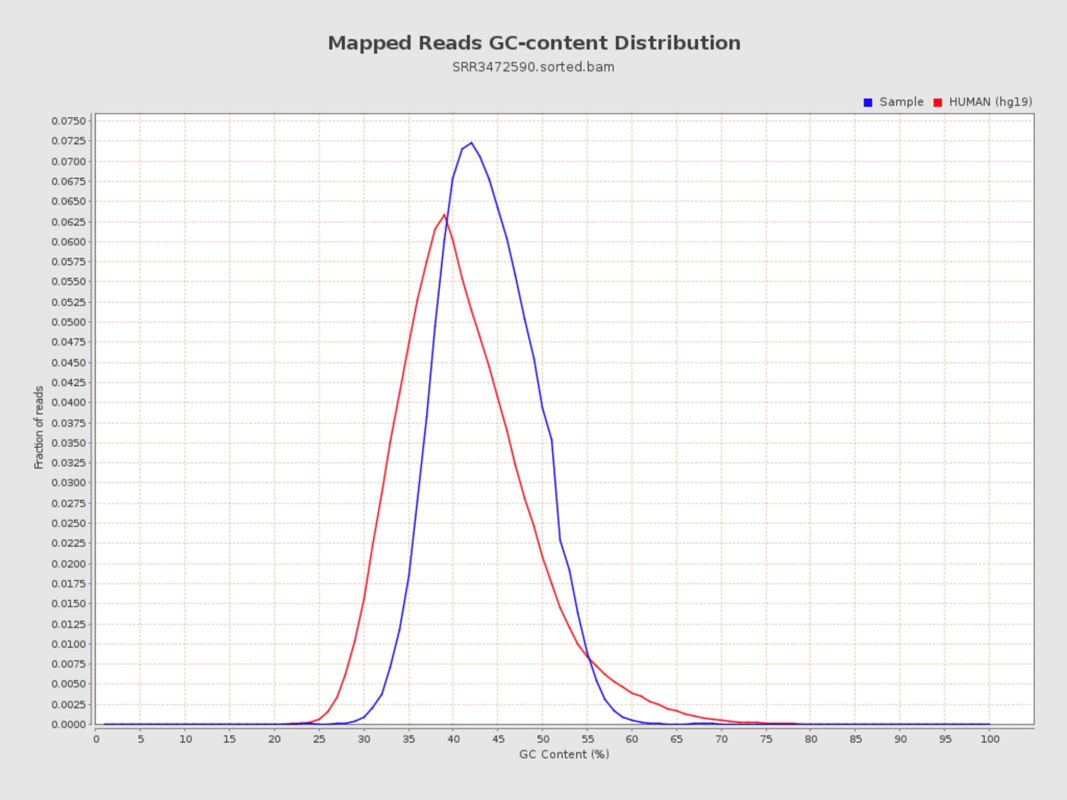
7. Results : Duplication Rate Histogram



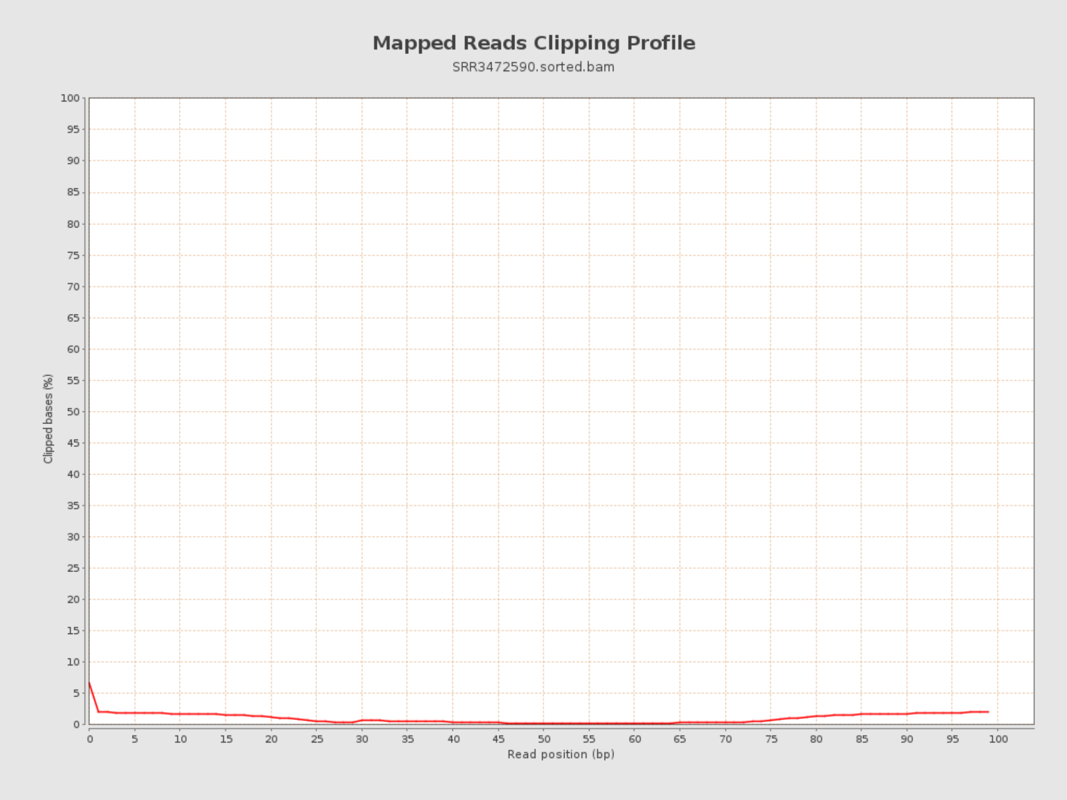
8. Results : Mapped Reads Nucleotide Content



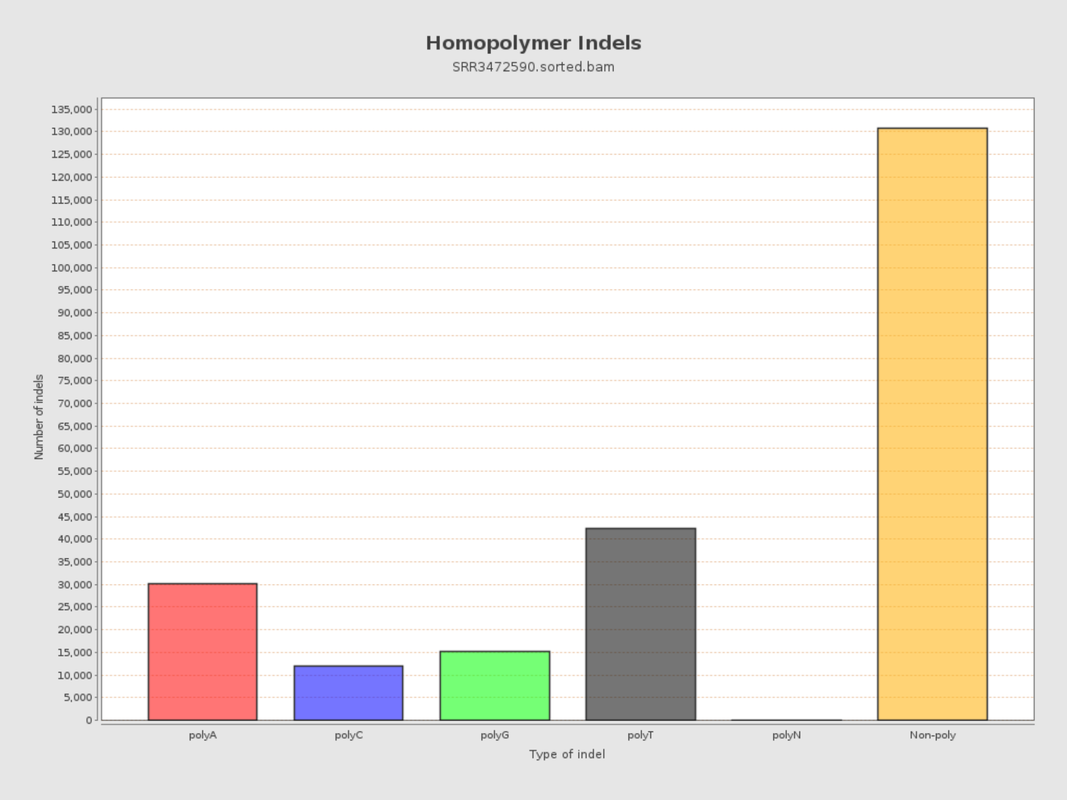
9. Results : Mapped Reads GC-content Distribution



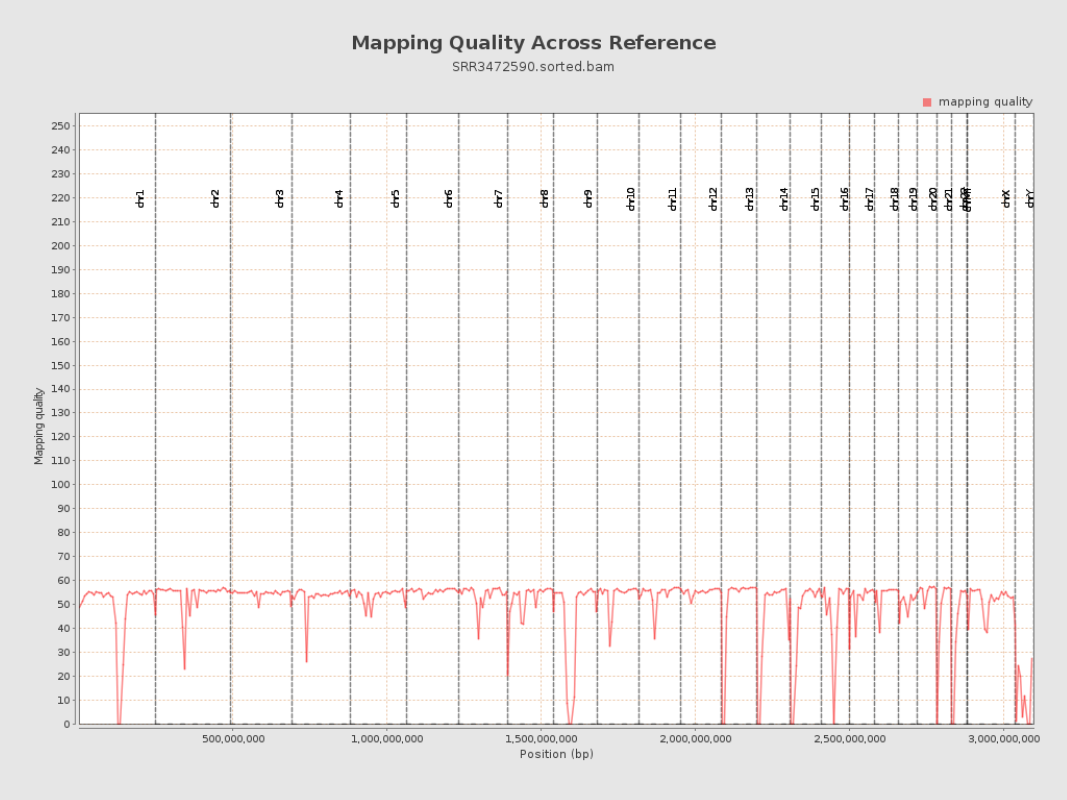
10. Results : Mapped Reads Clipping Profile



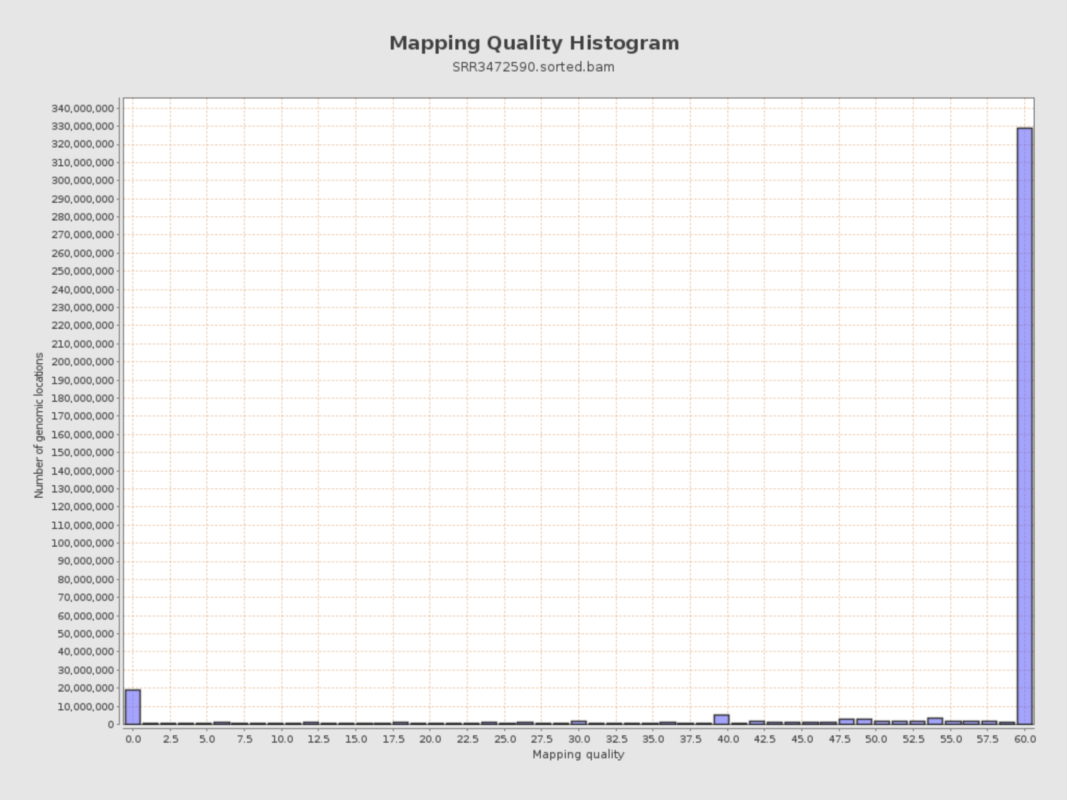
11. Results : Homopolymer Indels



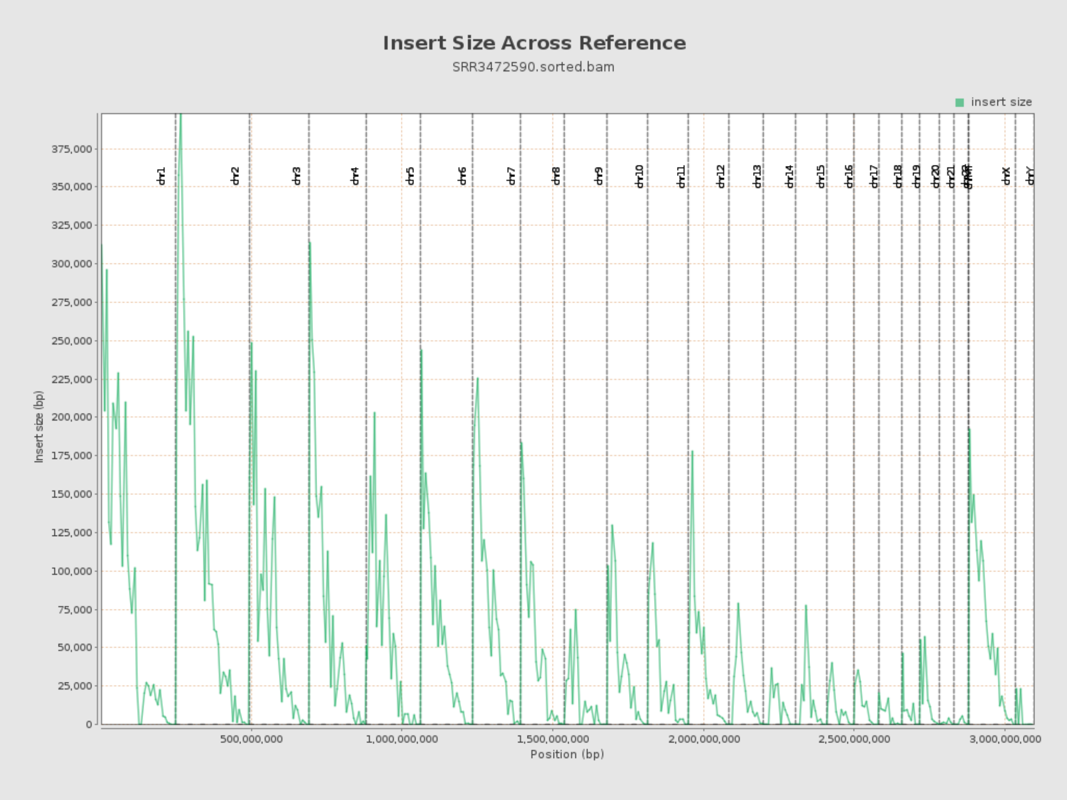
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram