Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:51:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472468.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_SRR3472468 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472468_1.fastq.gz SRR3472468_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:51:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472468.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,282,660
Mapped reads	12,123,012 / 98.7%
Unmapped reads	159,648 / 1.3%
Mapped paired reads	12,123,012 / 98.7%
Mapped reads, first in pair	6,096,183 / 49.63%
Mapped reads, second in pair	6,026,829 / 49.07%
Mapped reads, both in pair	12,038,654 / 98.01%
Mapped reads, singletons	84,358 / 0.69%
Secondary alignments	0
Supplementary alignments	40,743 / 0.33%
Read min/max/mean length	30 / 100 / 98.9
Duplicated reads (estimated)	6,476,046 / 52.73%
Duplication rate	44.15%
Clipped reads	861,254 / 7.01%

2.2. ACGT Content

Number/percentage of A's	320,382,820 / 27.06%
Number/percentage of C's	271,631,308 / 22.94%
Number/percentage of T's	322,419,235 / 27.23%
Number/percentage of G's	269,358,691 / 22.75%
Number/percentage of N's	159,368 / 0.01%

GC Percentage	45.69%

2.3. Coverage

Mean	0.3825
Standard Deviation	9.9676

2.4. Mapping Quality

Mean Mapping Quality	55.13

2.5. Insert size

Mean	18,171.32
Standard Deviation	1,342,024.46
P25/Median/P75	145 / 202 / 272

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	5,276,120
Insertions	74,096
Mapped reads with at least one insertion	0.6%
Deletions	56,887
Mapped reads with at least one deletion	0.46%
Homopolymer indels	45.6%

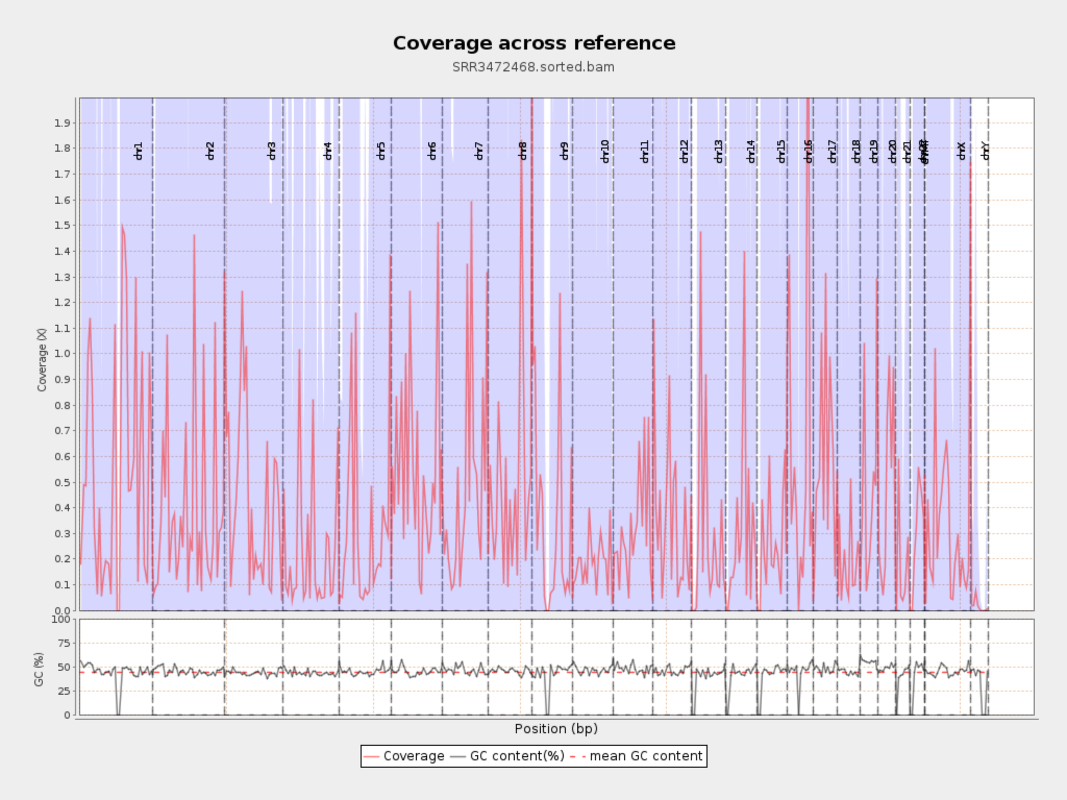
2.7. Chromosome stats

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

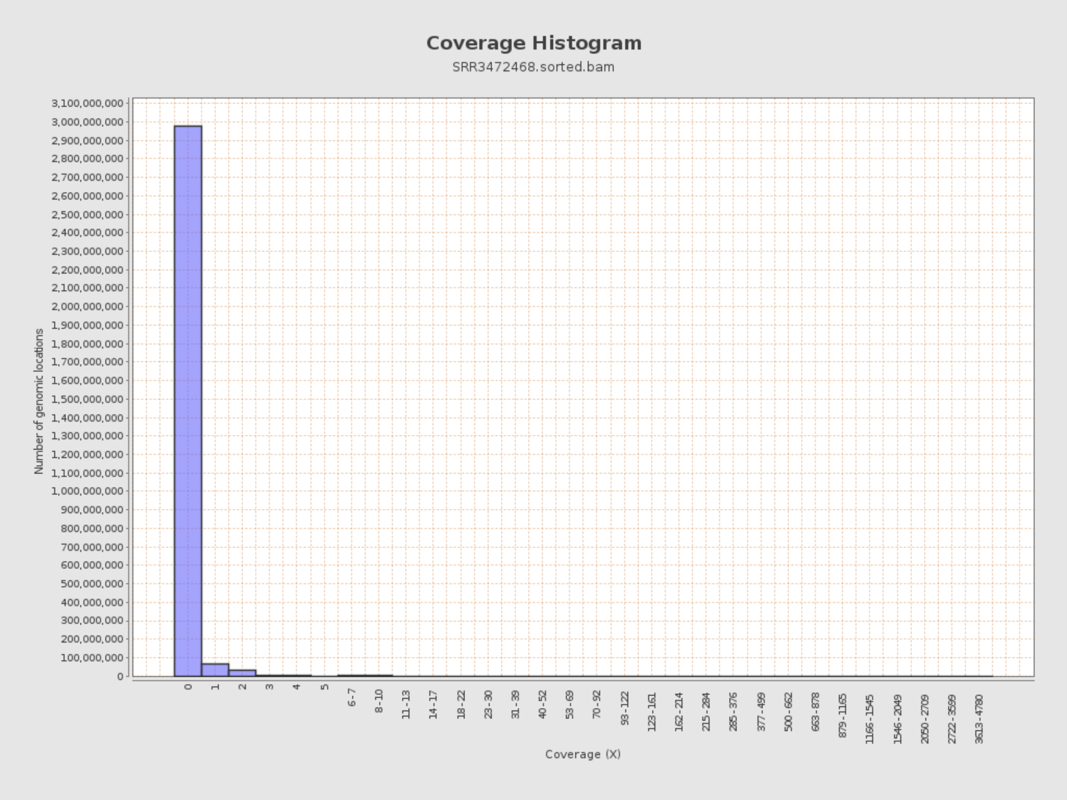
		bases	coverage	deviation
chr1	249250621	140327881	0.563	13.5376
chr2	243199373	92144486	0.3789	10.1246
chr3	198022430	88519523	0.447	8.7581
chr4	191154276	43220004	0.2261	7.9913
chr5	180915260	60054218	0.3319	9.8864
chr6	171115067	92599336	0.5412	10.5062
chr7	159138663	79770977	0.5013	13.5408
chr8	146364022	72585885	0.4959	11.3061
chr9	141213431	52263282	0.3701	9.8399
chr10	135534747	25299453	0.1867	5.0057
chr11	135006516	43048310	0.3189	8.7112
chr12	133851895	49080050	0.3667	7.7014
chr13	115169878	34138680	0.2964	8.9483
chr14	107349540	31338896	0.2919	8.9494
chr15	102531392	26478134	0.2582	6.9938
chr16	90354753	60044928	0.6645	16.5602
chr17	81195210	48165476	0.5932	12.3208
chr18	78077248	15066255	0.193	5.6926
chr19	59128983	26533130	0.4487	8.6695
chr20	63025520	30080842	0.4773	11.2026
chr21	48129895	8490100	0.1764	9.5867
chr22	51304566	14859136	0.2896	7.5666
chrMT	16571	8777	0.5297	1.0563
chrX	155270560	48913283	0.315	6.987

chrY	59373566	1060392	0.0179	0.7211

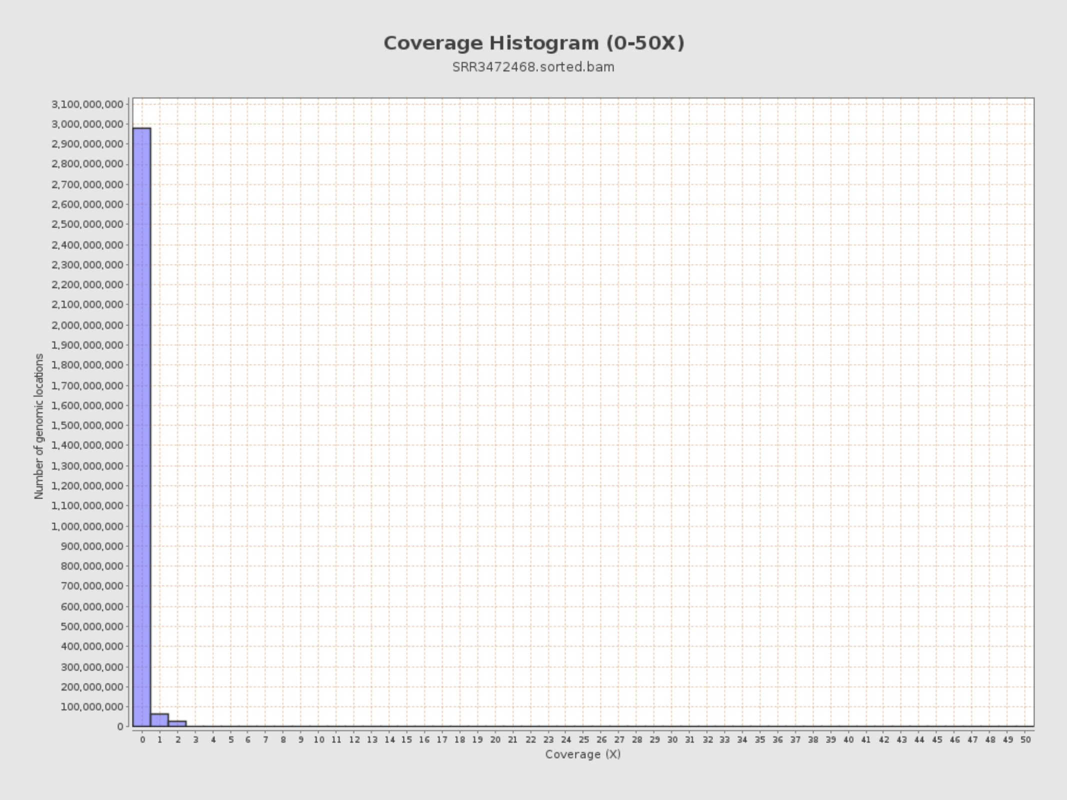
3. Results : Coverage across reference



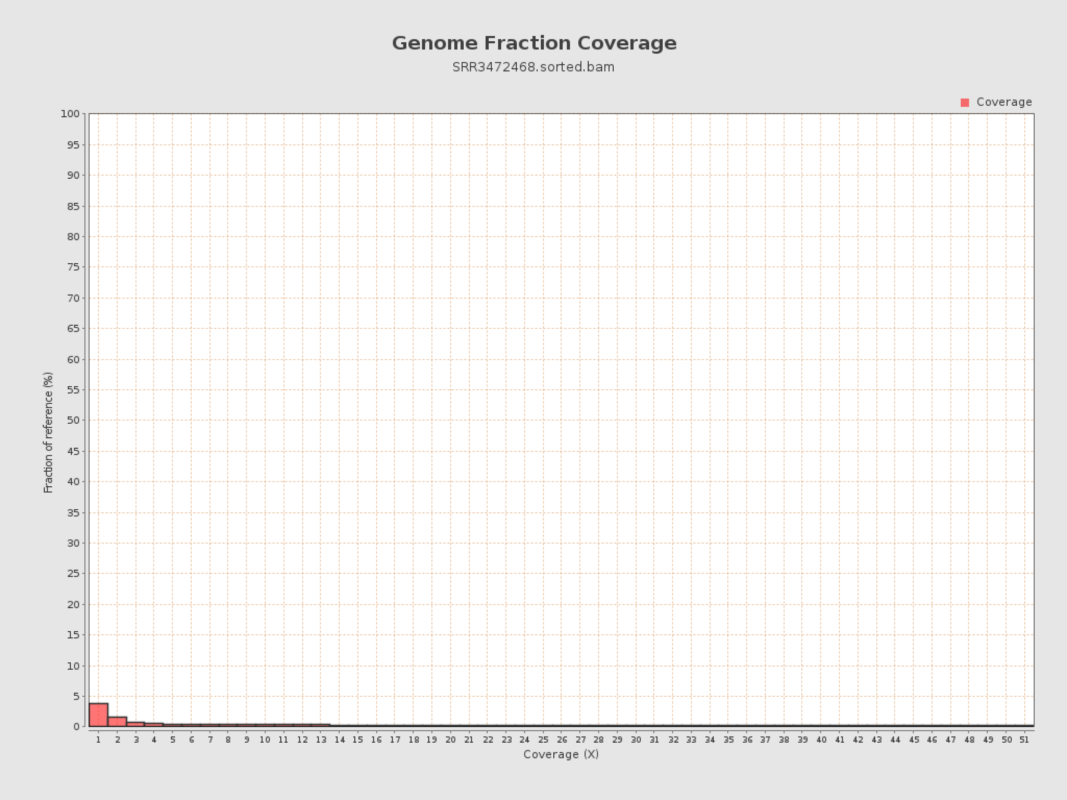
4. Results : Coverage Histogram



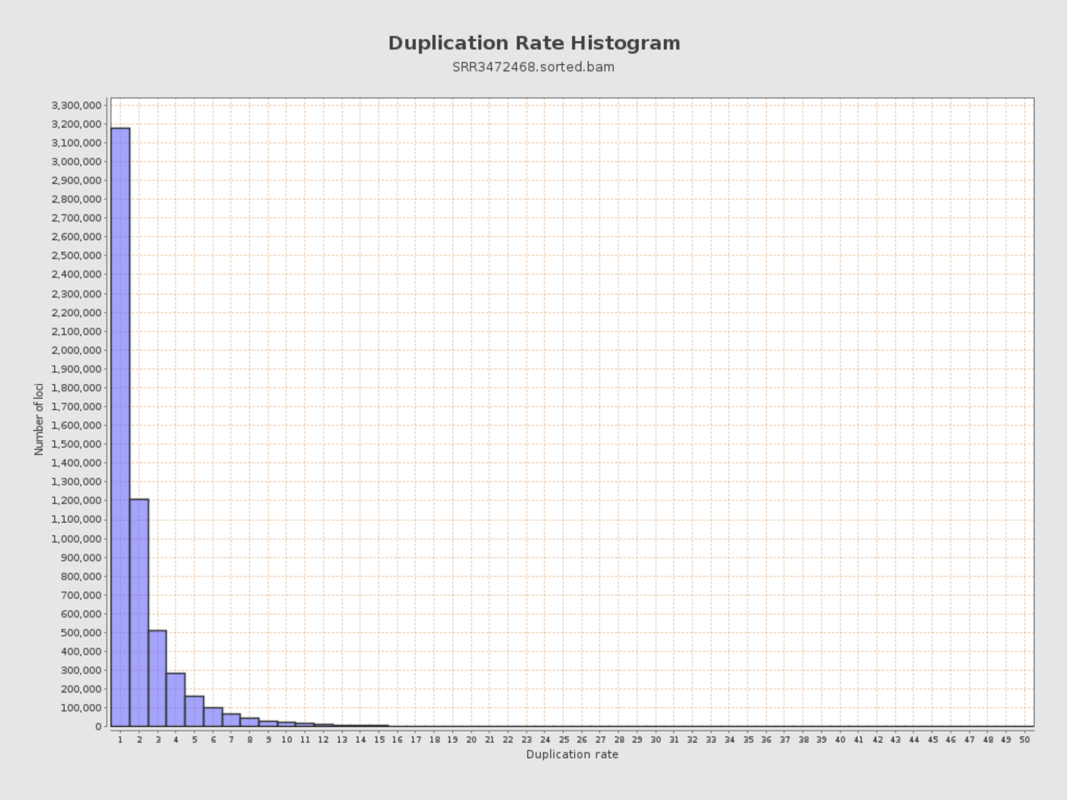
5. Results : Coverage Histogram (0-50X)



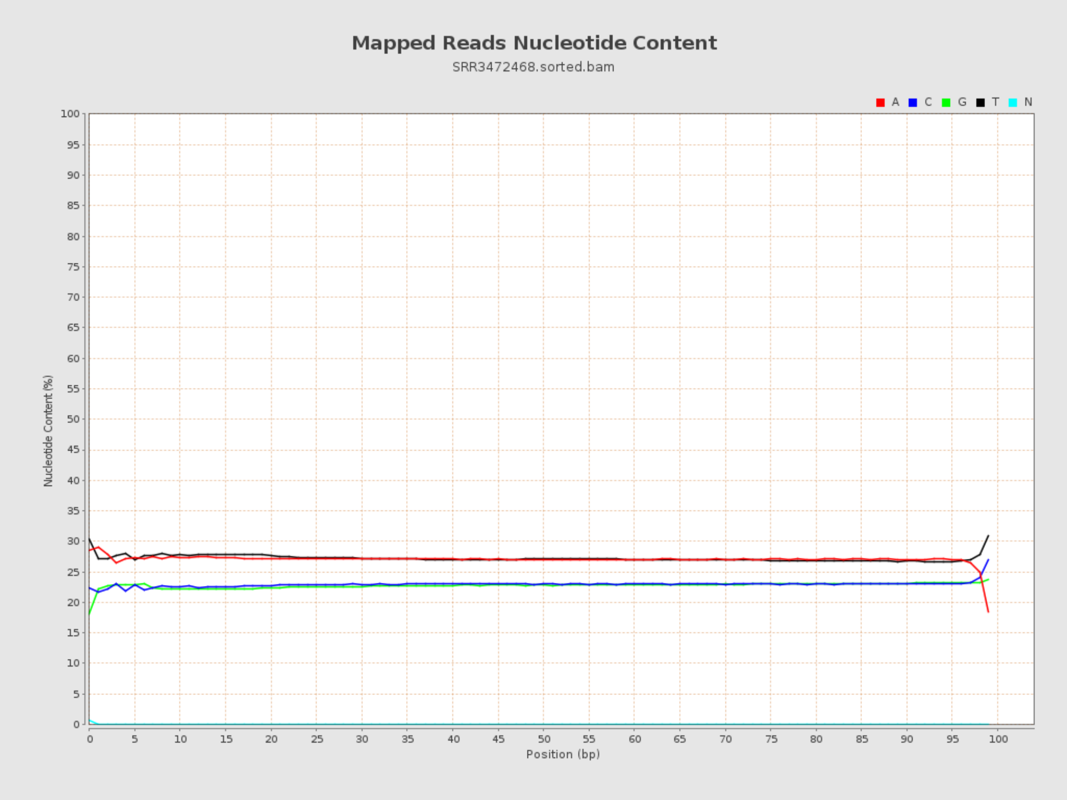
6. Results : Genome Fraction Coverage



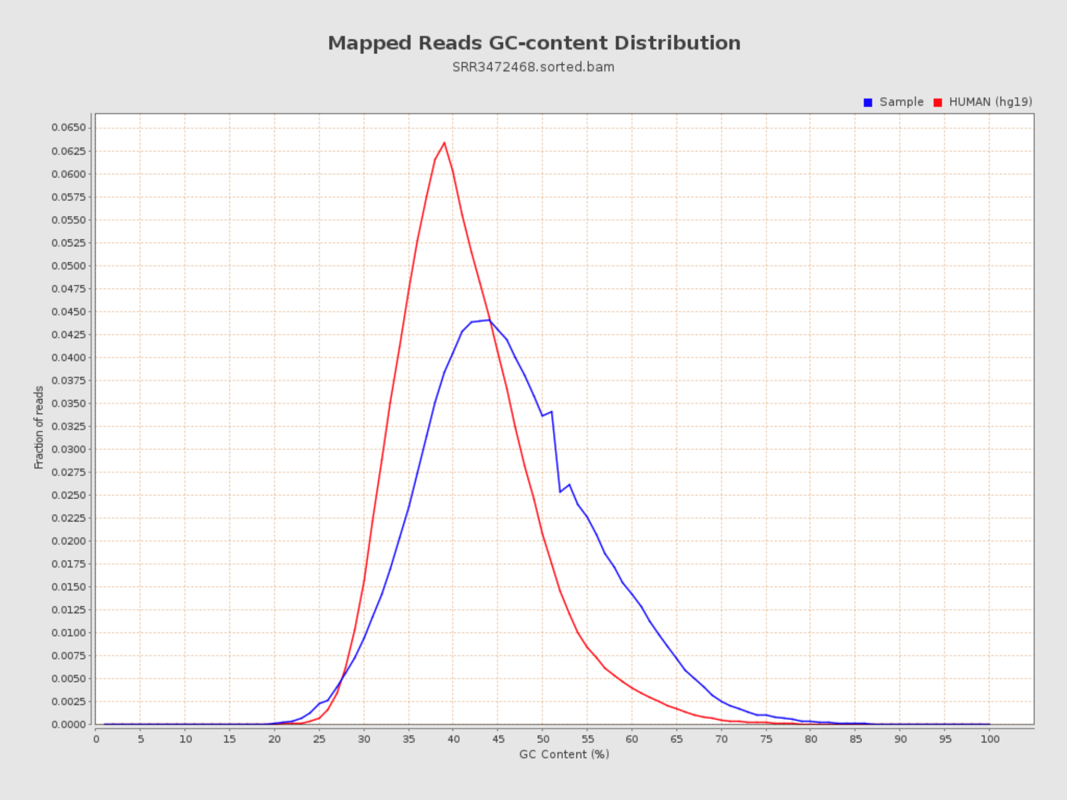
7. Results : Duplication Rate Histogram



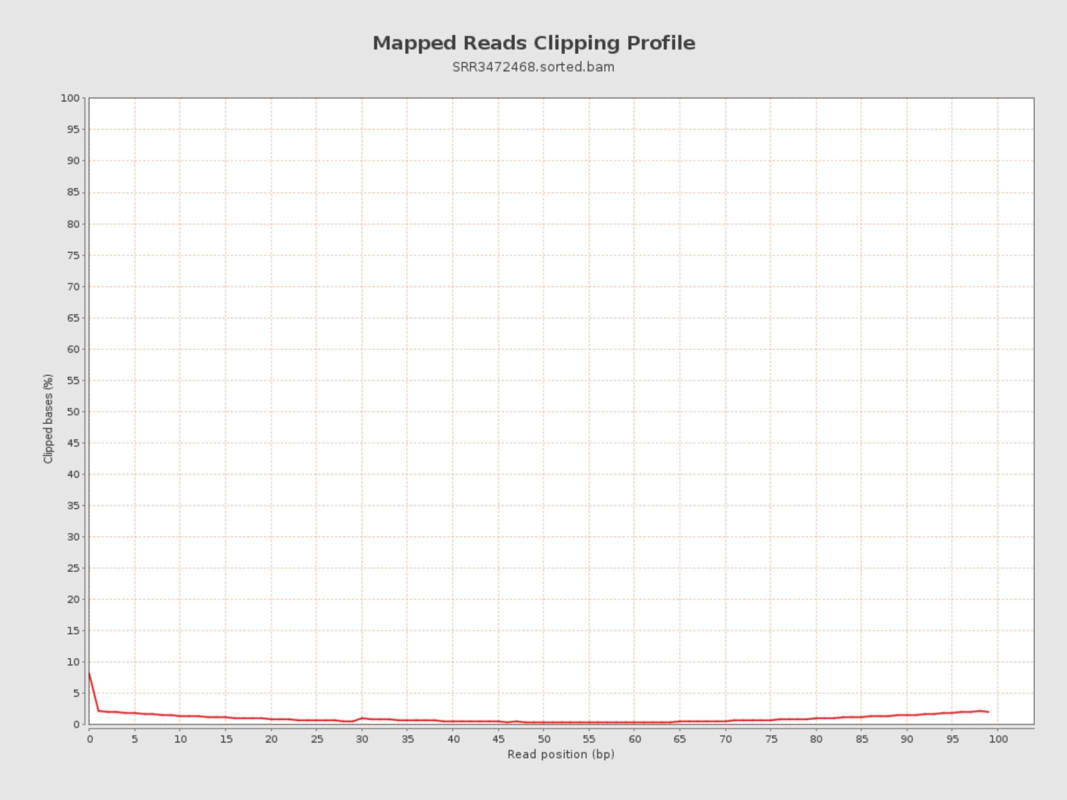
8. Results : Mapped Reads Nucleotide Content



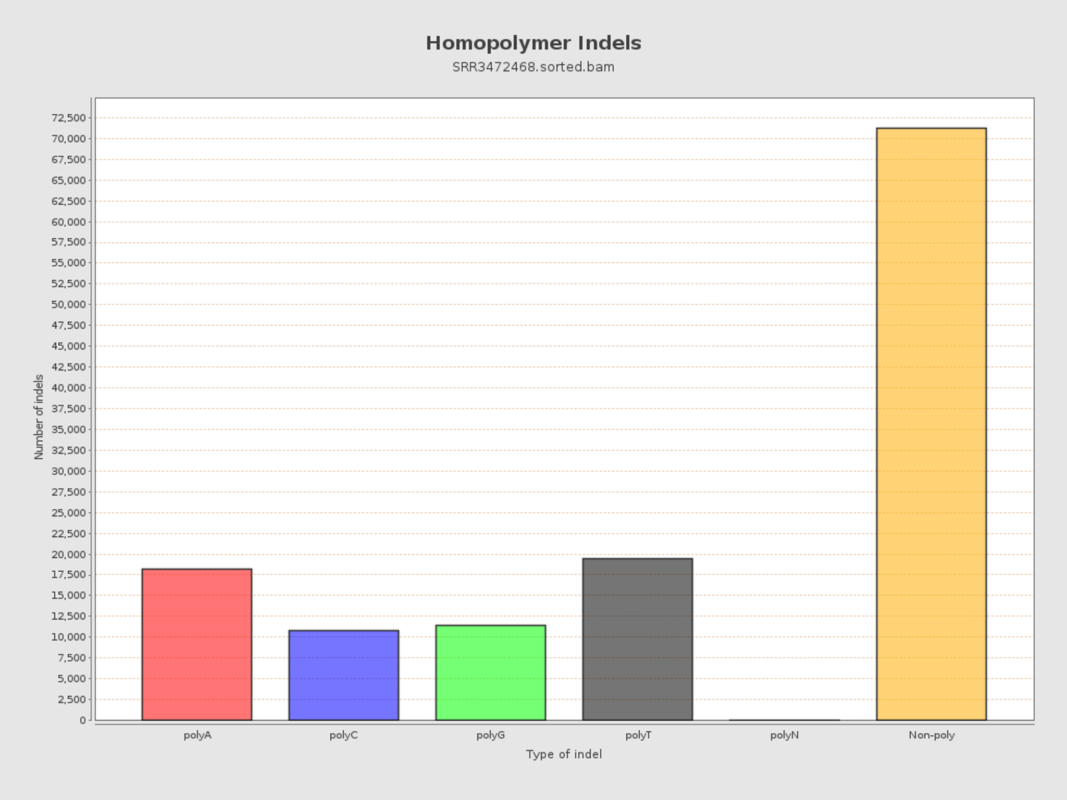
9. Results : Mapped Reads GC-content Distribution



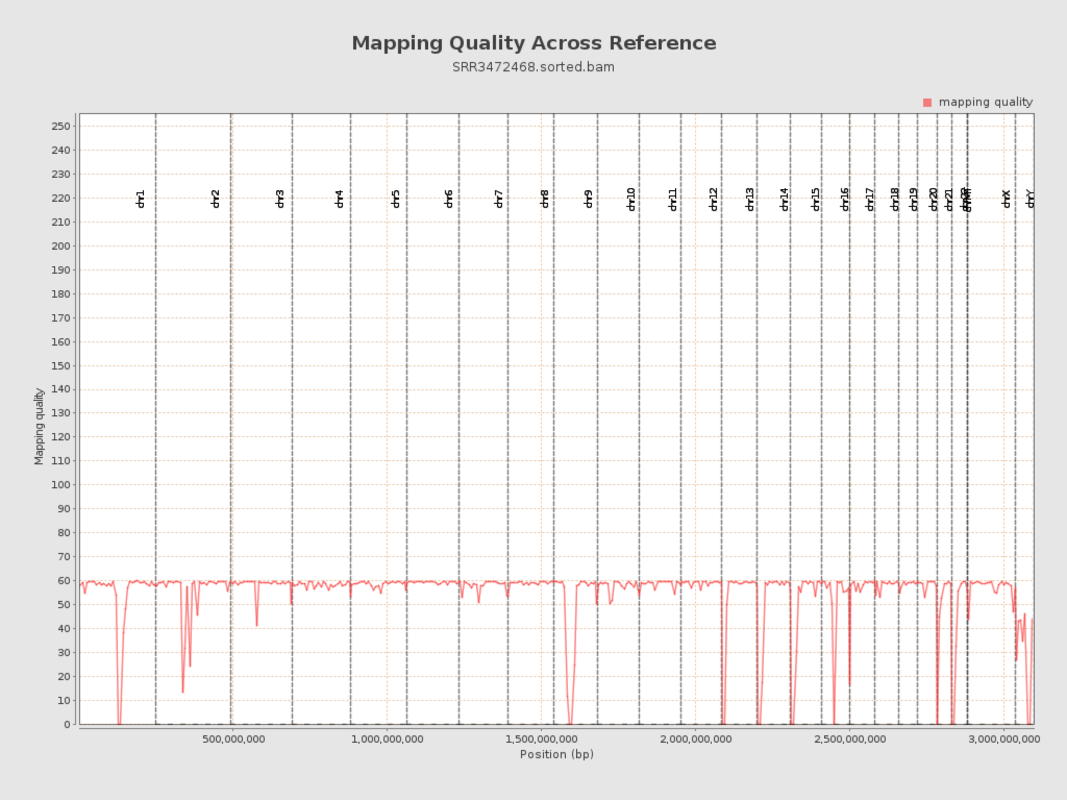
10. Results : Mapped Reads Clipping Profile



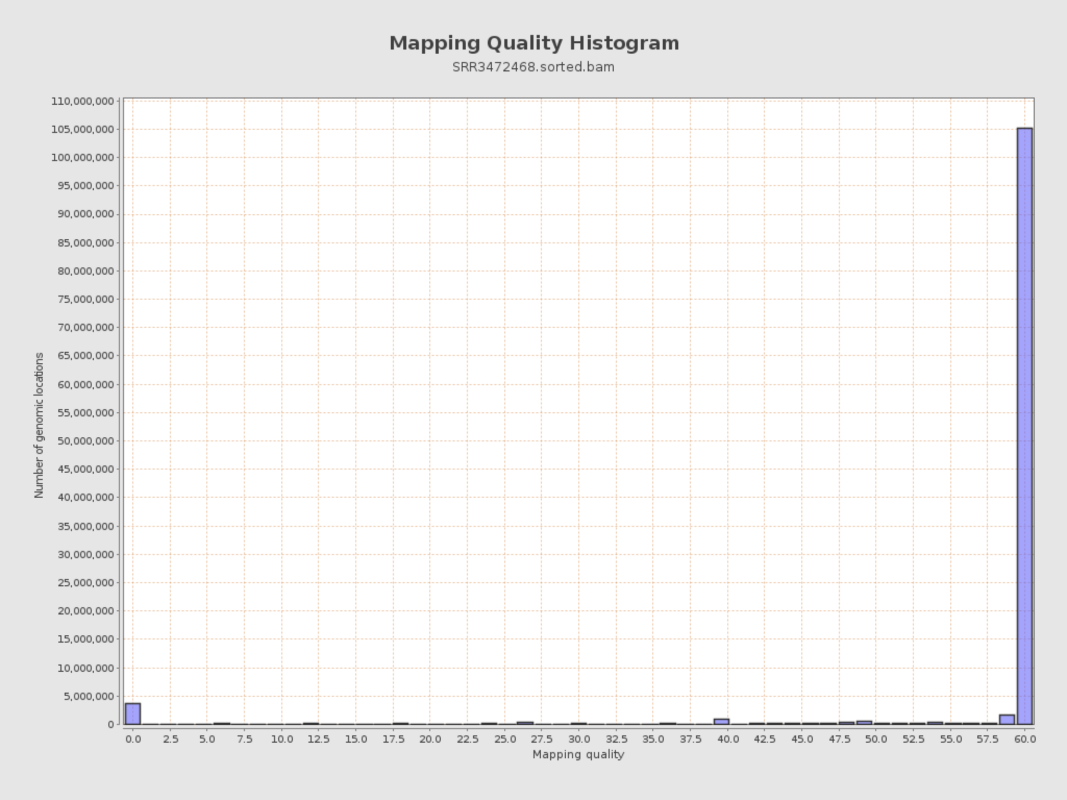
11. Results : Homopolymer Indels



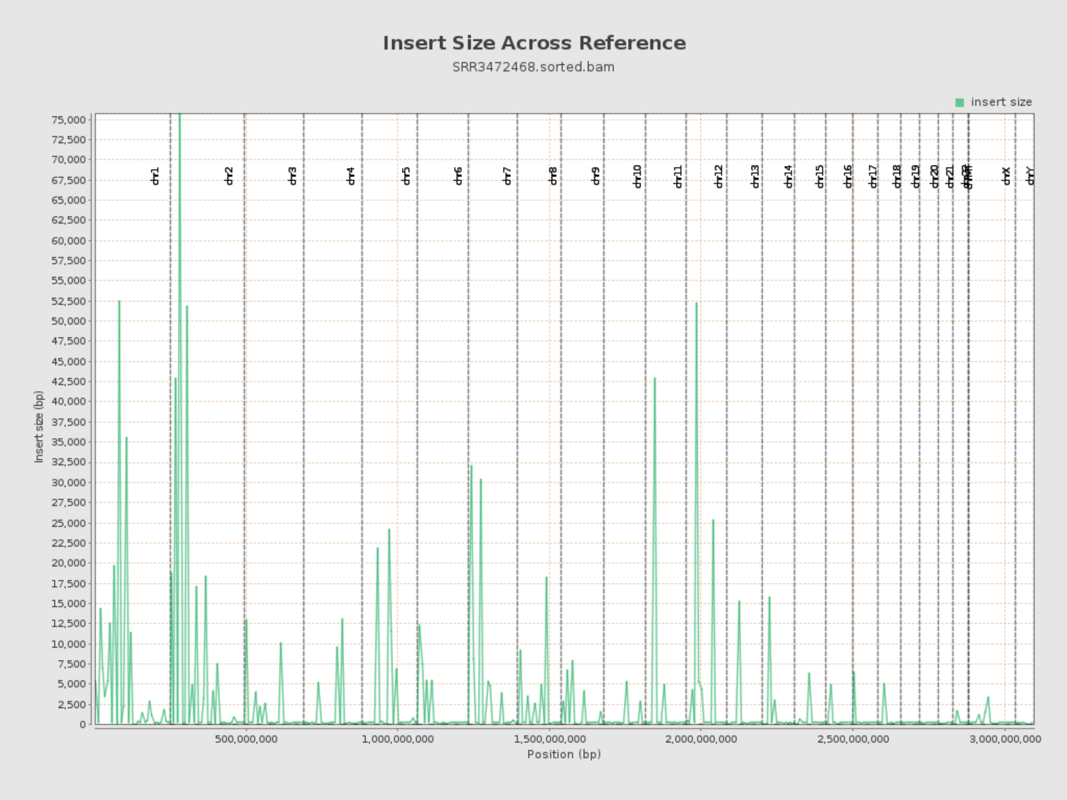
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram