Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 08:06:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472685.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_SRR3472685 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472685_1.fastq.gz SRR3472685_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 08:06:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472685.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,254,314
Mapped reads	16,123,868 / 99.2%
Unmapped reads	130,446 / 0.8%
Mapped paired reads	16,123,868 / 99.2%
Mapped reads, first in pair	8,082,246 / 49.72%
Mapped reads, second in pair	8,041,622 / 49.47%
Mapped reads, both in pair	16,039,030 / 98.68%
Mapped reads, singletons	84,838 / 0.52%
Secondary alignments	0
Supplementary alignments	102,804 / 0.63%
Read min/max/mean length	30 / 101 / 99.74
Duplicated reads (estimated)	11,277,280 / 69.38%
Duplication rate	47.47%
Clipped reads	1,191,468 / 7.33%

2.2. ACGT Content

Number/percentage of A's	437,868,576 / 27.62%
Number/percentage of C's	356,356,568 / 22.48%
Number/percentage of T's	438,664,576 / 27.67%
Number/percentage of G's	352,098,069 / 22.21%
Number/percentage of N's	300,560 / 0.02%

GC Percentage	44.69%

2.3. Coverage

Mean	0.5122
Standard Deviation	30.4207

2.4. Mapping Quality

Mean Mapping Quality	54.74

2.5. Insert size

Mean	22,704.27
Standard Deviation	1,447,854.05
P25/Median/P75	150 / 206 / 277

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	9,534,493
Insertions	96,063
Mapped reads with at least one insertion	0.59%
Deletions	91,628
Mapped reads with at least one deletion	0.56%
Homopolymer indels	46.9%

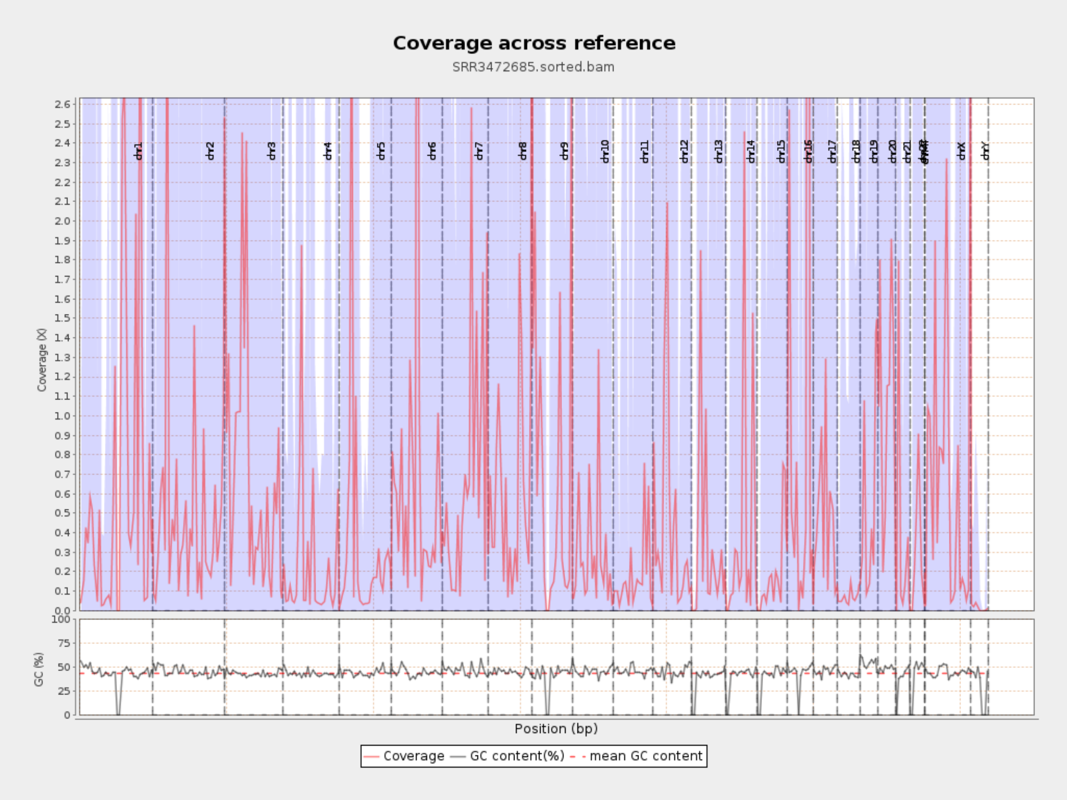
2.7. Chromosome stats

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

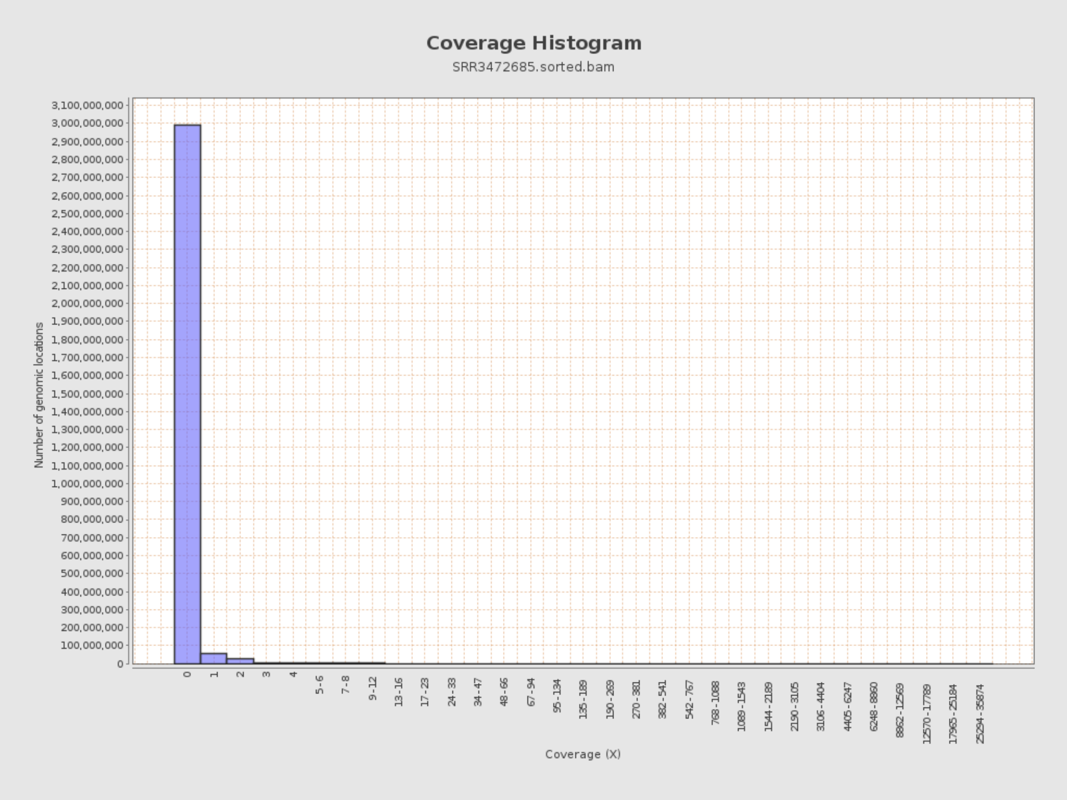
		bases	**coverage**	**deviation**
chr1	249250621	166333236	0.6673	56.2412
chr2	243199373	122596655	0.5041	25.8242
chr3	198022430	142761361	0.7209	21.1815
chr4	191154276	44695334	0.2338	21.0078
chr5	180915260	63572662	0.3514	27.8442
chr6	171115067	124239221	0.7261	38.3765
chr7	159138663	113224773	0.7115	34.3371
chr8	146364022	88492540	0.6046	28.4451
chr9	141213431	103190532	0.7307	37.725
chr10	135534747	40107983	0.2959	24.7691
chr11	135006516	24489948	0.1814	10.3207
chr12	133851895	59170160	0.4421	18.2309
chr13	115169878	40168826	0.3488	13.2136
chr14	107349540	42449511	0.3954	18.456
chr15	102531392	20328426	0.1983	11.8791
chr16	90354753	109760112	1.2148	60.314
chr17	81195210	39081510	0.4813	20.1715
chr18	78077248	5445323	0.0697	2.5638
chr19	59128983	31784389	0.5375	16.2444
chr20	63025520	69192371	1.0978	40.1226
chr21	48129895	18927653	0.3933	35.811
chr22	51304566	14410529	0.2809	12.0677
chrMT	16571	3247	0.1959	0.5961
chrX	155270560	100220683	0.6455	22.6759

chrY	59373566	865263	0.0146	0.5021

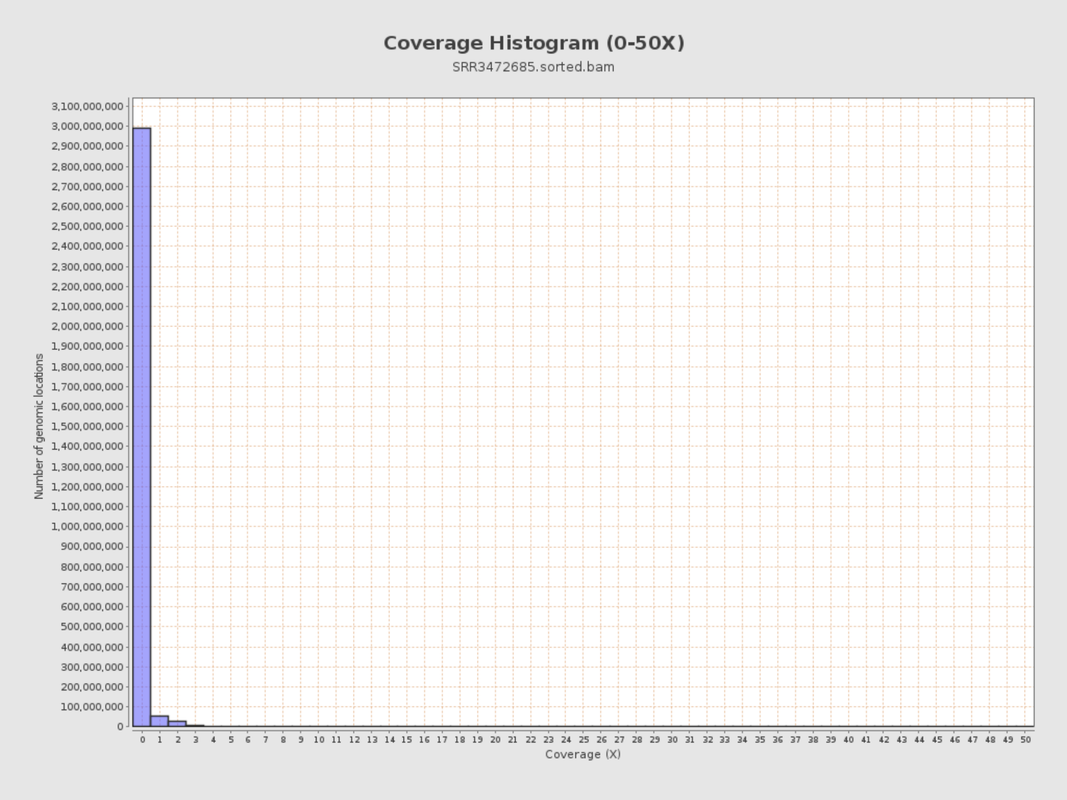
3. Results : Coverage across reference



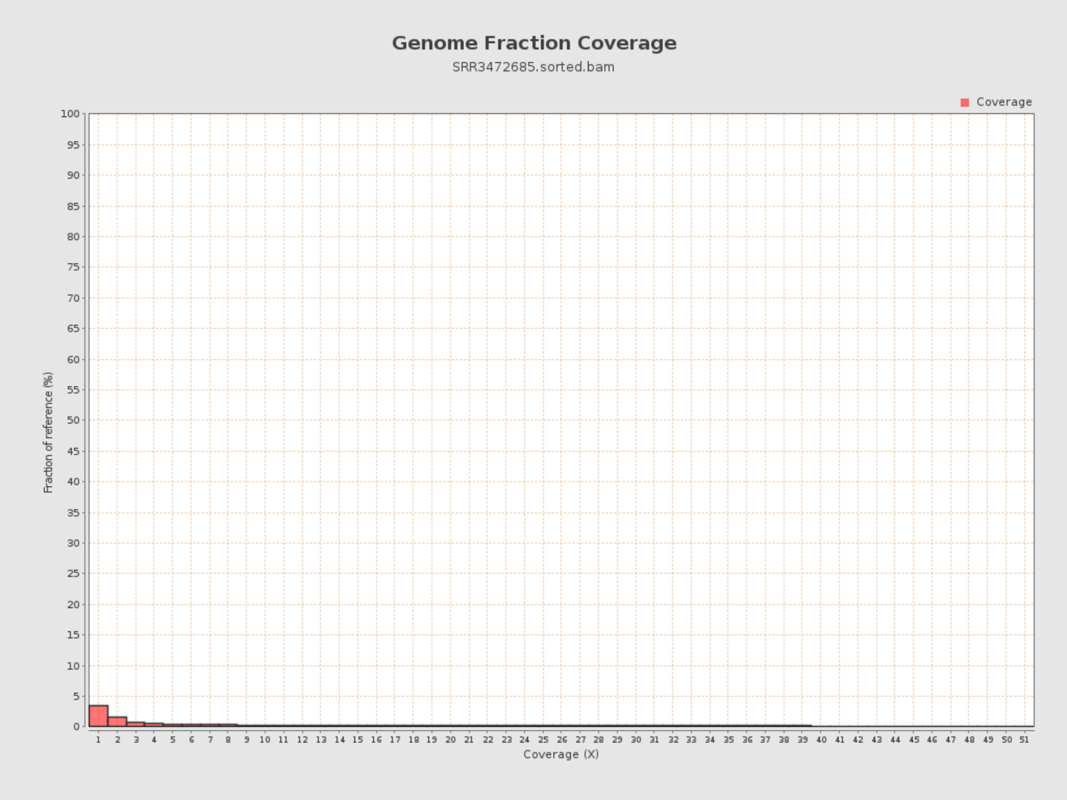
4. Results : Coverage Histogram



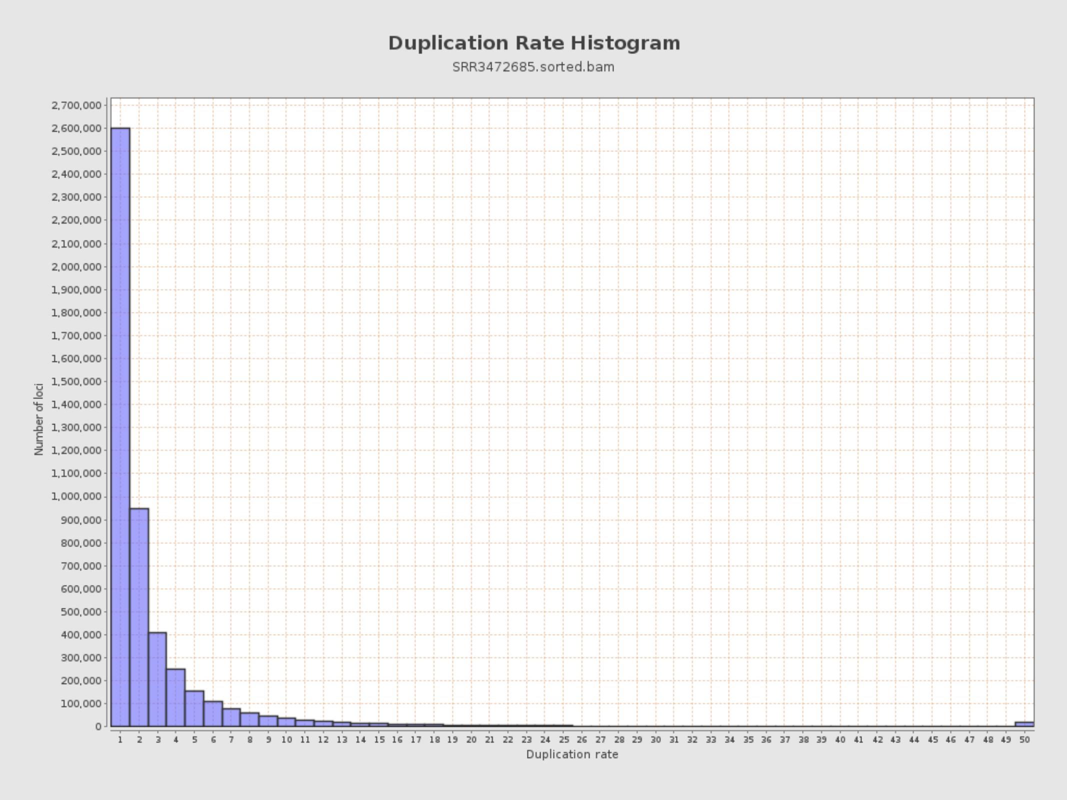
5. Results : Coverage Histogram (0-50X)



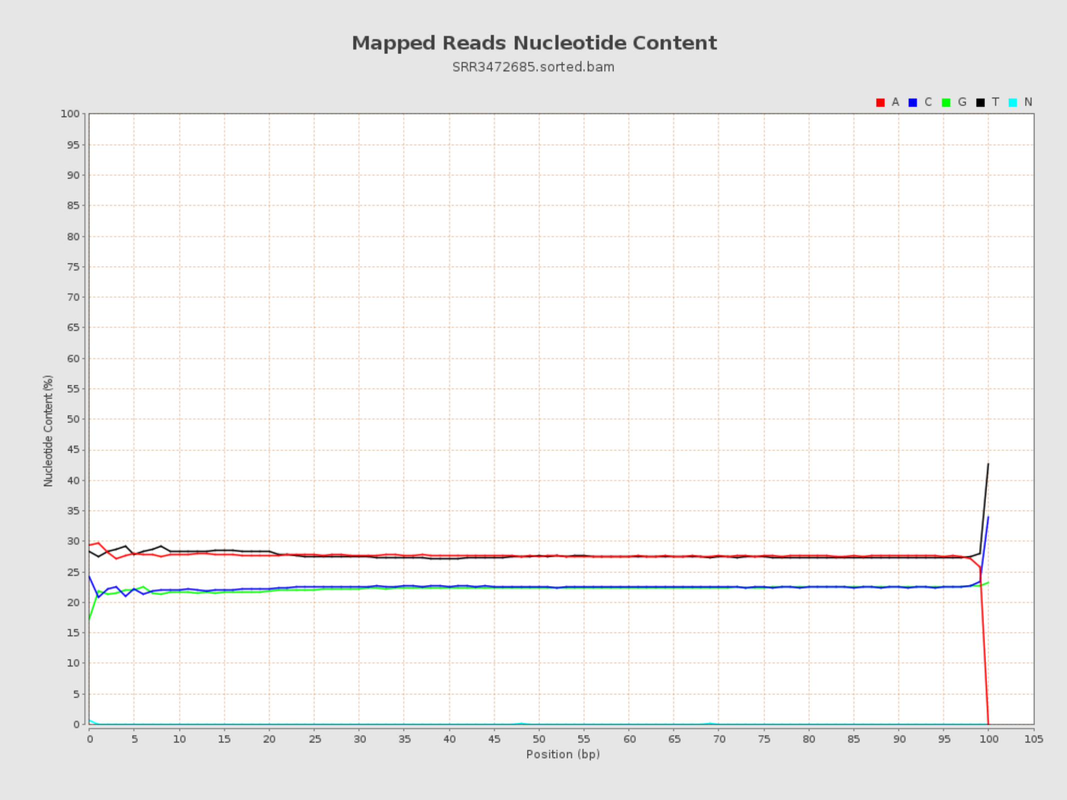
6. Results : Genome Fraction Coverage



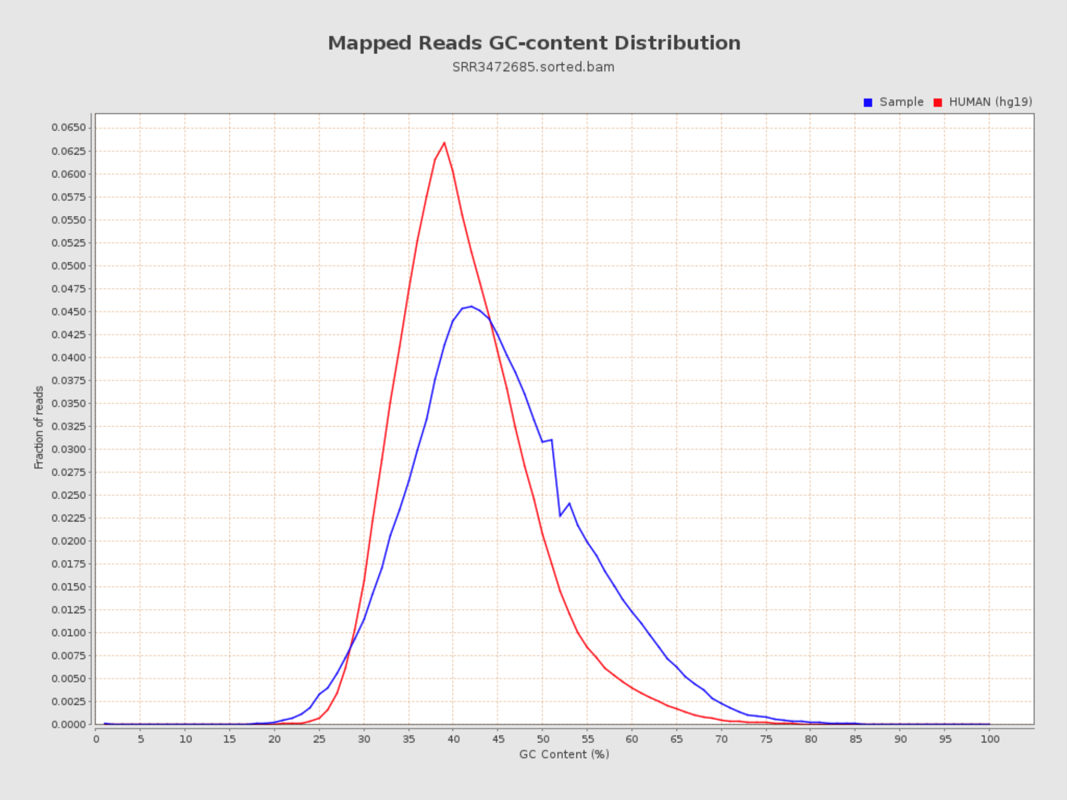
7. Results : Duplication Rate Histogram



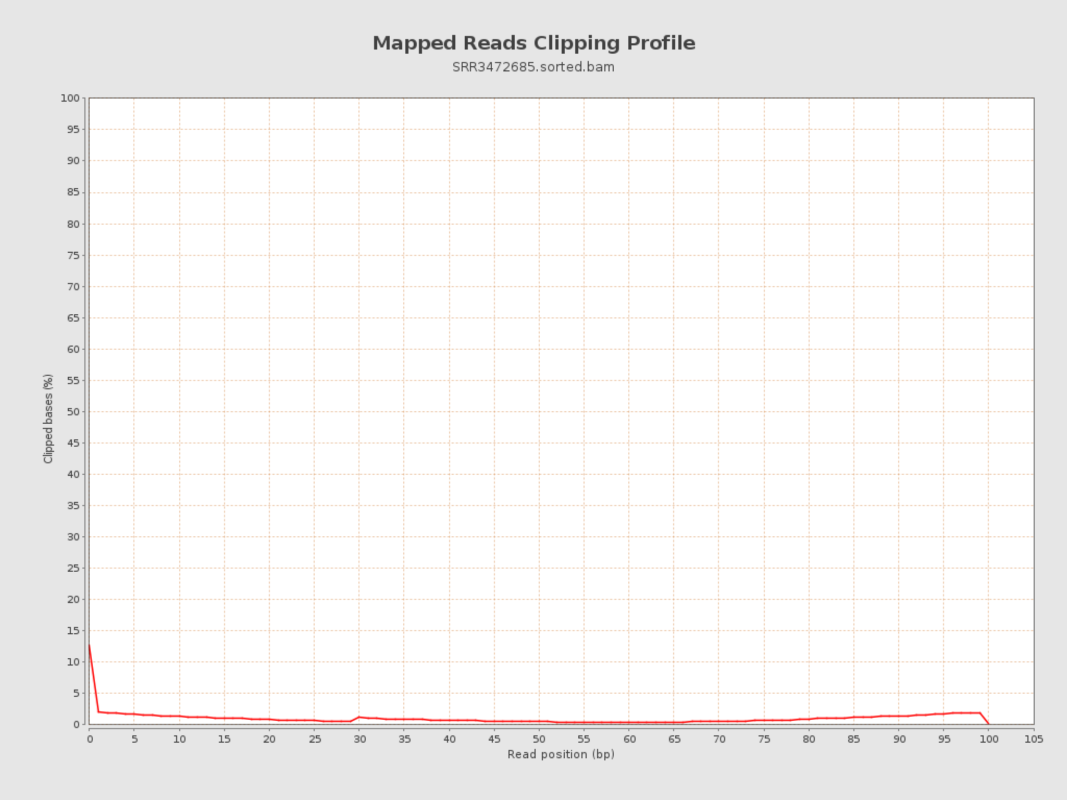
8. Results : Mapped Reads Nucleotide Content



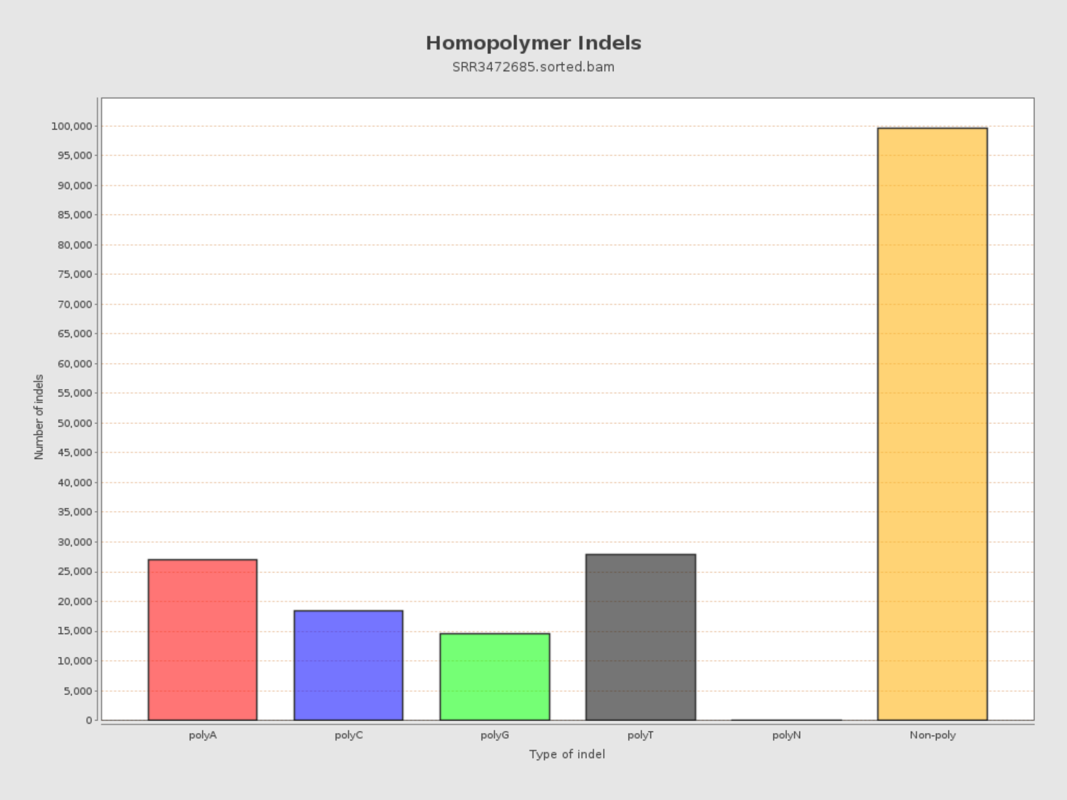
9. Results : Mapped Reads GC-content Distribution



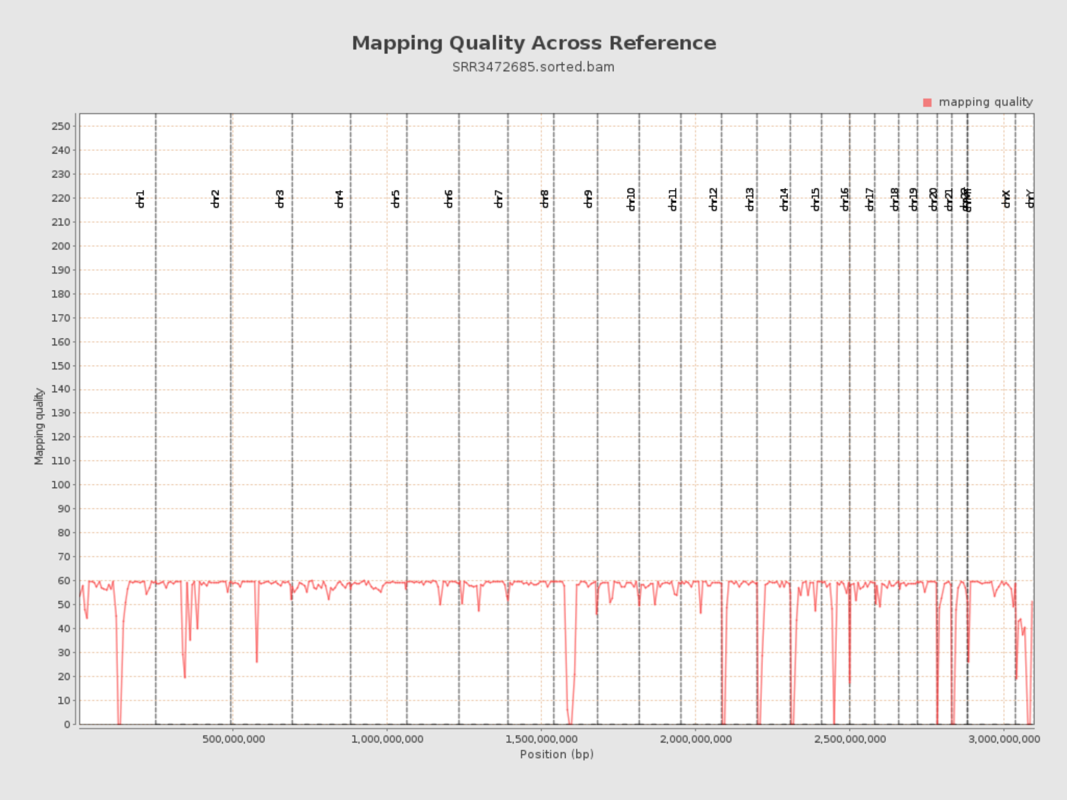
10. Results : Mapped Reads Clipping Profile



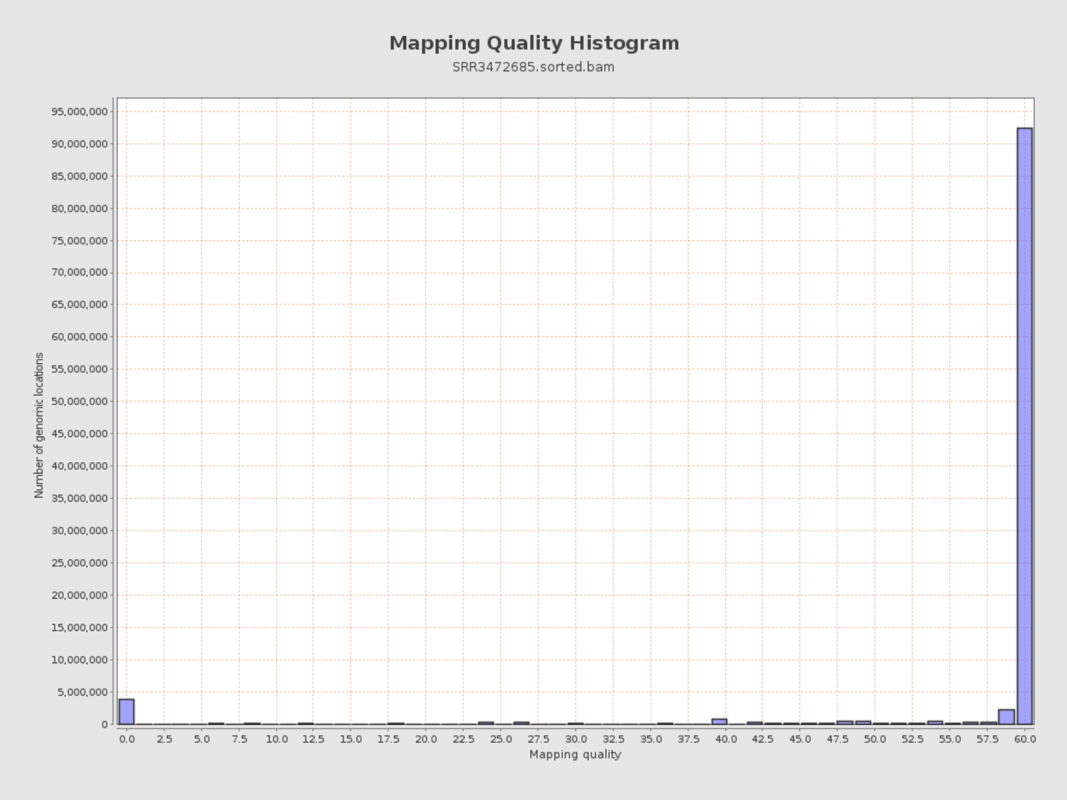
11. Results : Homopolymer Indels



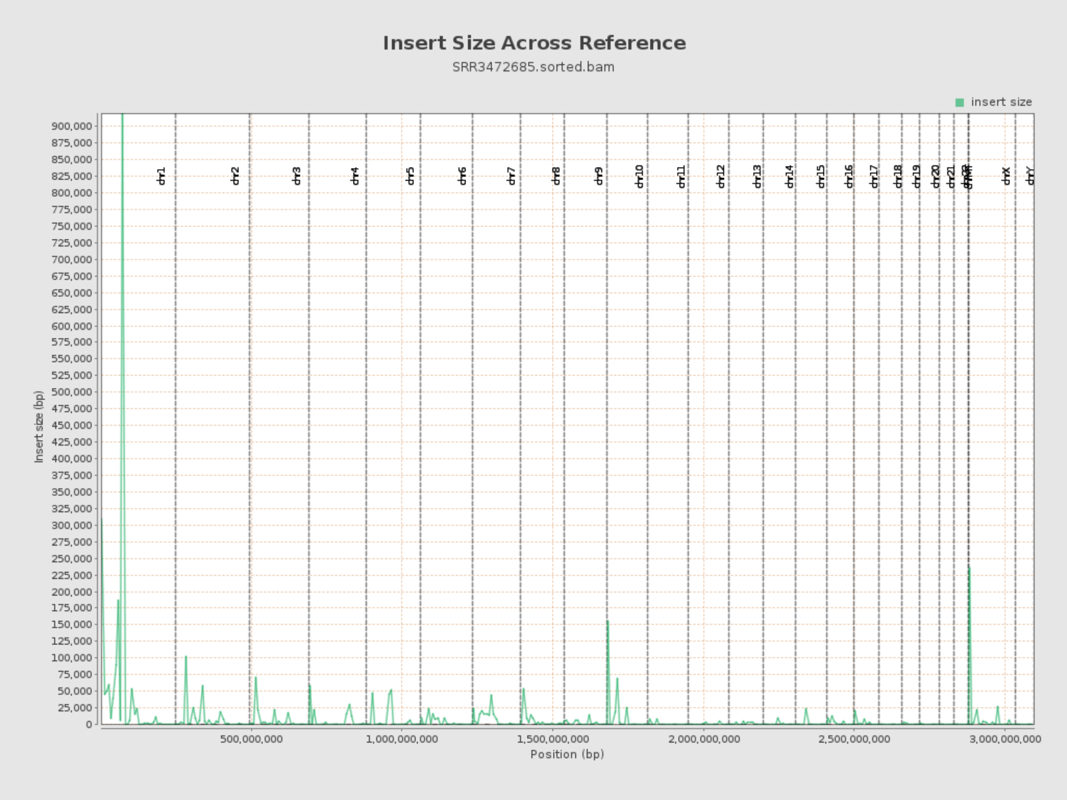
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



Insert Size Across Reference

SRR3472685.sorted.bam

15. Results : Insert Size Histogram