Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 05:02:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472748.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_SRR3472748 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472748_1.fastq.gz SRR3472748_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 05:02:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472748.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,567,986
Mapped reads	10,437,460 / 98.76%
Unmapped reads	130,526 / 1.24%
Mapped paired reads	10,437,460 / 98.76%
Mapped reads, first in pair	5,242,321 / 49.61%
Mapped reads, second in pair	5,195,139 / 49.16%
Mapped reads, both in pair	10,363,112 / 98.06%
Mapped reads, singletons	74,348 / 0.7%
Secondary alignments	0
Supplementary alignments	37,109 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	6,027,464 / 57.04%
Duplication rate	44.54%
Clipped reads	861,197 / 8.15%

2.2. ACGT Content

Number/percentage of A's	287,349,468 / 27.98%
Number/percentage of C's	227,851,069 / 22.18%
Number/percentage of T's	284,708,458 / 27.72%
Number/percentage of G's	226,959,125 / 22.1%
Number/percentage of N's	196,811 / 0.02%

GC Percentage	44.28%

2.3. Coverage

Mean	0.3318
Standard Deviation	12.2434

2.4. Mapping Quality

Mean Mapping Quality	55.26

2.5. Insert size

Mean	28,123.82
Standard Deviation	1,625,563.32
P25/Median/P75	178 / 254 / 346

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	6,644,339
Insertions	59,157
Mapped reads with at least one insertion	0.56%
Deletions	57,433
Mapped reads with at least one deletion	0.54%
Homopolymer indels	45.91%

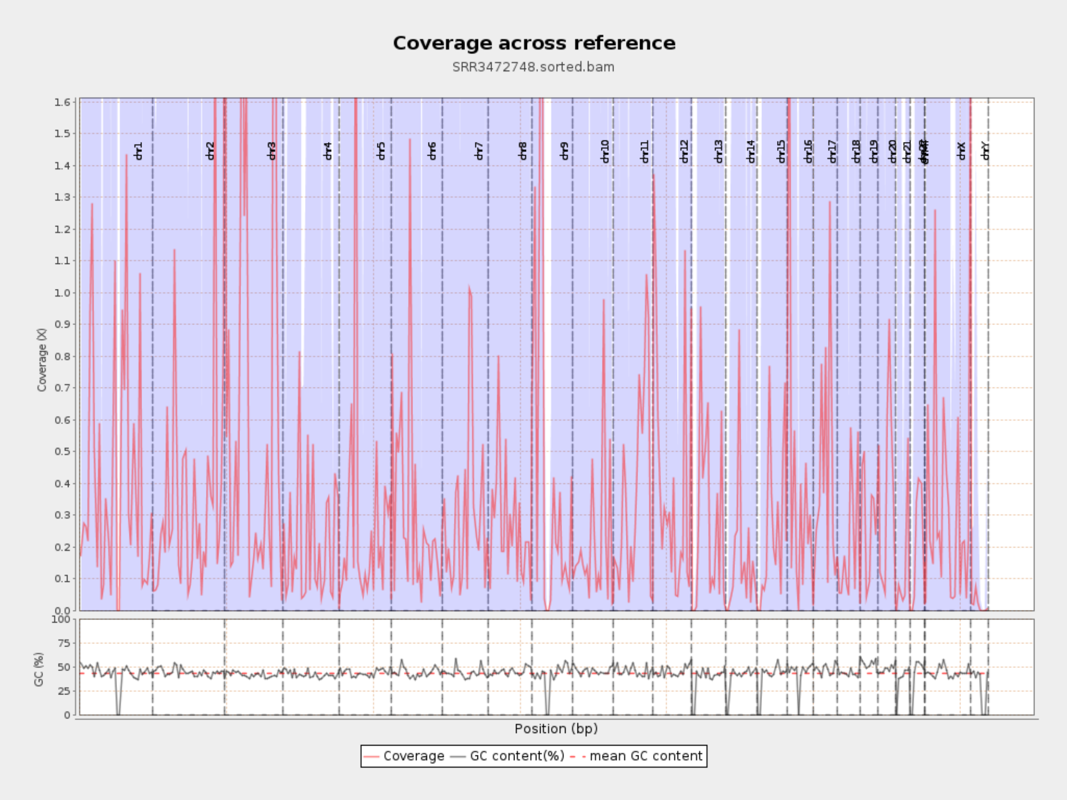
2.7. Chromosome stats

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

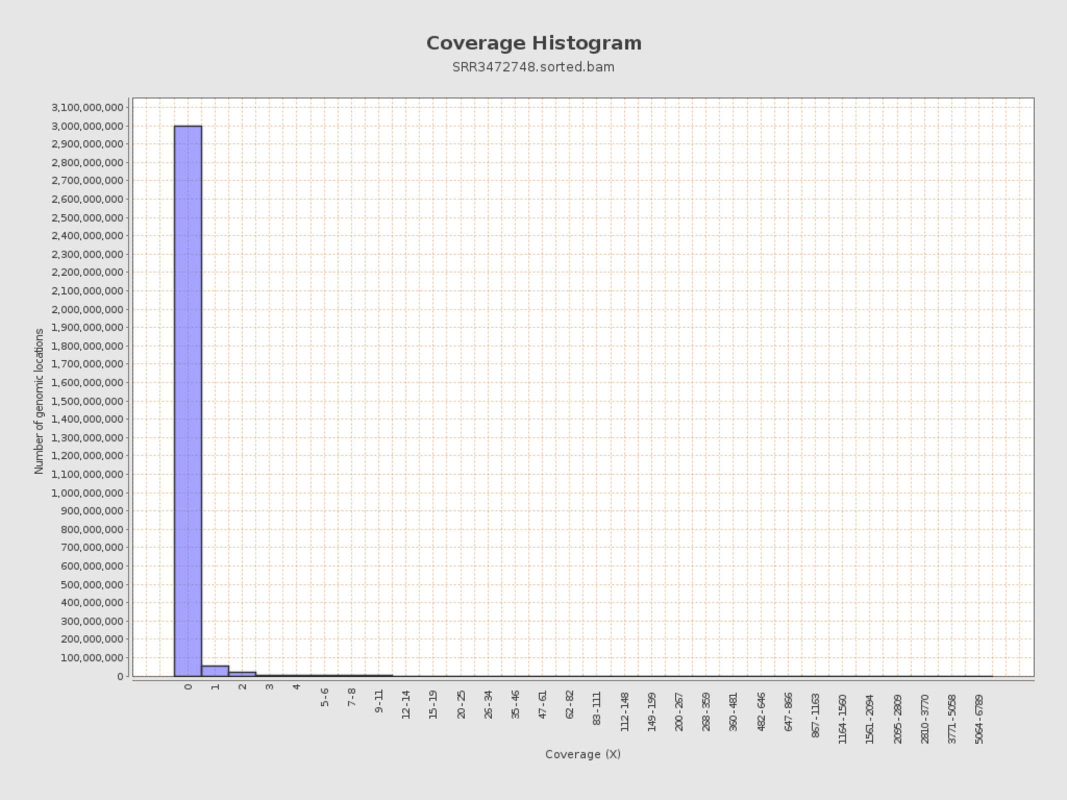
		bases	coverage	deviation
chr1	249250621	103072663	0.4135	14.8405
chr2	243199373	85224008	0.3504	17.1411
chr3	198022430	133488674	0.6741	16.6535
chr4	191154276	40527102	0.212	8.4391
chr5	180915260	53675601	0.2967	9.2993
chr6	171115067	51277430	0.2997	8.5088
chr7	159138663	49355835	0.3101	10.6303
chr8	146364022	38816185	0.2652	8.6043
chr9	141213431	63094791	0.4468	17.5984
chr10	135534747	28994161	0.2139	8.5734
chr11	135006516	50901051	0.377	14.4696
chr12	133851895	54880549	0.41	15.7668
chr13	115169878	32536195	0.2825	12.3304
chr14	107349540	17579430	0.1638	7.1315
chr15	102531392	26437263	0.2578	10.3517
chr16	90354753	38138481	0.4221	12.9643
chr17	81195210	34515820	0.4251	9.7003
chr18	78077248	16712573	0.2141	8.9889
chr19	59128983	16543008	0.2798	7.194
chr20	63025520	24324533	0.3859	10.8404
chr21	48129895	6252379	0.1299	6.3156
chr22	51304566	10473397	0.2041	5.7774
chrMT	16571	2547	0.1537	0.5467
chrX	155270560	49288631	0.3174	11.296

chrY	59373566	1092882	0.0184	0.5622

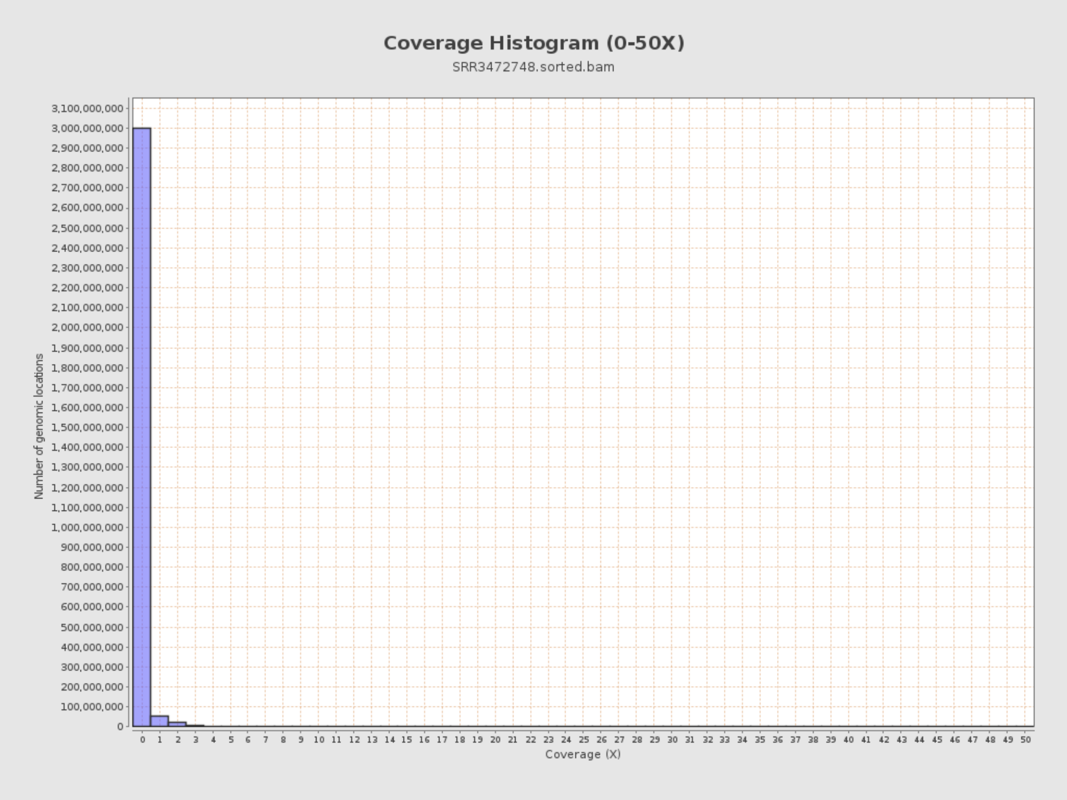
3. Results : Coverage across reference



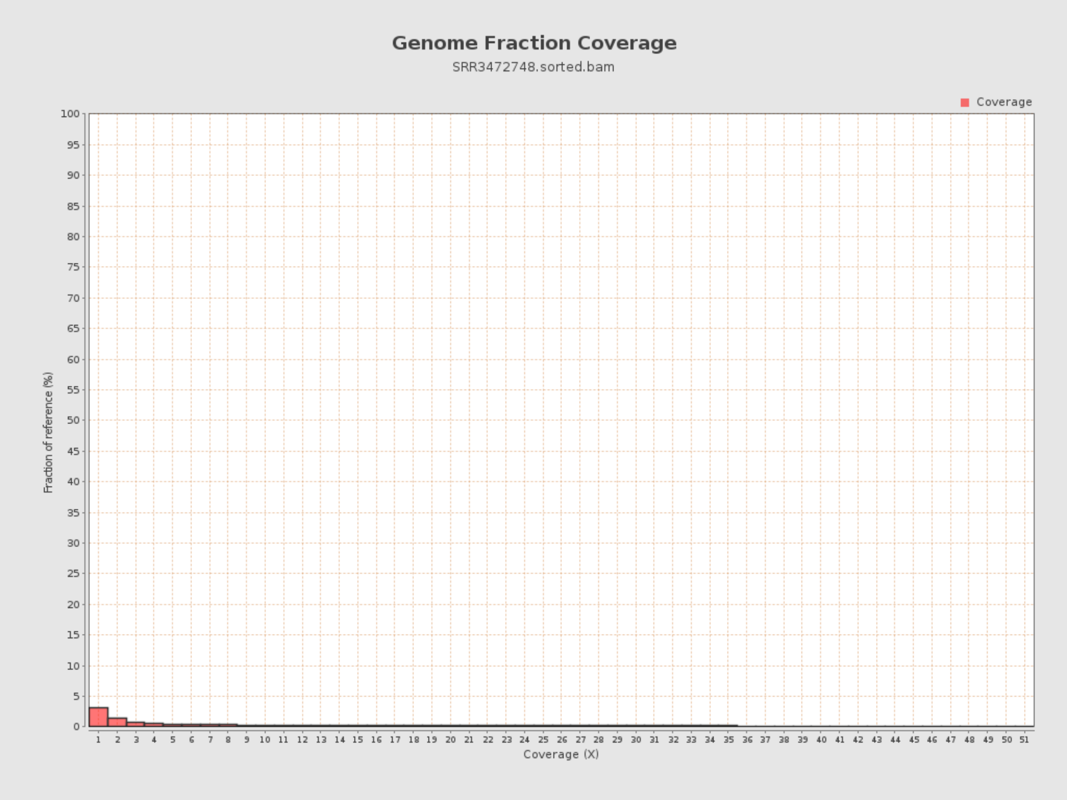
4. Results : Coverage Histogram



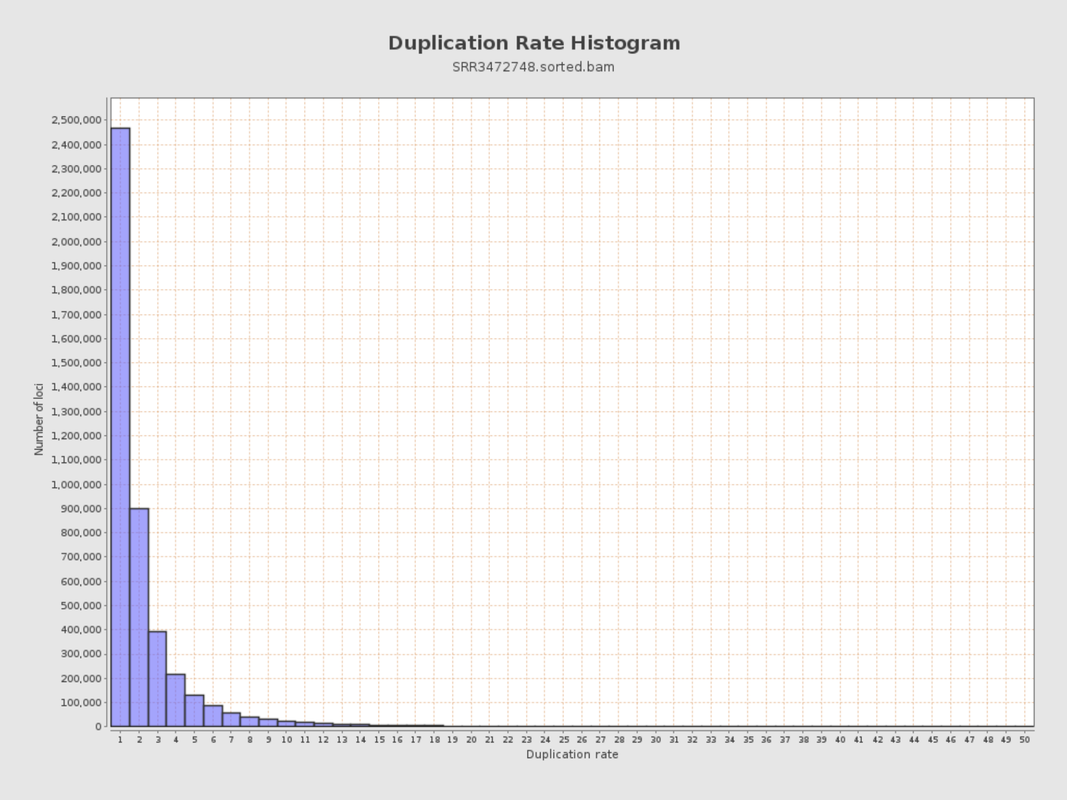
5. Results : Coverage Histogram (0-50X)



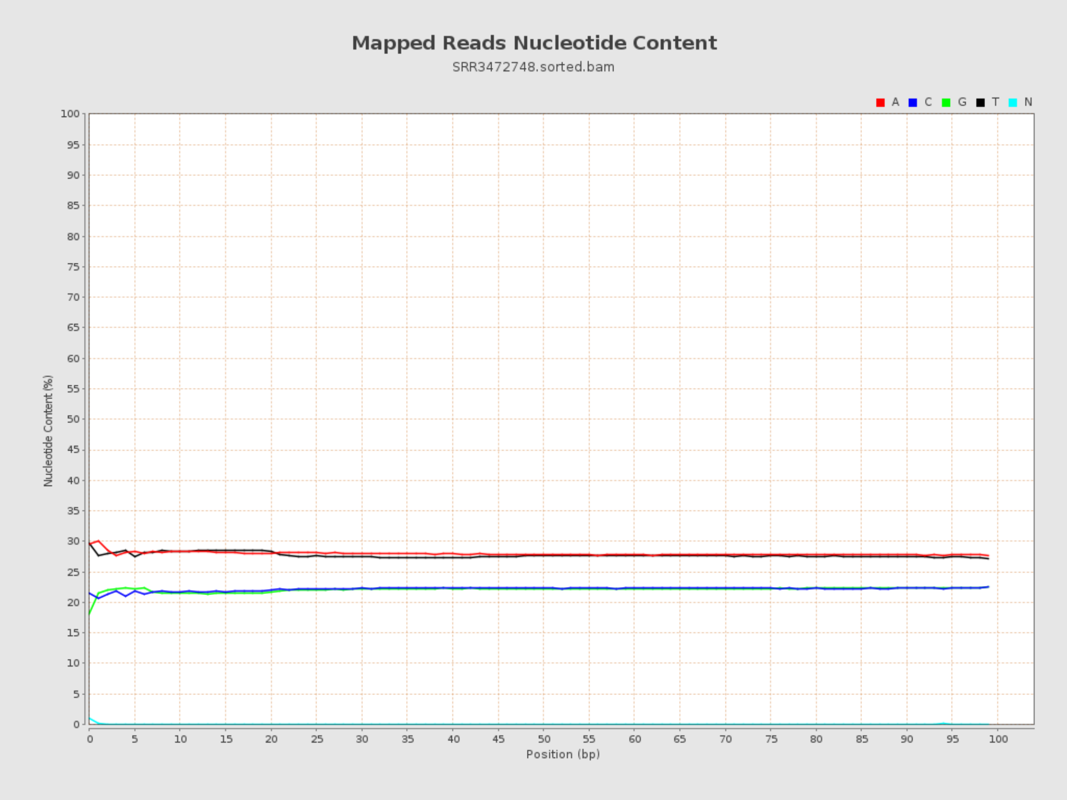
6. Results : Genome Fraction Coverage



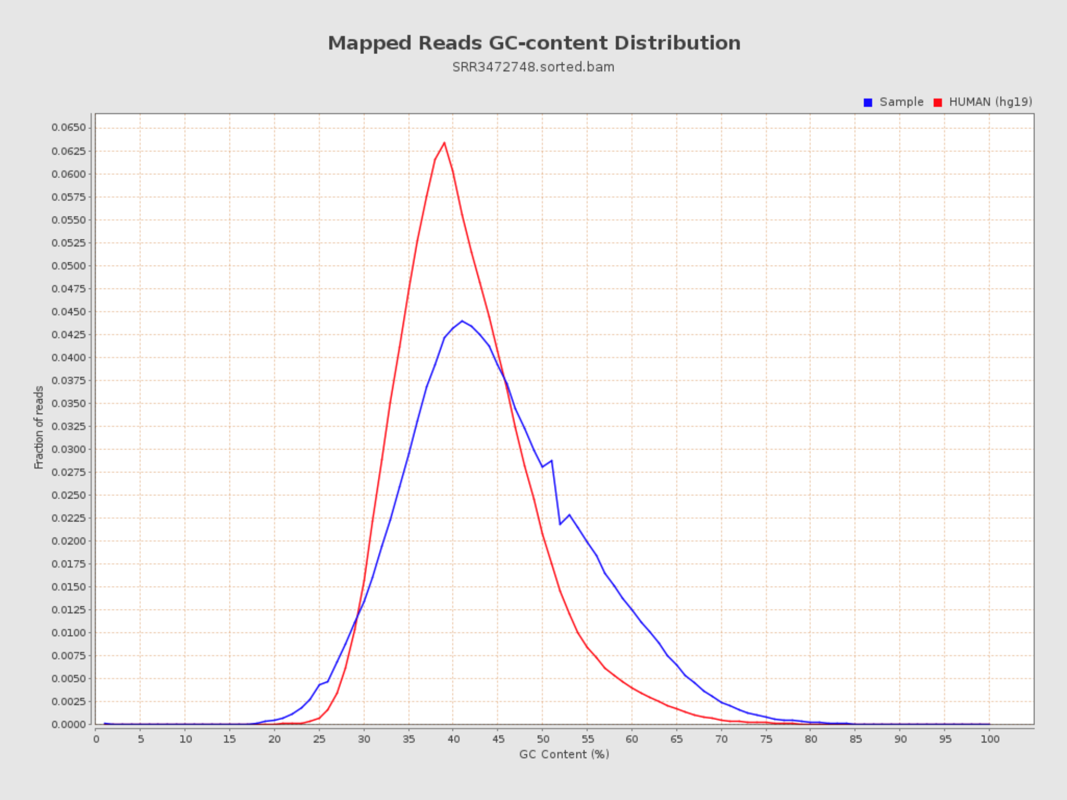
7. Results : Duplication Rate Histogram



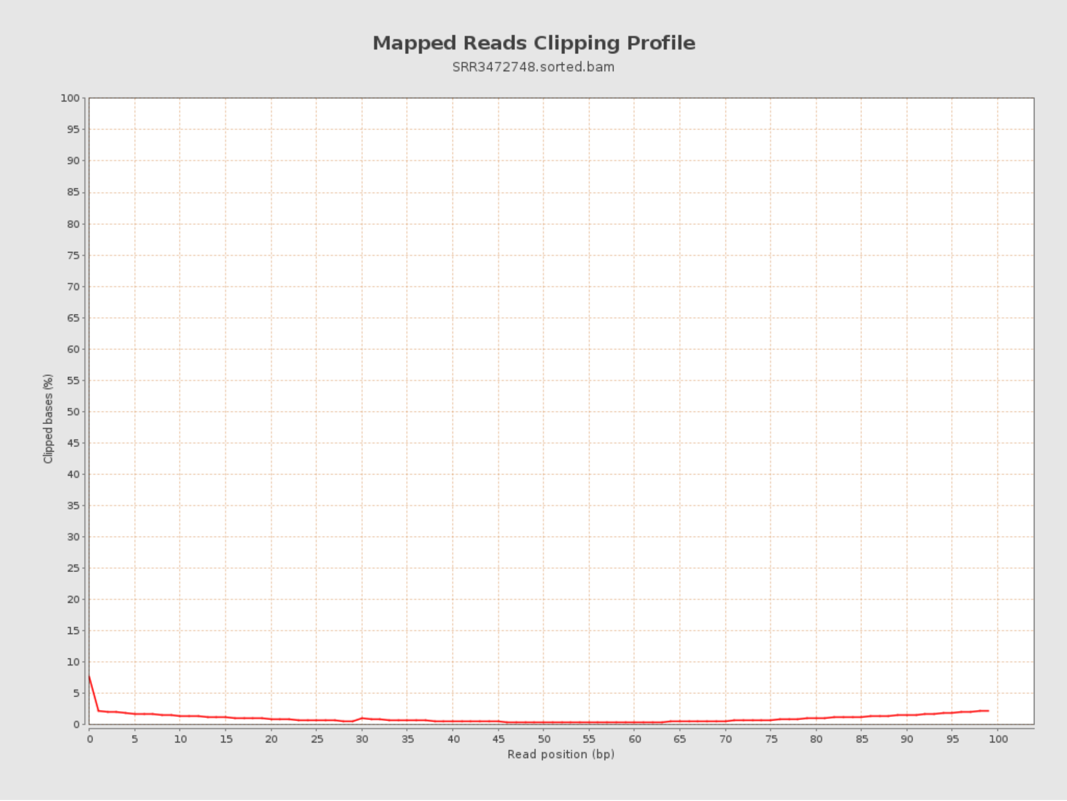
8. Results : Mapped Reads Nucleotide Content



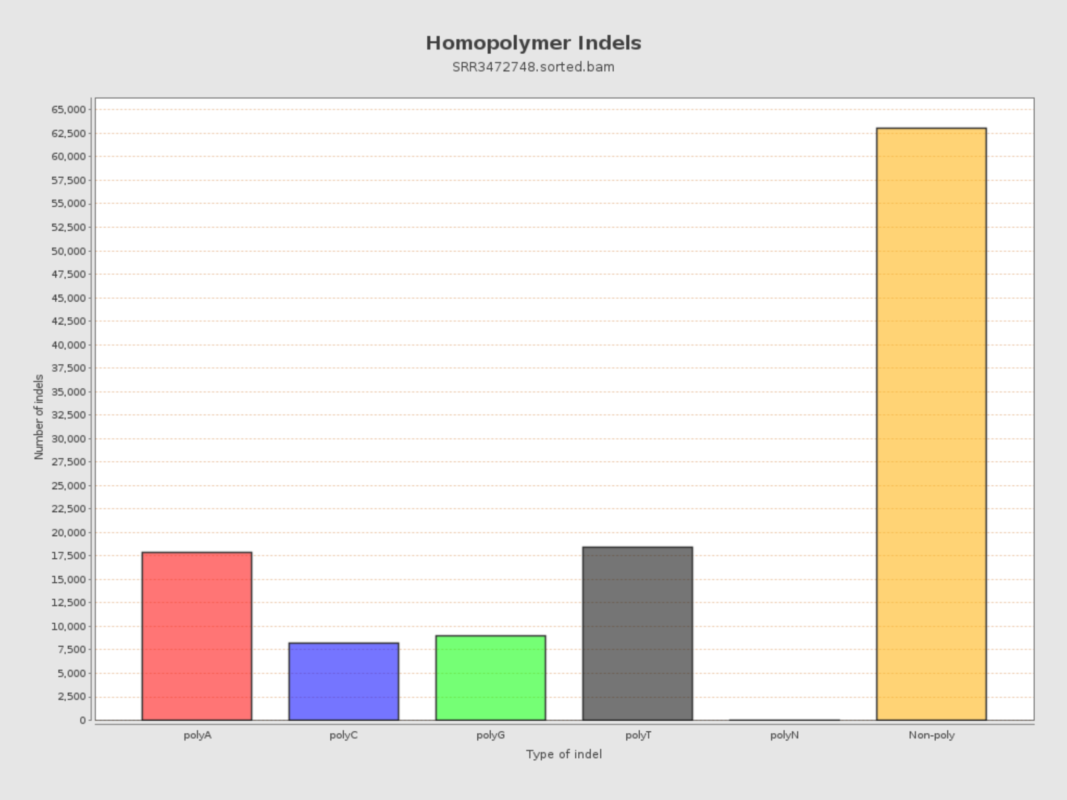
9. Results : Mapped Reads GC-content Distribution



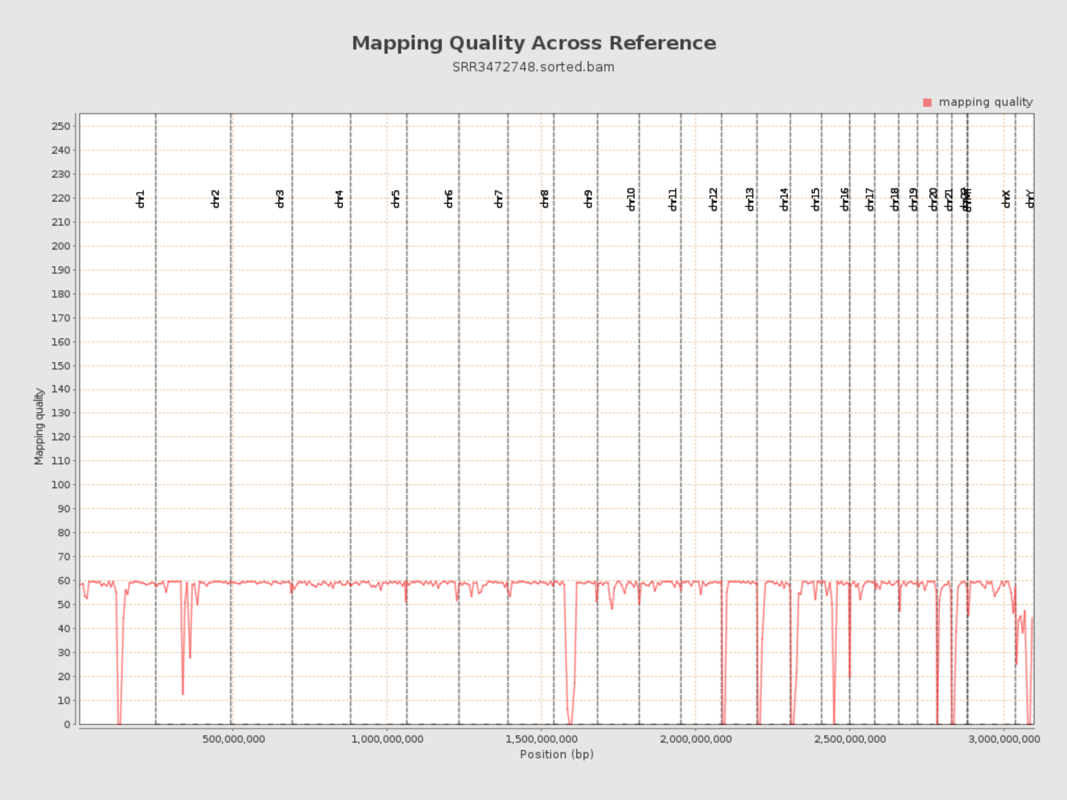
10. Results : Mapped Reads Clipping Profile



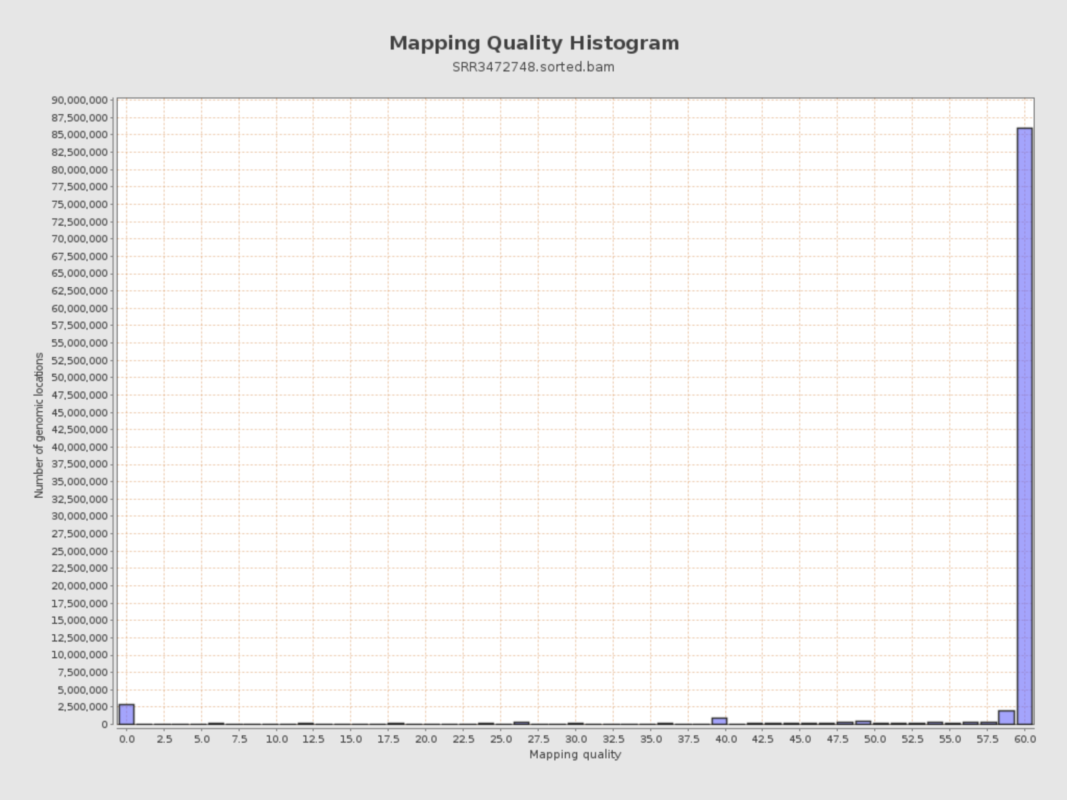
11. Results : Homopolymer Indels



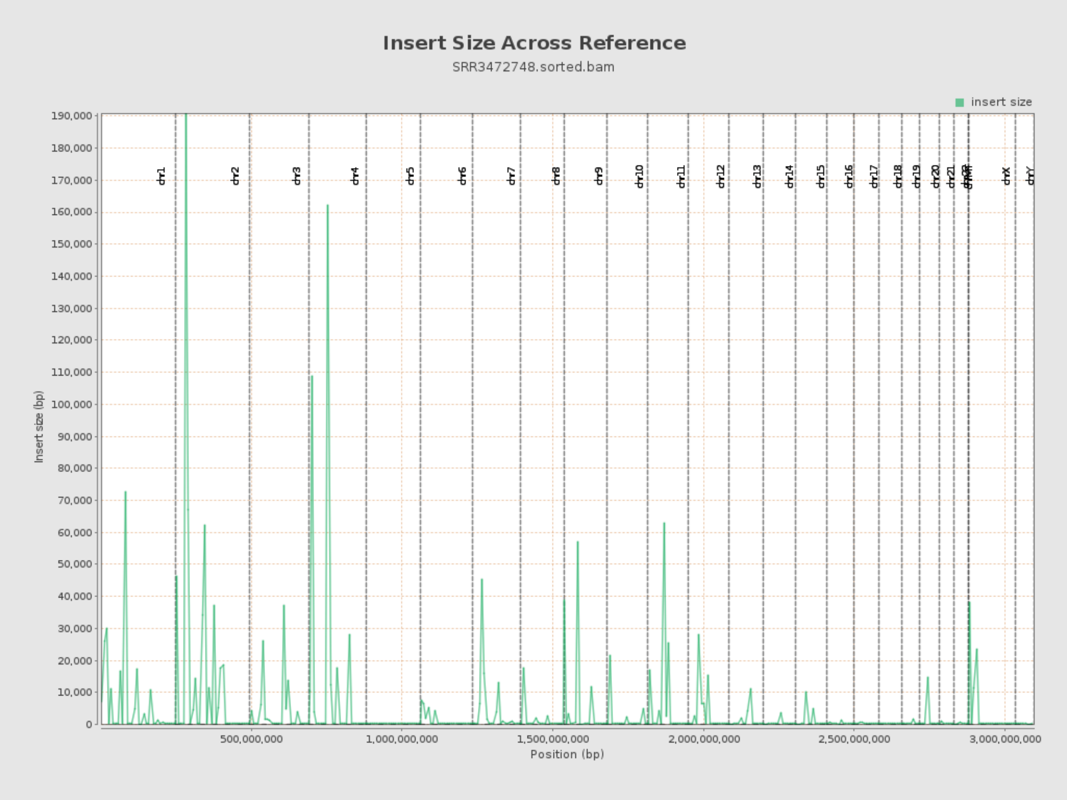
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram