Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:16:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472462.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_SRR3472462 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472462_1.fastq.gz SRR3472462_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:16:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472462.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,015,584
Mapped reads	9,894,396 / 98.79%
Unmapped reads	121,188 / 1.21%
Mapped paired reads	9,894,396 / 98.79%
Mapped reads, first in pair	4,964,935 / 49.57%
Mapped reads, second in pair	4,929,461 / 49.22%
Mapped reads, both in pair	9,827,892 / 98.13%
Mapped reads, singletons	66,504 / 0.66%
Secondary alignments	0
Supplementary alignments	38,108 / 0.38%
Read min/max/mean length	30 / 100 / 99.3
Duplicated reads (estimated)	5,699,111 / 56.9%
Duplication rate	45.4%
Clipped reads	912,954 / 9.12%

2.2. ACGT Content

Number/percentage of A's	263,073,952 / 27.29%
Number/percentage of C's	220,204,607 / 22.85%
Number/percentage of T's	262,292,762 / 27.21%
Number/percentage of G's	218,129,219 / 22.63%
Number/percentage of N's	118,890 / 0.01%

GC Percentage	45.48%

2.3. Coverage

Mean	0.3114
Standard Deviation	10.5106

2.4. Mapping Quality

Mean Mapping Quality	54.89

2.5. Insert size

Mean	16,382.23
Standard Deviation	1,276,525.32
P25/Median/P75	141 / 196 / 262

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	5,842,870
Insertions	55,366
Mapped reads with at least one insertion	0.55%
Deletions	48,973
Mapped reads with at least one deletion	0.49%
Homopolymer indels	45.72%

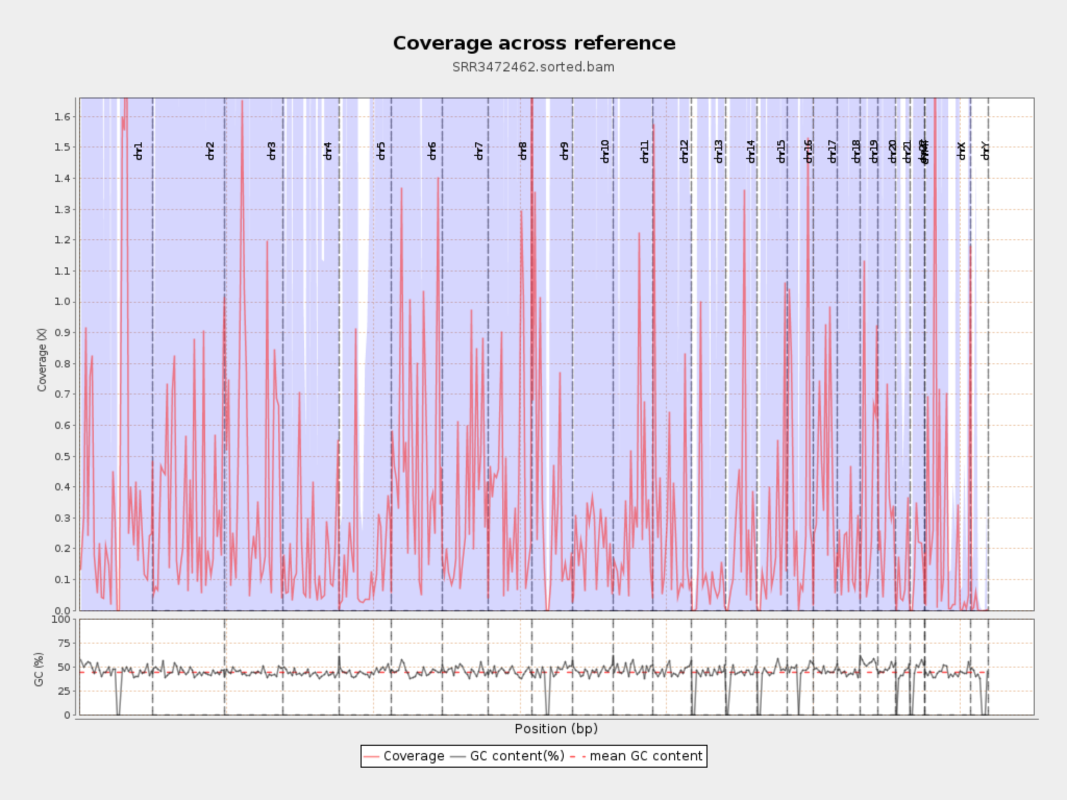
2.7. Chromosome stats

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

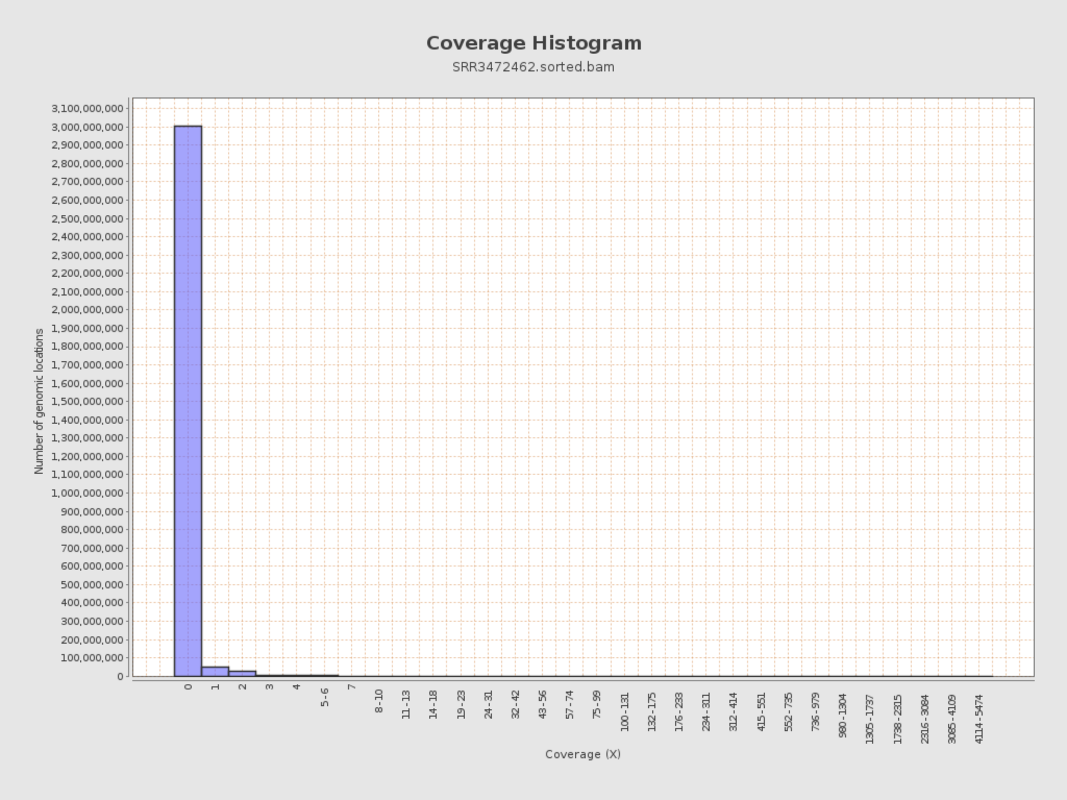
		bases	coverage	deviation
chr1	249250621	100537632	0.4034	13.4341
chr2	243199373	79961037	0.3288	10.6163
chr3	198022430	94246516	0.4759	13.9759
chr4	191154276	32598757	0.1705	5.9456
chr5	180915260	29374089	0.1624	7.4141
chr6	171115067	87668096	0.5123	14.6845
chr7	159138663	56347133	0.3541	11.9074
chr8	146364022	59710951	0.408	11.5252
chr9	141213431	51249717	0.3629	10.4823
chr10	135534747	28800794	0.2125	8.2388
chr11	135006516	40707162	0.3015	9.904
chr12	133851895	43862165	0.3277	11.4457
chr13	115169878	15755857	0.1368	6.1338
chr14	107349540	27775977	0.2587	7.9405
chr15	102531392	23885487	0.233	8.7842
chr16	90354753	37390988	0.4138	11.3464
chr17	81195210	35937937	0.4426	11.9208
chr18	78077248	15664961	0.2006	7.477
chr19	59128983	26839210	0.4539	11.3476
chr20	63025520	18780281	0.298	12.2634
chr21	48129895	5491757	0.1141	4.7349
chr22	51304566	7921211	0.1544	4.2054
chrMT	16571	3134	0.1891	0.502
chrX	155270560	42828248	0.2758	9.54

chrY	59373566	595411	0.01	0.535

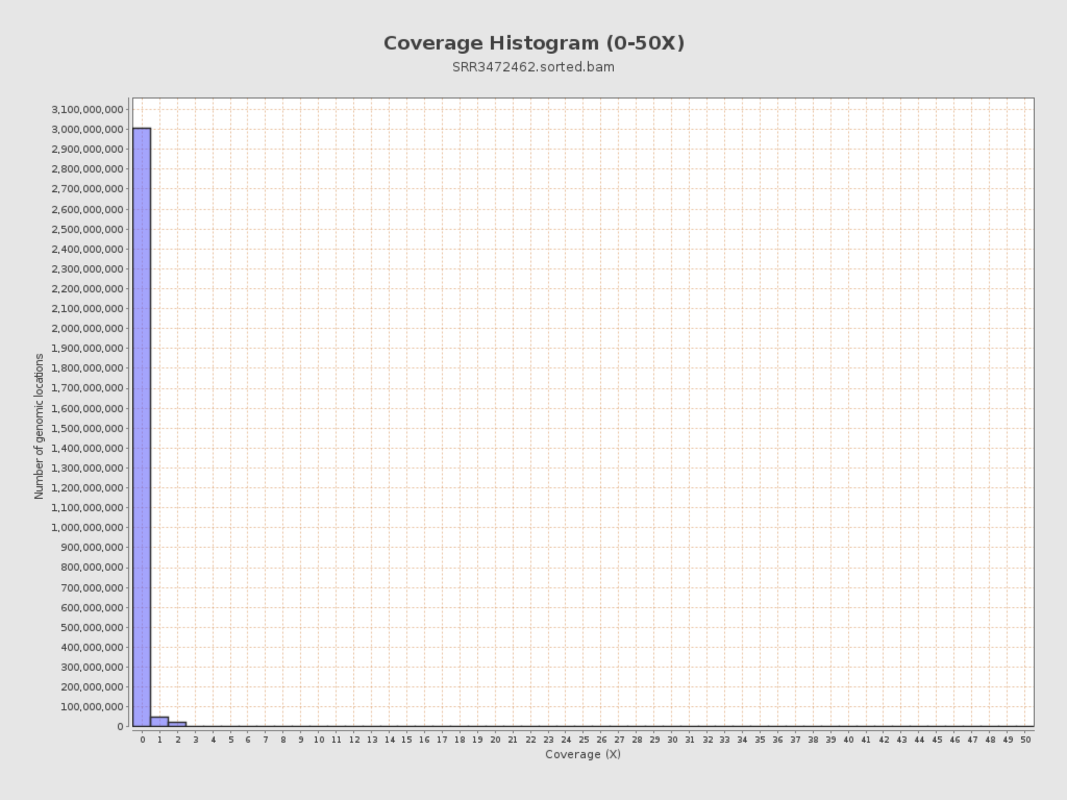
3. Results : Coverage across reference



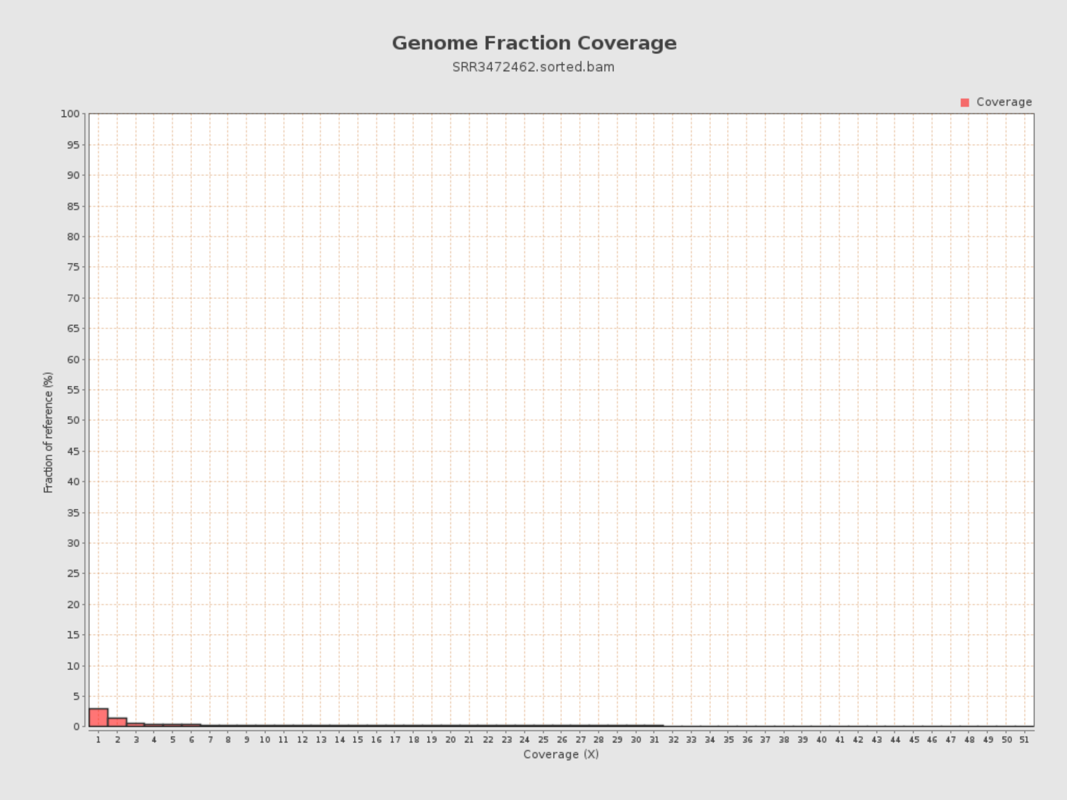
4. Results : Coverage Histogram



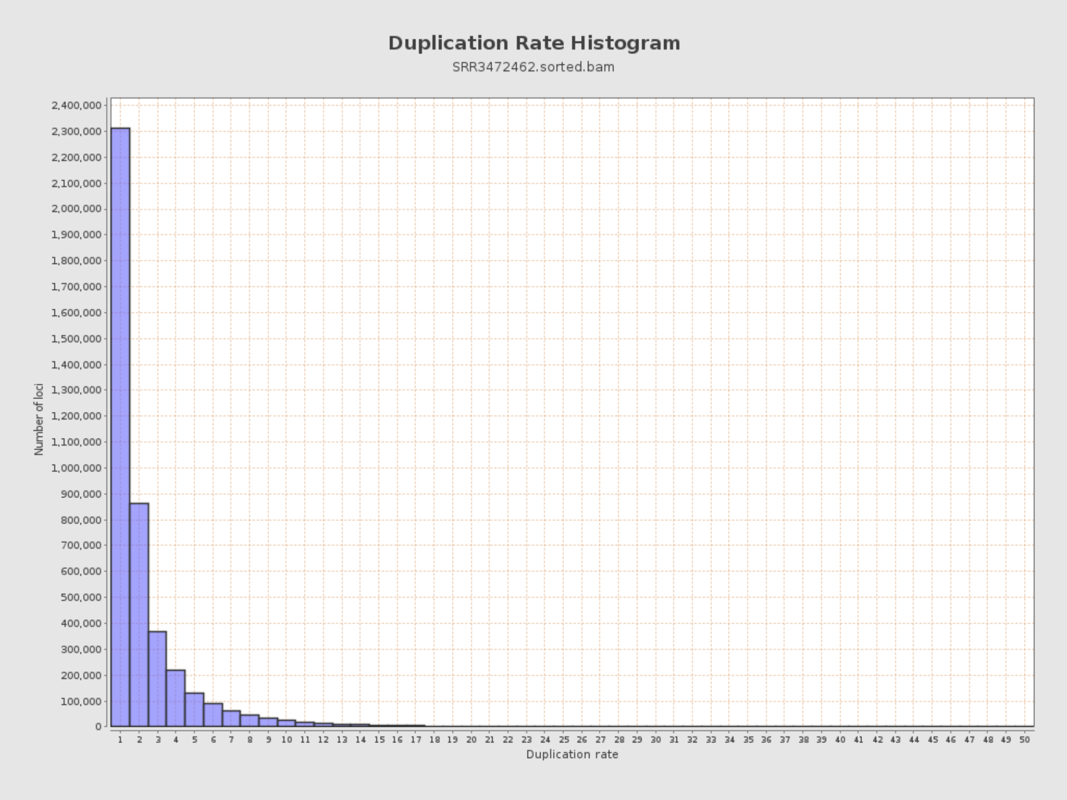
5. Results : Coverage Histogram (0-50X)



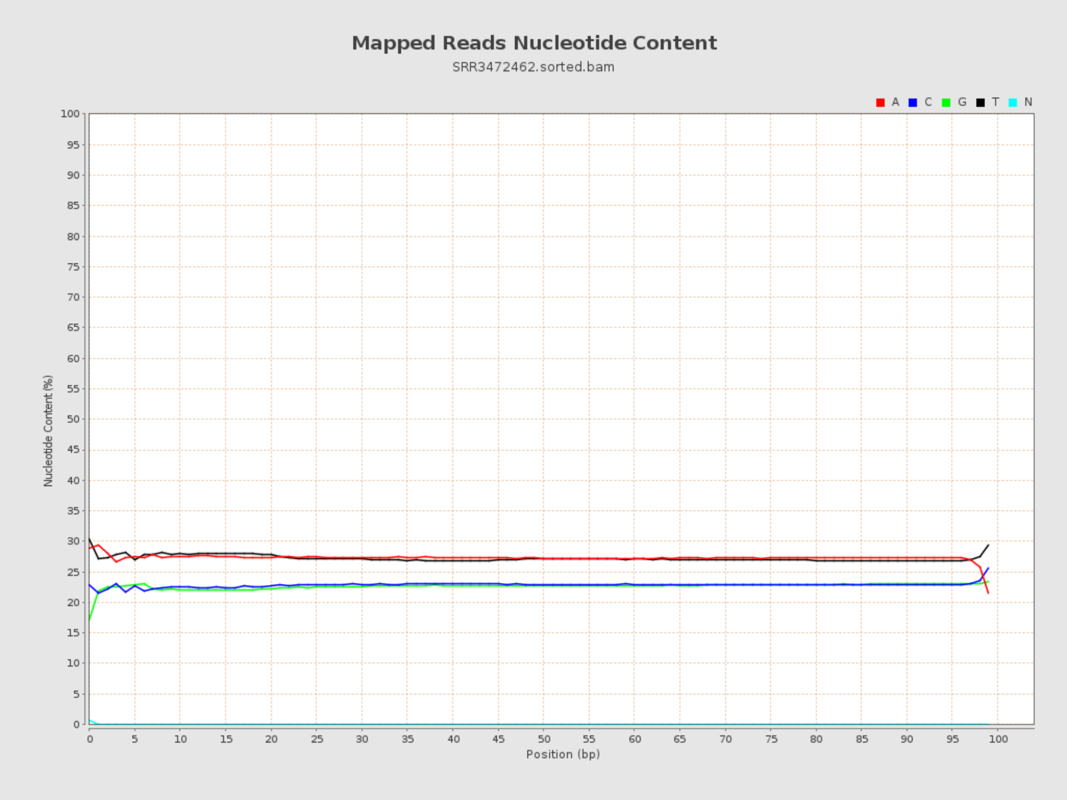
6. Results : Genome Fraction Coverage



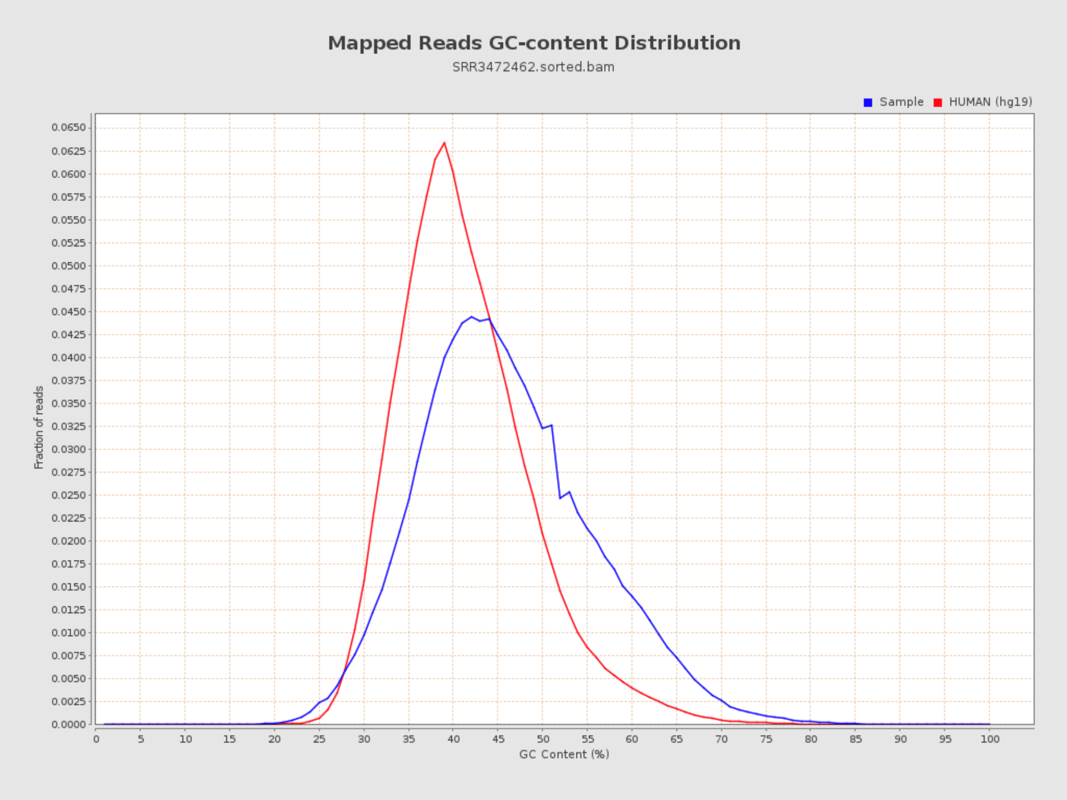
7. Results : Duplication Rate Histogram



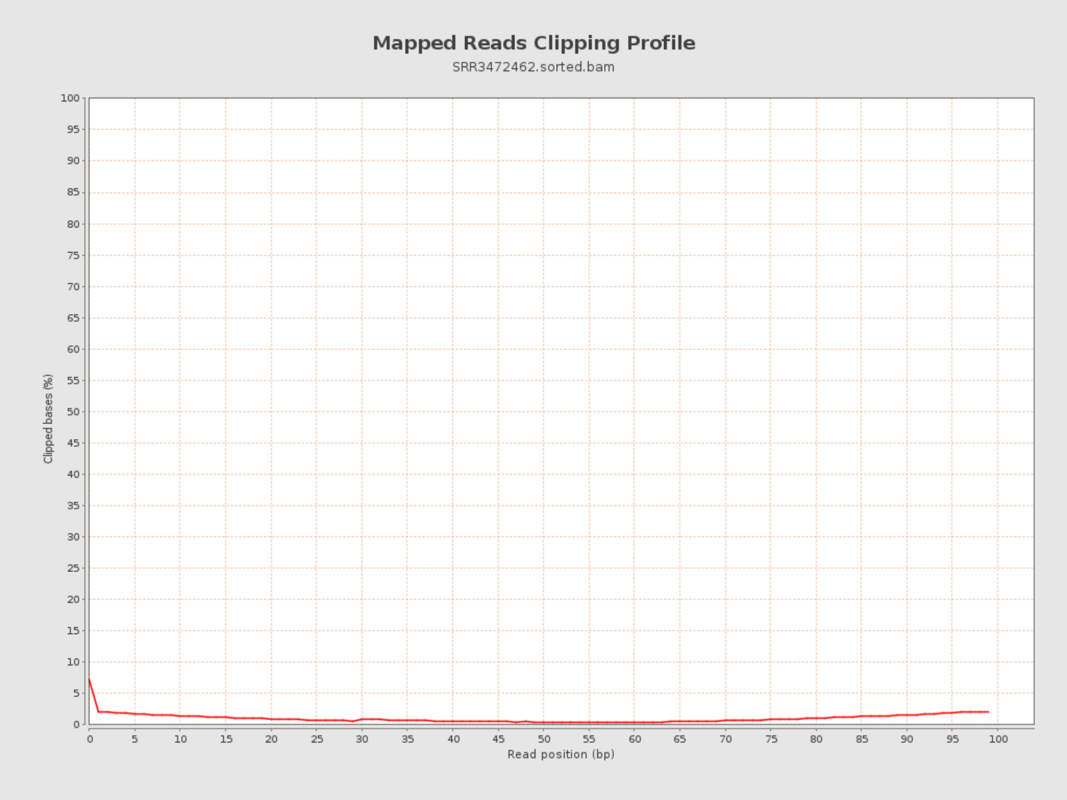
8. Results : Mapped Reads Nucleotide Content



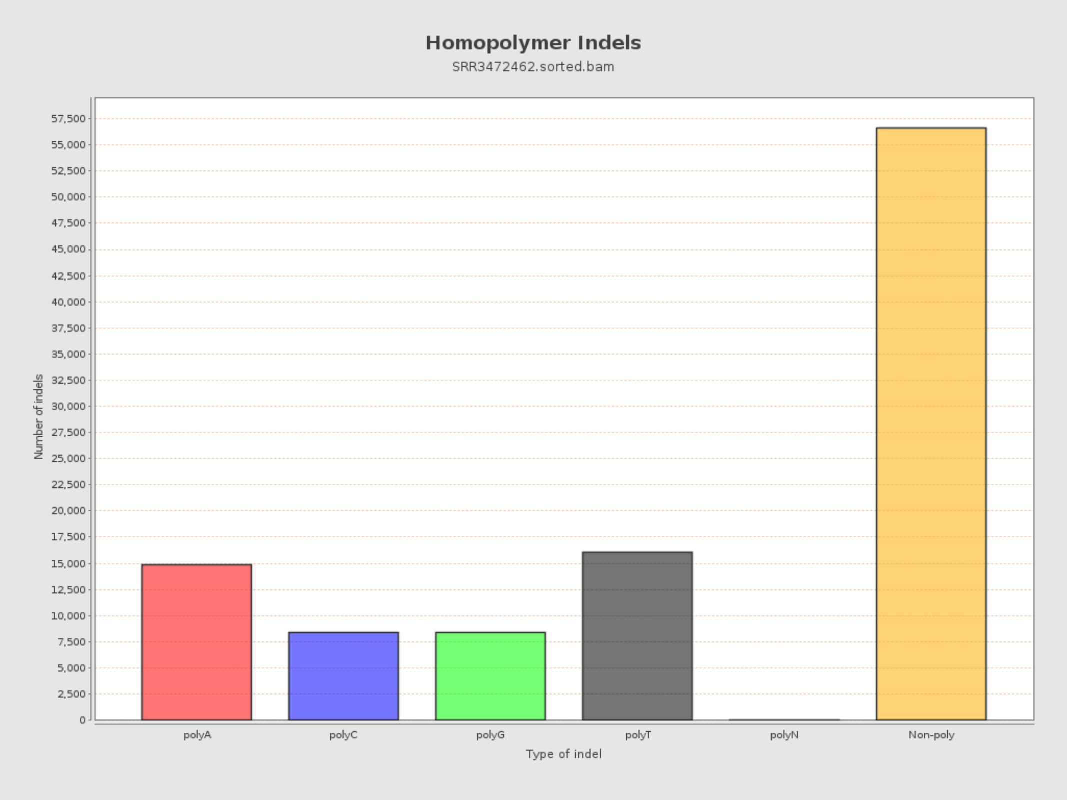
9. Results : Mapped Reads GC-content Distribution



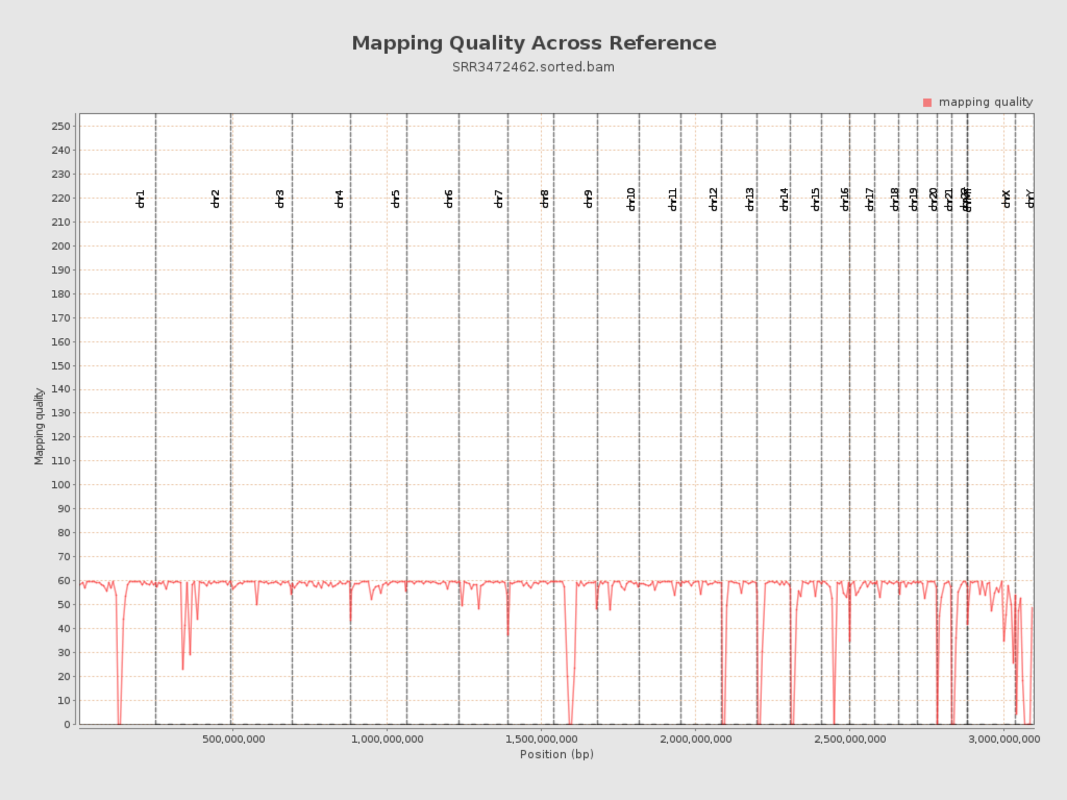
10. Results : Mapped Reads Clipping Profile



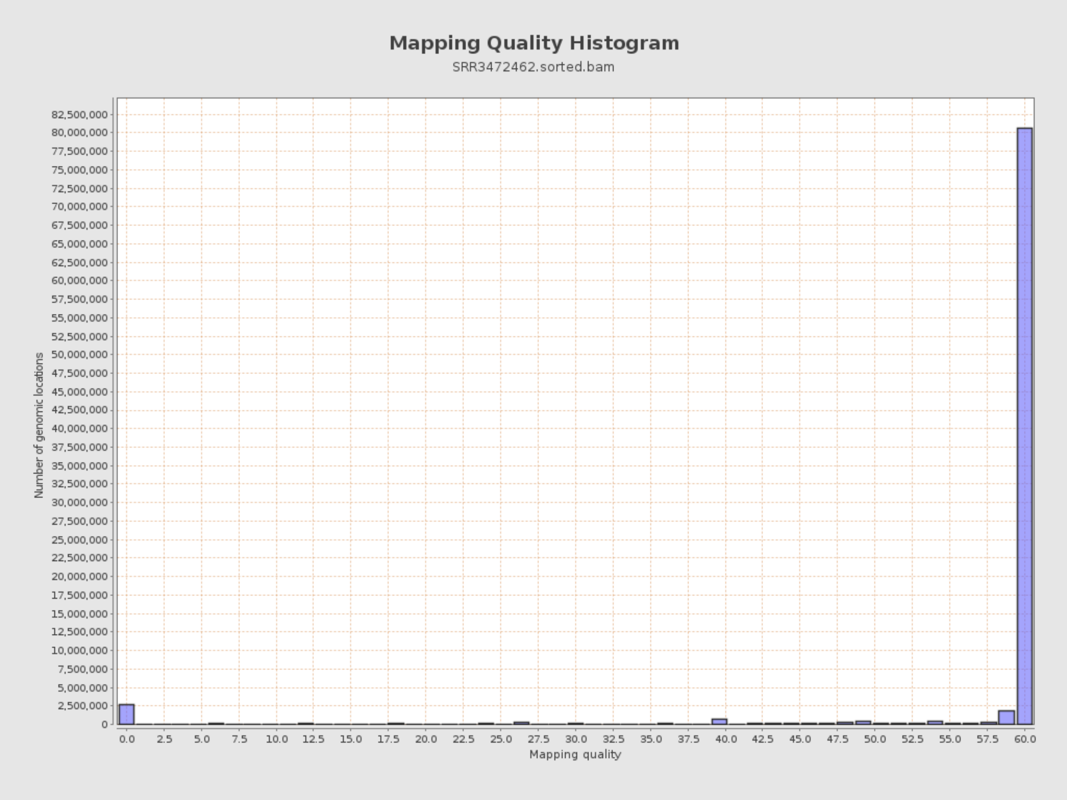
11. Results : Homopolymer Indels



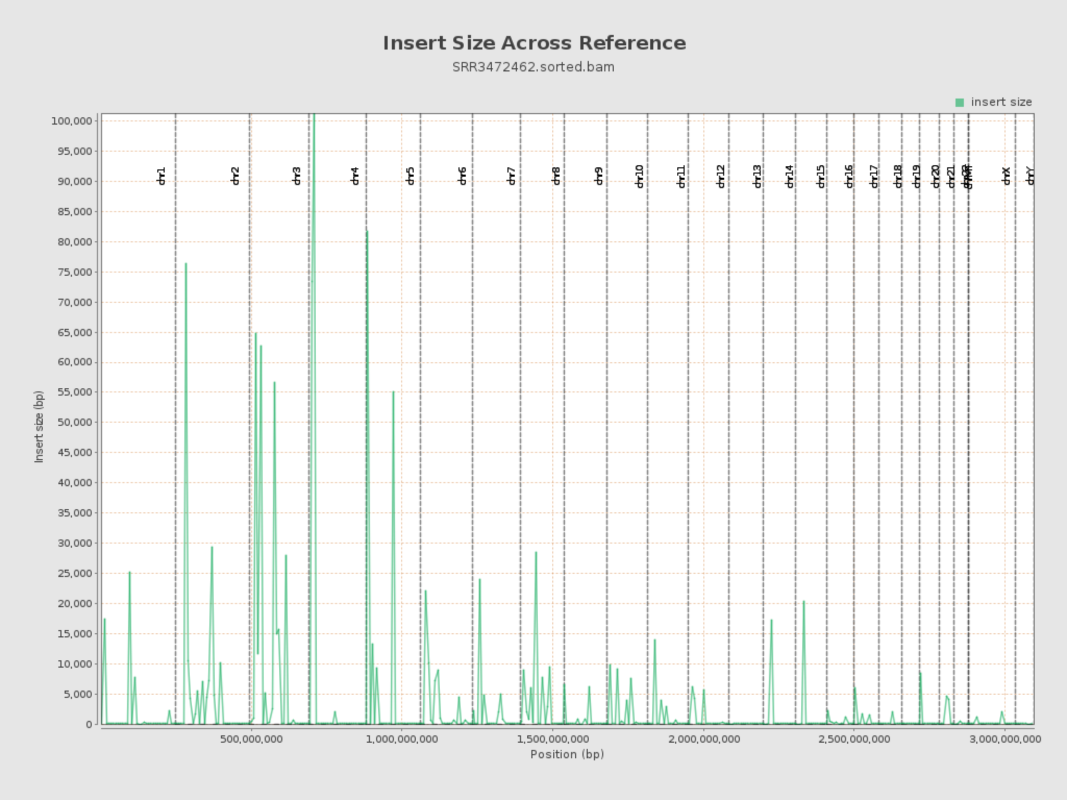
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram