Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:09:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472562.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_SRR3472562 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472562_1.fastq.gz SRR3472562_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:09:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472562.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,155,966
Mapped reads	11,974,778 / 98.51%
Unmapped reads	181,188 / 1.49%
Mapped paired reads	11,974,778 / 98.51%
Mapped reads, first in pair	6,013,537 / 49.47%
Mapped reads, second in pair	5,961,241 / 49.04%
Mapped reads, both in pair	11,879,180 / 97.72%
Mapped reads, singletons	95,598 / 0.79%
Secondary alignments	0
Supplementary alignments	42,262 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	7,213,633 / 59.34%
Duplication rate	45.39%
Clipped reads	1,017,814 / 8.37%

2.2. ACGT Content

Number/percentage of A's	318,897,276 / 27.1%
Number/percentage of C's	271,818,470 / 23.1%
Number/percentage of T's	315,969,904 / 26.85%
Number/percentage of G's	269,802,094 / 22.93%
Number/percentage of N's	178,599 / 0.02%

GC Percentage	46.03%

2.3. Coverage

Mean	0.3801
Standard Deviation	13.9244

2.4. Mapping Quality

Mean Mapping Quality	54.11

2.5. Insert size

Mean	29,761.85
Standard Deviation	1,725,838.86
P25/Median/P75	175 / 249 / 341

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	7,646,551
Insertions	67,909
Mapped reads with at least one insertion	0.56%
Deletions	55,248
Mapped reads with at least one deletion	0.46%
Homopolymer indels	44.49%

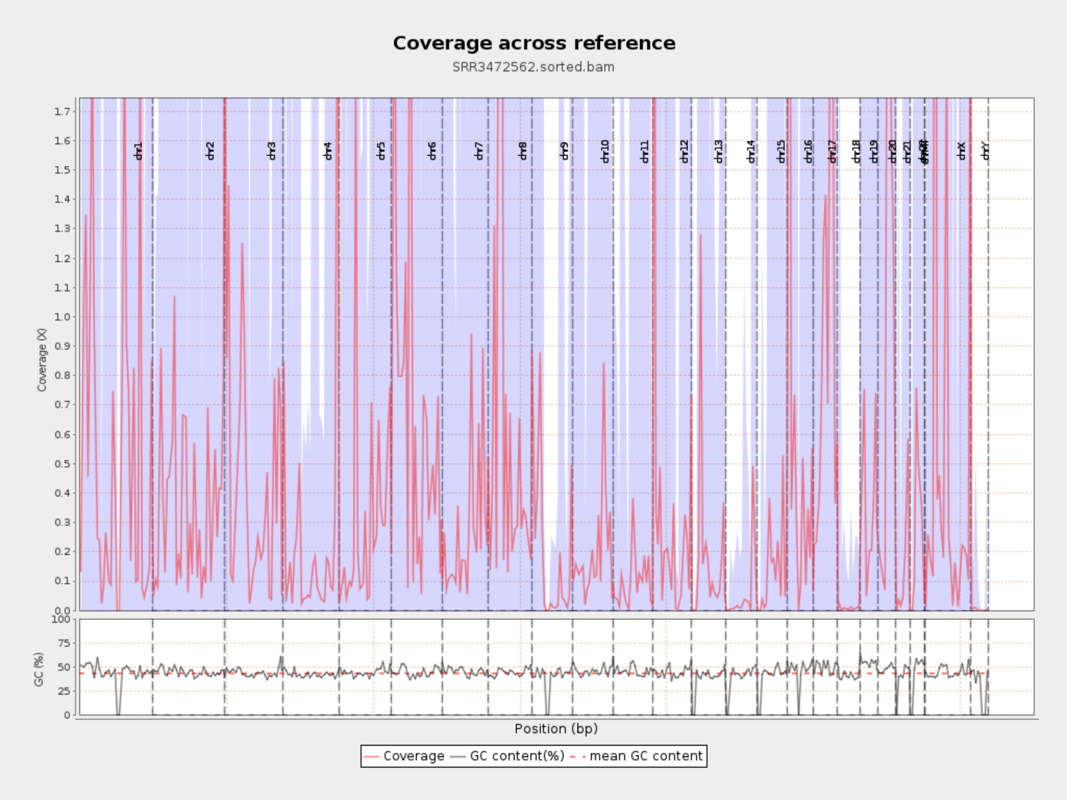
2.7. Chromosome stats

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

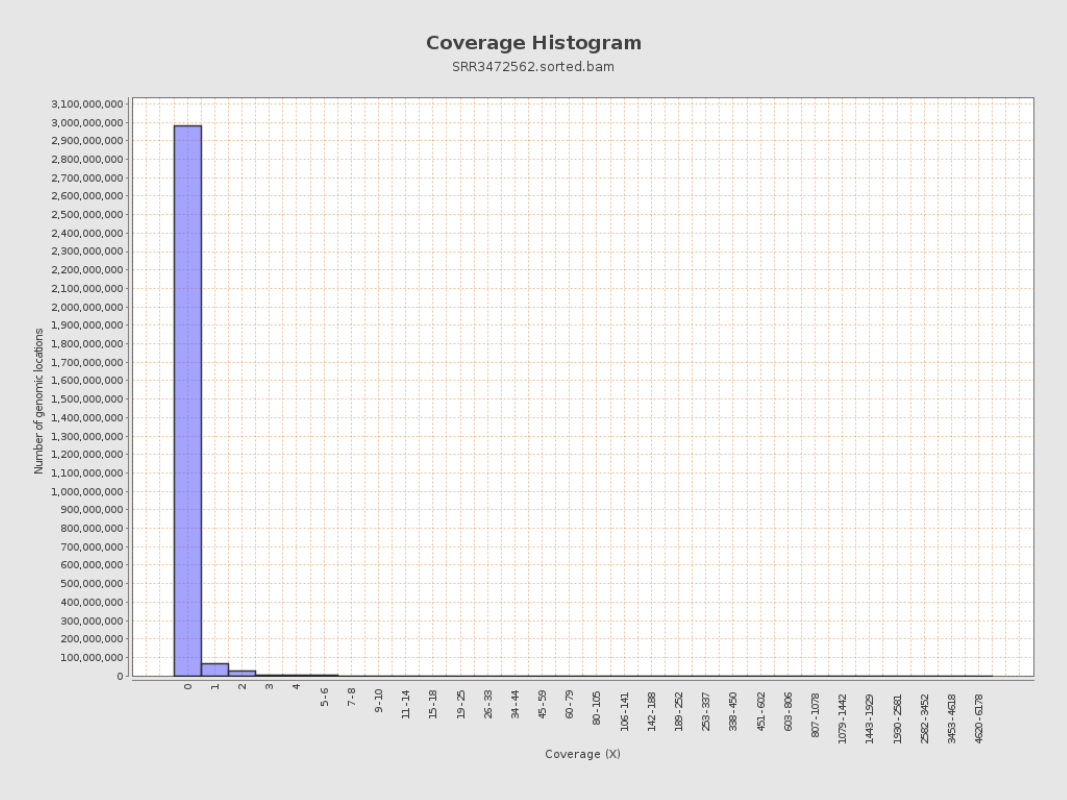
		bases	coverage	deviation
chr1	249250621	140055291	0.5619	17.9413
chr2	243199373	84227766	0.3463	10.645
chr3	198022430	93537456	0.4724	12.4965
chr4	191154276	47115359	0.2465	9.9428
chr5	180915260	57484685	0.3177	10.1588
chr6	171115067	125549727	0.7337	21.0308
chr7	159138663	44265238	0.2782	8.5156
chr8	146364022	95462136	0.6522	21.5446
chr9	141213431	26987455	0.1911	7.6373
chr10	135534747	27350225	0.2018	6.6092
chr11	135006516	14514867	0.1075	3.2599
chr12	133851895	55088381	0.4116	26.425
chr13	115169878	22324205	0.1938	8.1558
chr14	107349540	6017452	0.0561	5.6588
chr15	102531392	13956750	0.1361	4.803
chr16	90354753	57919227	0.641	16.8387
chr17	81195210	72732332	0.8958	18.4184
chr18	78077248	700467	0.009	0.7237
chr19	59128983	22910498	0.3875	9.7676
chr20	63025520	67546178	1.0717	25.9034
chr21	48129895	7197004	0.1495	6.4428
chr22	51304566	14183344	0.2765	9.8315
chrMT	16571	3109	0.1876	0.5392
chrX	155270560	79422400	0.5115	15.641

chrY	59373566	251846	0.0042	0.2705

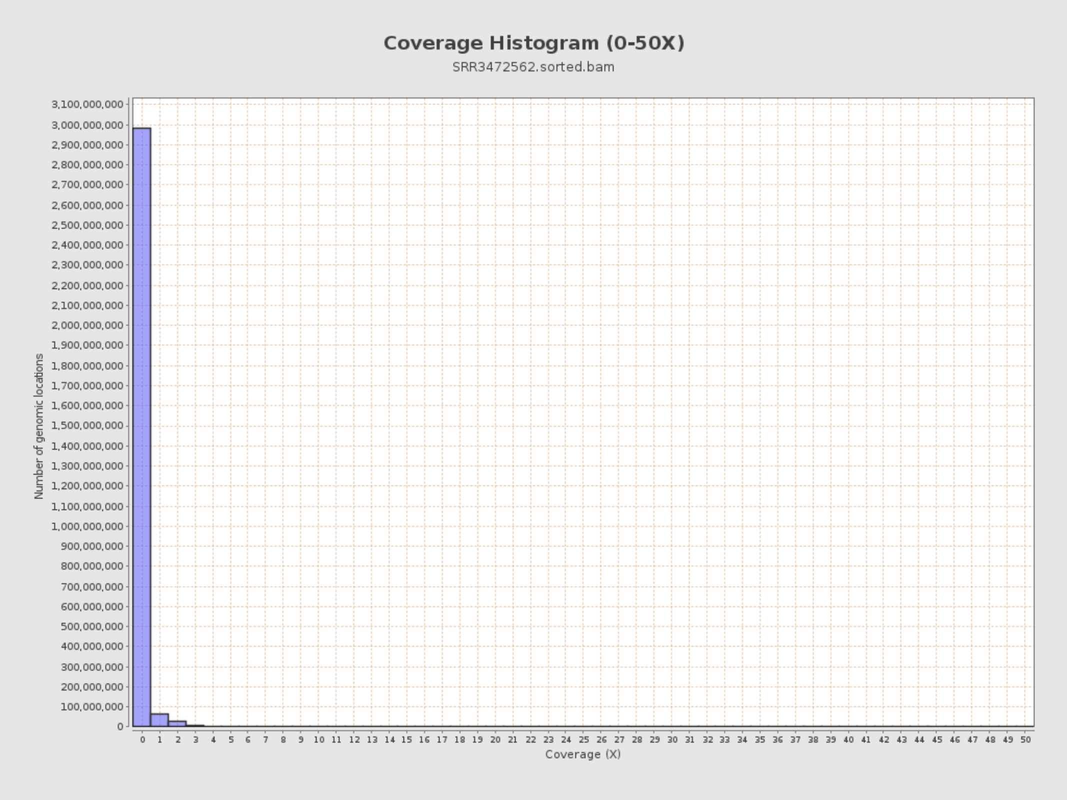
3. Results : Coverage across reference



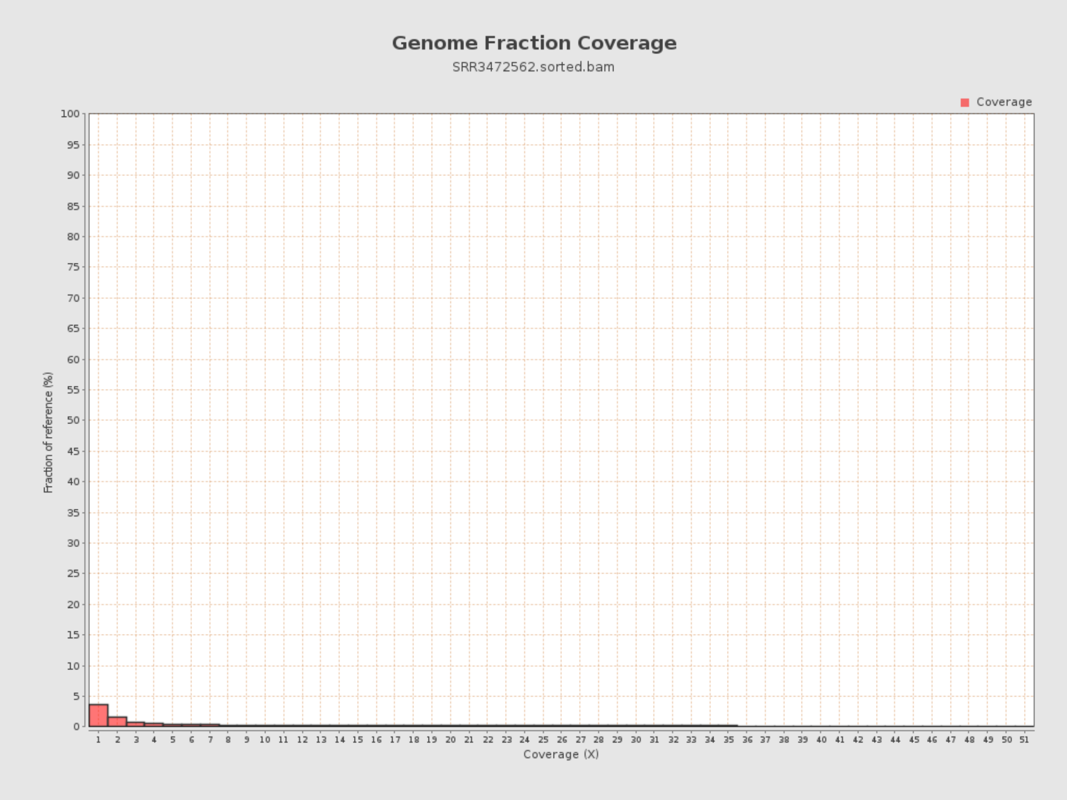
4. Results : Coverage Histogram



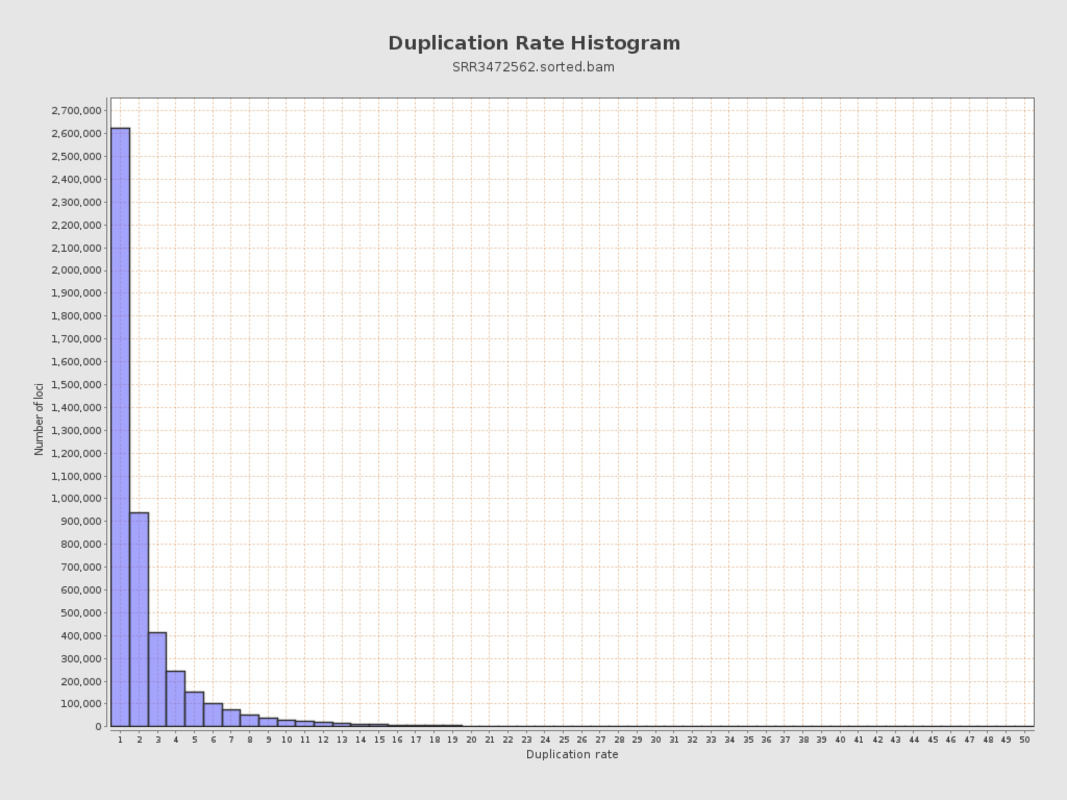
5. Results : Coverage Histogram (0-50X)



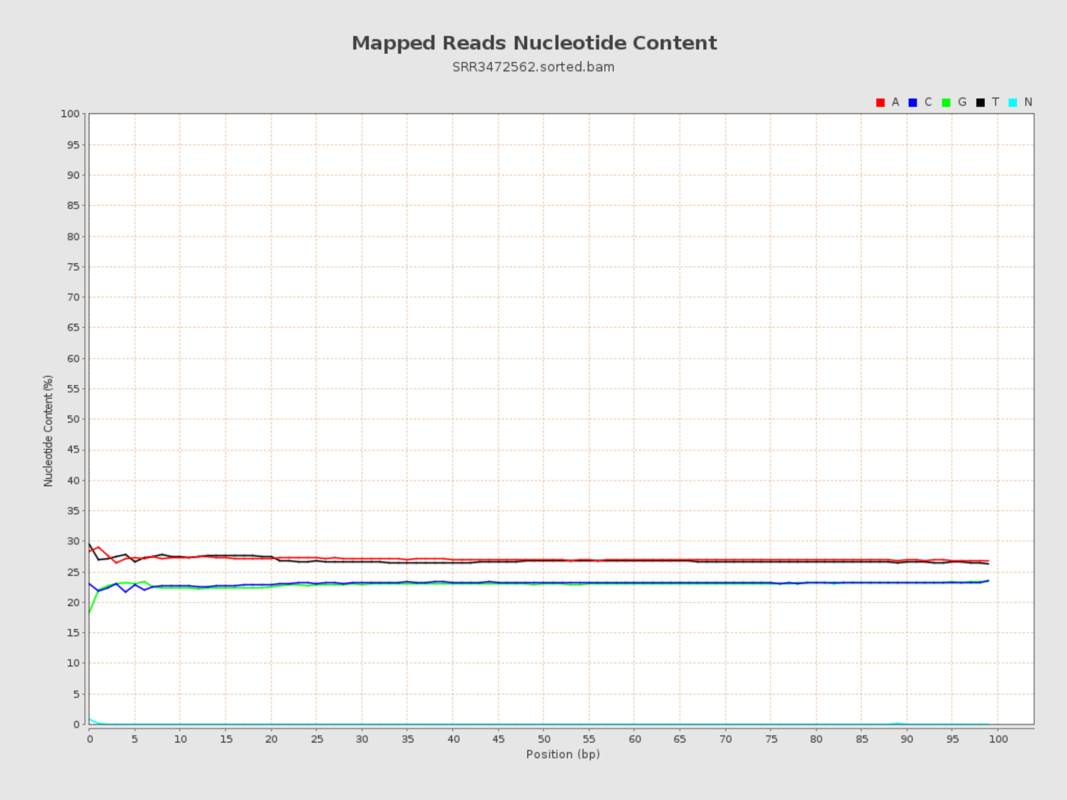
6. Results : Genome Fraction Coverage



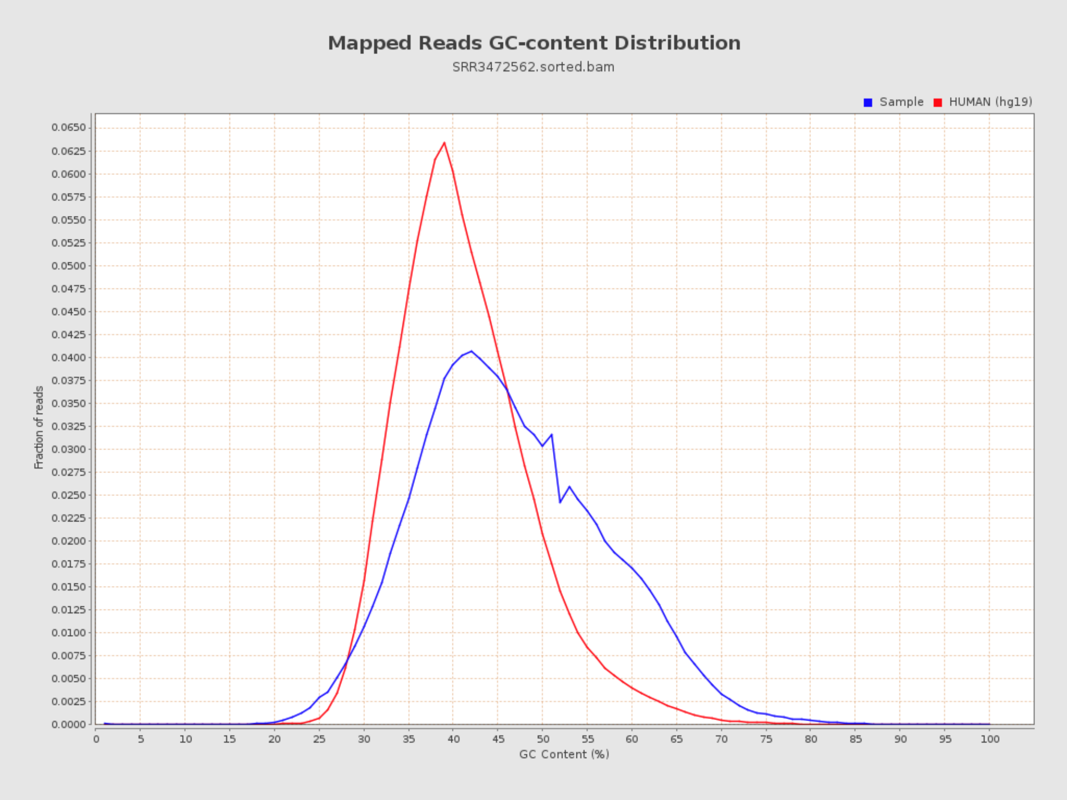
7. Results : Duplication Rate Histogram



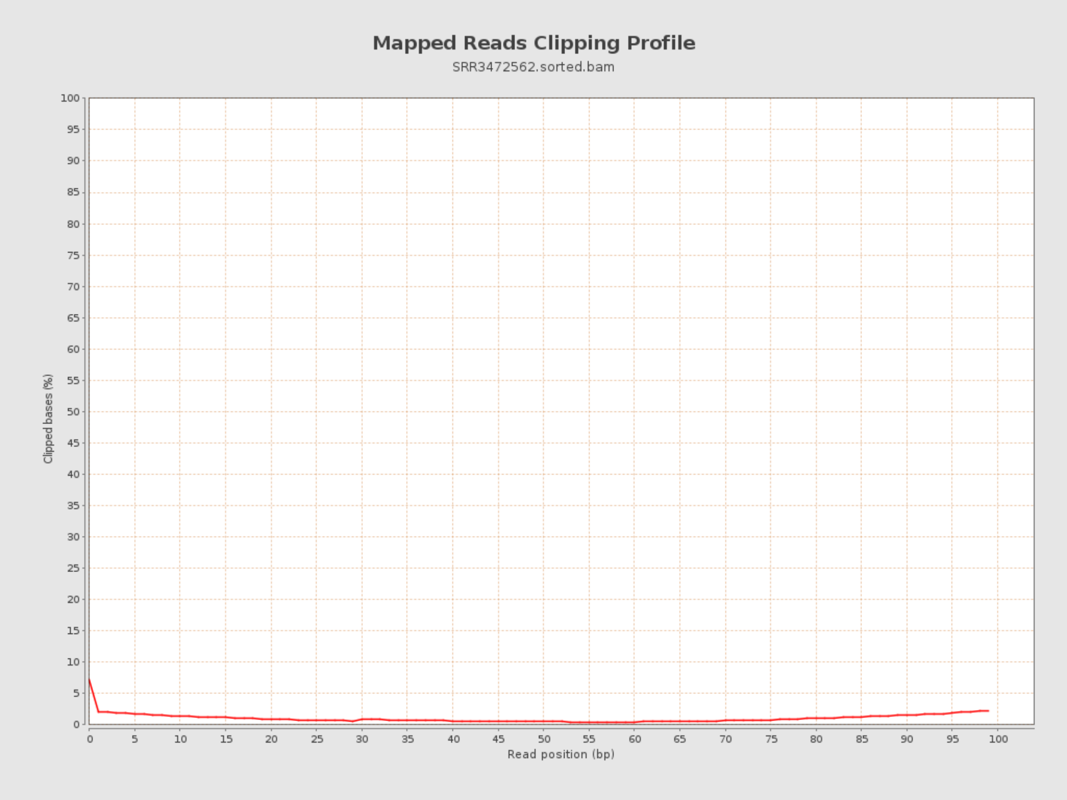
8. Results : Mapped Reads Nucleotide Content



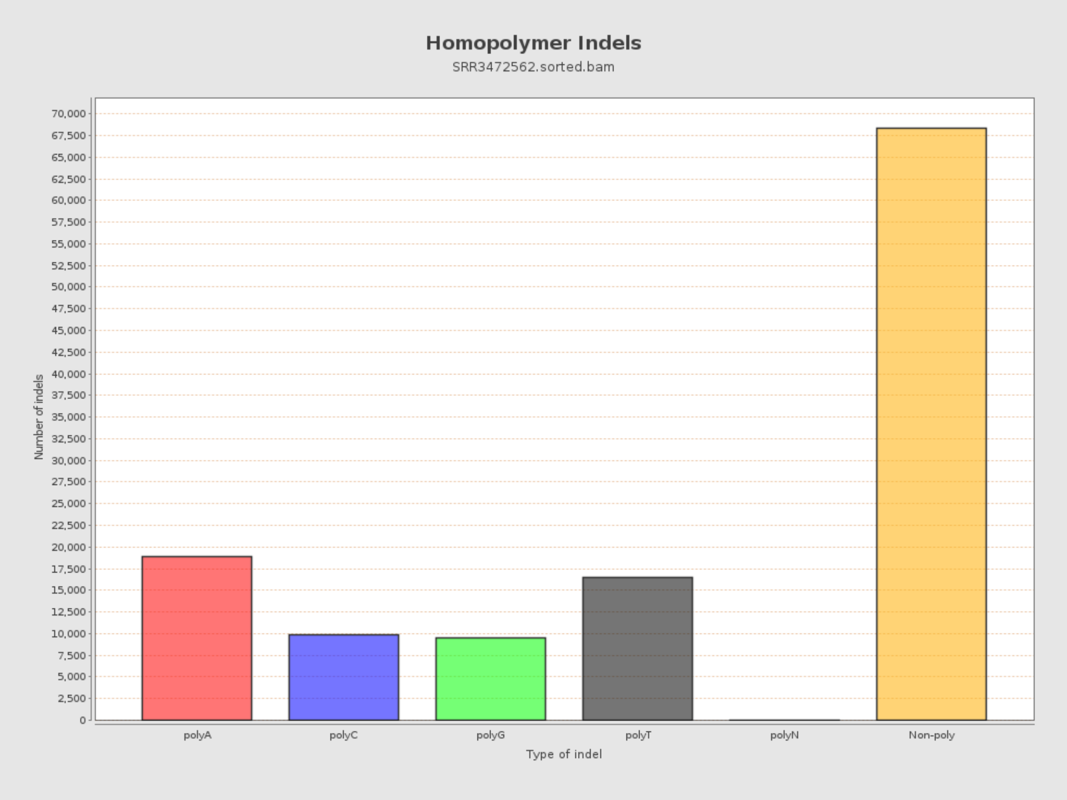
9. Results : Mapped Reads GC-content Distribution



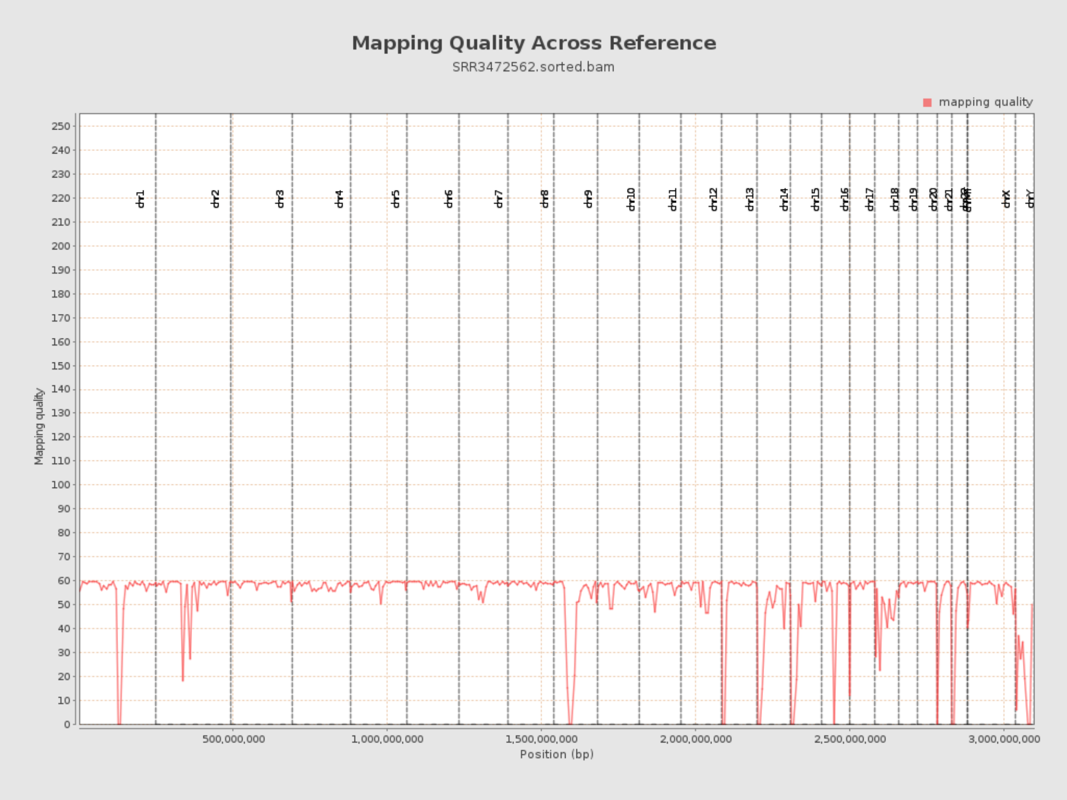
10. Results : Mapped Reads Clipping Profile



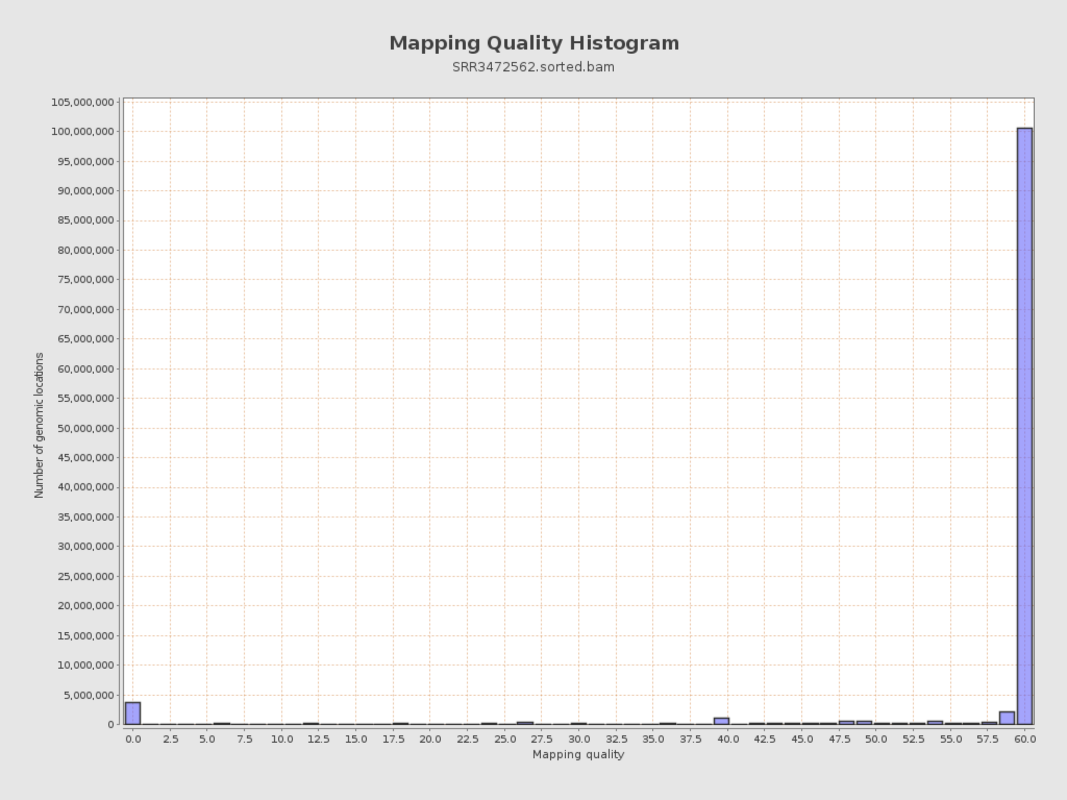
11. Results : Homopolymer Indels



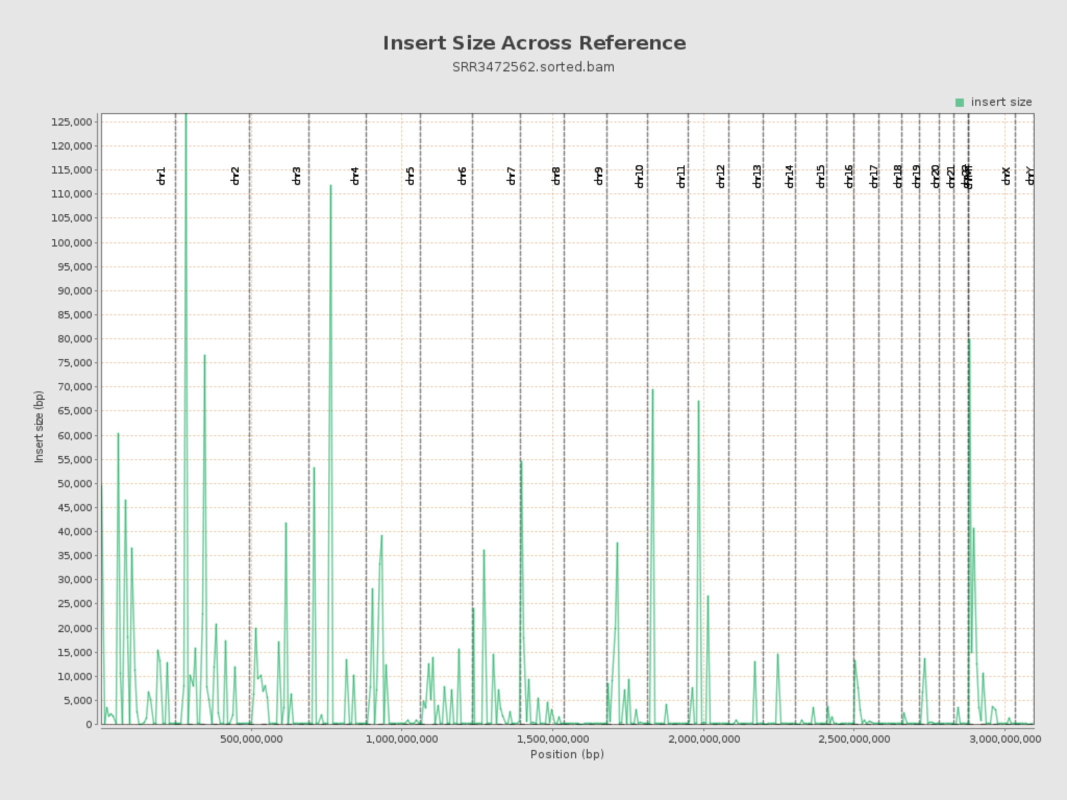
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram