Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 12:54:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472619.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_SRR3472619 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472619_1.fastq.gz SRR3472619_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 12:54:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472619.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,404,364
Mapped reads	18,284,118 / 99.35%
Unmapped reads	120,246 / 0.65%
Mapped paired reads	18,284,118 / 99.35%
Mapped reads, first in pair	9,161,390 / 49.78%
Mapped reads, second in pair	9,122,728 / 49.57%
Mapped reads, both in pair	18,200,540 / 98.89%
Mapped reads, singletons	83,578 / 0.45%
Secondary alignments	0
Supplementary alignments	90,302 / 0.49%
Read min/max/mean length	30 / 101 / 99.85
Duplicated reads (estimated)	12,407,189 / 67.41%
Duplication rate	50.44%
Clipped reads	1,281,289 / 6.96%

2.2. ACGT Content

Number/percentage of A's	491,385,166 / 27.29%
Number/percentage of C's	411,700,485 / 22.86%
Number/percentage of T's	491,010,910 / 27.27%
Number/percentage of G's	406,340,078 / 22.56%
Number/percentage of N's	327,099 / 0.02%

GC Percentage	45.43%

2.3. Coverage

Mean	0.5818
Standard Deviation	21.9103

2.4. Mapping Quality

Mean Mapping Quality	54.99

2.5. Insert size

Mean	21,646.99
Standard Deviation	1,422,559.28
P25/Median/P75	161 / 220 / 295

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	10,957,447
Insertions	111,174
Mapped reads with at least one insertion	0.6%
Deletions	93,483
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.88%

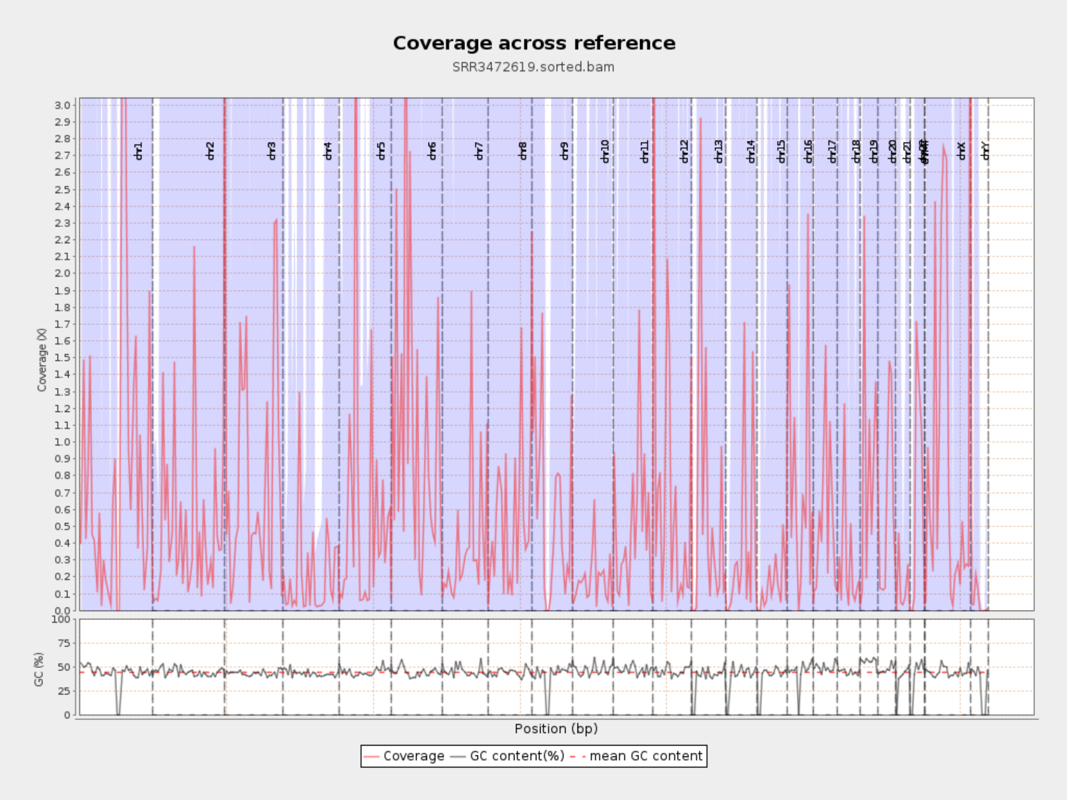
2.7. Chromosome stats

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

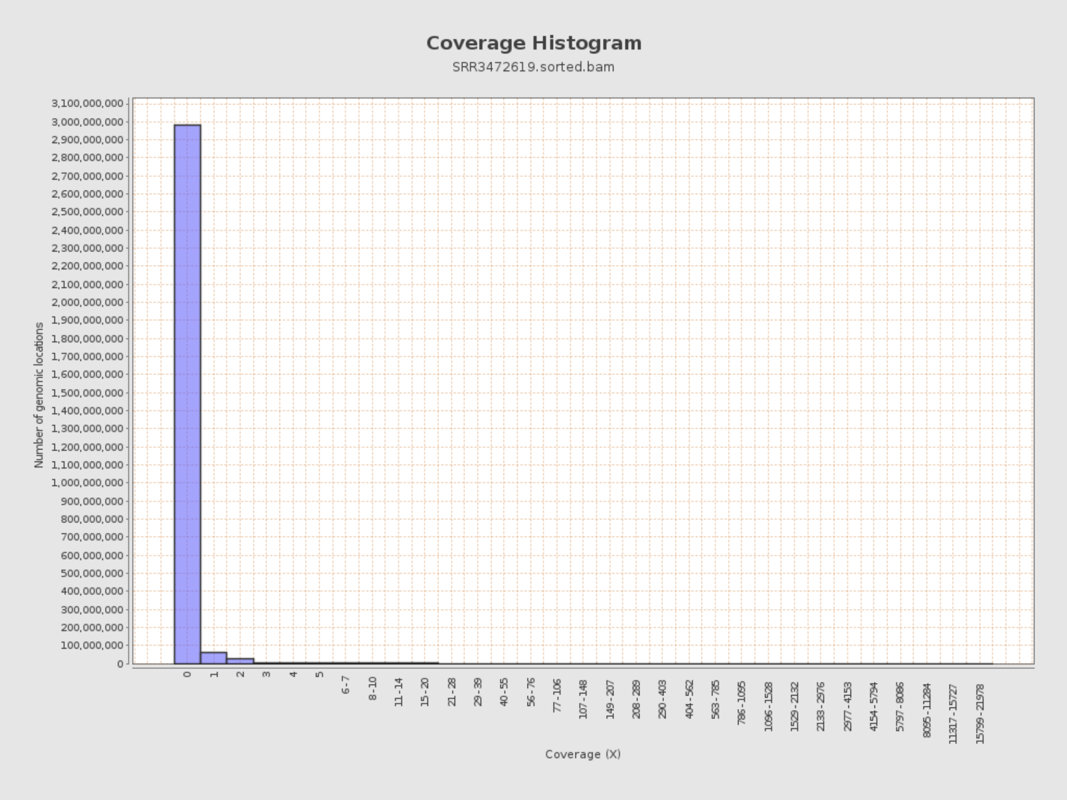
		bases	coverage	deviation
chr1	249250621	216604433	0.869	26.1566
chr2	243199373	117947207	0.485	18.3695
chr3	198022430	160887028	0.8125	23.1701
chr4	191154276	38606029	0.202	9.1314
chr5	180915260	106657238	0.5895	21.934
chr6	171115067	194836318	1.1386	42.2818
chr7	159138663	65247727	0.41	19.102
chr8	146364022	79576686	0.5437	17.6847
chr9	141213431	88561156	0.6271	18.3057
chr10	135534747	25308346	0.1867	11.0515
chr11	135006516	67723193	0.5016	15.0721
chr12	133851895	98727351	0.7376	21.2917
chr13	115169878	70665107	0.6136	21.5005
chr14	107349540	38363903	0.3574	17.446
chr15	102531392	16261274	0.1586	6.4705
chr16	90354753	70853264	0.7842	21.8031
chr17	81195210	45223089	0.557	16.3199
chr18	78077248	21640439	0.2772	16.4708
chr19	59128983	52691918	0.8911	26.6154
chr20	63025520	39452674	0.626	23.177
chr21	48129895	7229573	0.1502	8.2676
chr22	51304566	35912321	0.7	22.5537
chrMT	16571	3994	0.241	0.6296
chrX	155270560	138778650	0.8938	33.7302

chrY	59373566	3233888	0.0545	4.6653

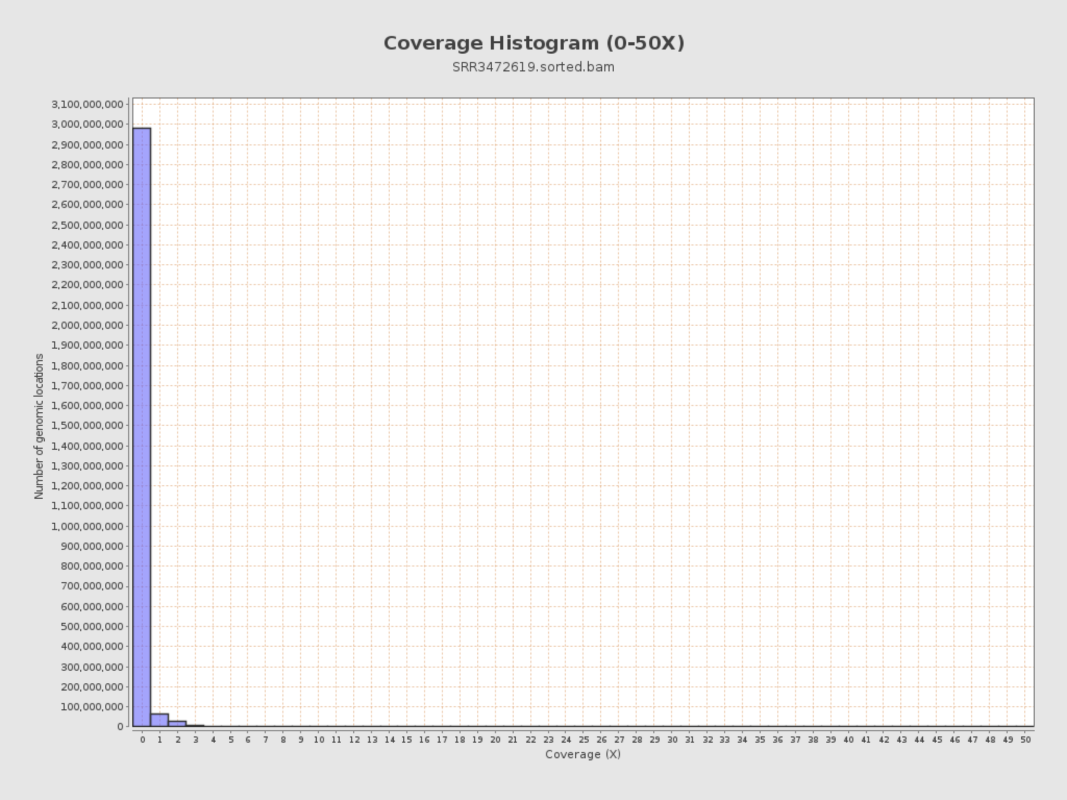
3. Results : Coverage across reference



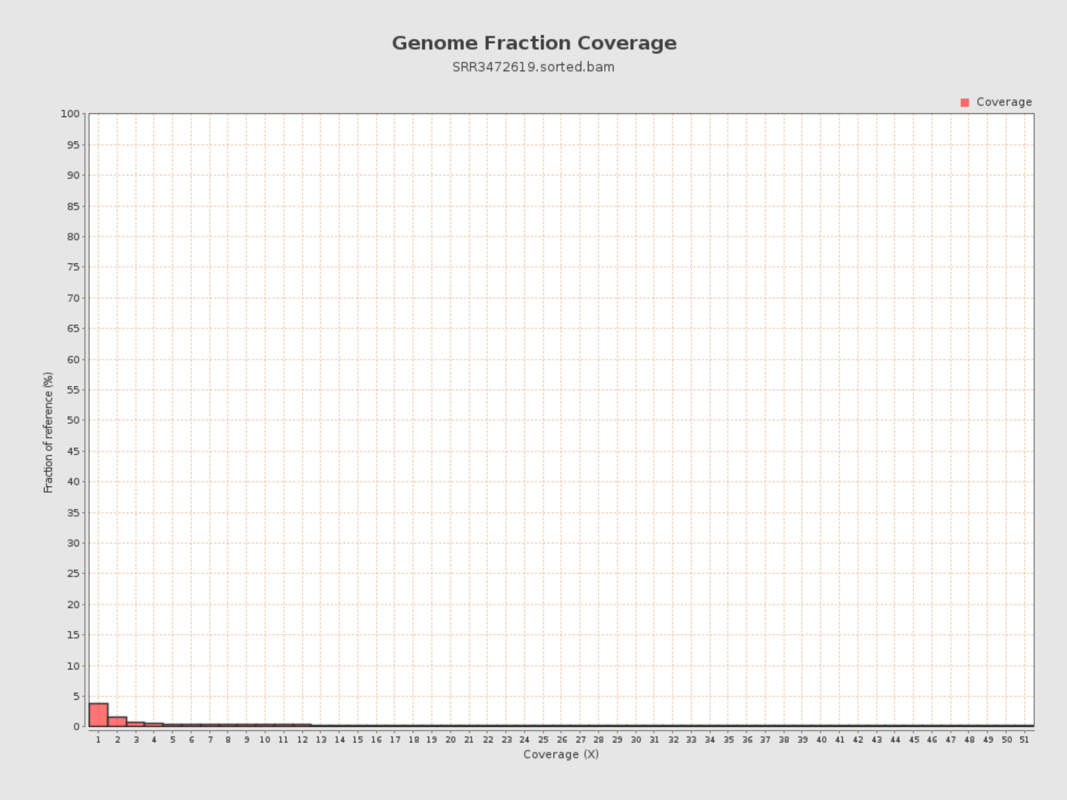
4. Results : Coverage Histogram



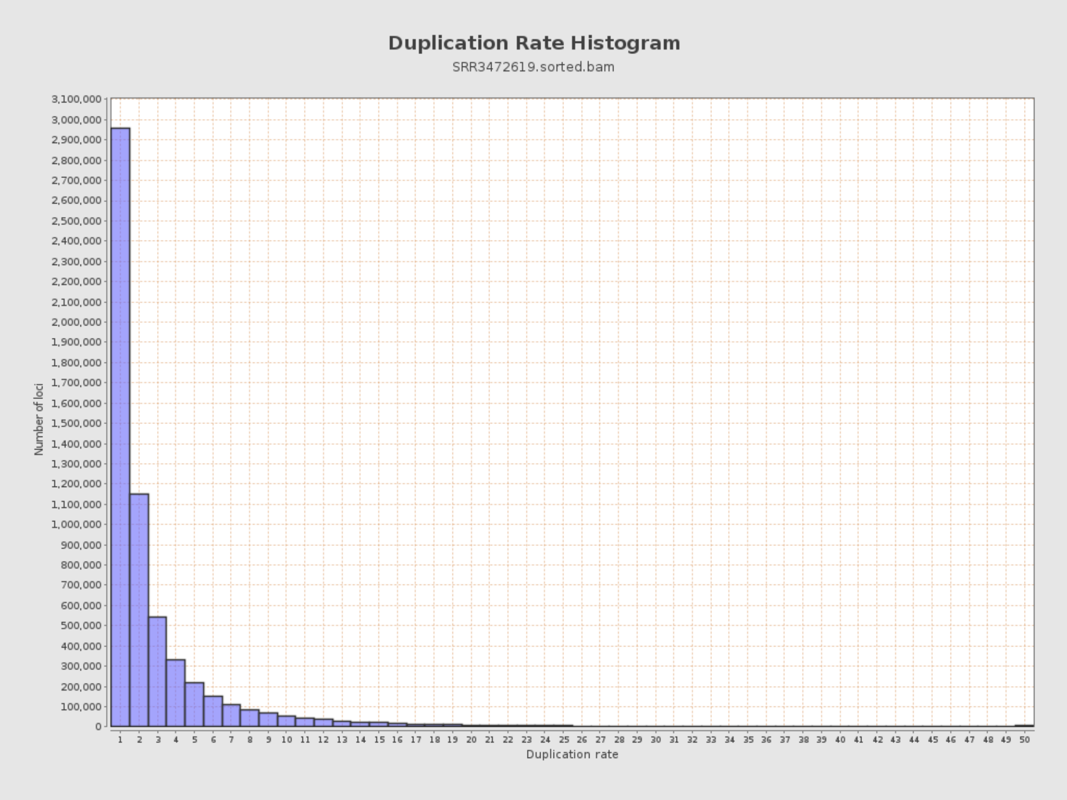
5. Results : Coverage Histogram (0-50X)



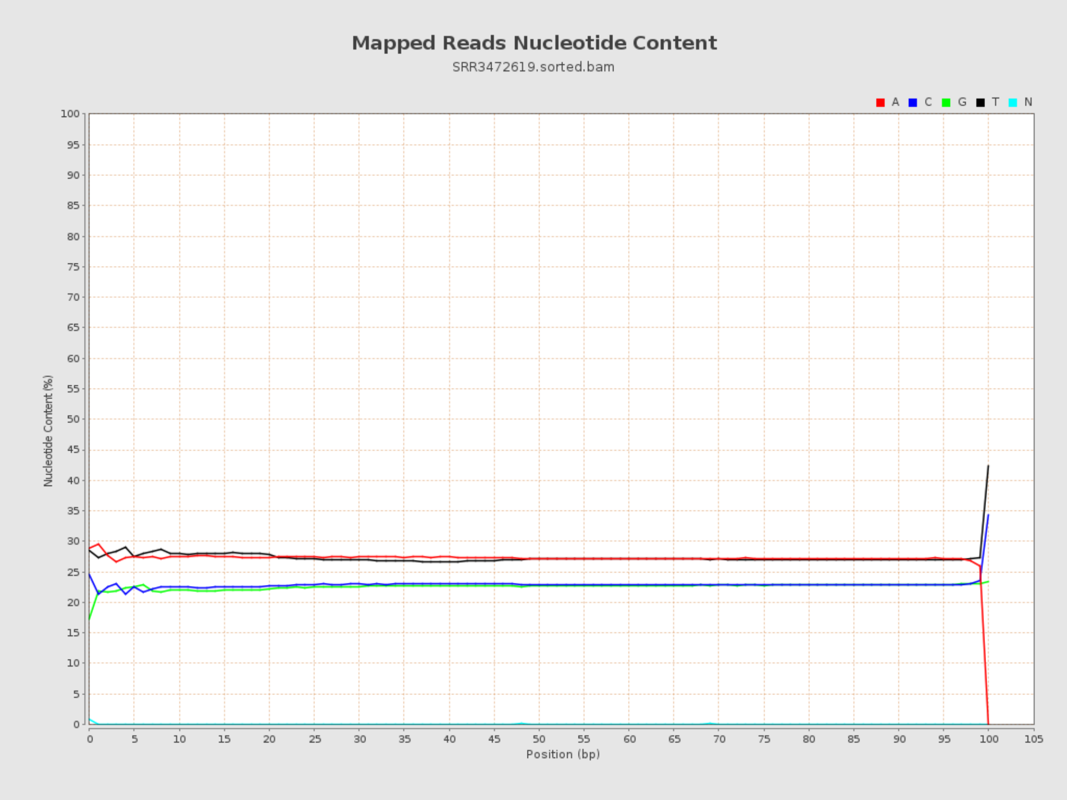
6. Results : Genome Fraction Coverage



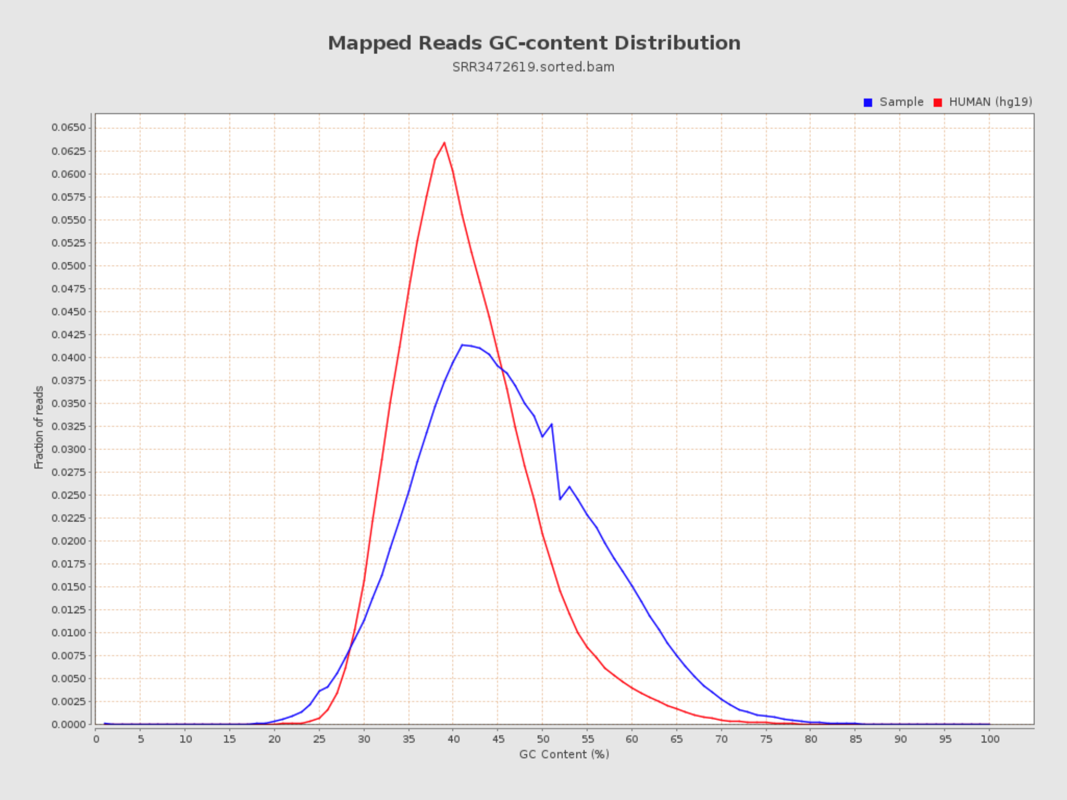
7. Results : Duplication Rate Histogram



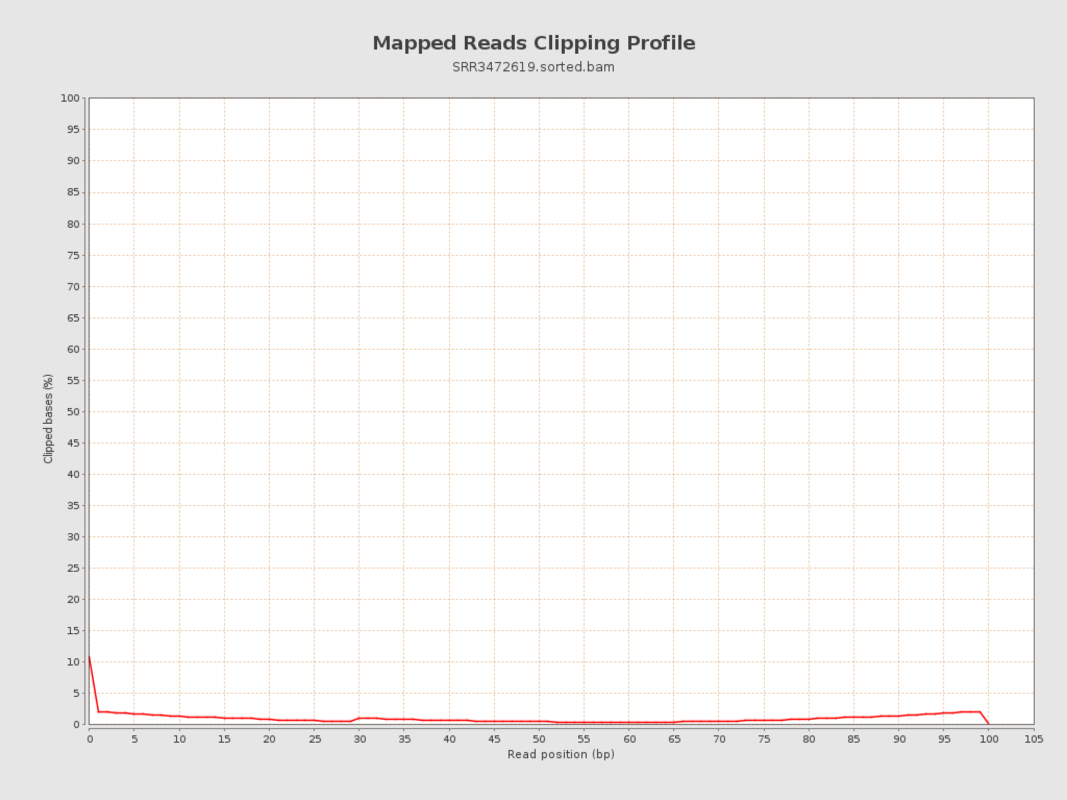
8. Results : Mapped Reads Nucleotide Content



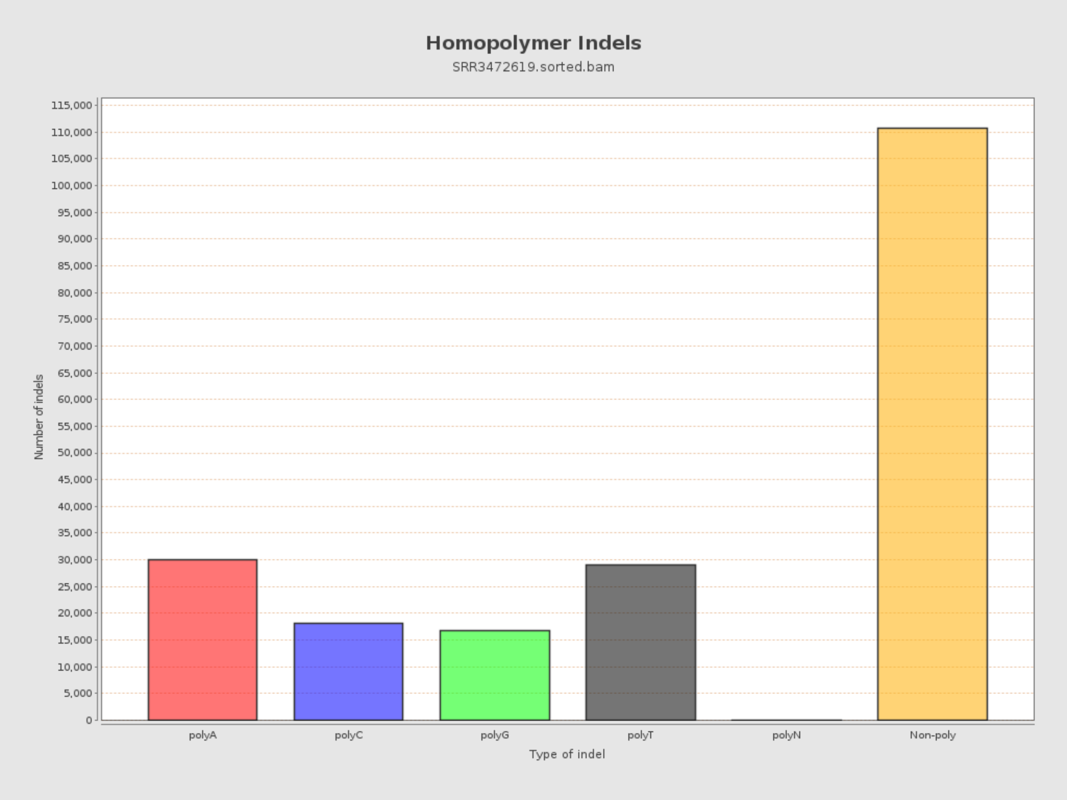
9. Results : Mapped Reads GC-content Distribution



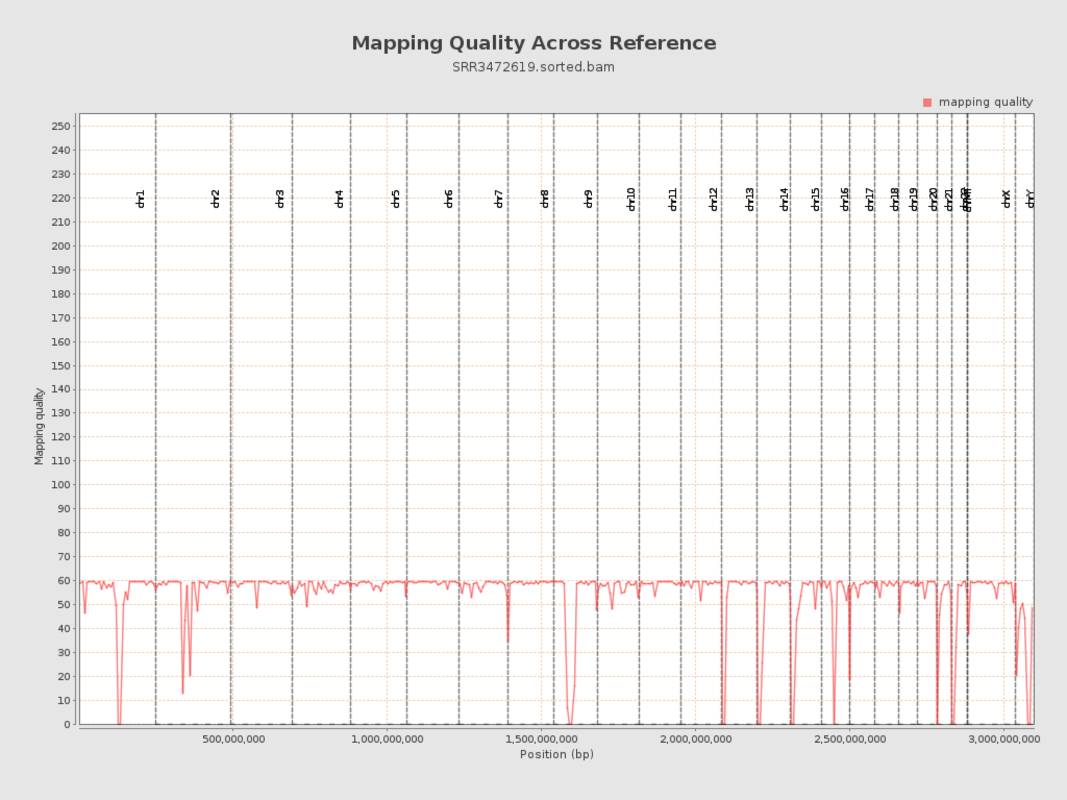
10. Results : Mapped Reads Clipping Profile



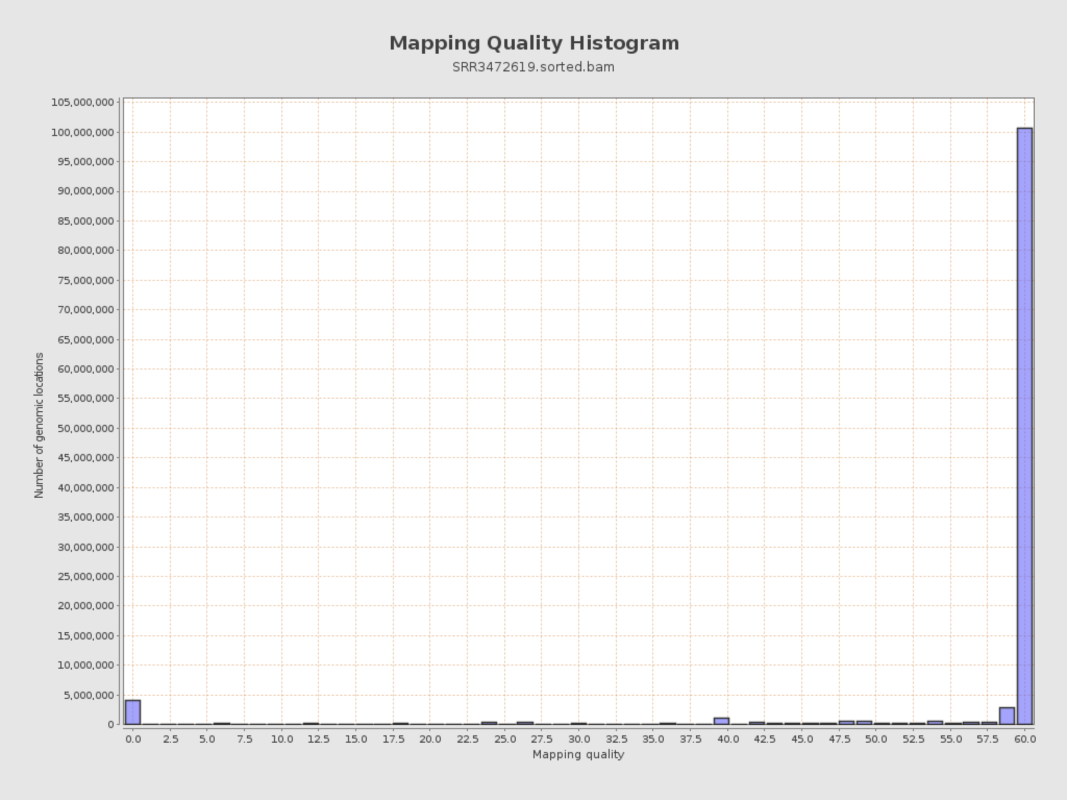
11. Results : Homopolymer Indels



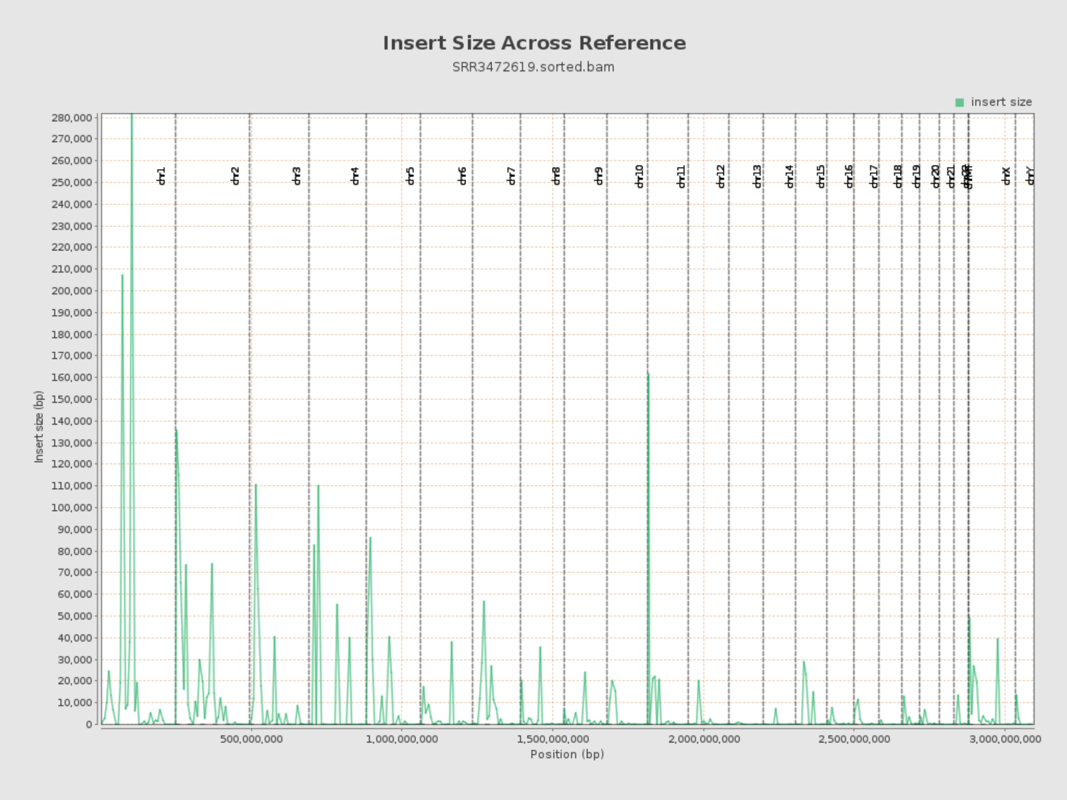
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram