

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 13:55:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472622.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_SRR3472622 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472622_1.fastq.gz SRR3472622_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 13:55:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472622.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,428,788
Mapped reads	16,293,837 / 99.18%
Unmapped reads	134,951 / 0.82%
Mapped paired reads	16,293,837 / 99.18%
Mapped reads, first in pair	8,169,331 / 49.73%
Mapped reads, second in pair	8,124,506 / 49.45%
Mapped reads, both in pair	16,202,572 / 98.62%
Mapped reads, singletons	91,265 / 0.56%
Secondary alignments	0
Supplementary alignments	85,638 / 0.52%
Read min/max/mean length	30 / 101 / 99.75
Duplicated reads (estimated)	11,150,612 / 67.87%
Duplication rate	49.62%
Clipped reads	1,090,919 / 6.64%

2.2. ACGT Content

Number/percentage of A's	428,874,108 / 26.73%
Number/percentage of C's	375,475,235 / 23.4%
Number/percentage of T's	429,748,260 / 26.79%
Number/percentage of G's	369,970,998 / 23.06%
Number/percentage of N's	294,088 / 0.02%

GC Percentage	46.46%
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2.3. Coverage

Mean	0.5183
Standard Deviation	22.1528

2.4. Mapping Quality

Mean Mapping Quality	54.64
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2.5. Insert size

Mean	20,473.58
Standard Deviation	1,413,404.03
P25/Median/P75	163 / 226 / 299

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	10,117,528
Insertions	99,550
Mapped reads with at least one insertion	0.6%
Deletions	91,595
Mapped reads with at least one deletion	0.56%
Homopolymer indels	46.18%

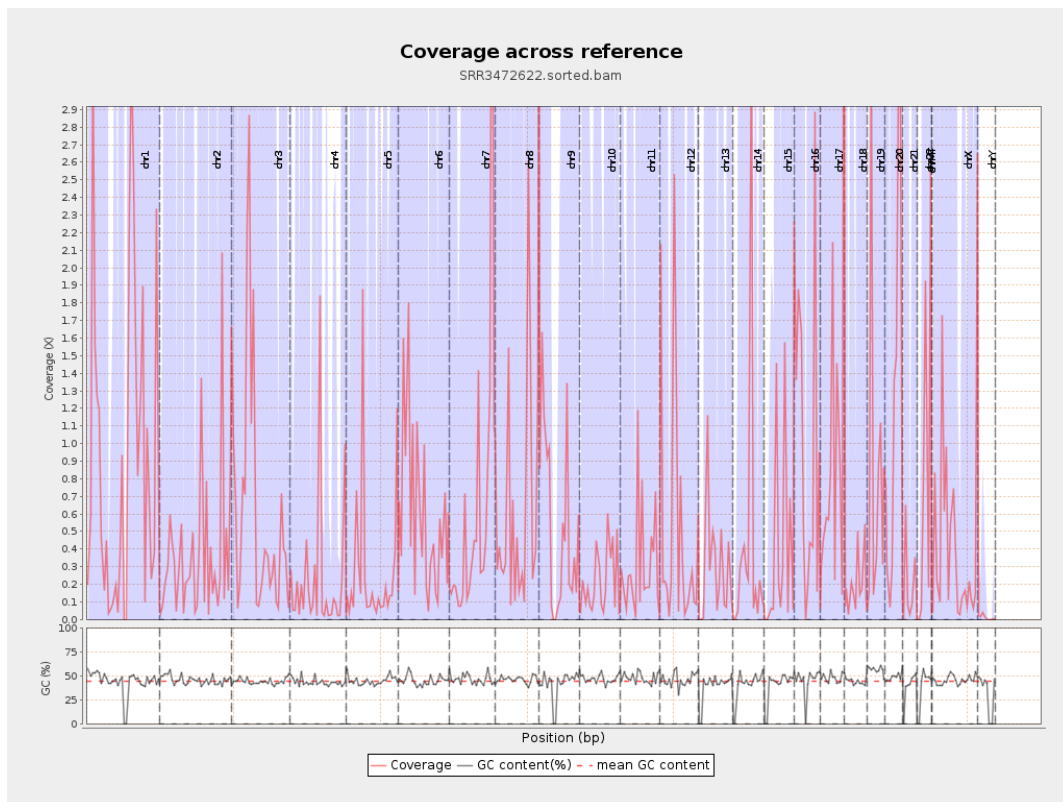
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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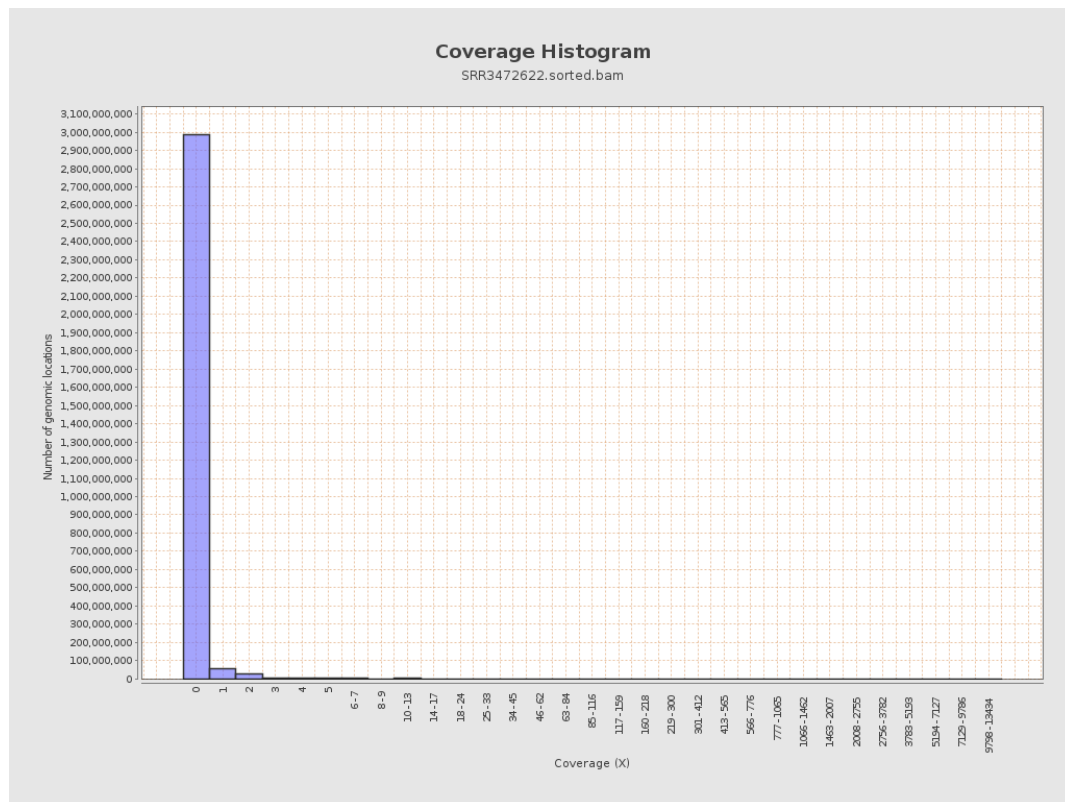
		bases	coverage	deviation
chr1	249250621	233691493	0.9376	30.9586
chr2	243199373	88837248	0.3653	17.4206
chr3	198022430	124759295	0.63	18.2515
chr4	191154276	41189306	0.2155	15.0144
chr5	180915260	50561567	0.2795	12.3464
chr6	171115067	102244991	0.5975	17.2339
chr7	159138663	106136281	0.6669	40.8899
chr8	146364022	92291763	0.6306	22.0863
chr9	141213431	77960986	0.5521	16.3944
chr10	135534747	29791613	0.2198	12.0305
chr11	135006516	42638339	0.3158	14.3548
chr12	133851895	68115445	0.5089	16.5227
chr13	115169878	35562288	0.3088	10.1522
chr14	107349540	43173318	0.4022	17.164
chr15	102531392	37168235	0.3625	17.7183
chr16	90354753	91350615	1.011	31.9917
chr17	81195210	77991359	0.9605	24.5944
chr18	78077248	16143613	0.2068	6.718
chr19	59128983	50364106	0.8518	35.6254
chr20	63025520	78206404	1.2409	48.3723
chr21	48129895	10211111	0.2122	13.0761
chr22	51304566	42589489	0.8301	38.7639
chrMT	16571	2375	0.1433	0.4863
chrX	155270560	62893318	0.4051	14.0791

chrY	59373566	704549	0.0119	0.3799
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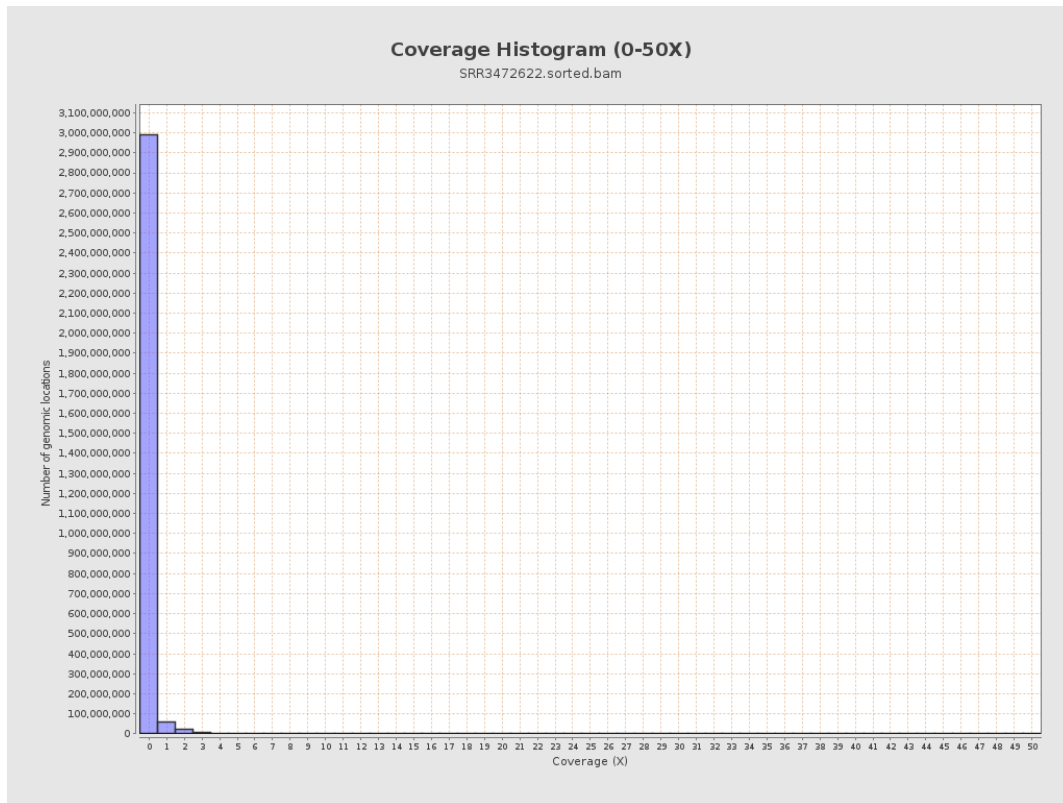
3. Results : Coverage across reference



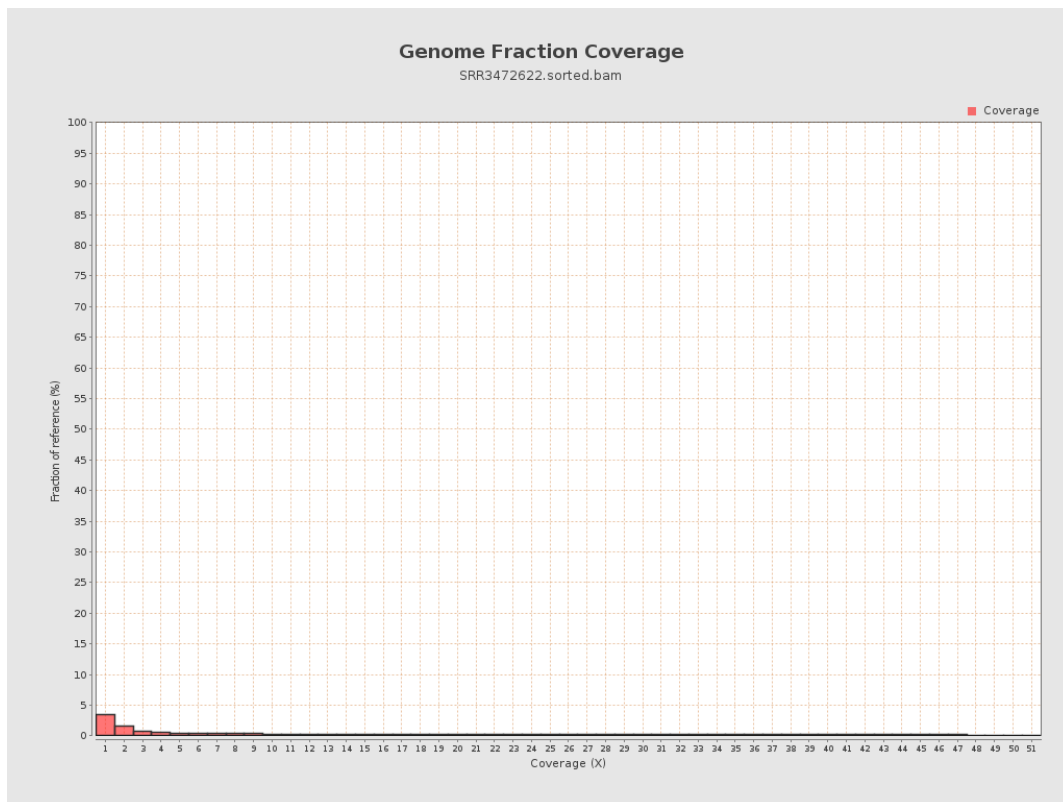
4. Results : Coverage Histogram



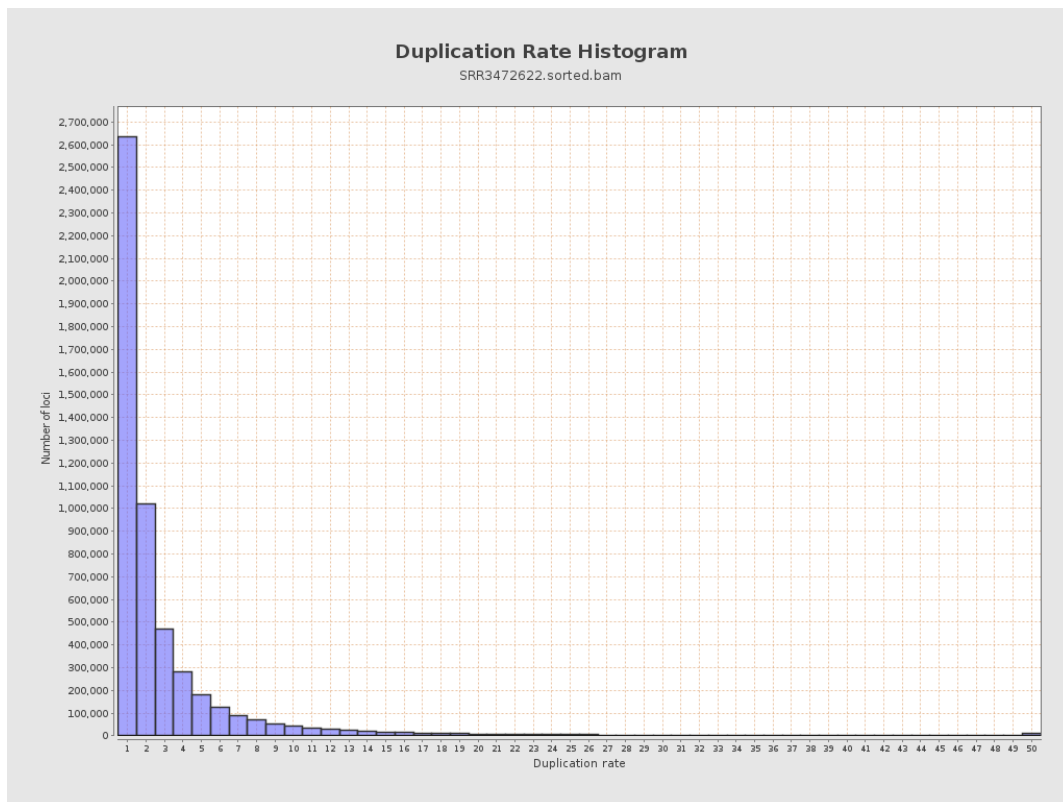
5. Results : Coverage Histogram (0-50X)



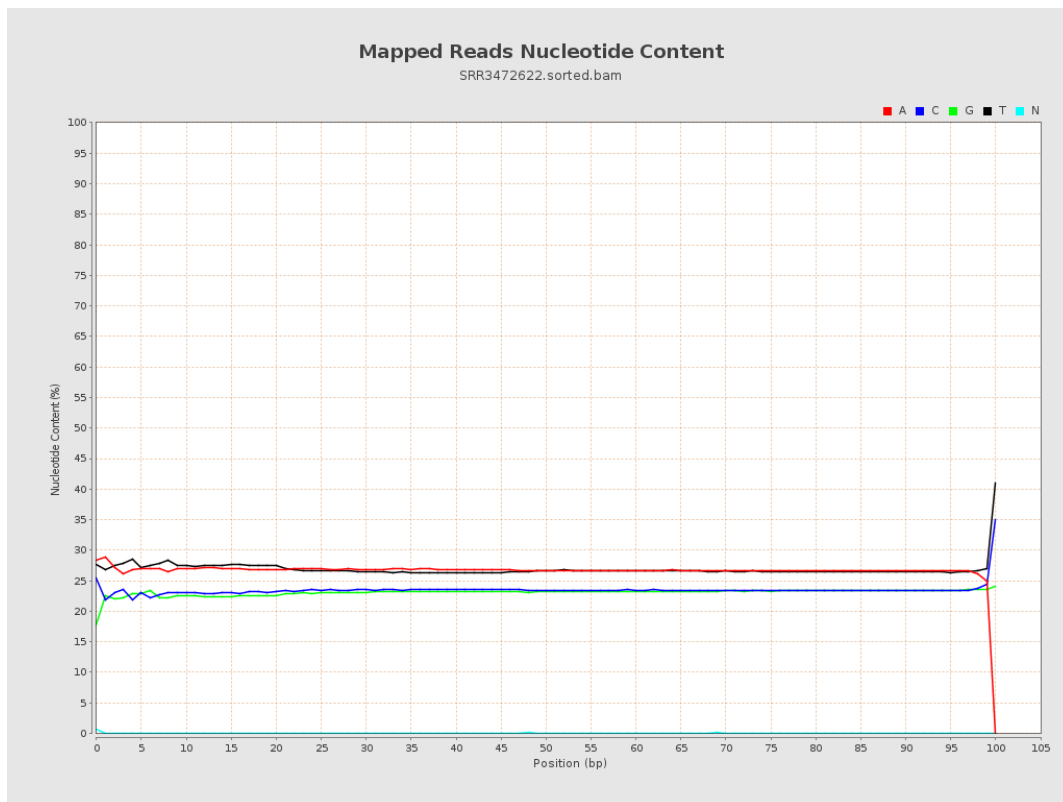
6. Results : Genome Fraction Coverage



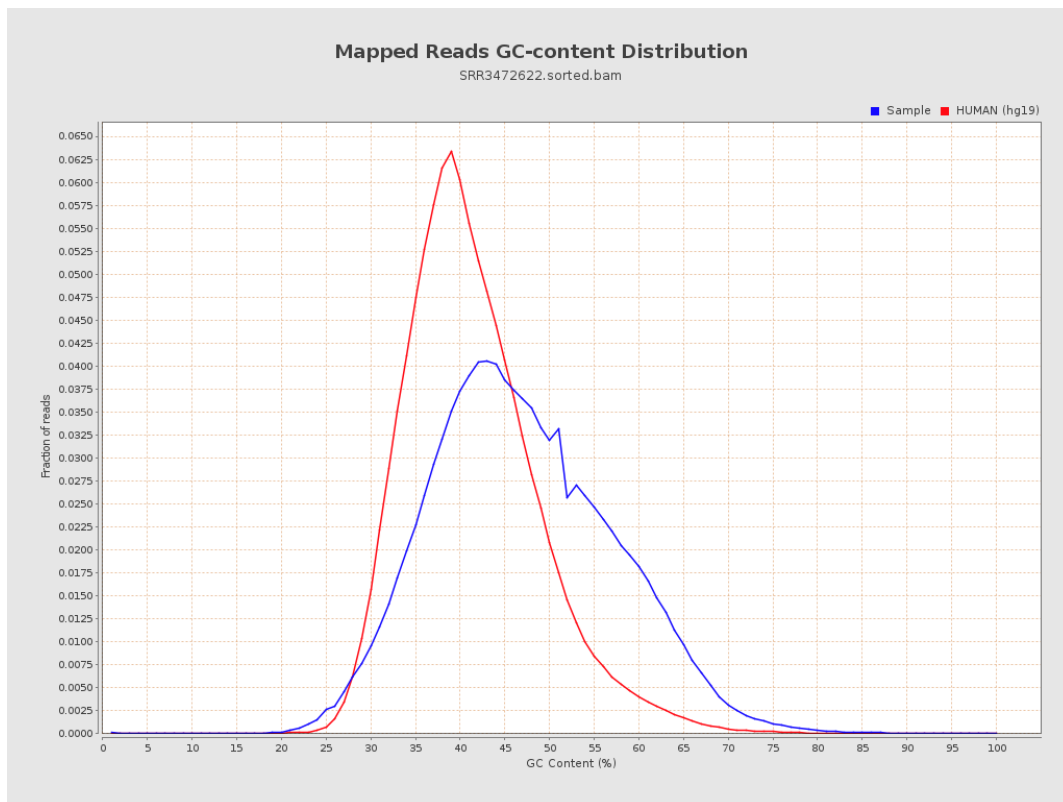
7. Results : Duplication Rate Histogram



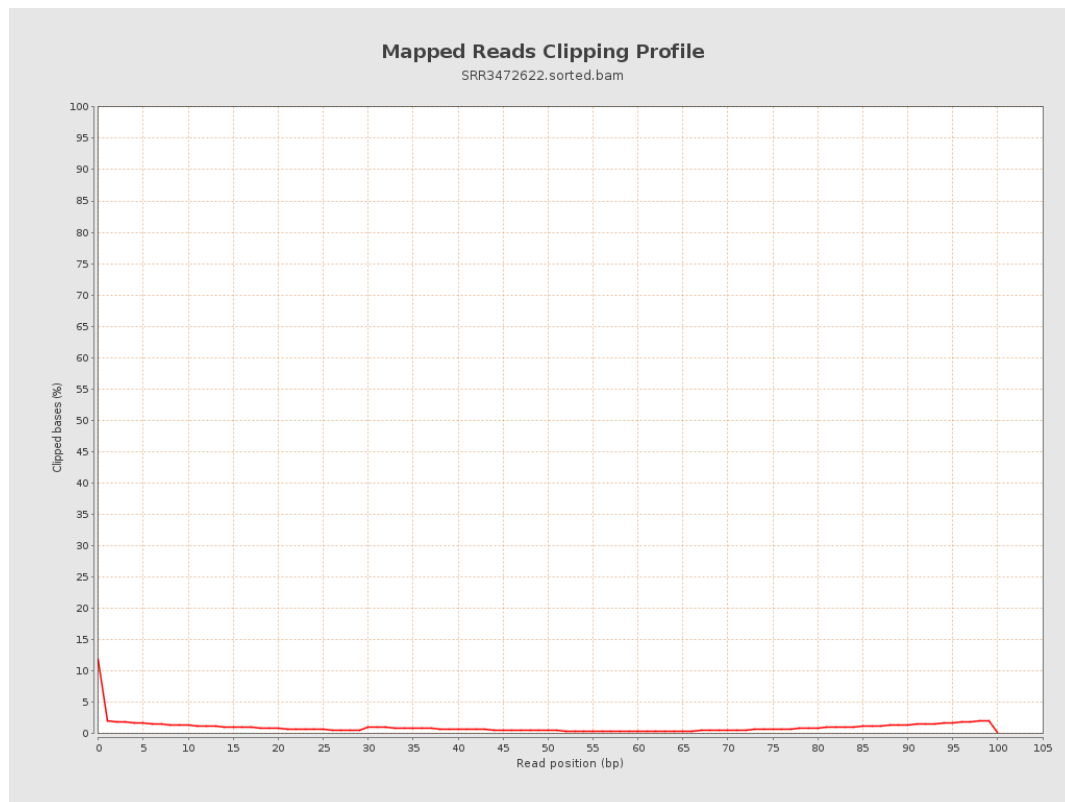
8. Results : Mapped Reads Nucleotide Content



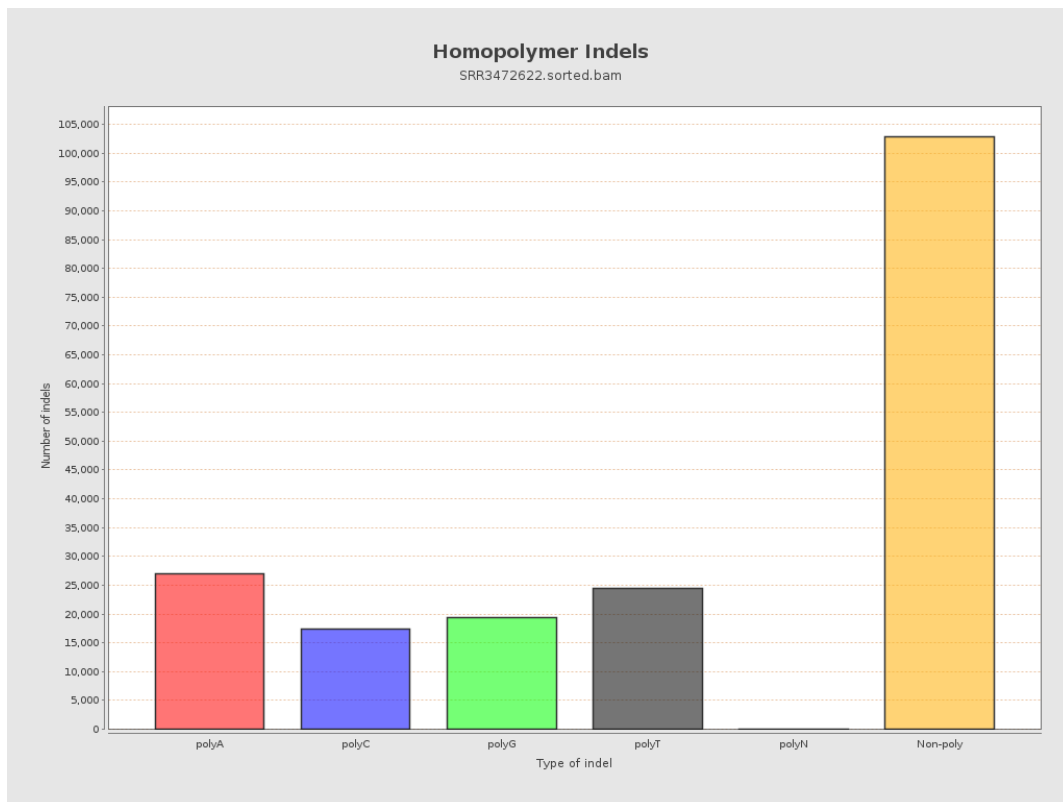
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



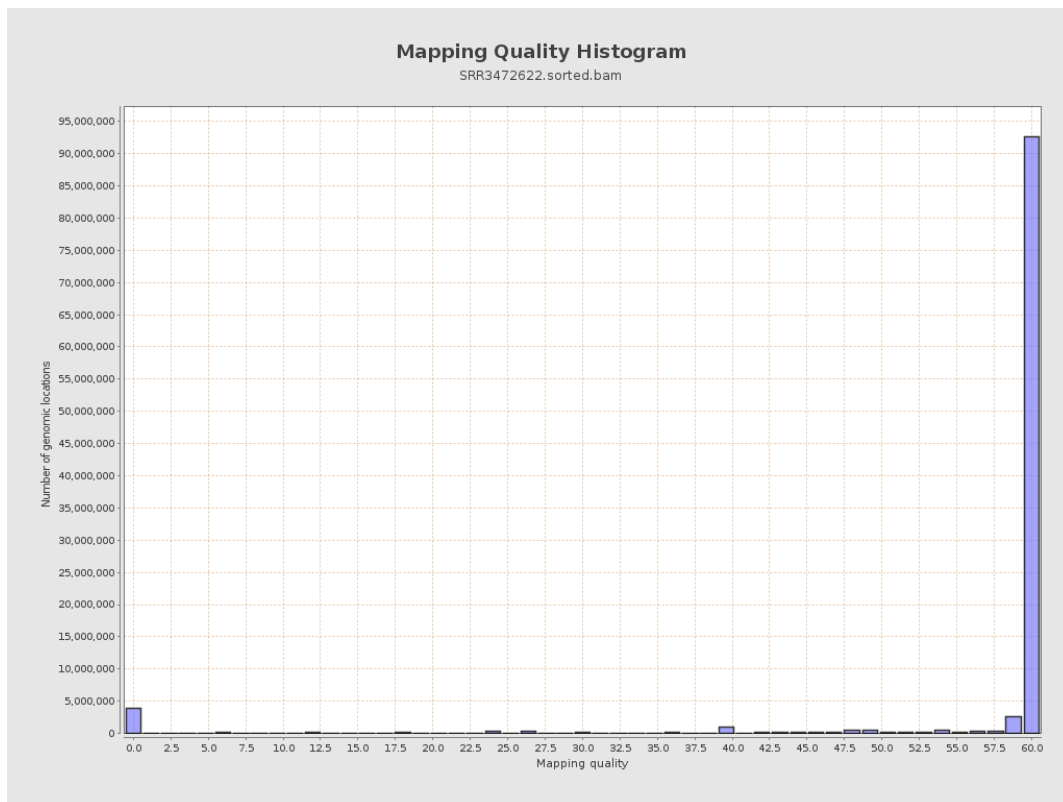
11. Results : Homopolymer Indels



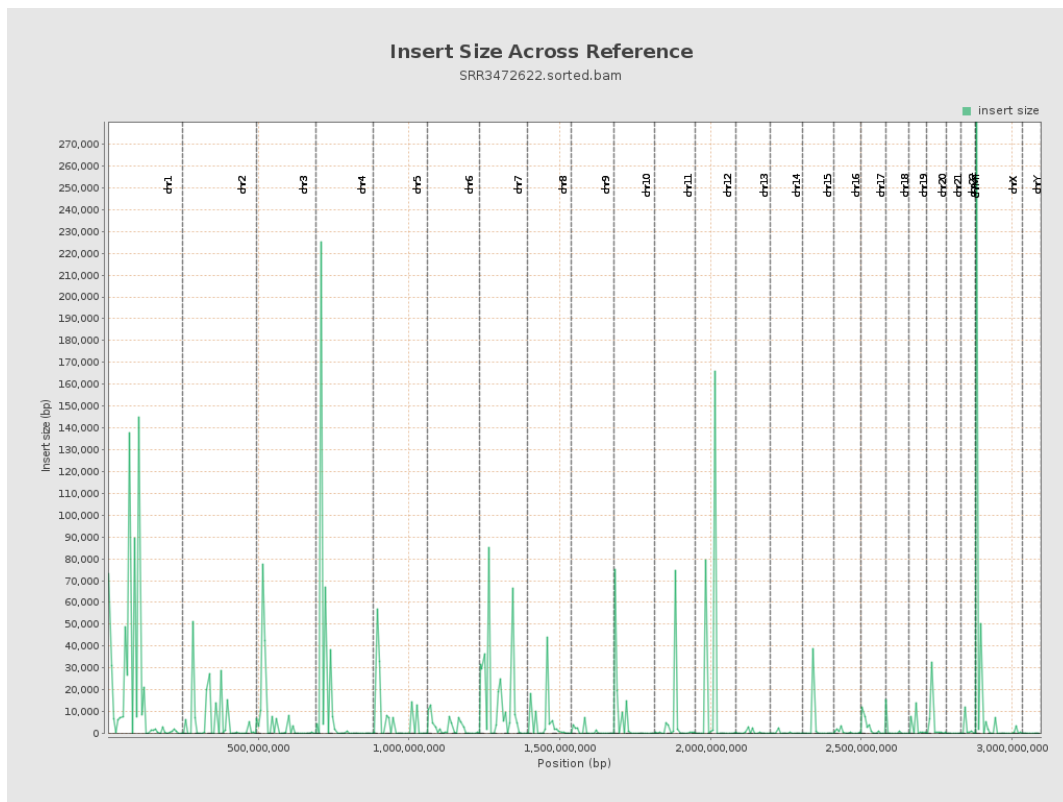
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

