

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 08:40:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472607.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_SRR3472607 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472607_1.fastq.gz SRR3472607_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 08:40:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472607.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,405,820
Mapped reads	15,267,478 / 99.1%
Unmapped reads	138,342 / 0.9%
Mapped paired reads	15,267,478 / 99.1%
Mapped reads, first in pair	7,657,062 / 49.7%
Mapped reads, second in pair	7,610,416 / 49.4%
Mapped reads, both in pair	15,179,648 / 98.53%
Mapped reads, singletons	87,830 / 0.57%
Secondary alignments	0
Supplementary alignments	69,993 / 0.45%
Read min/max/mean length	30 / 101 / 99.75
Duplicated reads (estimated)	10,145,862 / 65.86%
Duplication rate	49.12%
Clipped reads	984,071 / 6.39%

2.2. ACGT Content

Number/percentage of A's	397,208,255 / 26.41%
Number/percentage of C's	356,570,935 / 23.7%
Number/percentage of T's	398,885,246 / 26.52%
Number/percentage of G's	351,322,080 / 23.36%
Number/percentage of N's	279,804 / 0.02%

GC Percentage	47.06%
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2.3. Coverage

Mean	0.486
Standard Deviation	21.066

2.4. Mapping Quality

Mean Mapping Quality	54.92
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2.5. Insert size

Mean	20,154.07
Standard Deviation	1,388,408.45
P25/Median/P75	161 / 220 / 292

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	9,469,972
Insertions	88,664
Mapped reads with at least one insertion	0.57%
Deletions	82,023
Mapped reads with at least one deletion	0.52%
Homopolymer indels	45.24%

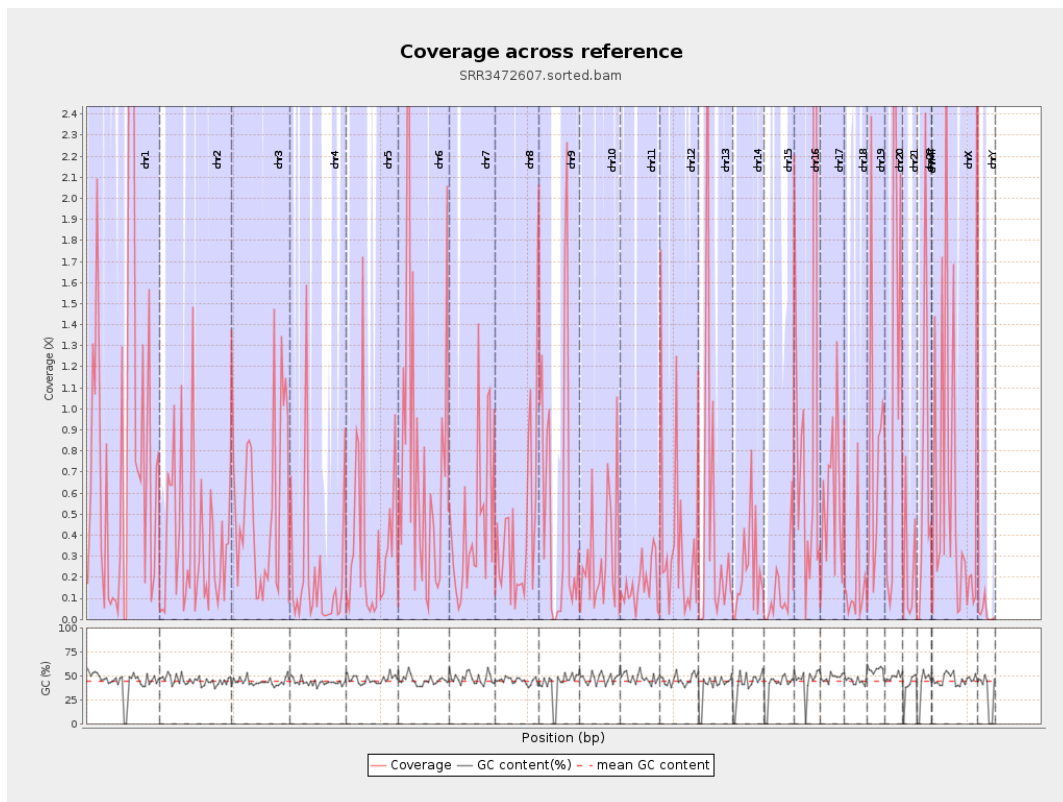
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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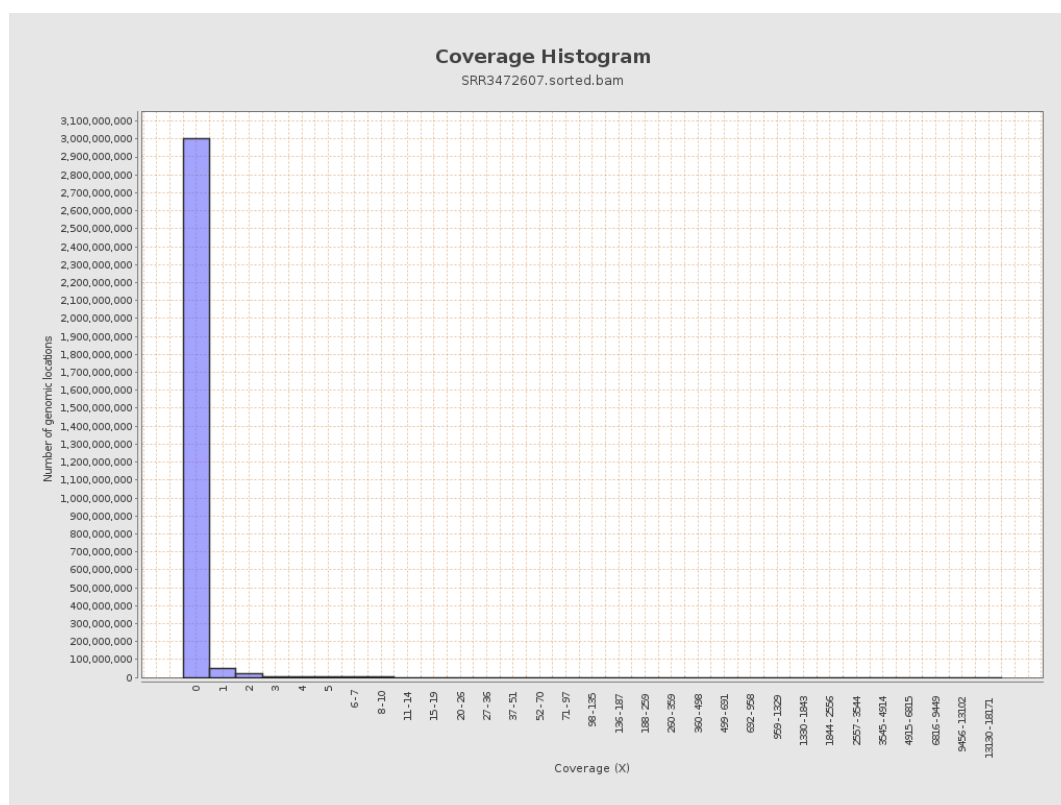
		bases	coverage	deviation
chr1	249250621	208337660	0.8359	27.2049
chr2	243199373	88961313	0.3658	12.9852
chr3	198022430	110765567	0.5594	16.3659
chr4	191154276	38288081	0.2003	10.0315
chr5	180915260	63138645	0.349	11.6914
chr6	171115067	129363122	0.756	31.7188
chr7	159138663	73308278	0.4607	14.3687
chr8	146364022	62101859	0.4243	20.4564
chr9	141213431	77495157	0.5488	24.1227
chr10	135534747	40041895	0.2954	11.8486
chr11	135006516	23203565	0.1719	6.435
chr12	133851895	50620295	0.3782	12.1918
chr13	115169878	53463046	0.4642	21.1566
chr14	107349540	24331059	0.2267	11.6079
chr15	102531392	14835422	0.1447	5.732
chr16	90354753	114794978	1.2705	56.6033
chr17	81195210	47402338	0.5838	14.2983
chr18	78077248	12908588	0.1653	9.3197
chr19	59128983	49414096	0.8357	20.4856
chr20	63025520	75779030	1.2024	39.3461
chr21	48129895	11102037	0.2307	13.1488
chr22	51304566	34817764	0.6786	21.9765
chrMT	16571	2906	0.1754	0.4647
chrX	155270560	98165503	0.6322	27.8215

chrY	59373566	1836413	0.0309	1.8648
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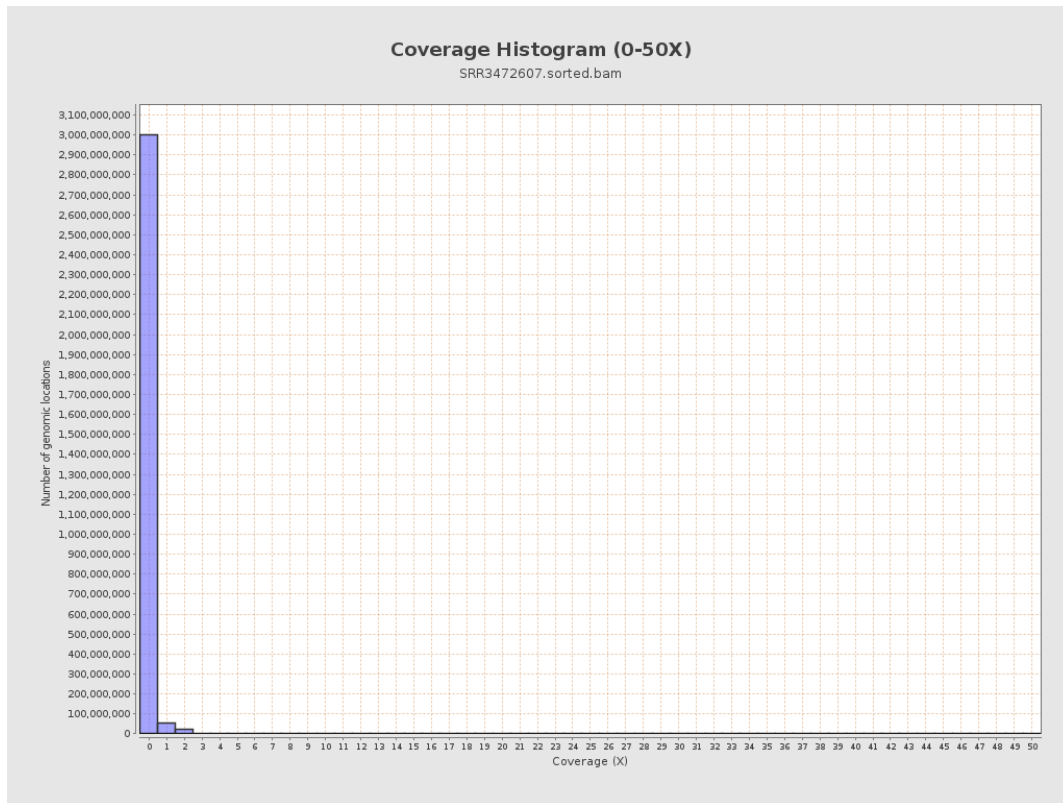
3. Results : Coverage across reference



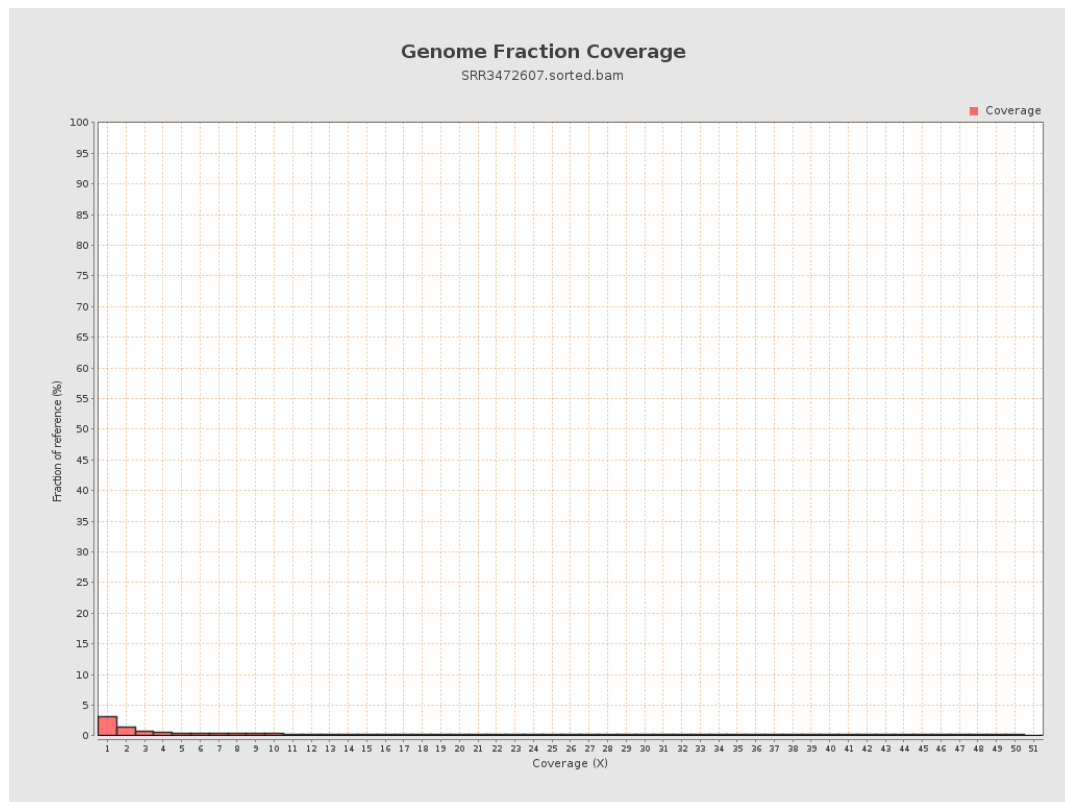
4. Results : Coverage Histogram



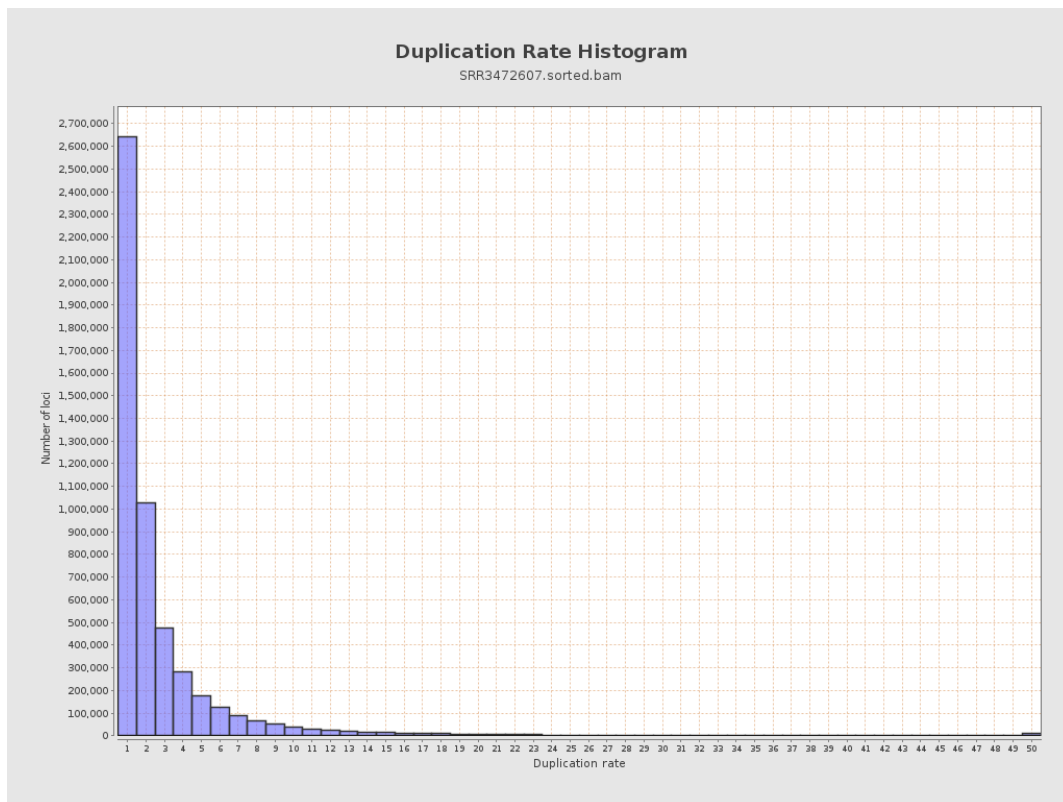
5. Results : Coverage Histogram (0-50X)



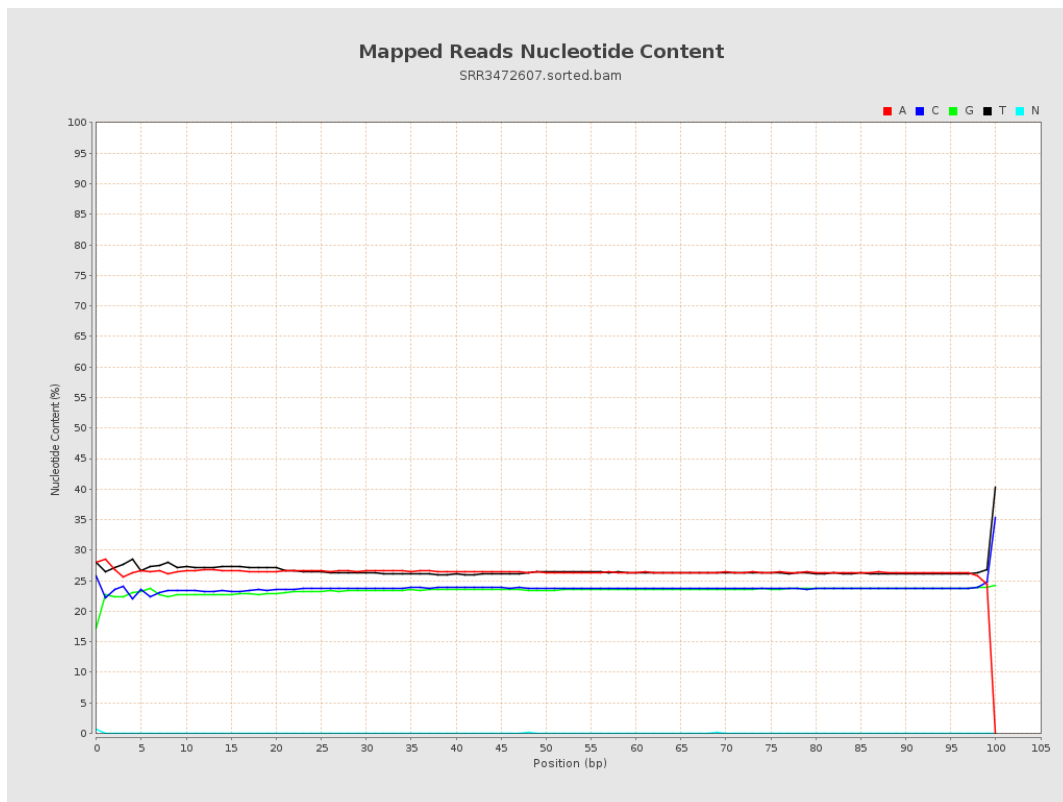
6. Results : Genome Fraction Coverage



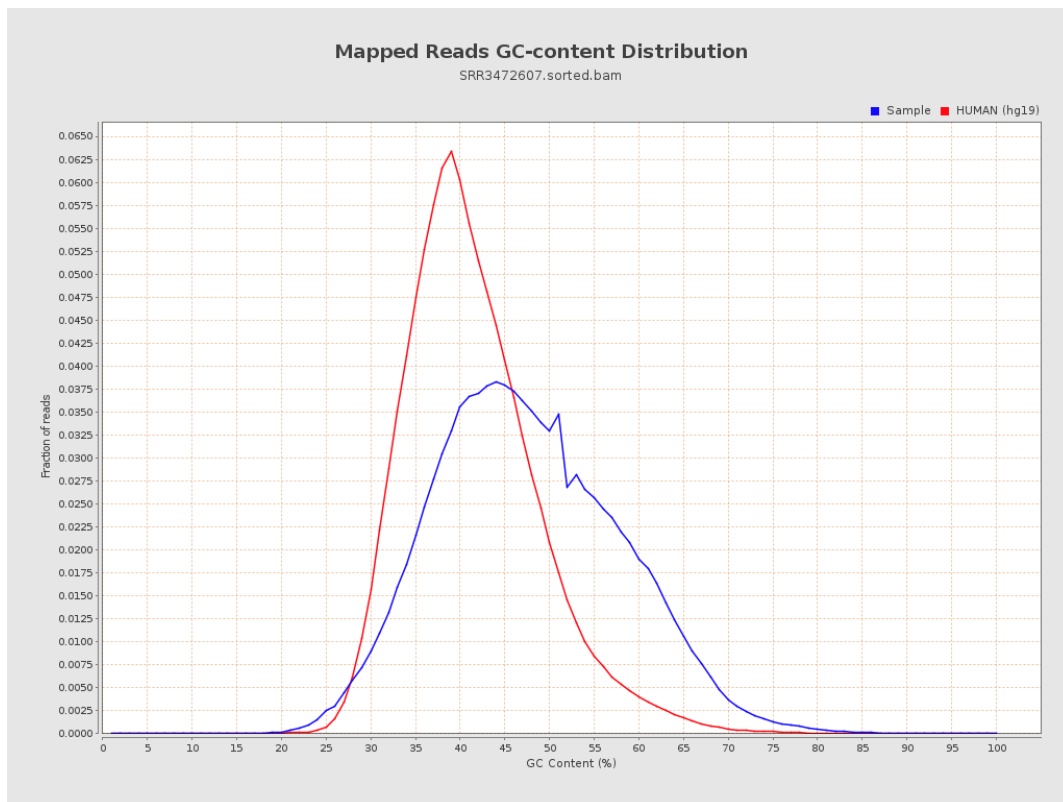
7. Results : Duplication Rate Histogram



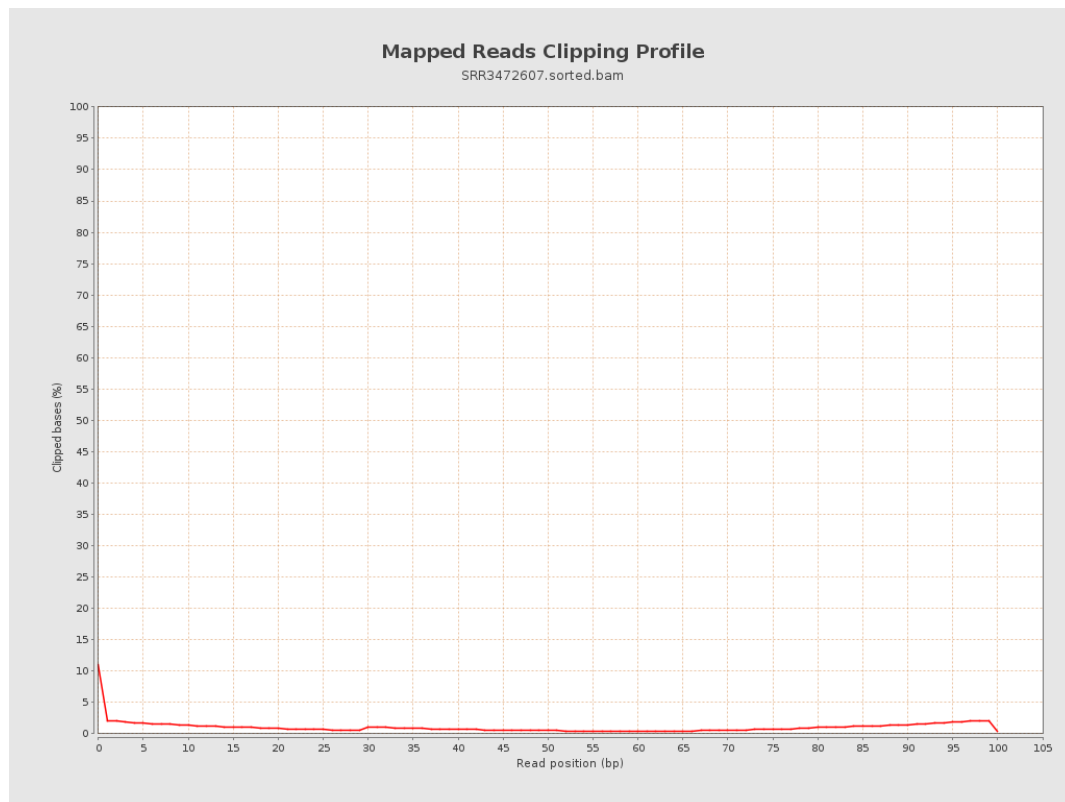
8. Results : Mapped Reads Nucleotide Content



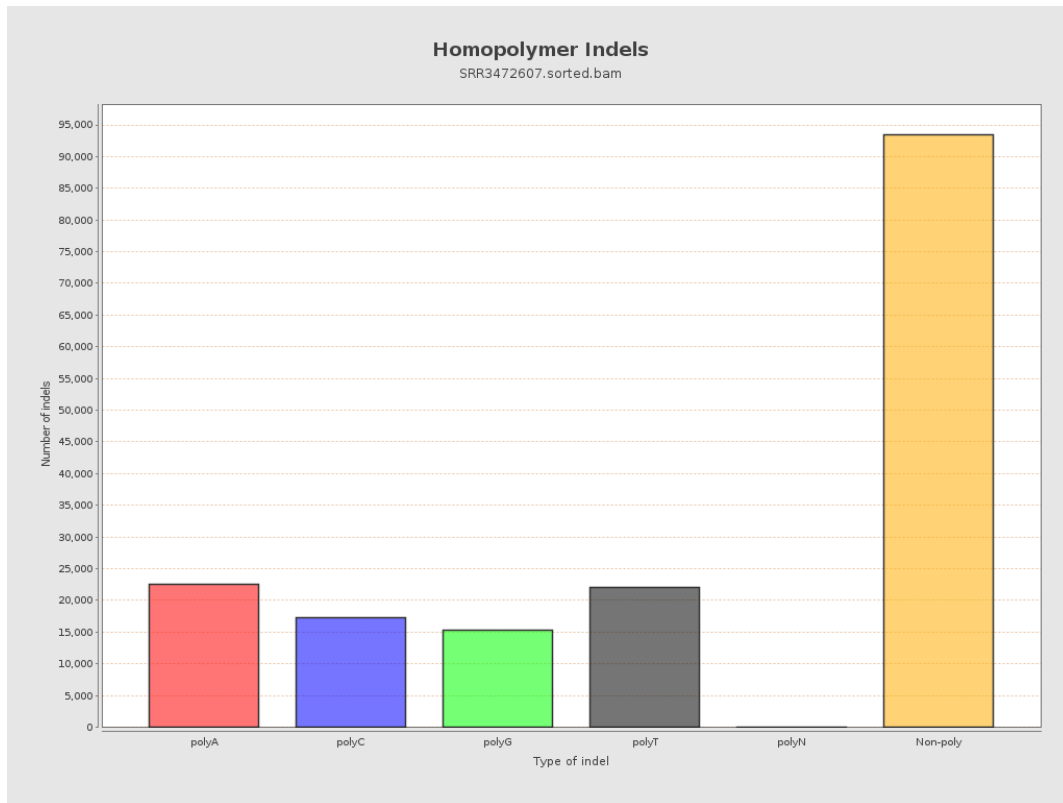
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



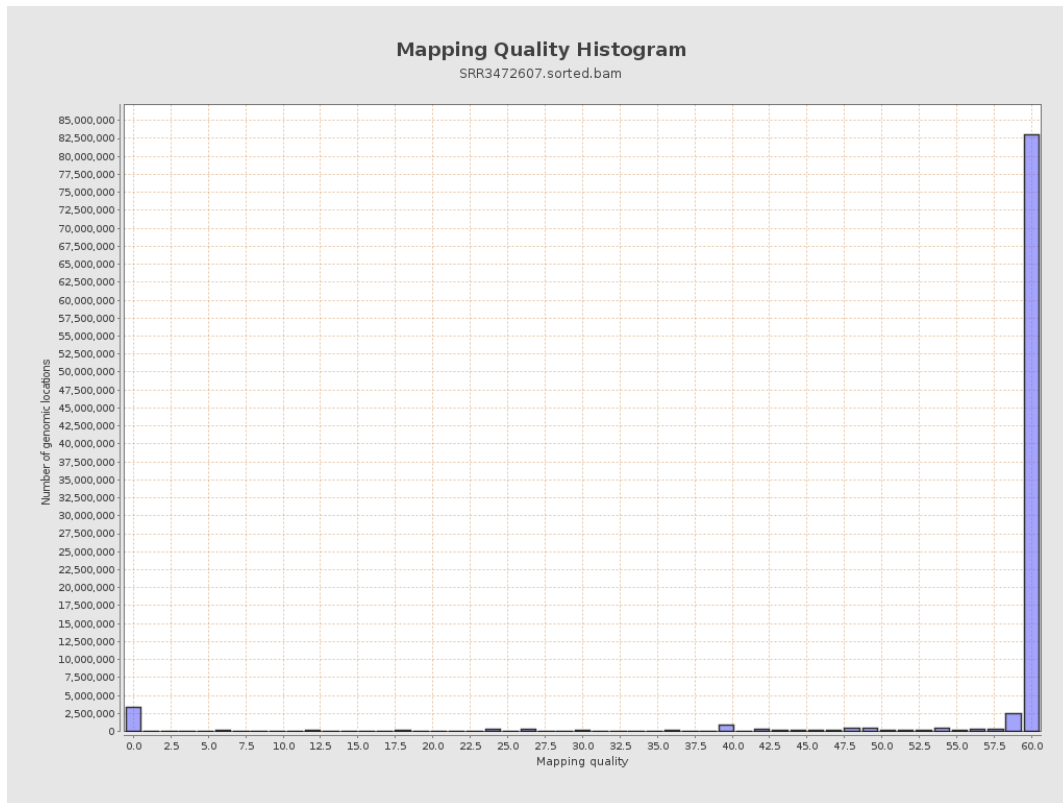
11. Results : Homopolymer Indels



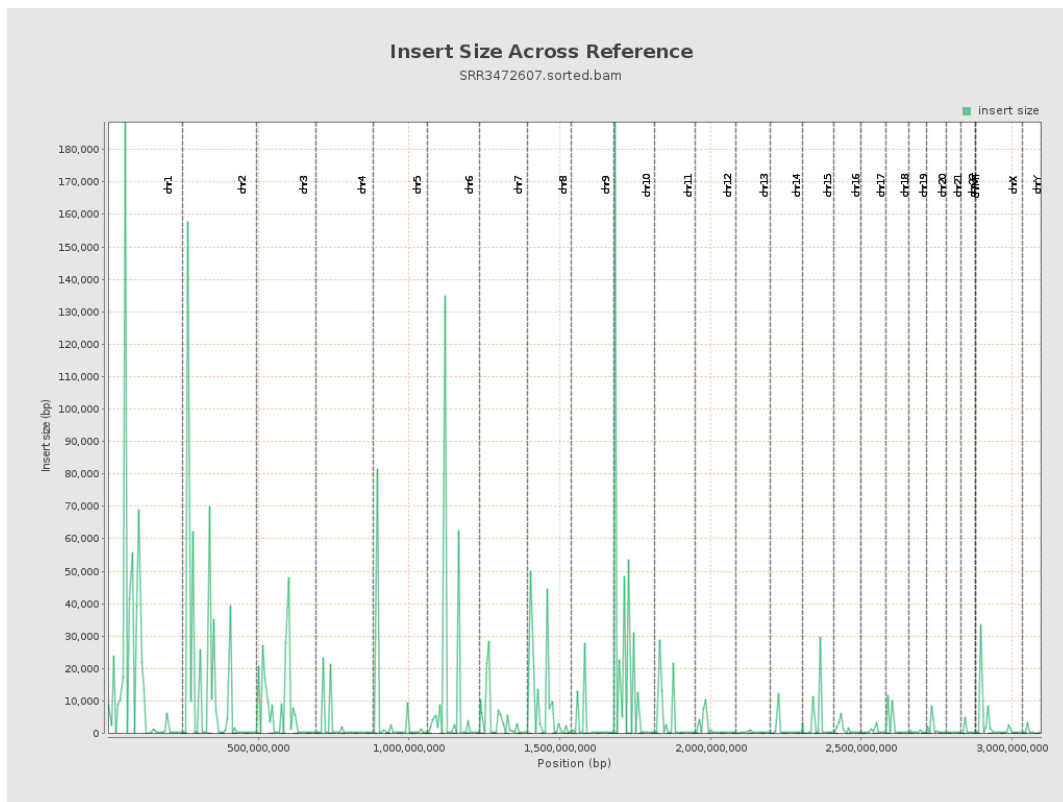
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

