

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 04:45:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472546.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_SRR3472546 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472546_1.fastq.gz SRR3472546_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 04:45:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472546.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,856,508
Mapped reads	15,680,236 / 98.89%
Unmapped reads	176,272 / 1.11%
Mapped paired reads	15,680,236 / 98.89%
Mapped reads, first in pair	7,857,548 / 49.55%
Mapped reads, second in pair	7,822,688 / 49.33%
Mapped reads, both in pair	15,594,662 / 98.35%
Mapped reads, singletons	85,574 / 0.54%
Secondary alignments	0
Supplementary alignments	68,263 / 0.43%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	9,615,482 / 60.64%
Duplication rate	45.05%
Clipped reads	1,561,751 / 9.85%

2.2. ACGT Content

Number/percentage of A's	421,362,842 / 27.41%
Number/percentage of C's	349,846,265 / 22.75%
Number/percentage of T's	418,738,794 / 27.24%
Number/percentage of G's	347,269,431 / 22.59%
Number/percentage of N's	236,161 / 0.02%

GC Percentage	45.34%
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2.3. Coverage

Mean	0.4967
Standard Deviation	16.9113

2.4. Mapping Quality

Mean Mapping Quality	55.01
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2.5. Insert size

Mean	30,679.24
Standard Deviation	1,713,443.71
P25/Median/P75	157 / 221 / 300

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	8,858,127
Insertions	80,535
Mapped reads with at least one insertion	0.51%
Deletions	75,792
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.25%

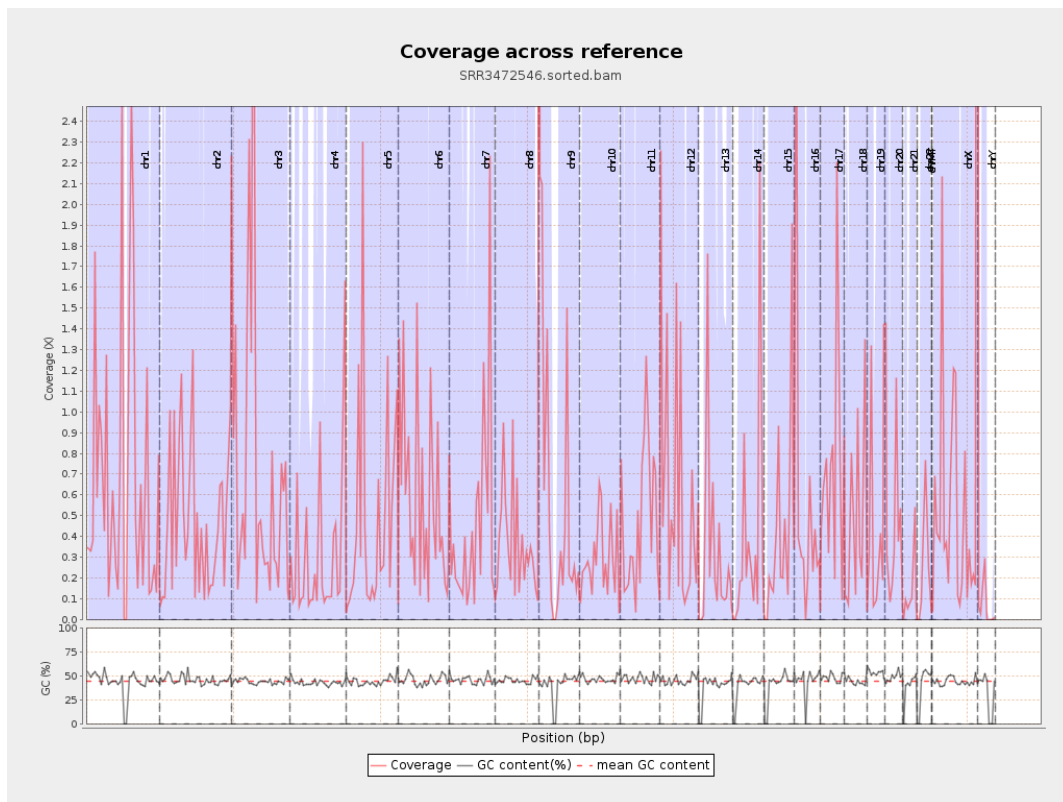
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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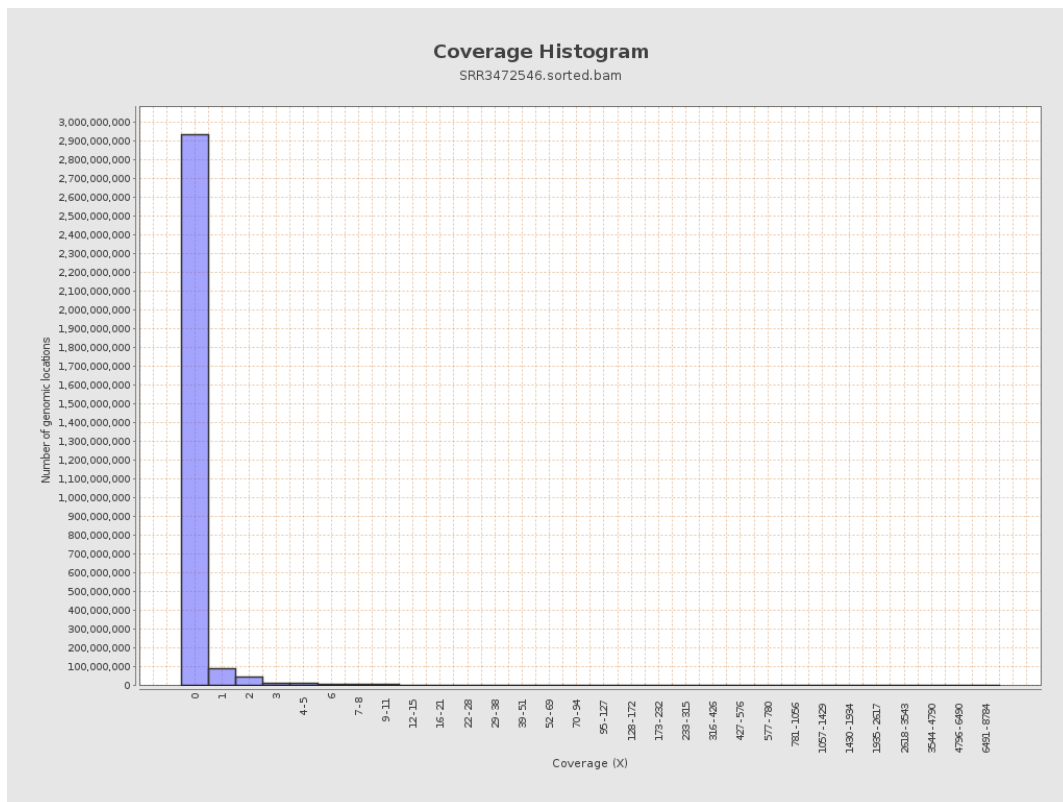
		bases	coverage	deviation
chr1	249250621	174064780	0.6984	20.4505
chr2	243199373	114713528	0.4717	17.468
chr3	198022430	146756863	0.7411	16.3698
chr4	191154276	56764692	0.297	12.0706
chr5	180915260	89874514	0.4968	18.8543
chr6	171115067	97733446	0.5712	15.3481
chr7	159138663	72411652	0.455	16.5912
chr8	146364022	54663949	0.3735	12.7171
chr9	141213431	84911578	0.6013	15.9211
chr10	135534747	39866616	0.2941	9.9132
chr11	135006516	64535085	0.478	14.4977
chr12	133851895	84877647	0.6341	18.9796
chr13	115169878	37055921	0.3218	11.9037
chr14	107349540	38955849	0.3629	14.8454
chr15	102531392	44839494	0.4373	16.7207
chr16	90354753	51338364	0.5682	15.6701
chr17	81195210	58099950	0.7156	17.3398
chr18	78077248	38375212	0.4915	16.8866
chr19	59128983	23549474	0.3983	13.291
chr20	63025520	31122782	0.4938	16.1886
chr21	48129895	7048423	0.1464	5.3327
chr22	51304566	12601070	0.2456	6.9071
chrMT	16571	1579	0.0953	0.356
chrX	155270560	109274988	0.7038	31.9728

chrY	59373566	4211850	0.0709	4.257
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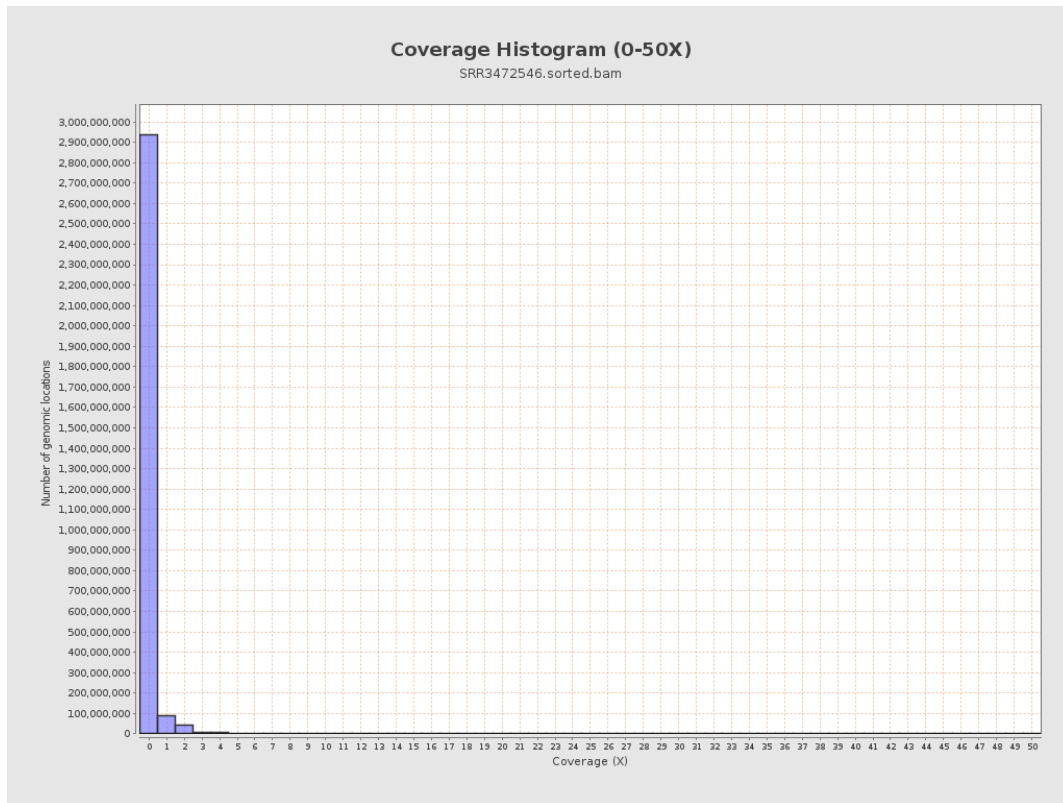
3. Results : Coverage across reference



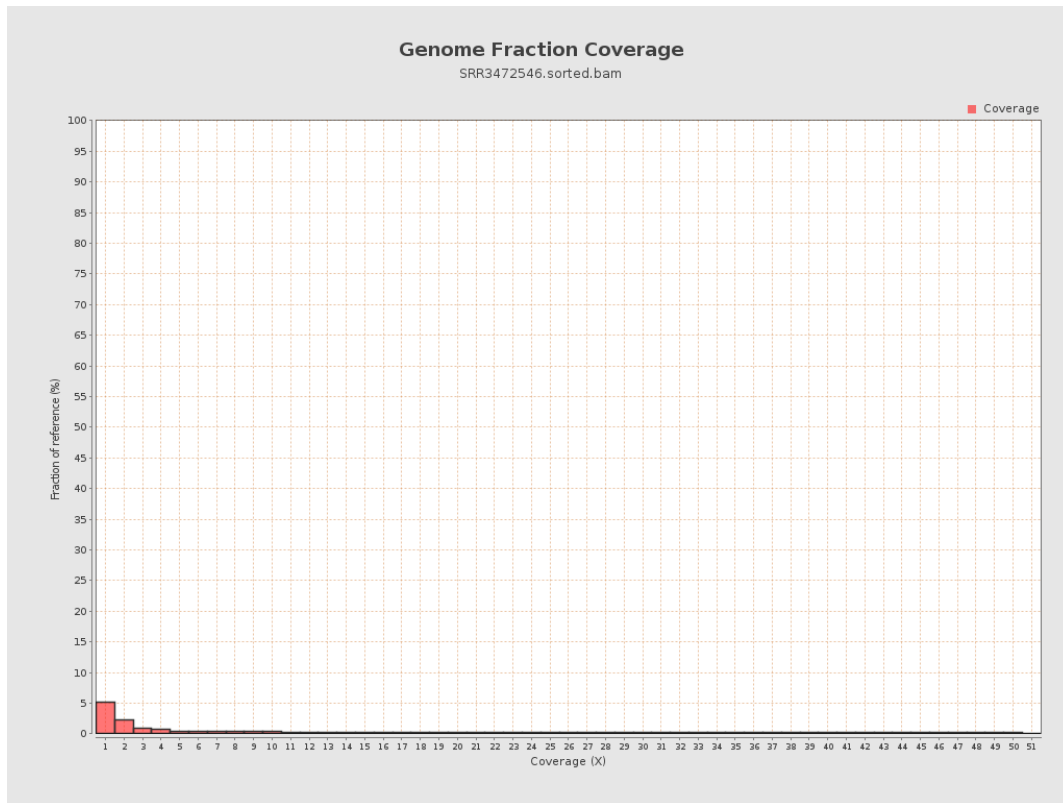
4. Results : Coverage Histogram



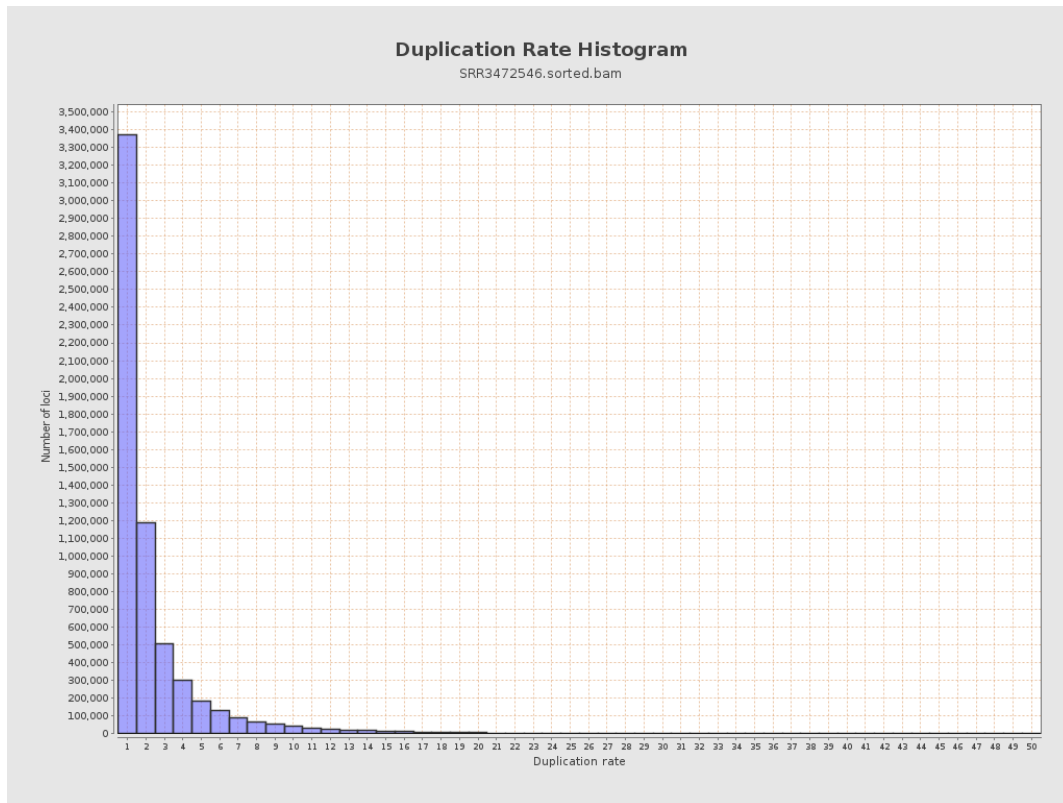
5. Results : Coverage Histogram (0-50X)



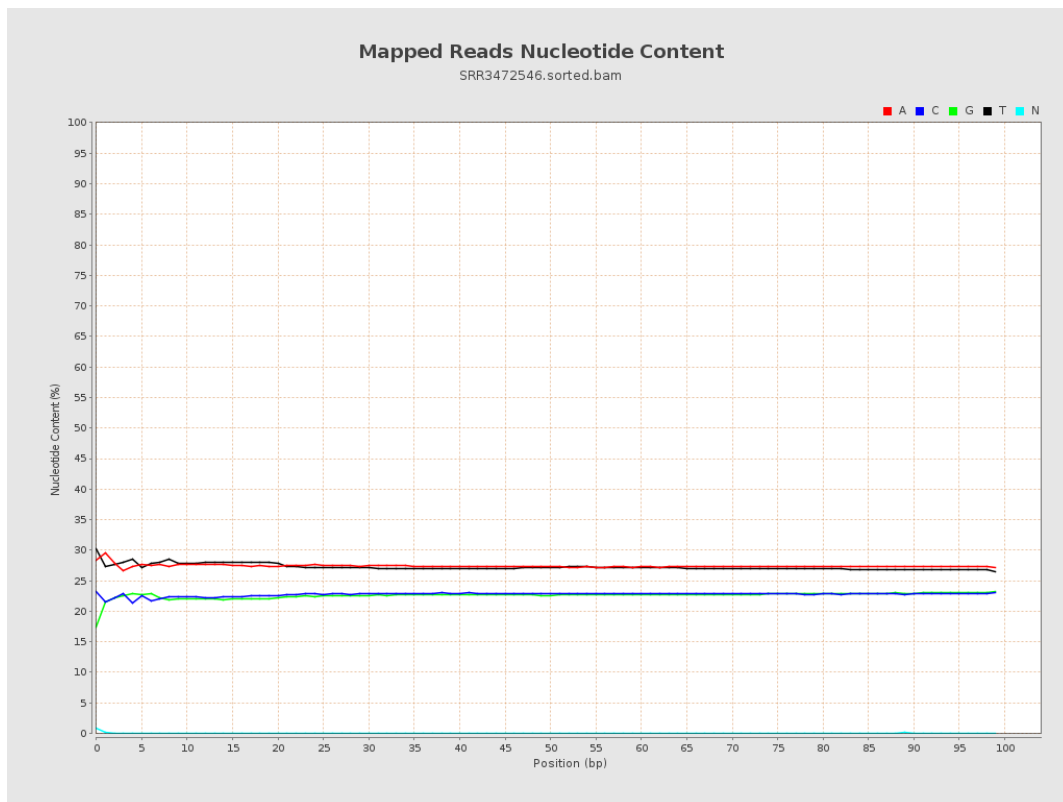
6. Results : Genome Fraction Coverage



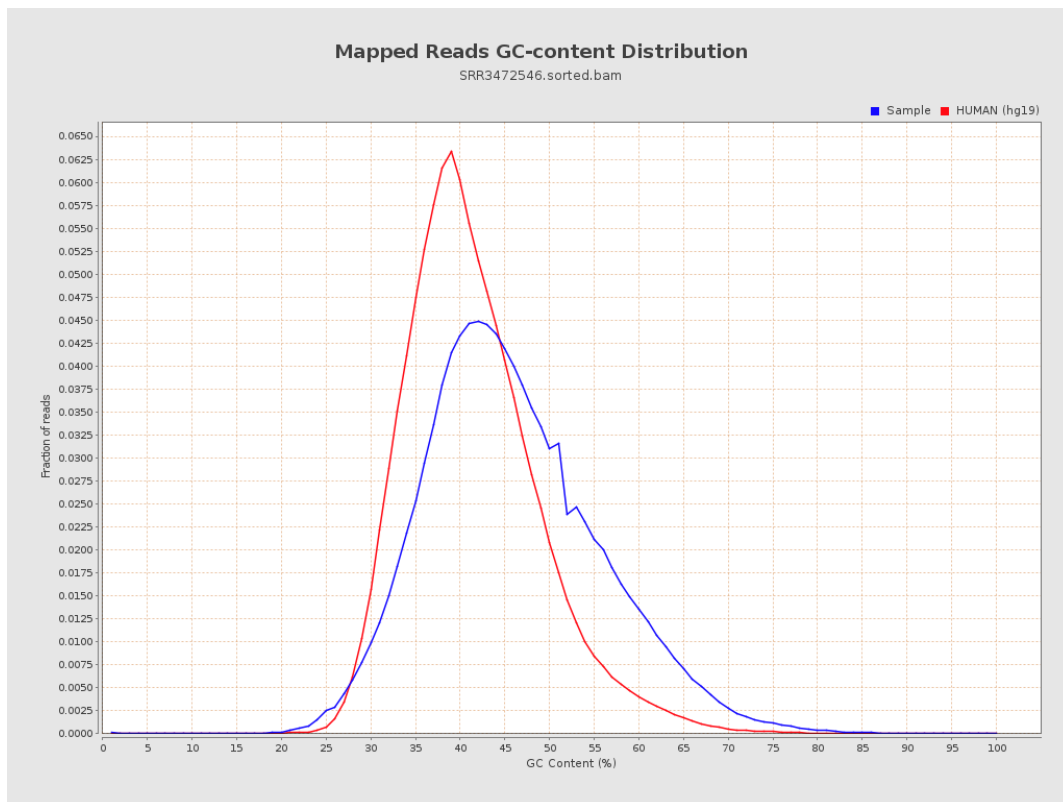
7. Results : Duplication Rate Histogram



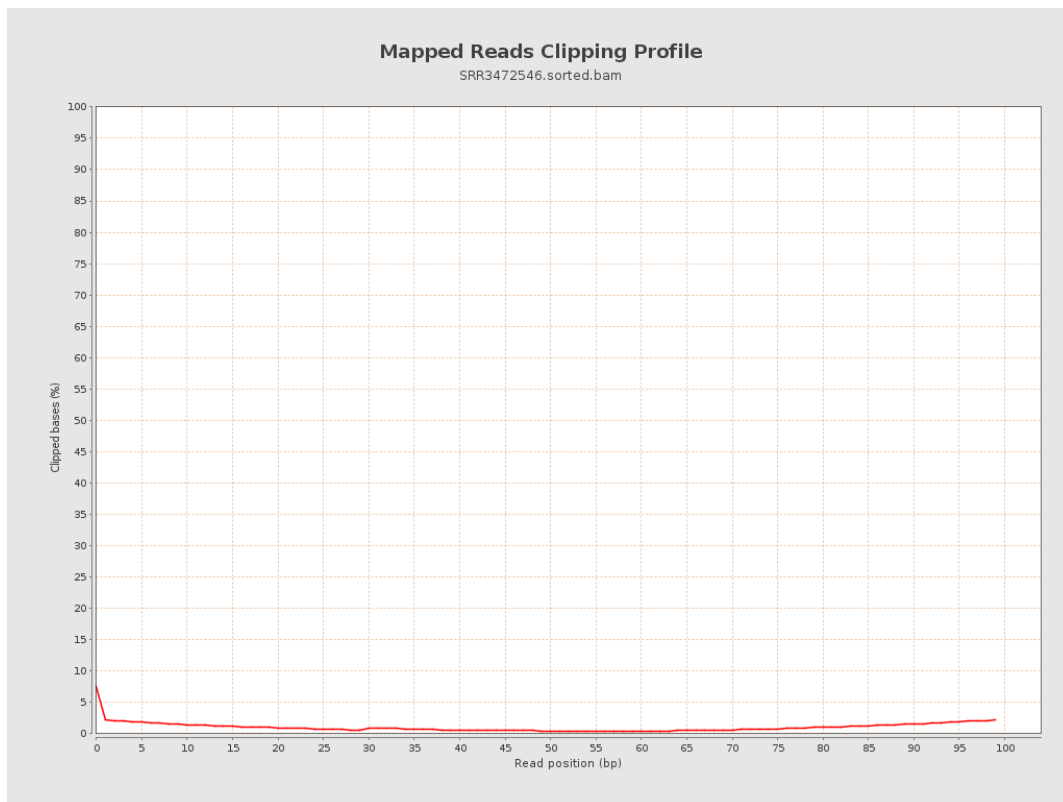
8. Results : Mapped Reads Nucleotide Content



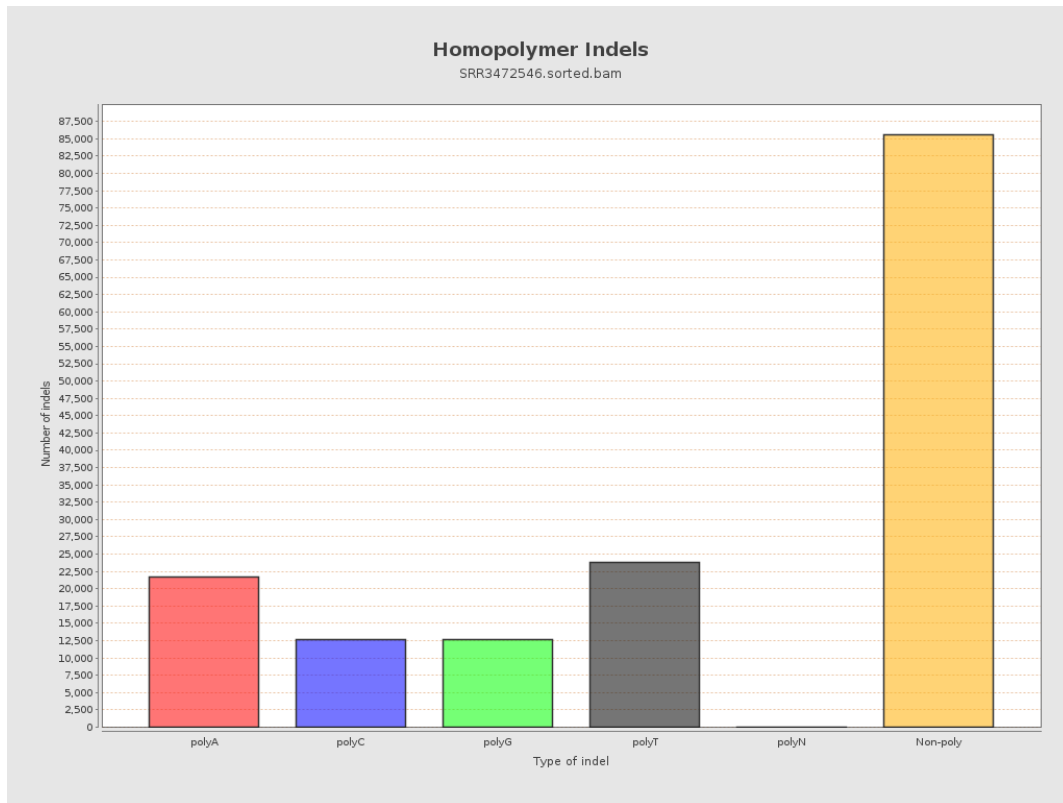
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



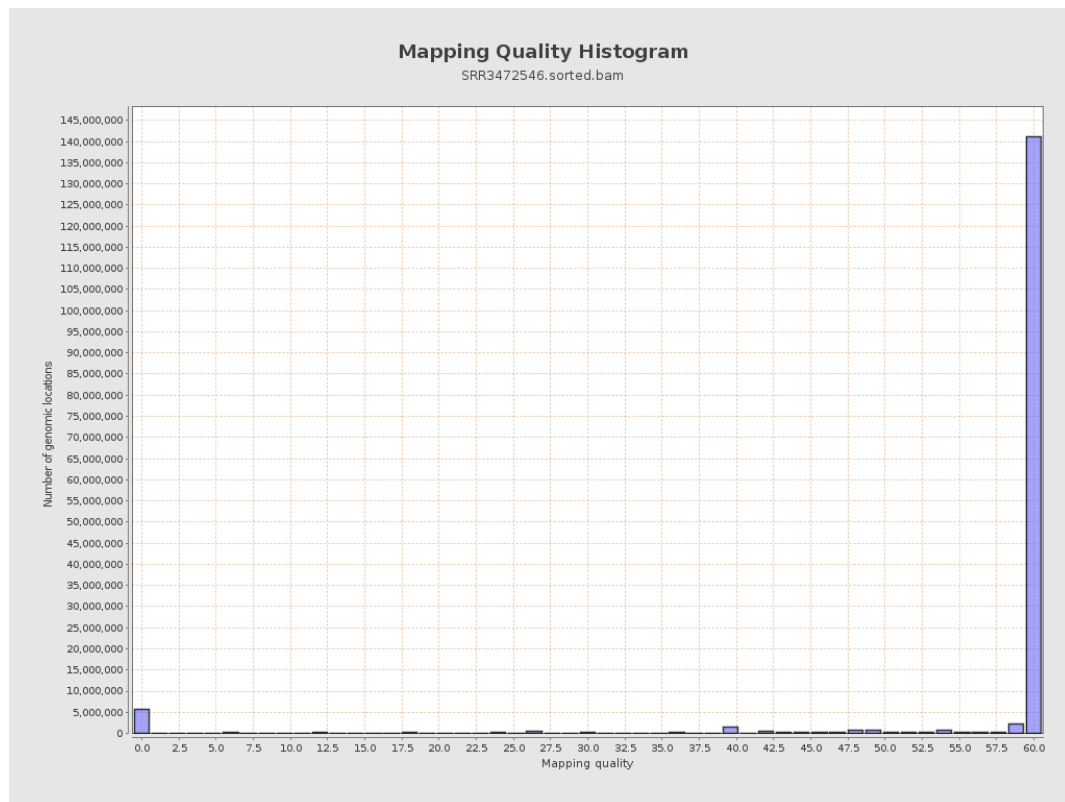
11. Results : Homopolymer Indels



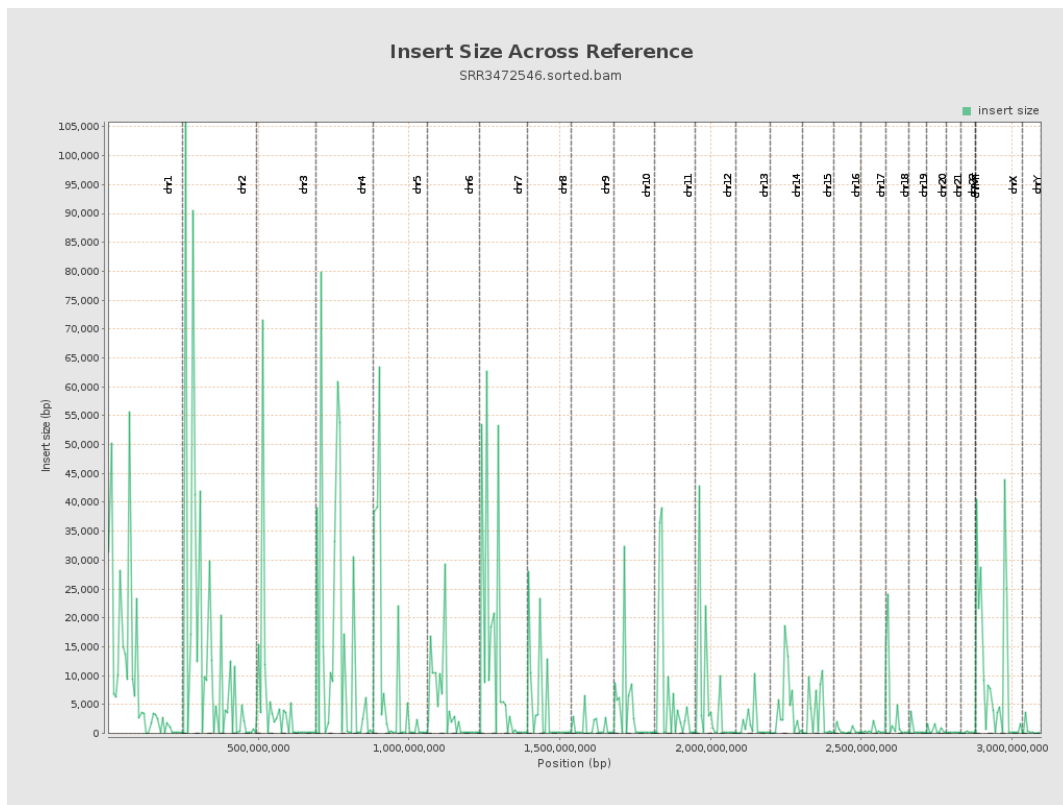
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

