

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:09:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472400.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_SRR3472400 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472400_1.fastq.gz SRR3472400_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:09:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472400.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,013,022
Mapped reads	21,844,006 / 99.23%
Unmapped reads	169,016 / 0.77%
Mapped paired reads	21,844,006 / 99.23%
Mapped reads, first in pair	10,952,785 / 49.76%
Mapped reads, second in pair	10,891,221 / 49.48%
Mapped reads, both in pair	21,739,314 / 98.76%
Mapped reads, singletons	104,692 / 0.48%
Secondary alignments	0
Supplementary alignments	109,467 / 0.5%
Read min/max/mean length	30 / 100 / 99.45
Duplicated reads (estimated)	15,340,747 / 69.69%
Duplication rate	45.76%
Clipped reads	1,585,551 / 7.2%

2.2. ACGT Content

Number/percentage of A's	569,530,151 / 26.58%
Number/percentage of C's	502,768,968 / 23.47%
Number/percentage of T's	571,208,019 / 26.66%
Number/percentage of G's	498,583,613 / 23.27%
Number/percentage of N's	265,757 / 0.01%

GC Percentage	46.74%
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2.3. Coverage

Mean	0.6921
Standard Deviation	32.119

2.4. Mapping Quality

Mean Mapping Quality	55
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2.5. Insert size

Mean	19,818.28
Standard Deviation	1,447,872.62
P25/Median/P75	154 / 213 / 286

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	11,381,514
Insertions	136,660
Mapped reads with at least one insertion	0.62%
Deletions	102,842
Mapped reads with at least one deletion	0.46%
Homopolymer indels	46%

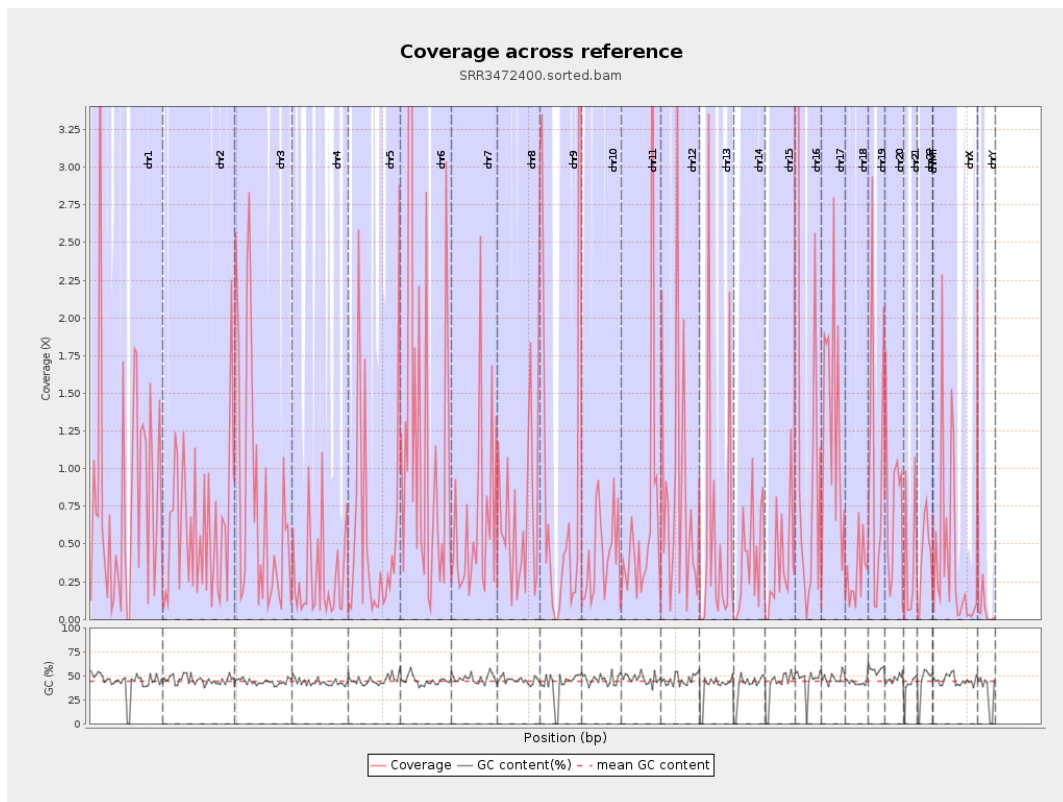
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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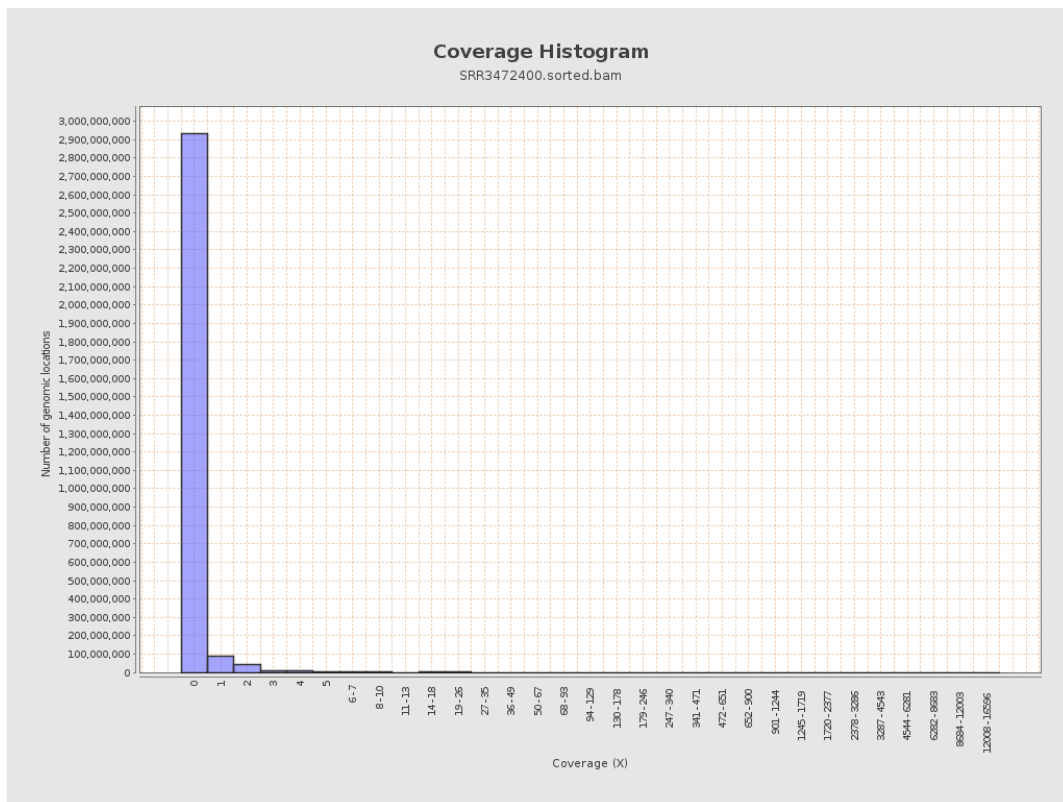
		bases	coverage	deviation
chr1	249250621	197207200	0.7912	32.4858
chr2	243199373	149438479	0.6145	23.6709
chr3	198022430	149247002	0.7537	32.1573
chr4	191154276	56635810	0.2963	12.0391
chr5	180915260	107409160	0.5937	27.725
chr6	171115067	223793439	1.3079	54.5508
chr7	159138663	102848697	0.6463	22.2224
chr8	146364022	101909288	0.6963	25.0716
chr9	141213431	131523907	0.9314	51.4353
chr10	135534747	60255278	0.4446	17.1247
chr11	135006516	91568403	0.6783	37.3112
chr12	133851895	114297037	0.8539	27.6119
chr13	115169878	64428669	0.5594	30.3159
chr14	107349540	43090377	0.4014	16.0322
chr15	102531392	36137726	0.3525	16.3054
chr16	90354753	162289957	1.7961	79.0273
chr17	81195210	107836028	1.3281	38.6339
chr18	78077248	23338388	0.2989	11.3661
chr19	59128983	60595186	1.0248	27.9475
chr20	63025520	46988020	0.7455	23.6092
chr21	48129895	19462684	0.4044	22.0437
chr22	51304566	22252984	0.4337	16.7594
chrMT	16571	11698	0.7059	1.064
chrX	155270560	66418178	0.4278	20.1922

chrY	59373566	3607917	0.0608	3.1403
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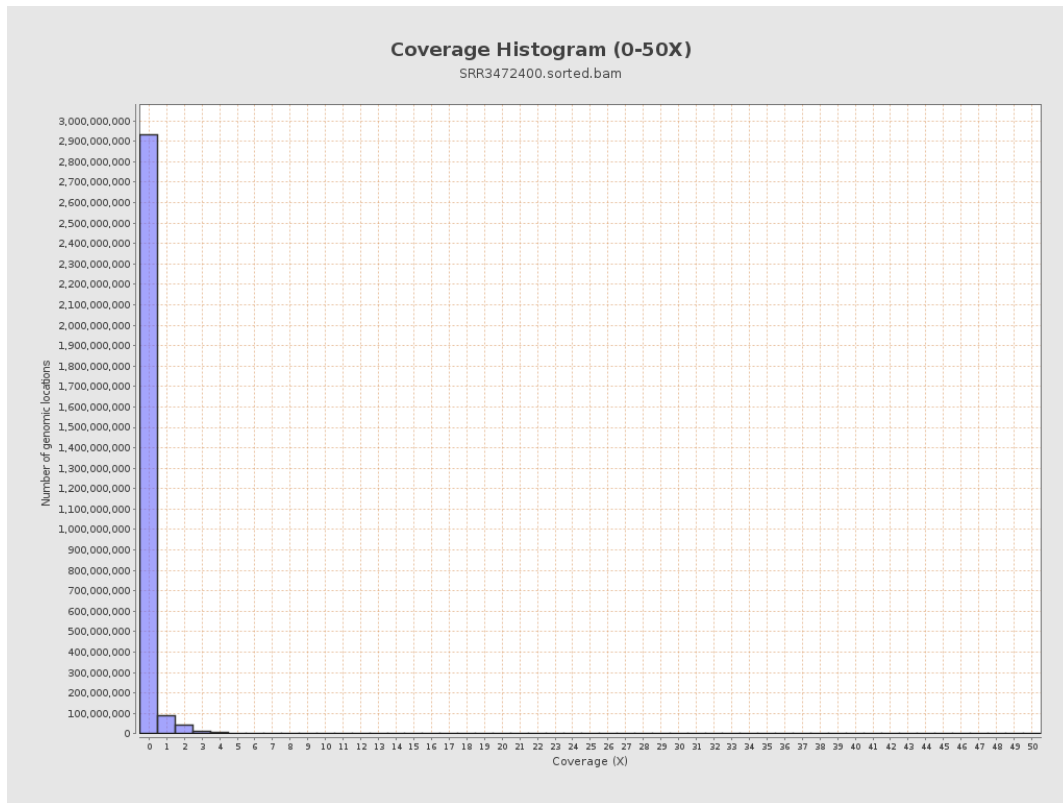
3. Results : Coverage across reference



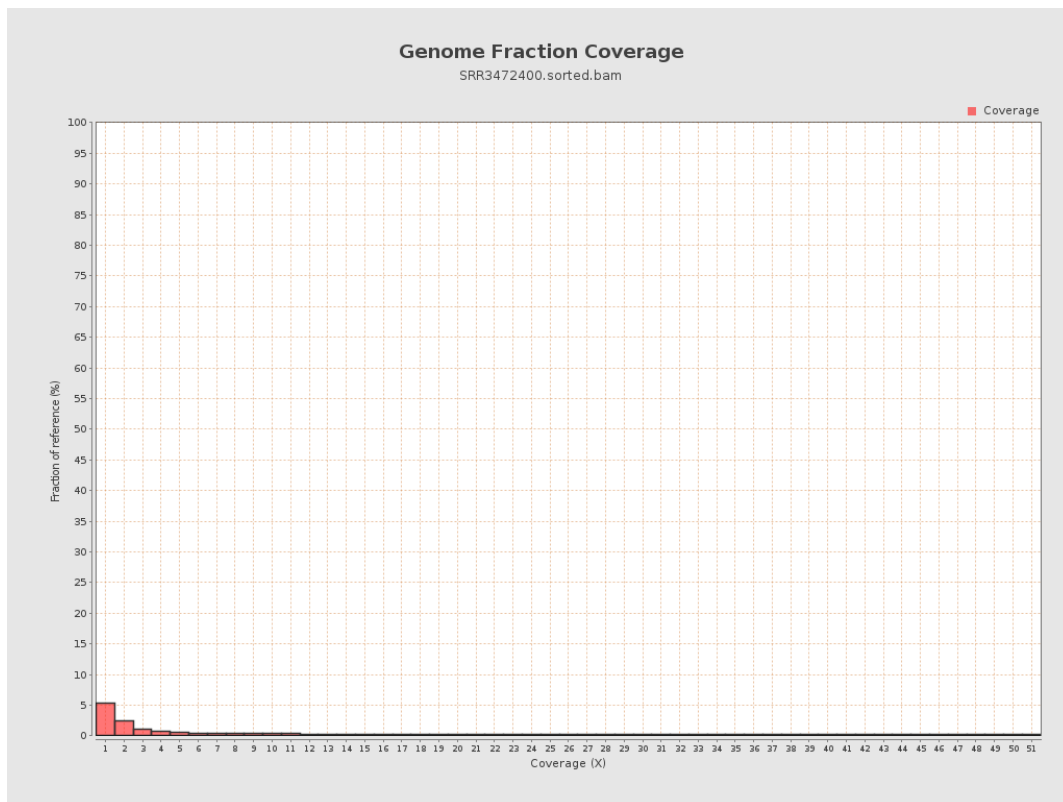
4. Results : Coverage Histogram



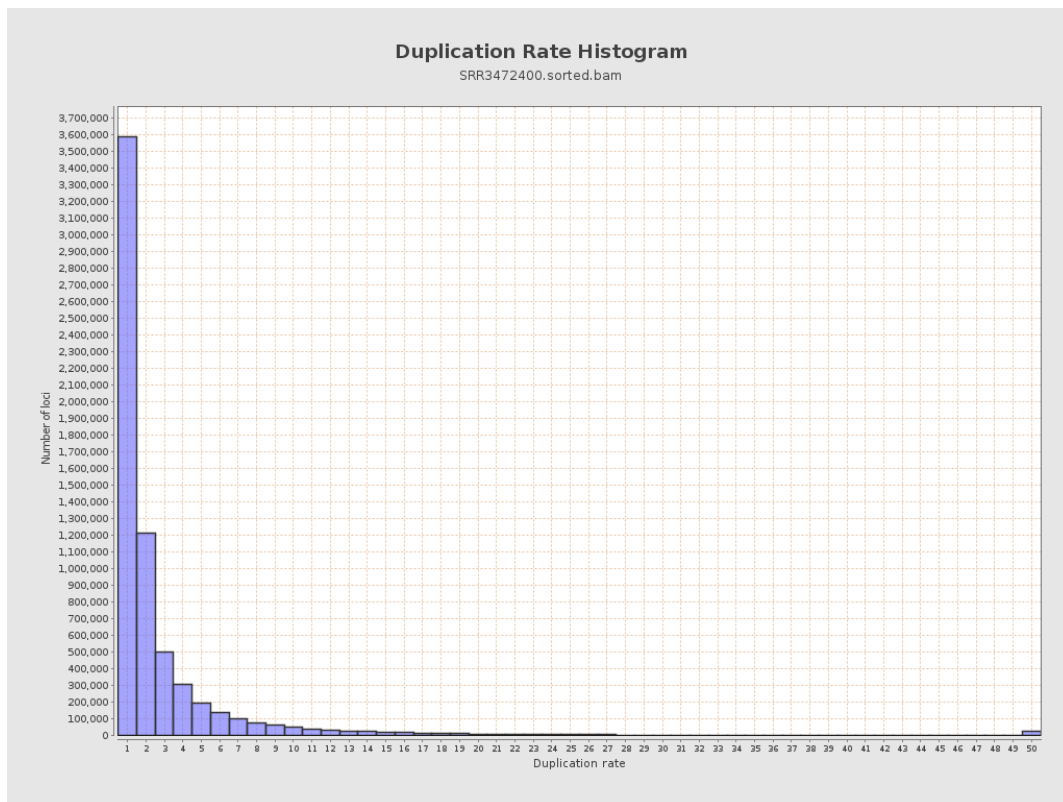
5. Results : Coverage Histogram (0-50X)



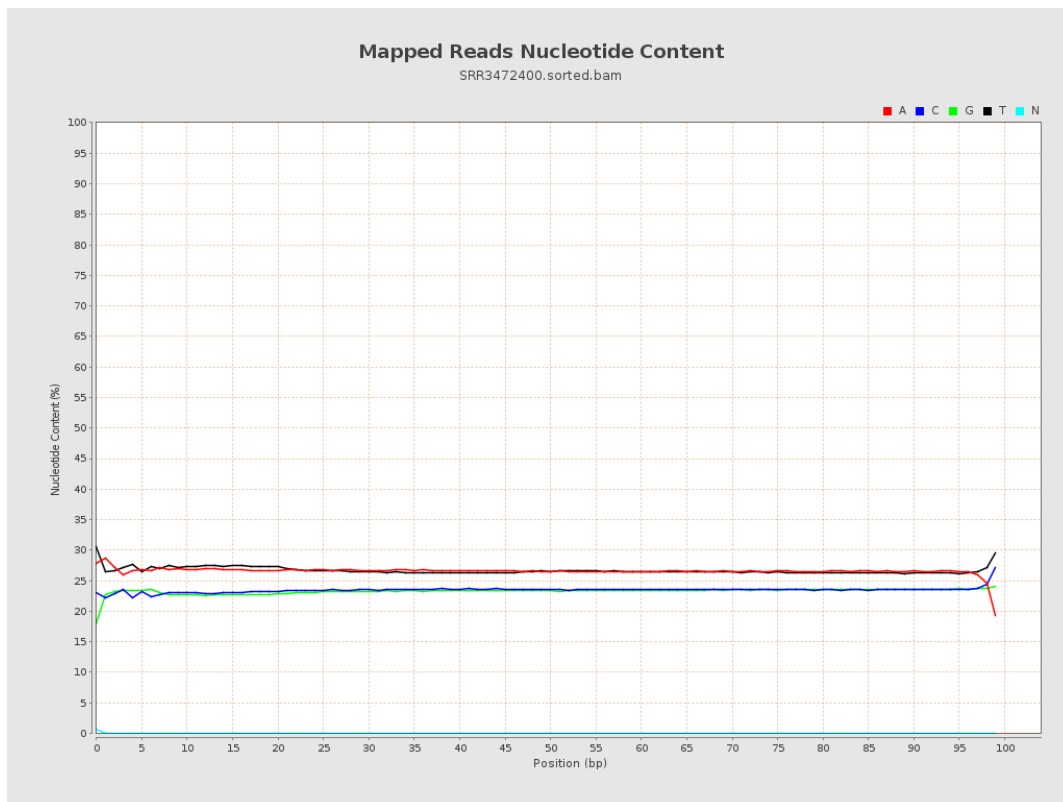
6. Results : Genome Fraction Coverage



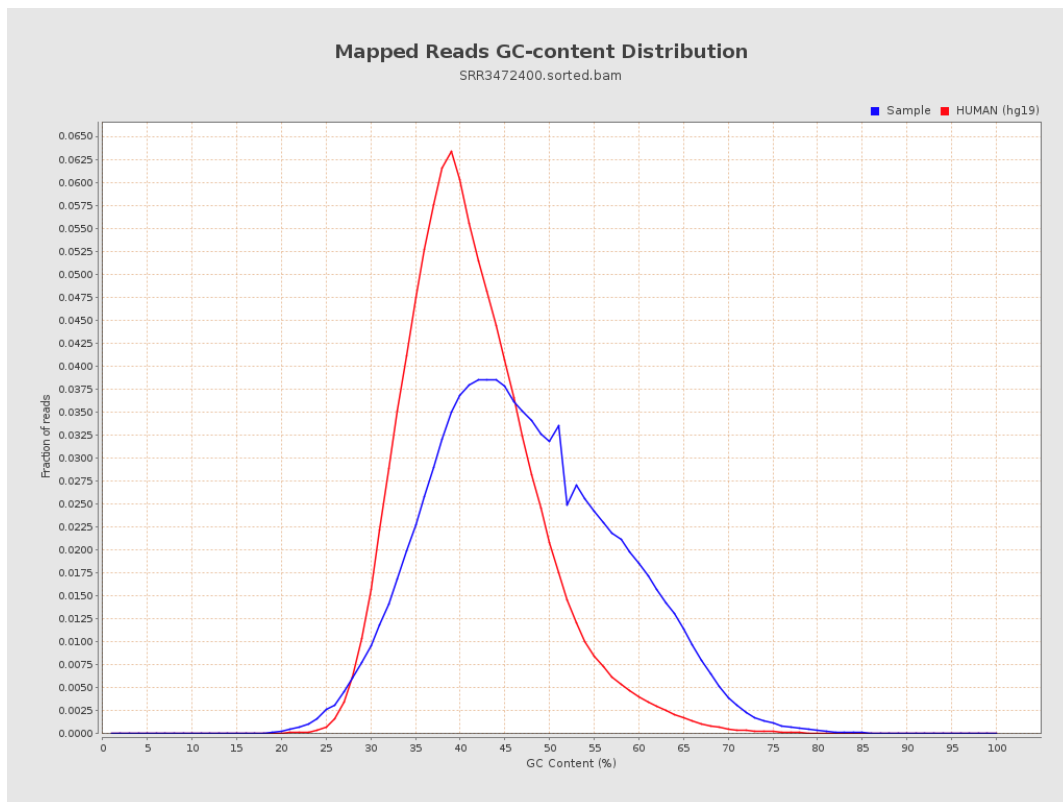
7. Results : Duplication Rate Histogram



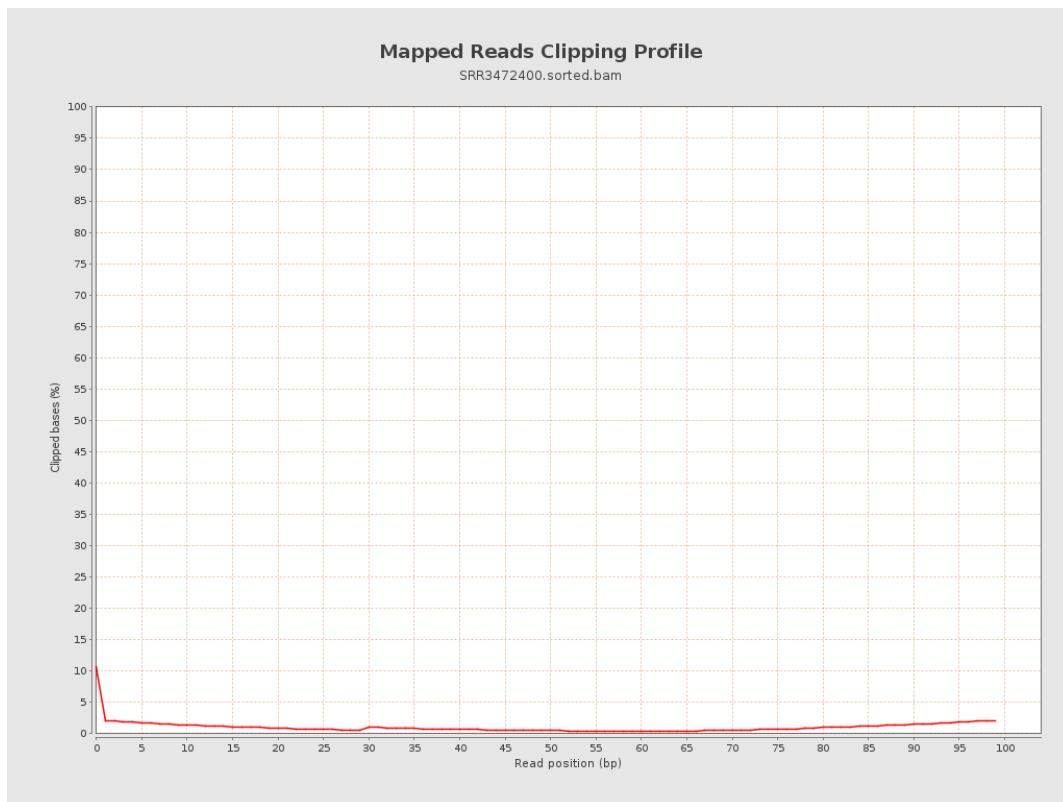
8. Results : Mapped Reads Nucleotide Content



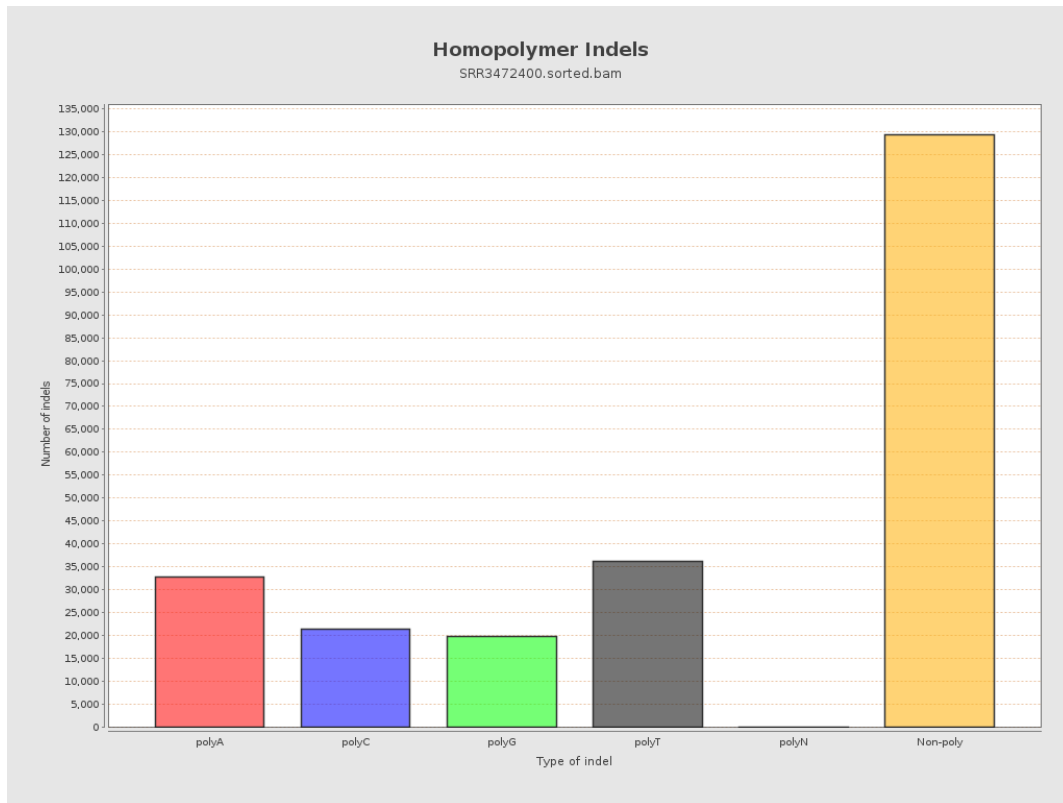
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



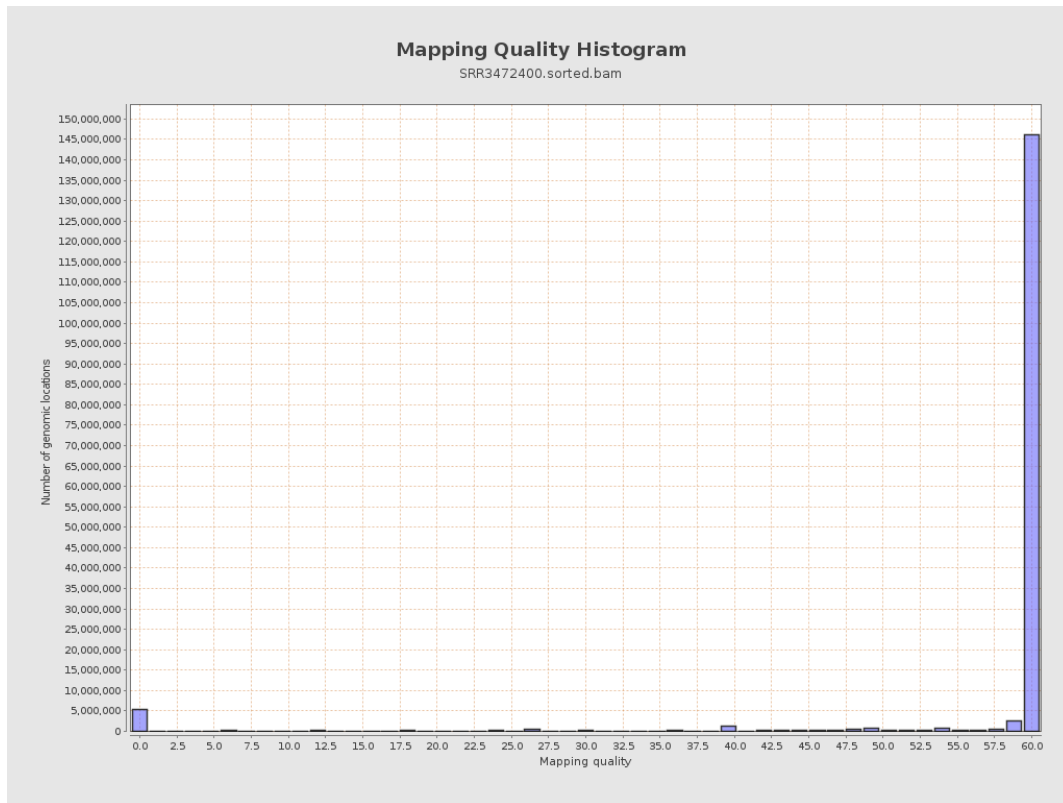
11. Results : Homopolymer Indels



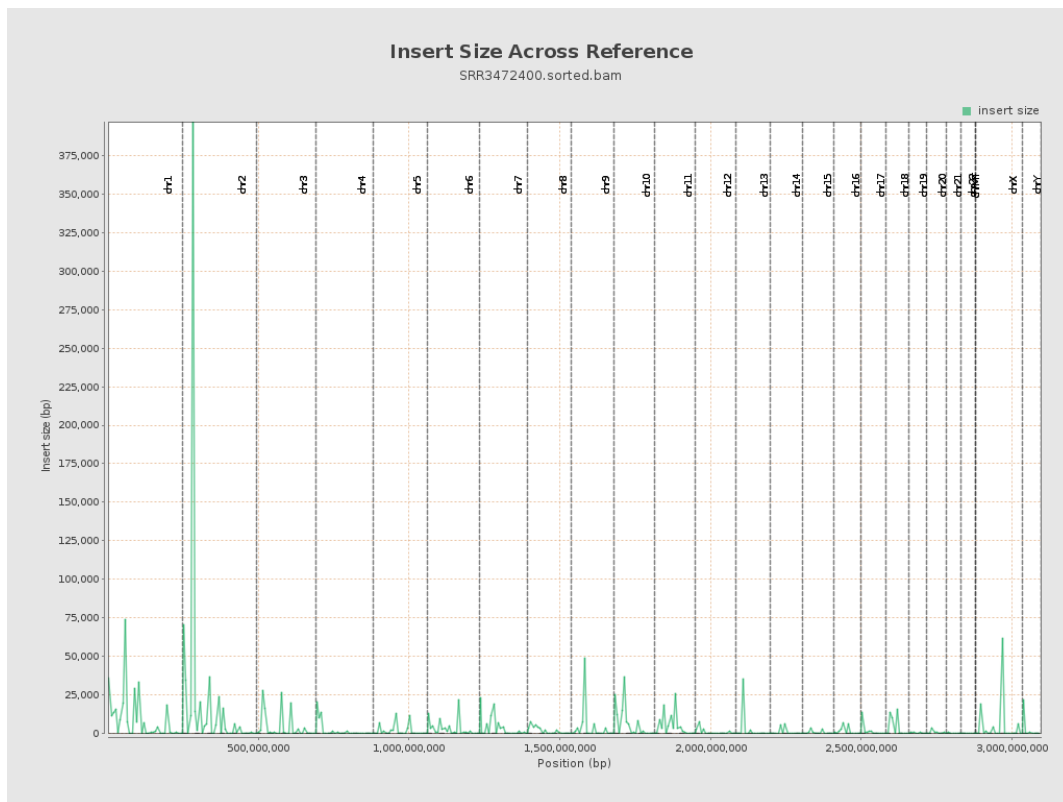
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

