

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:56:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472493.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_SRR3472493 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472493_1.fastq.gz SRR3472493_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:56:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472493.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,774,750
Mapped reads	16,517,788 / 98.47%
Unmapped reads	256,962 / 1.53%
Mapped paired reads	16,517,788 / 98.47%
Mapped reads, first in pair	8,298,882 / 49.47%
Mapped reads, second in pair	8,218,906 / 49%
Mapped reads, both in pair	16,378,188 / 97.64%
Mapped reads, singletons	139,600 / 0.83%
Secondary alignments	0
Supplementary alignments	65,279 / 0.39%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	10,202,186 / 60.82%
Duplication rate	46.48%
Clipped reads	1,350,783 / 8.05%

2.2. ACGT Content

Number/percentage of A's	454,360,550 / 27.96%
Number/percentage of C's	360,623,586 / 22.19%
Number/percentage of T's	451,856,886 / 27.8%
Number/percentage of G's	358,036,486 / 22.03%
Number/percentage of N's	250,989 / 0.02%

GC Percentage	44.22%
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2.3. Coverage

Mean	0.525
Standard Deviation	17.0249

2.4. Mapping Quality

Mean Mapping Quality	54.93
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2.5. Insert size

Mean	31,715.93
Standard Deviation	1,723,726.93
P25/Median/P75	177 / 249 / 337

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	10,274,257
Insertions	91,116
Mapped reads with at least one insertion	0.55%
Deletions	89,347
Mapped reads with at least one deletion	0.53%
Homopolymer indels	44.51%

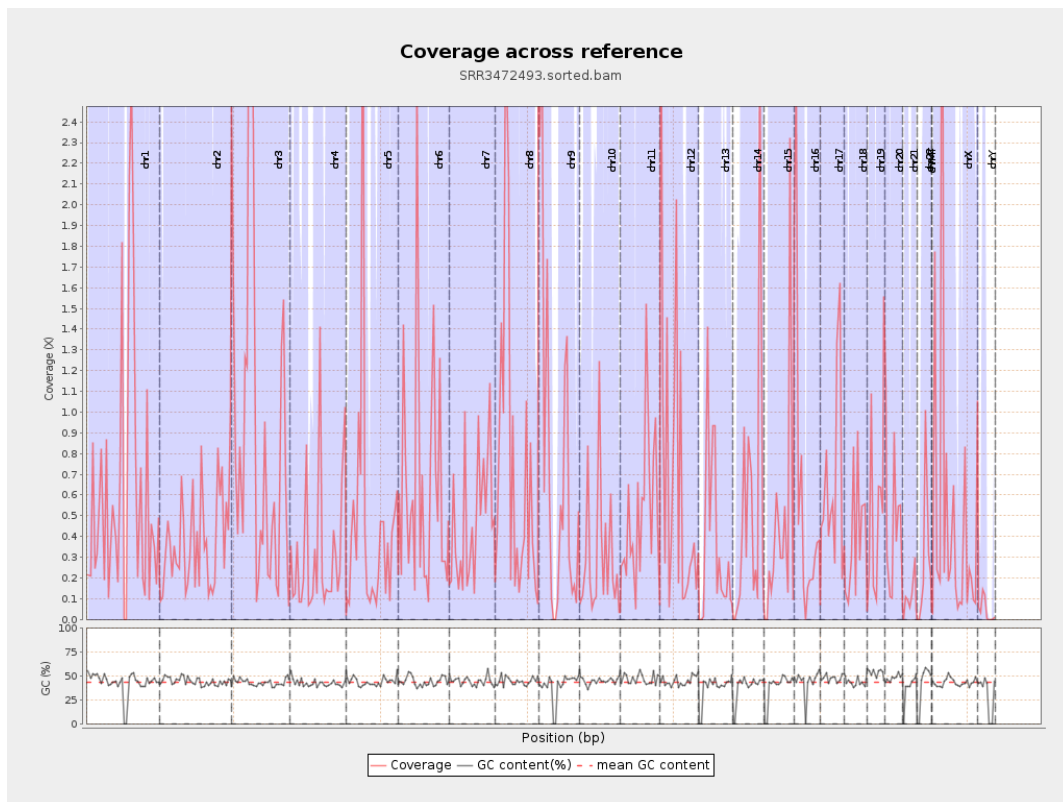
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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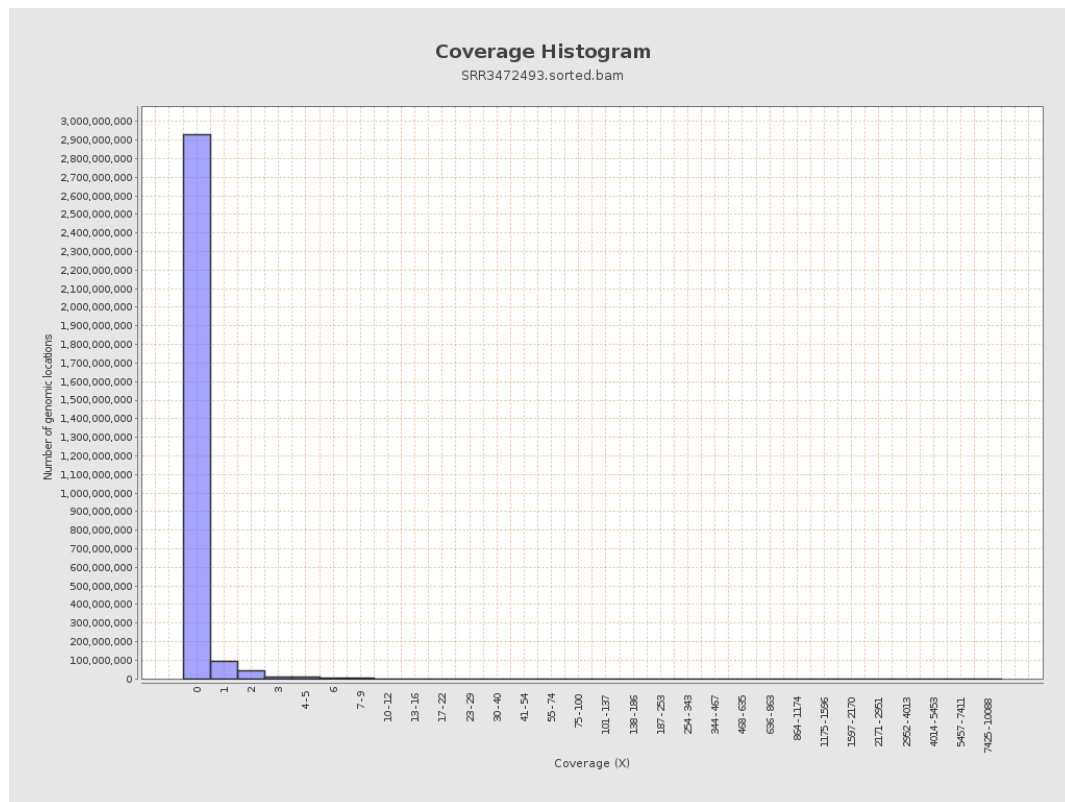
		bases	coverage	deviation
chr1	249250621	152454022	0.6116	22.3218
chr2	243199373	90794375	0.3733	11.0897
chr3	198022430	185252860	0.9355	21.1958
chr4	191154276	59248830	0.31	11.2296
chr5	180915260	84224766	0.4655	14.9597
chr6	171115067	109058890	0.6373	18.3554
chr7	159138663	77162043	0.4849	14.4021
chr8	146364022	108184931	0.7391	22.3412
chr9	141213431	110992799	0.786	20.181
chr10	135534747	40630444	0.2998	12.6359
chr11	135006516	69376668	0.5139	17.7894
chr12	133851895	96848534	0.7235	20.6974
chr13	115169878	42731367	0.371	13.1581
chr14	107349540	53135289	0.495	27.9599
chr15	102531392	45519478	0.444	13.2826
chr16	90354753	52619394	0.5824	16.1998
chr17	81195210	52705996	0.6491	14.7018
chr18	78077248	31132847	0.3987	14.5911
chr19	59128983	29410567	0.4974	11.6157
chr20	63025520	29017369	0.4604	13.4178
chr21	48129895	5536642	0.115	4.4074
chr22	51304566	13843934	0.2698	10.6311
chrMT	16571	1465	0.0884	0.3393
chrX	155270560	82776741	0.5331	16.164

chrY	59373566	2695992	0.0454	1.3909
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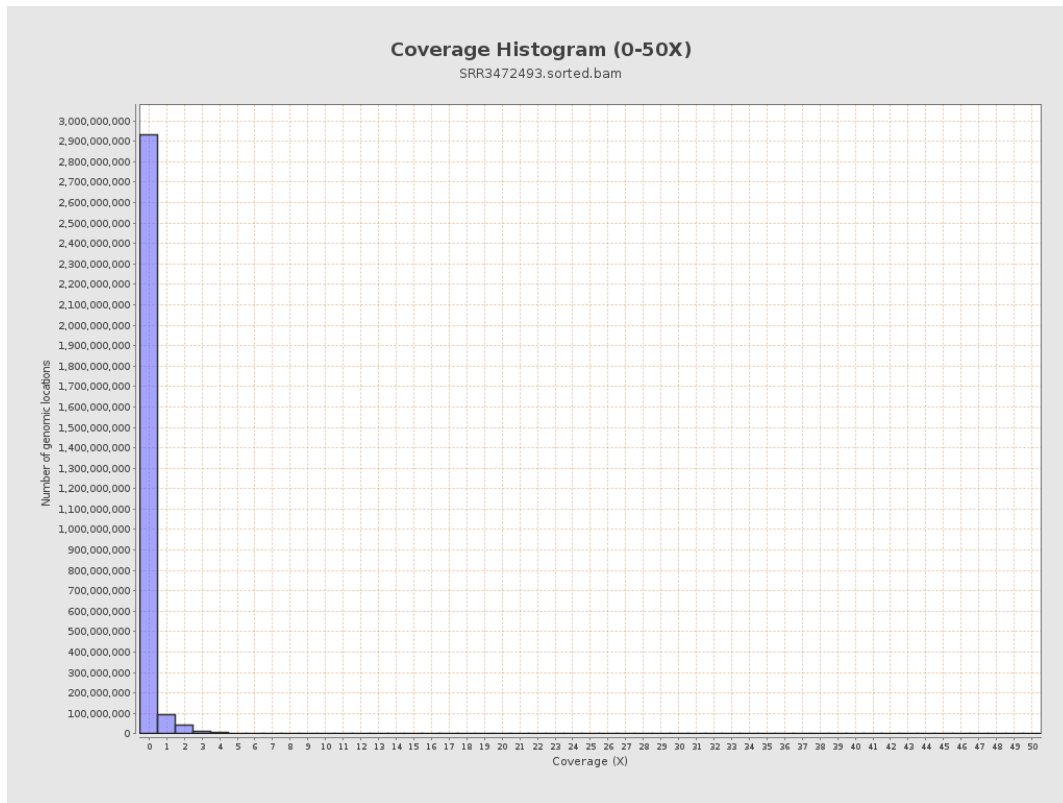
3. Results : Coverage across reference



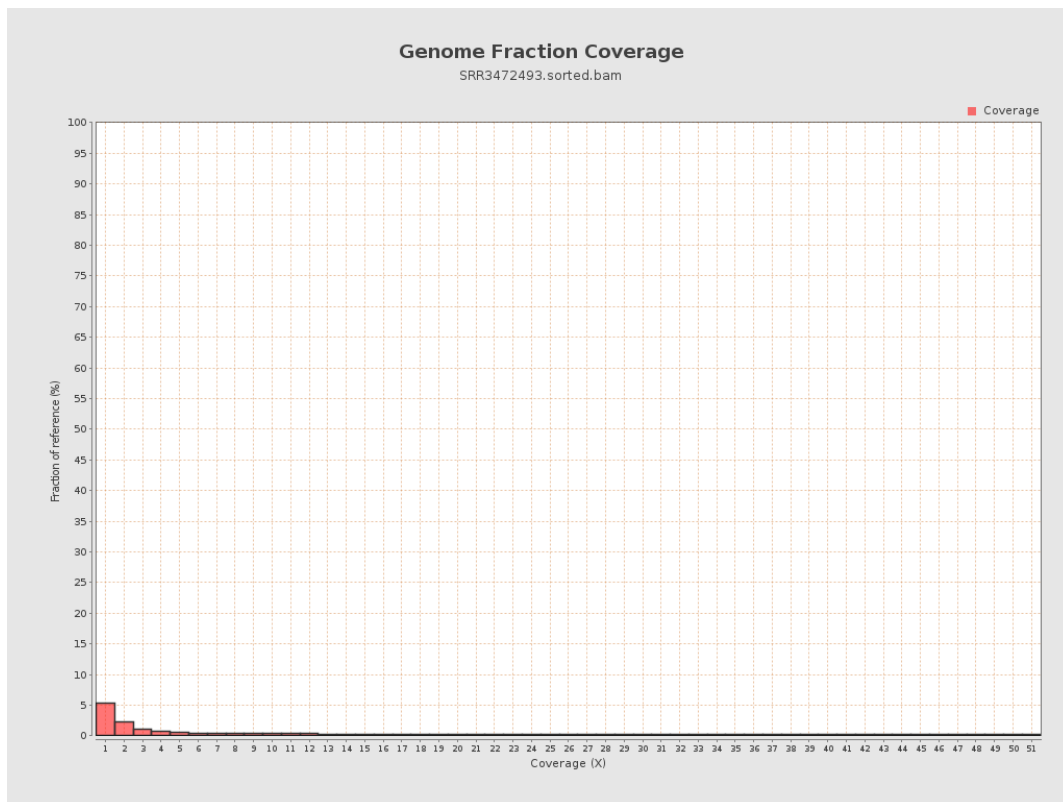
4. Results : Coverage Histogram



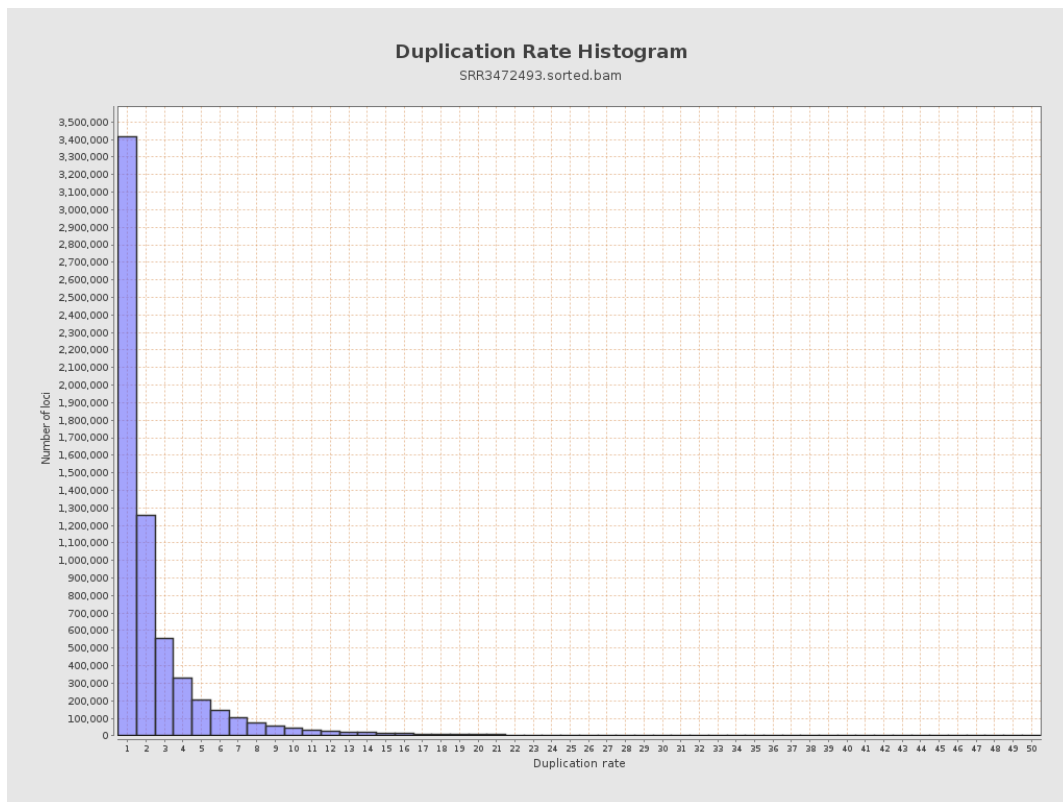
5. Results : Coverage Histogram (0-50X)



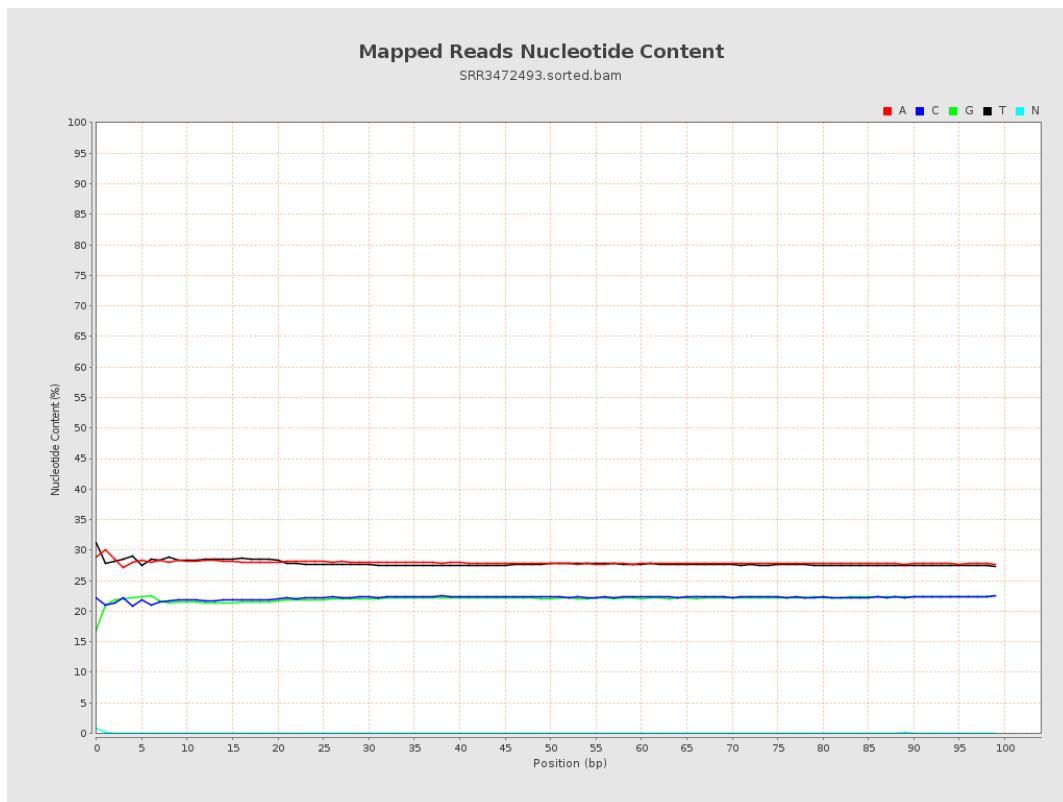
6. Results : Genome Fraction Coverage



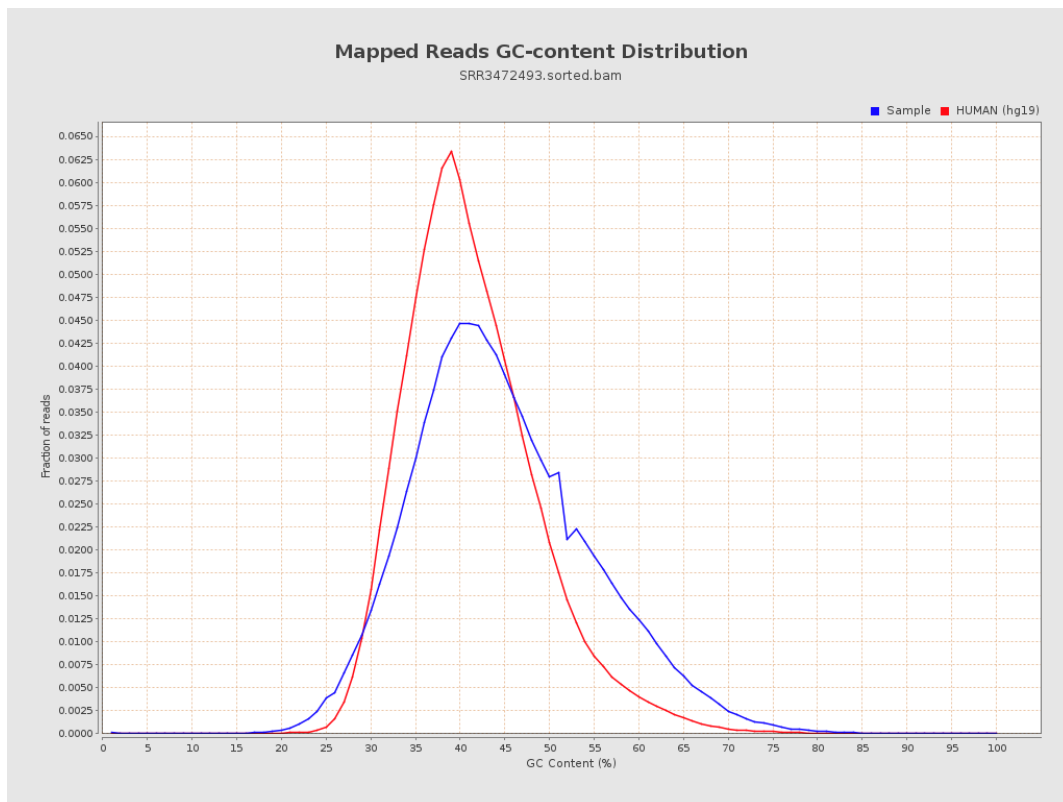
7. Results : Duplication Rate Histogram



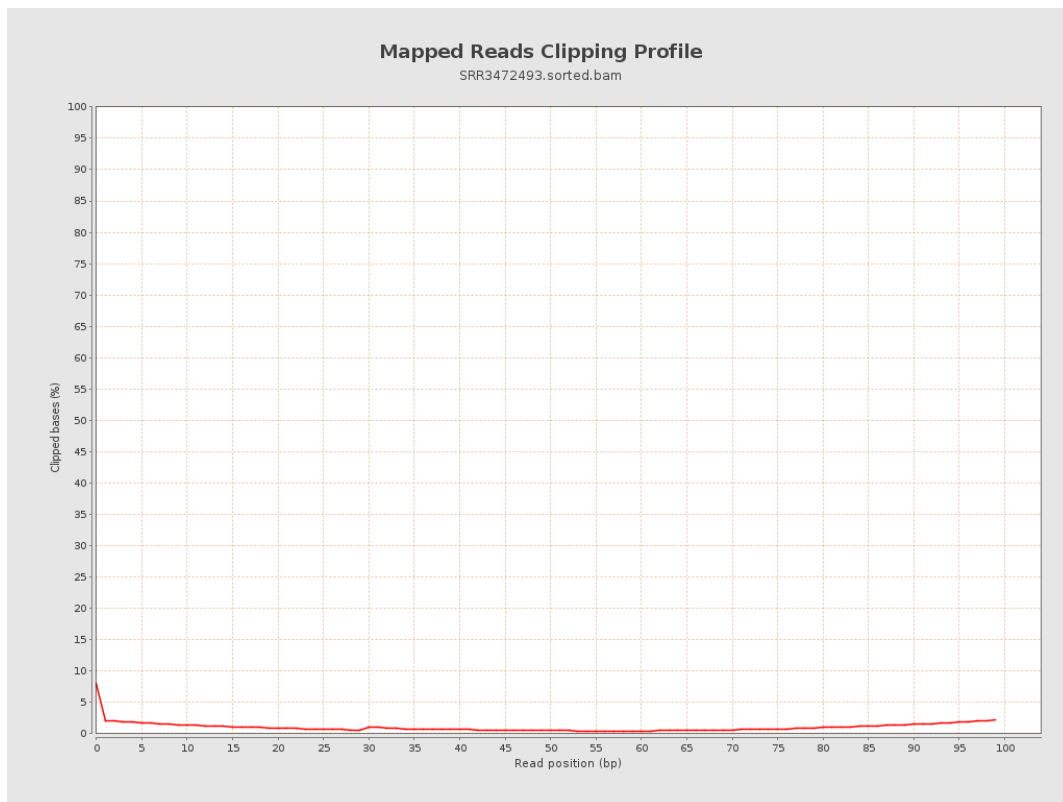
8. Results : Mapped Reads Nucleotide Content



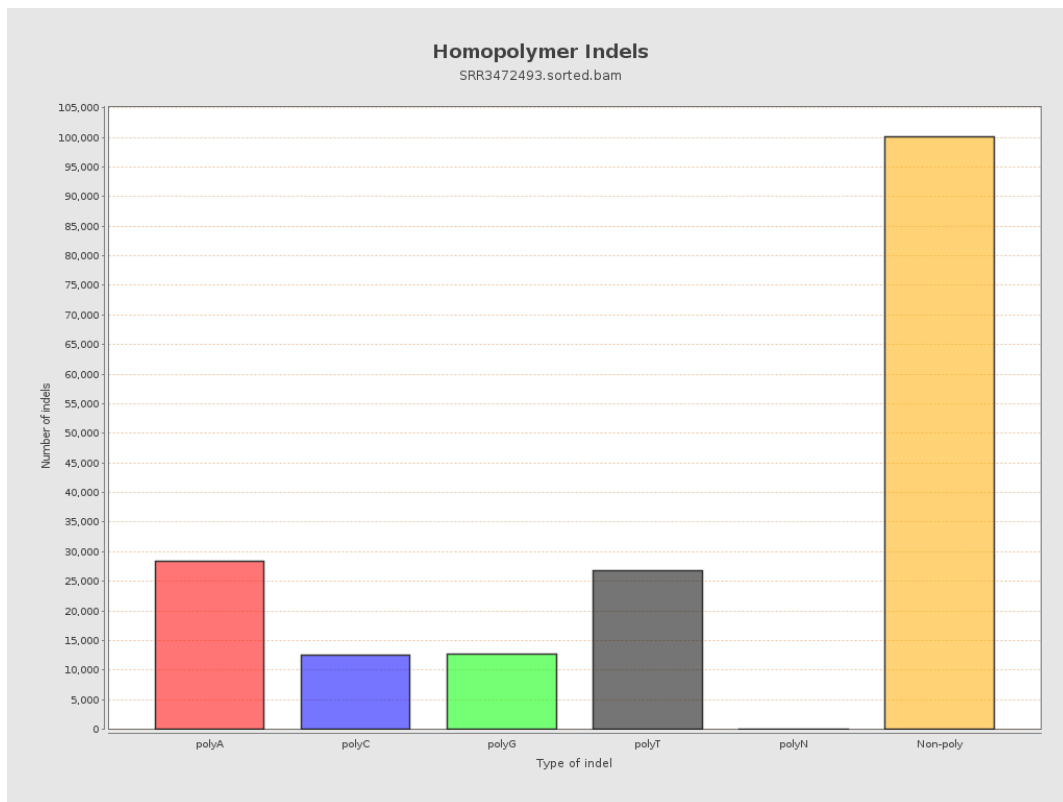
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



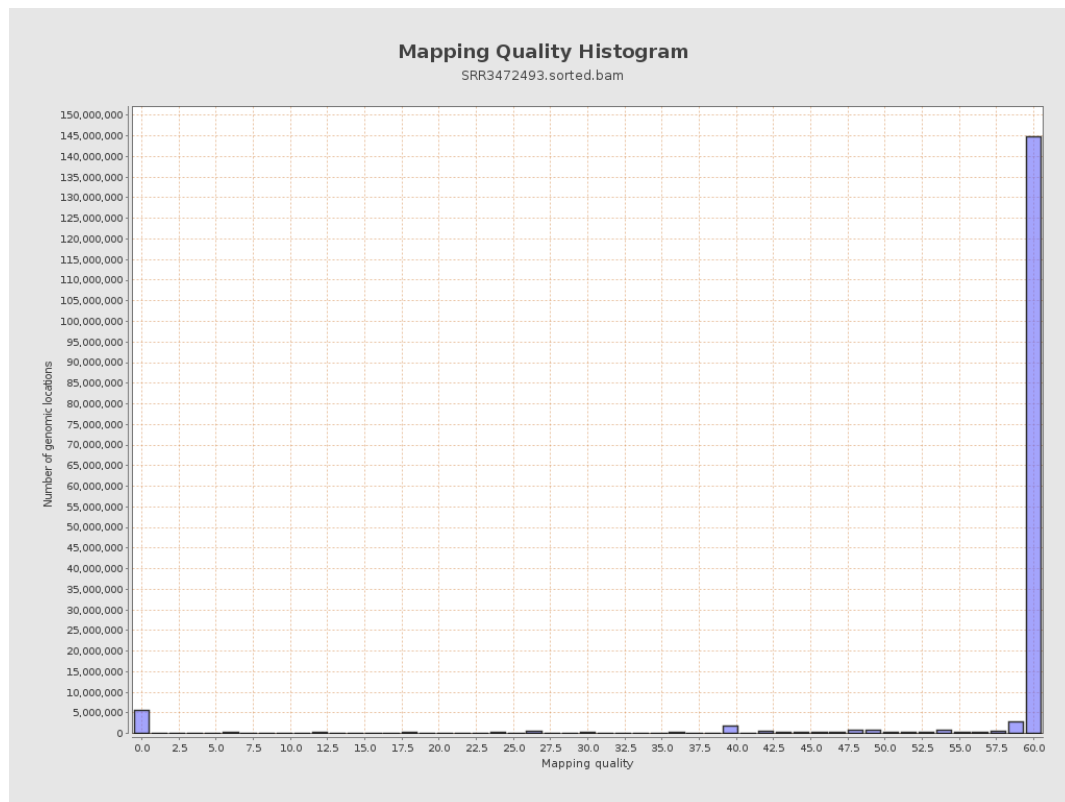
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

