

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 18:39:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472392.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_SRR3472392 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472392_1.fastq.gz SRR3472392_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 18:39:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472392.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,888,098
Mapped reads	19,710,991 / 99.11%
Unmapped reads	177,107 / 0.89%
Mapped paired reads	19,710,991 / 99.11%
Mapped reads, first in pair	9,892,453 / 49.74%
Mapped reads, second in pair	9,818,538 / 49.37%
Mapped reads, both in pair	19,595,698 / 98.53%
Mapped reads, singletons	115,293 / 0.58%
Secondary alignments	0
Supplementary alignments	79,962 / 0.4%
Read min/max/mean length	30 / 100 / 99.47
Duplicated reads (estimated)	12,294,988 / 61.82%
Duplication rate	46.17%
Clipped reads	1,296,868 / 6.52%

2.2. ACGT Content

Number/percentage of A's	527,164,686 / 27.22%
Number/percentage of C's	442,860,493 / 22.87%
Number/percentage of T's	527,705,793 / 27.25%
Number/percentage of G's	438,504,221 / 22.64%
Number/percentage of N's	232,207 / 0.01%

GC Percentage	45.51%
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2.3. Coverage

Mean	0.6256
Standard Deviation	19.3757

2.4. Mapping Quality

Mean Mapping Quality	54.78
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2.5. Insert size

Mean	21,262.6
Standard Deviation	1,447,500.57
P25/Median/P75	162 / 223 / 299

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	10,976,433
Insertions	112,923
Mapped reads with at least one insertion	0.57%
Deletions	100,193
Mapped reads with at least one deletion	0.5%
Homopolymer indels	46.57%

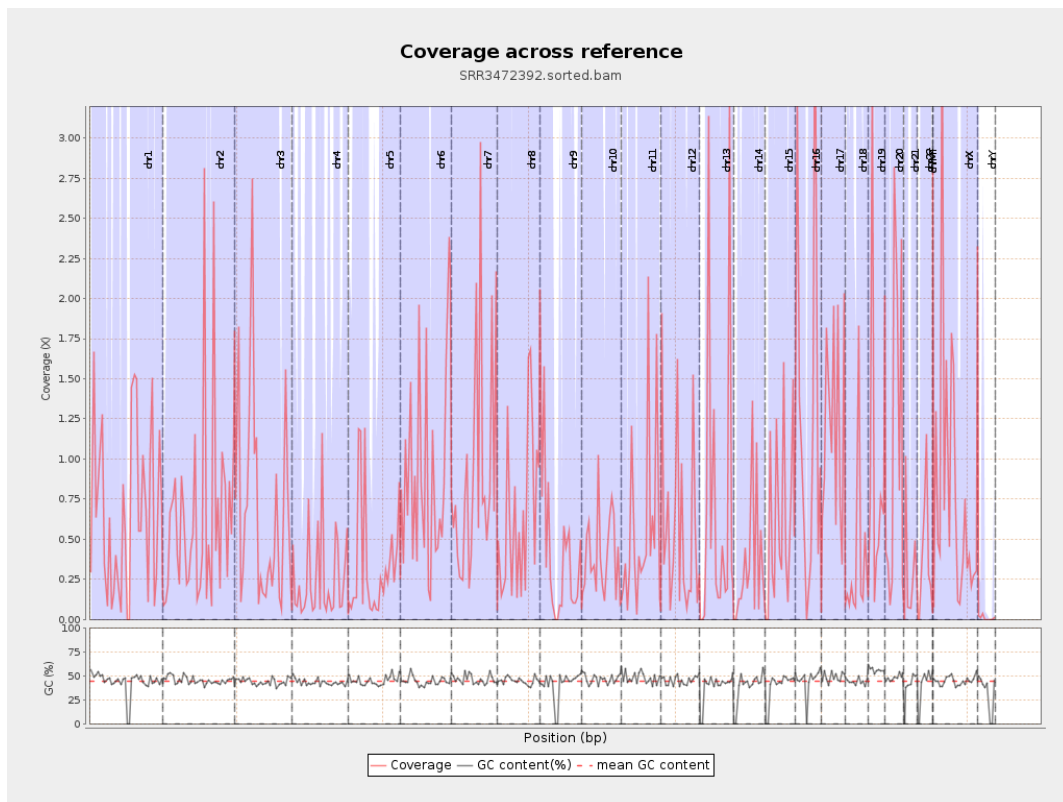
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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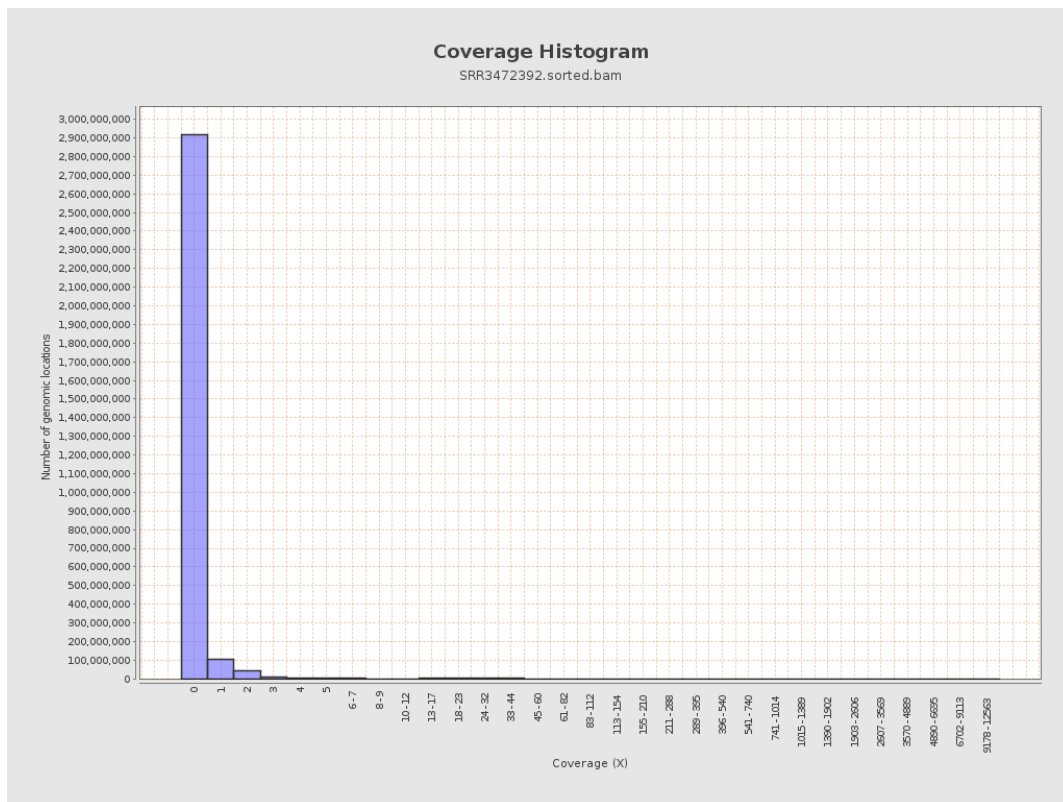
		bases	coverage	deviation
chr1	249250621	165451680	0.6638	16.2352
chr2	243199373	154035390	0.6334	18.3317
chr3	198022430	135256222	0.683	16.7376
chr4	191154276	50734320	0.2654	9.7791
chr5	180915260	63375604	0.3503	10.6264
chr6	171115067	155630008	0.9095	25.5692
chr7	159138663	148184387	0.9312	23.4957
chr8	146364022	96377139	0.6585	18.0314
chr9	141213431	53167940	0.3765	10.0801
chr10	135534747	55753580	0.4114	11.4831
chr11	135006516	73461332	0.5441	22.4938
chr12	133851895	79567380	0.5944	18.3434
chr13	115169878	82117898	0.713	30.8823
chr14	107349540	37575308	0.35	17.1182
chr15	102531392	62965283	0.6141	23.4045
chr16	90354753	108854607	1.2047	32.4941
chr17	81195210	96741551	1.1915	23.0976
chr18	78077248	27005696	0.3459	20.559
chr19	59128983	55404241	0.937	22.6317
chr20	63025520	70297566	1.1154	27.6138
chr21	48129895	15760956	0.3275	16.8834
chr22	51304566	20432001	0.3982	14.1665
chrMT	16571	46709	2.8187	2.5374
chrX	155270560	127921131	0.8239	18.9698

chrY	59373566	583293	0.0098	1.0198
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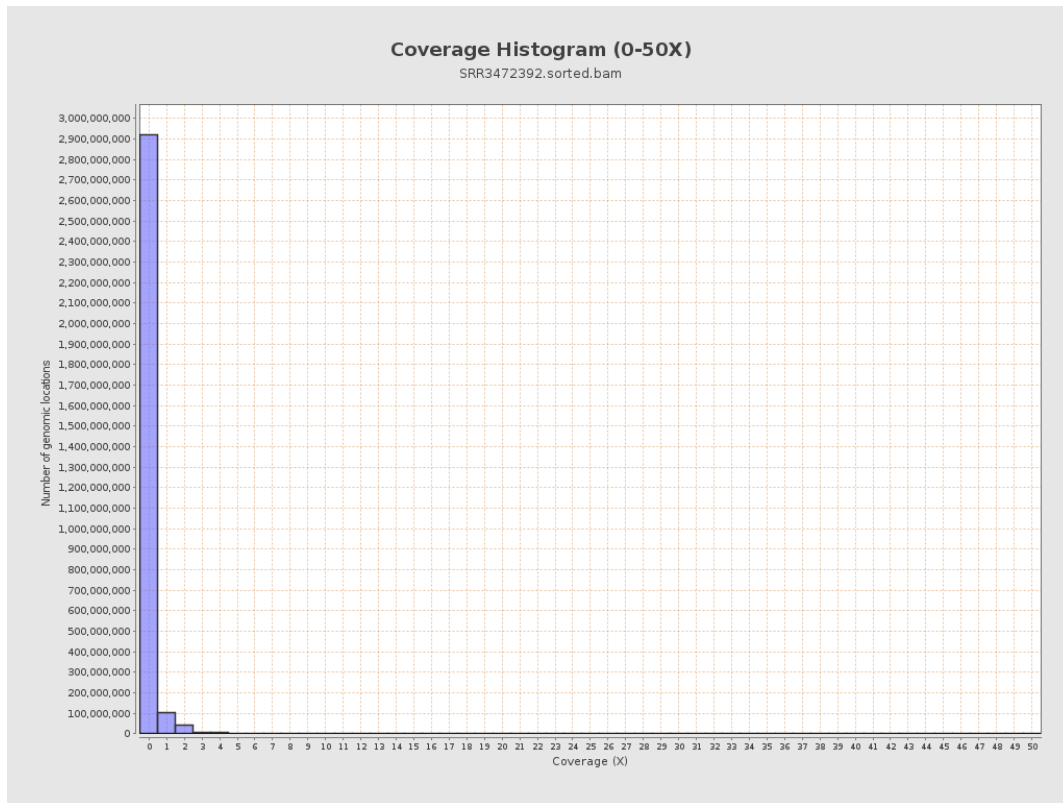
3. Results : Coverage across reference



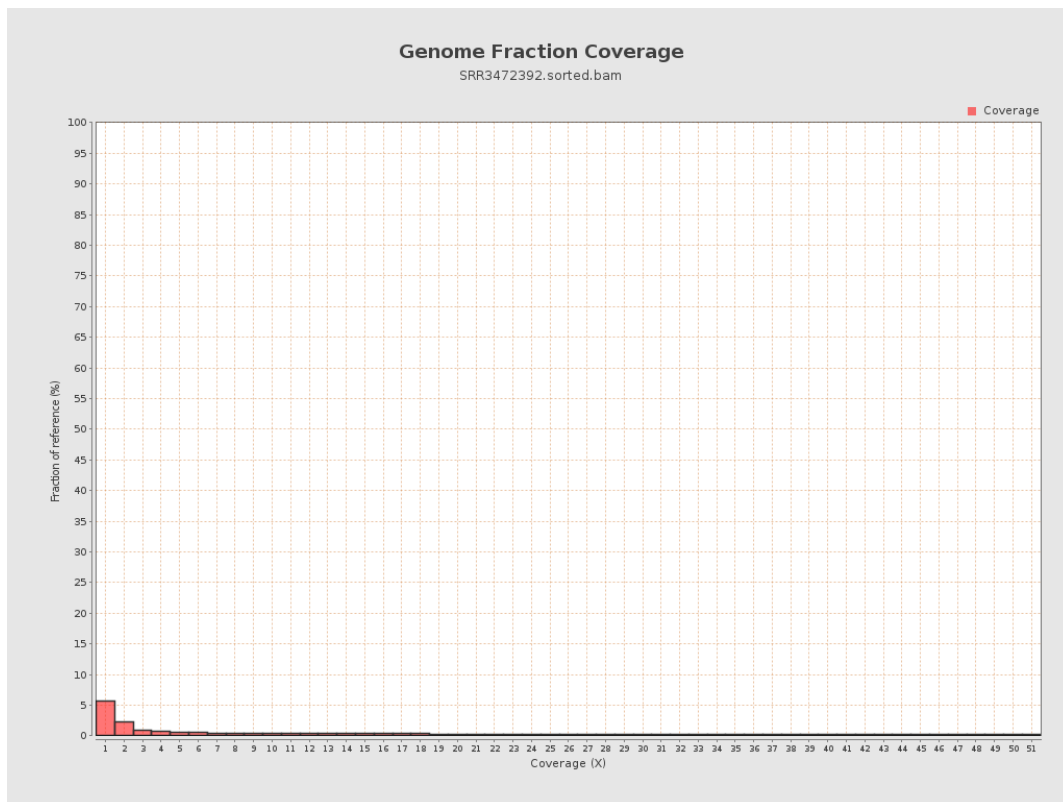
4. Results : Coverage Histogram



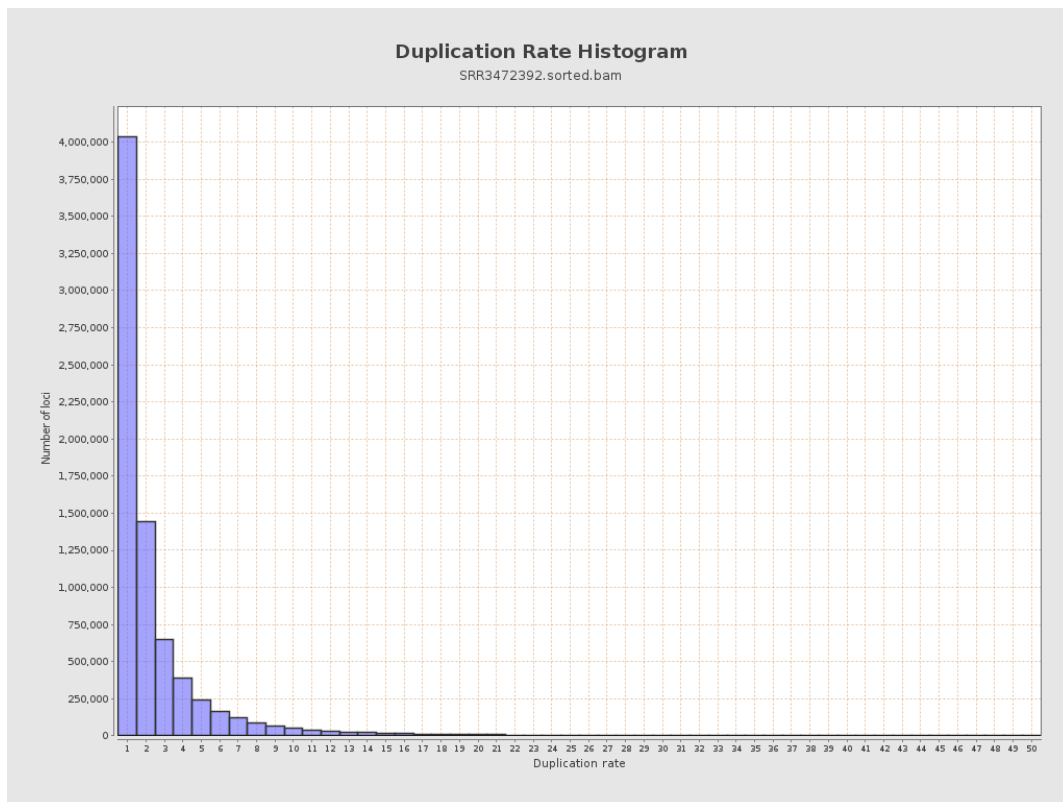
5. Results : Coverage Histogram (0-50X)



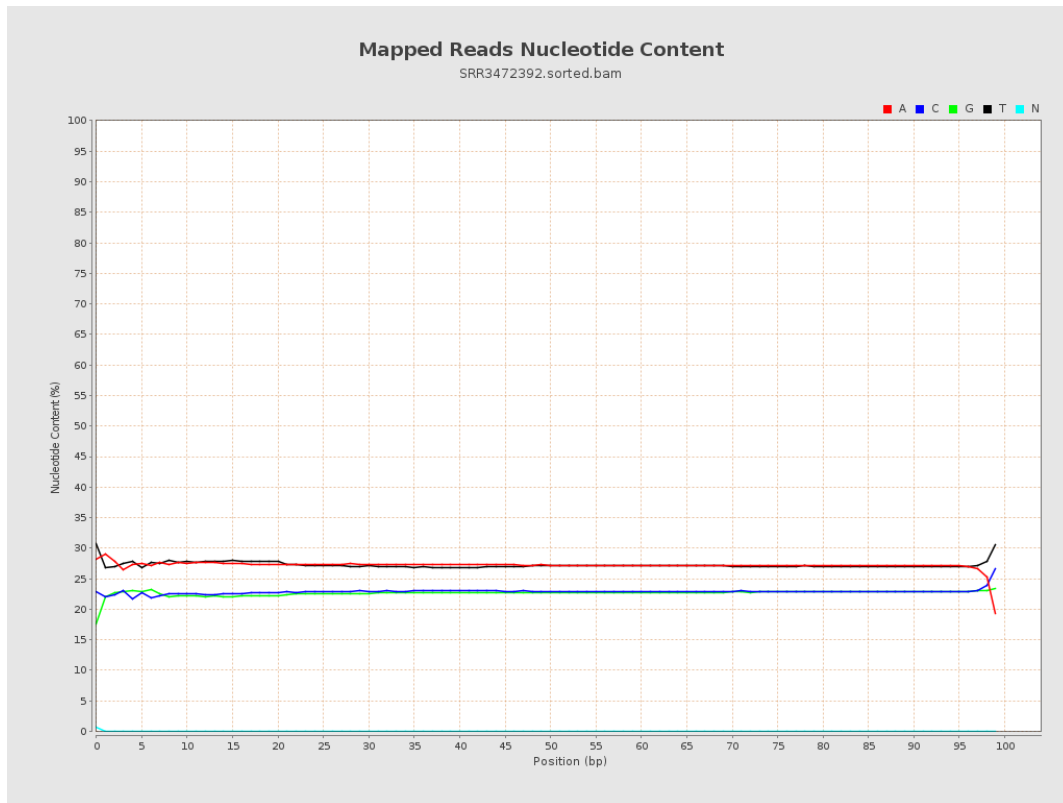
6. Results : Genome Fraction Coverage



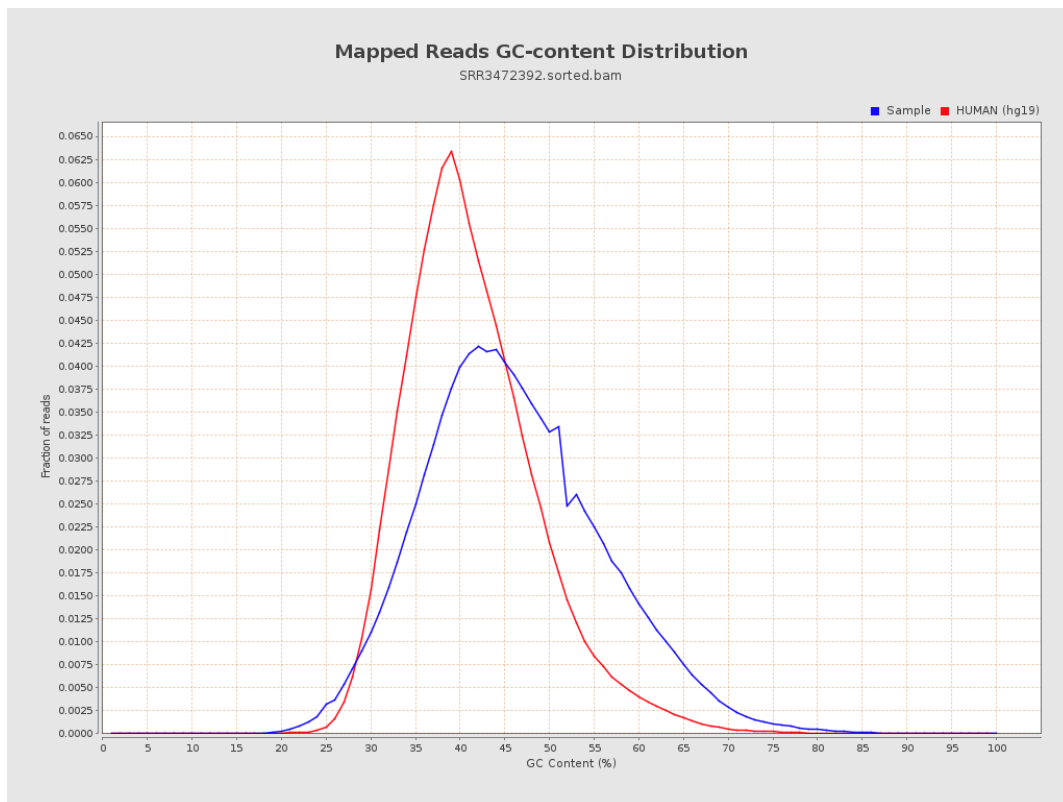
7. Results : Duplication Rate Histogram



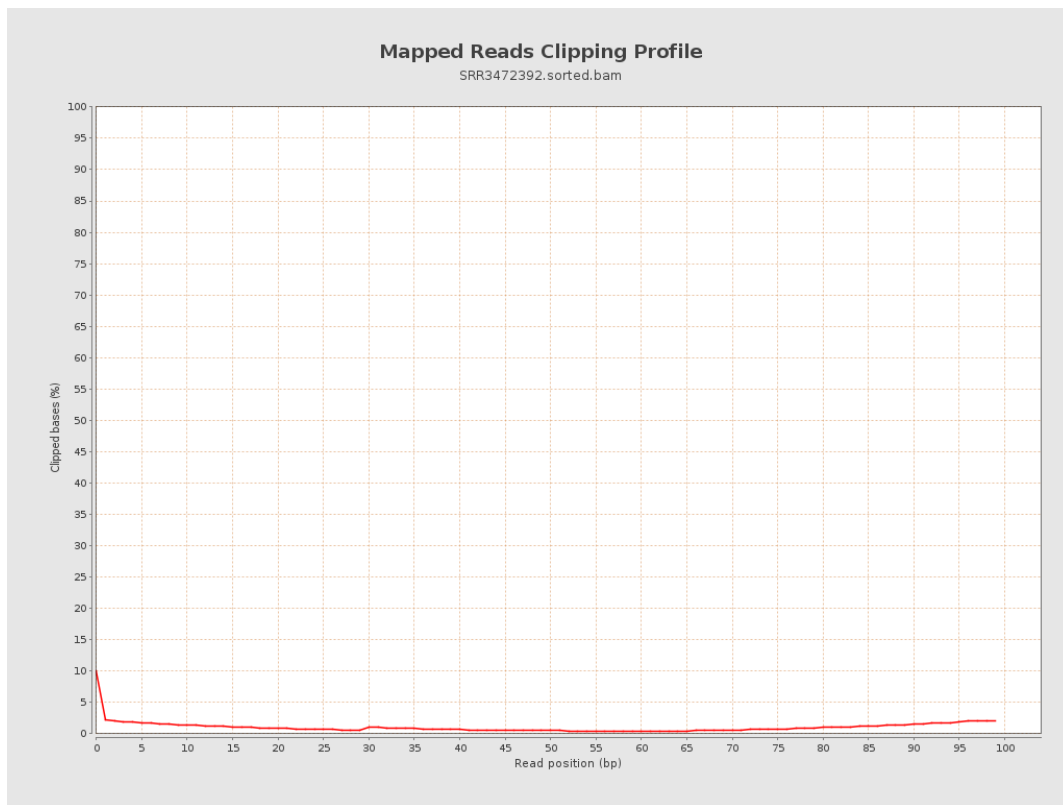
8. Results : Mapped Reads Nucleotide Content



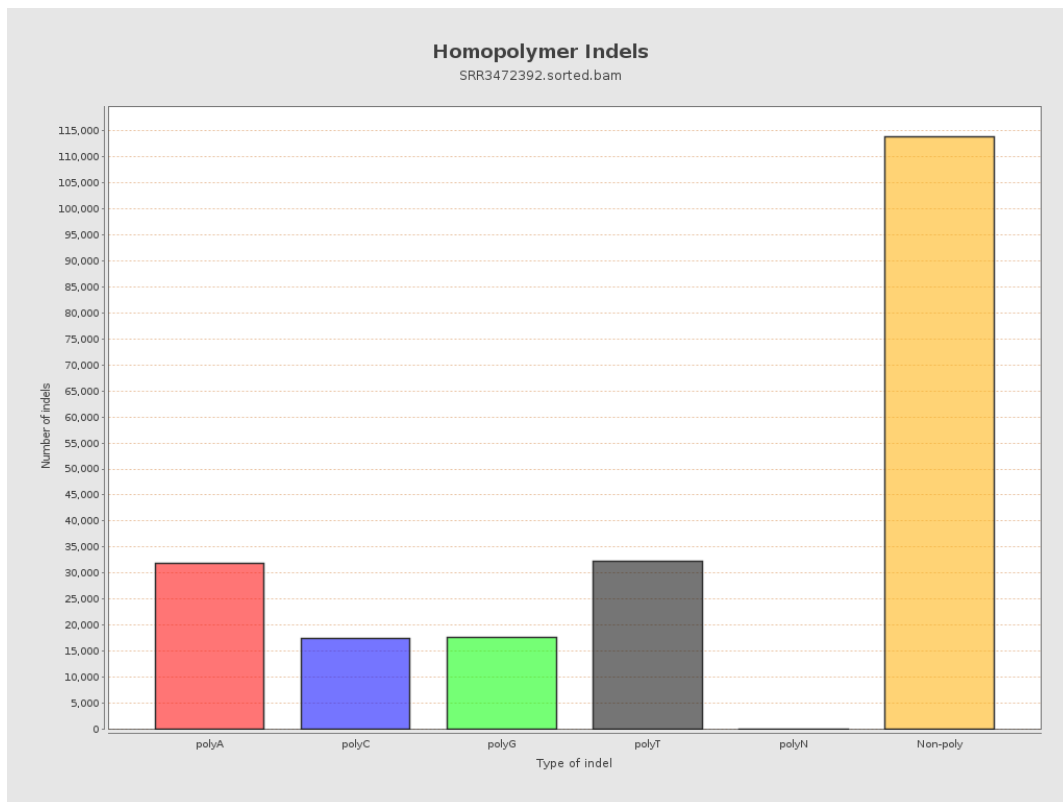
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



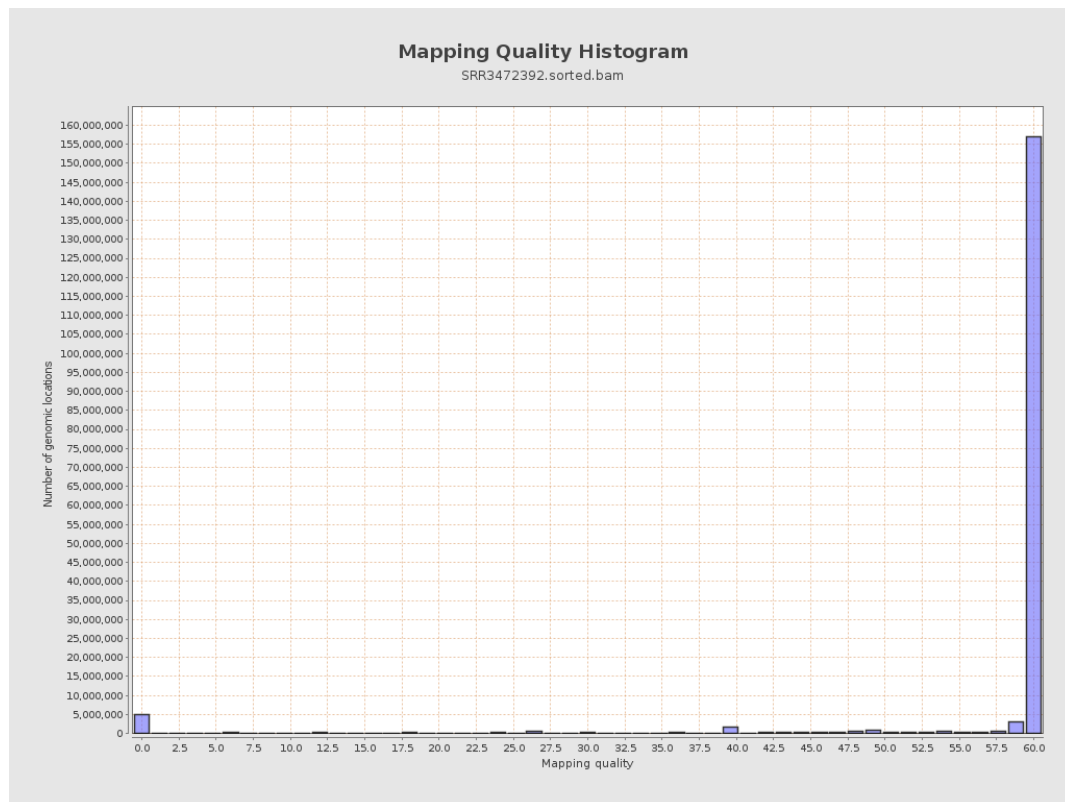
11. Results : Homopolymer Indels



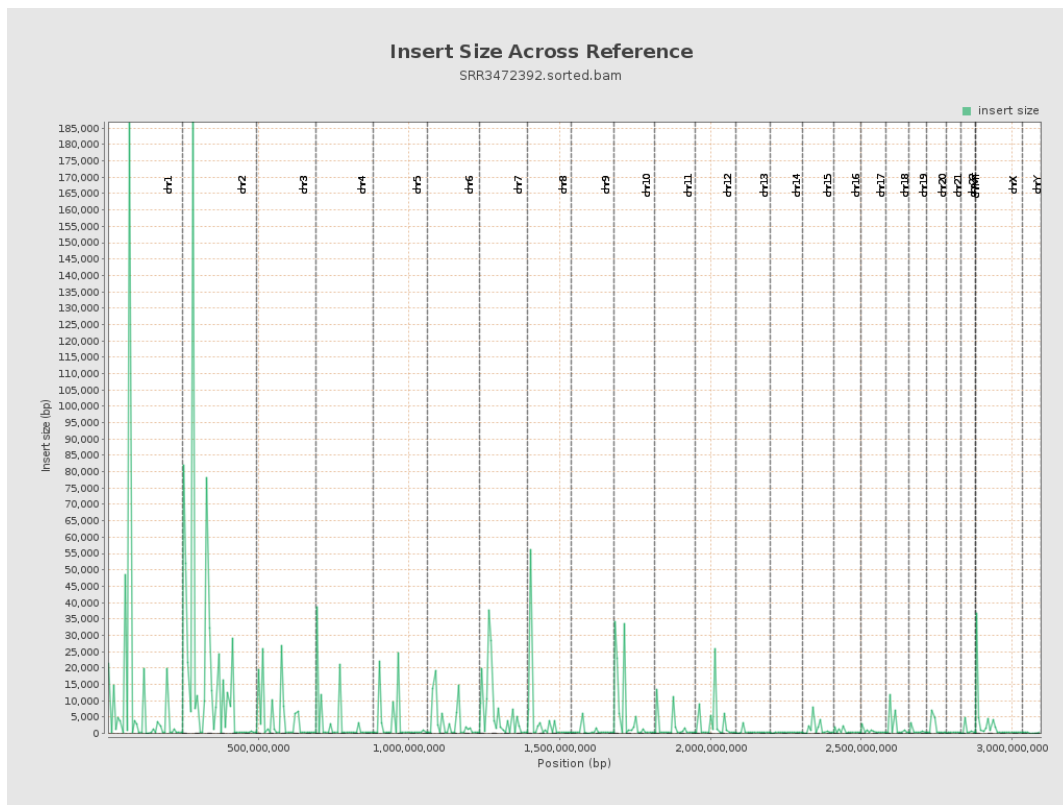
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

