

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 14:01:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046424.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_SRR2046424 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046424_1.fastq.gz SRR2046424_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 14:01:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046424.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,137,388
Mapped reads	7,109,081 / 99.6%
Unmapped reads	28,307 / 0.4%
Mapped paired reads	7,109,081 / 99.6%
Mapped reads, first in pair	3,558,843 / 49.86%
Mapped reads, second in pair	3,550,238 / 49.74%
Mapped reads, both in pair	7,088,994 / 99.32%
Mapped reads, singletons	20,087 / 0.28%
Secondary alignments	0
Supplementary alignments	42,024 / 0.59%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	5,404,790 / 75.73%
Duplication rate	36.35%
Clipped reads	1,302,135 / 18.24%

2.2. ACGT Content

Number/percentage of A's	202,132,659 / 29.38%
Number/percentage of C's	142,084,878 / 20.65%
Number/percentage of T's	200,597,496 / 29.16%
Number/percentage of G's	143,111,540 / 20.8%
Number/percentage of N's	58,831 / 0.01%

GC Percentage	41.45%
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2.3. Coverage

Mean	0.2223
Standard Deviation	23.4135

2.4. Mapping Quality

Mean Mapping Quality	52.46
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2.5. Insert size

Mean	53,547.4
Standard Deviation	2,431,949.51
P25/Median/P75	113 / 148 / 190

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	2,497,031
Insertions	57,830
Mapped reads with at least one insertion	0.8%
Deletions	66,653
Mapped reads with at least one deletion	0.91%
Homopolymer indels	49.74%

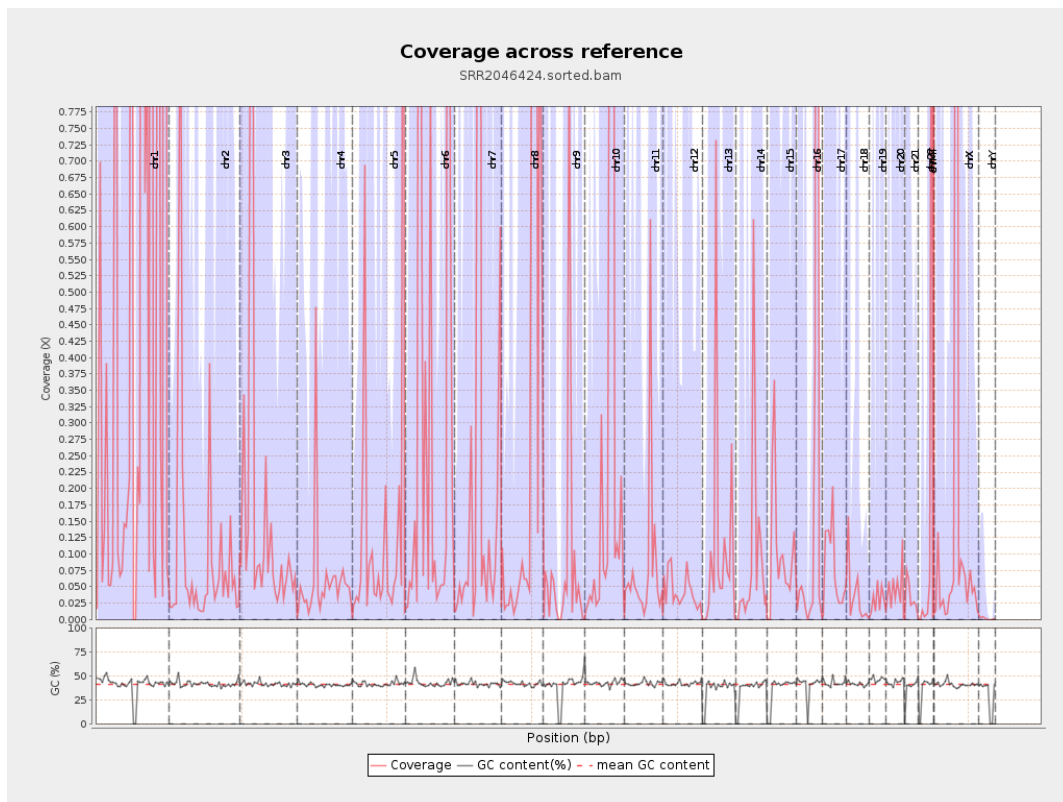
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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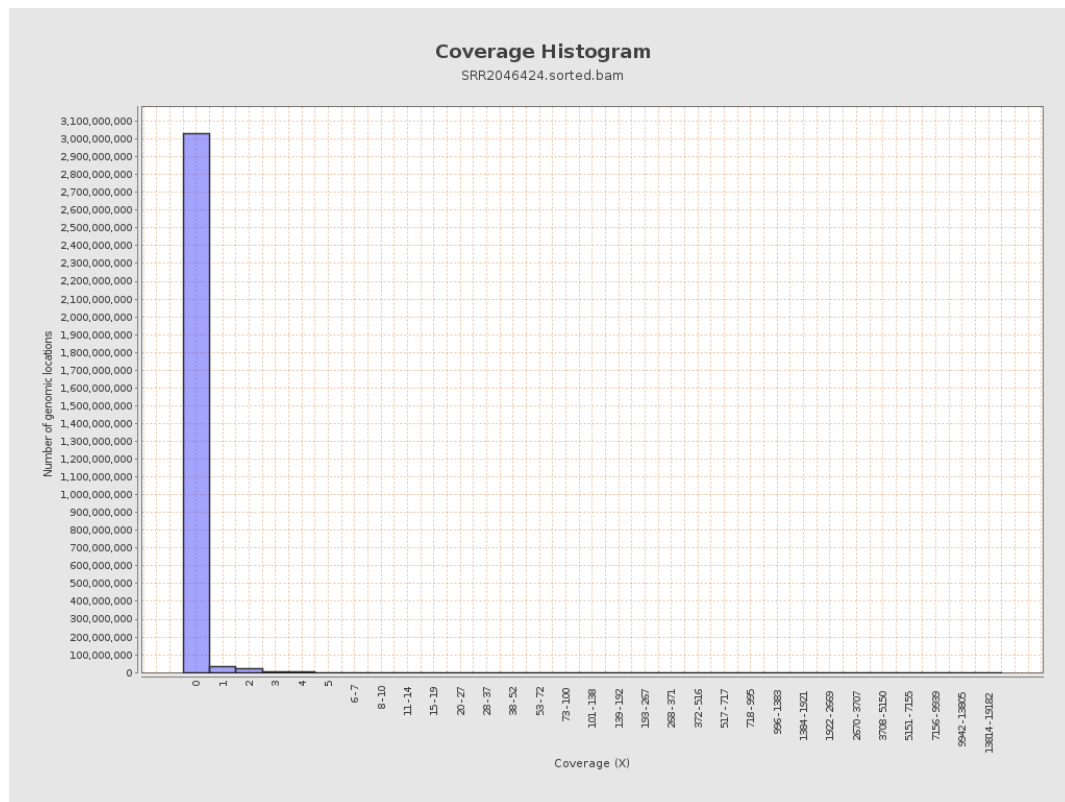
		bases	coverage	deviation
chr1	249250621	217162781	0.8713	53.7263
chr2	243199373	26325809	0.1082	9.4972
chr3	198022430	35319777	0.1784	14.6107
chr4	191154276	11537015	0.0604	6.6219
chr5	180915260	31212719	0.1725	18.7496
chr6	171115067	63145641	0.369	32.3058
chr7	159138663	44665029	0.2807	26.8009
chr8	146364022	75502064	0.5159	31.8161
chr9	141213431	11558011	0.0818	22.7576
chr10	135534747	43836429	0.3234	36.0642
chr11	135006516	10784185	0.0799	4.5404
chr12	133851895	5828741	0.0435	1.7151
chr13	115169878	12687291	0.1102	9.4955
chr14	107349540	9442663	0.088	8.6123
chr15	102531392	10768903	0.105	8.3441
chr16	90354753	30077982	0.3329	26.9733
chr17	81195210	6280104	0.0773	5.3712
chr18	78077248	2761119	0.0354	2.0555
chr19	59128983	1663353	0.0281	1.3777
chr20	63025520	3088898	0.049	2.8449
chr21	48129895	1611172	0.0335	1.7606
chr22	51304566	10462847	0.2039	15.9318
chrMT	16571	71255	4.3	3.3274
chrX	155270560	22285002	0.1435	16.0248

chrY	59373566	88060	0.0015	0.0898
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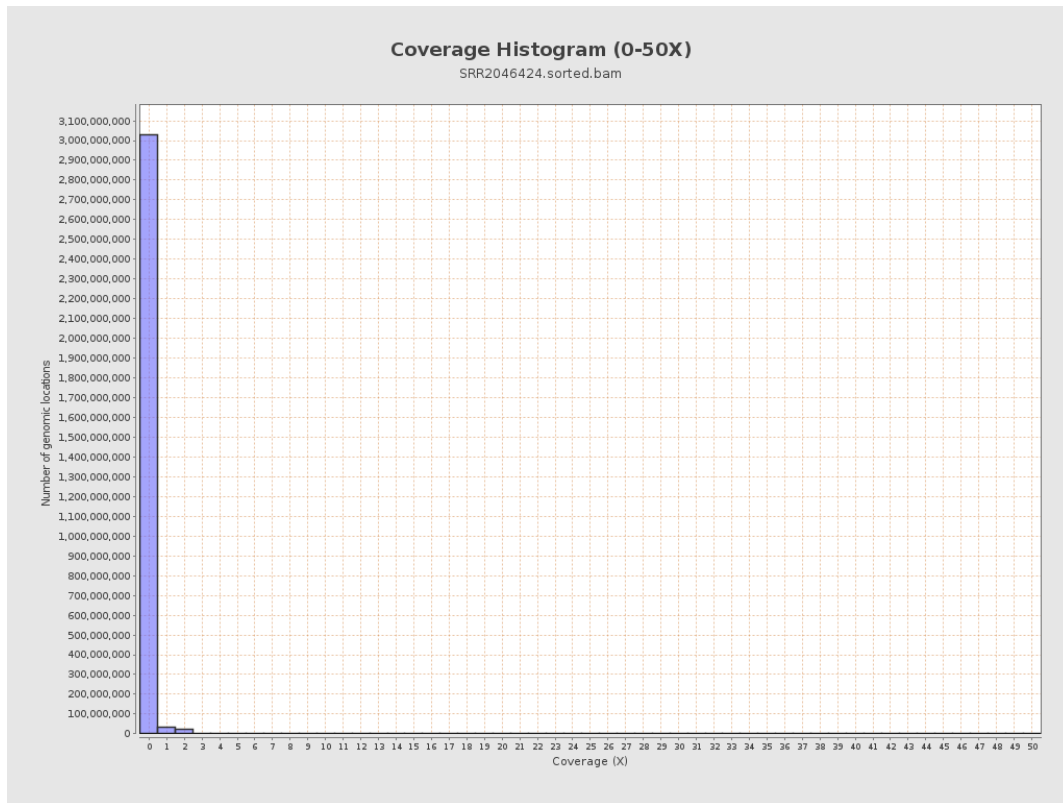
3. Results : Coverage across reference



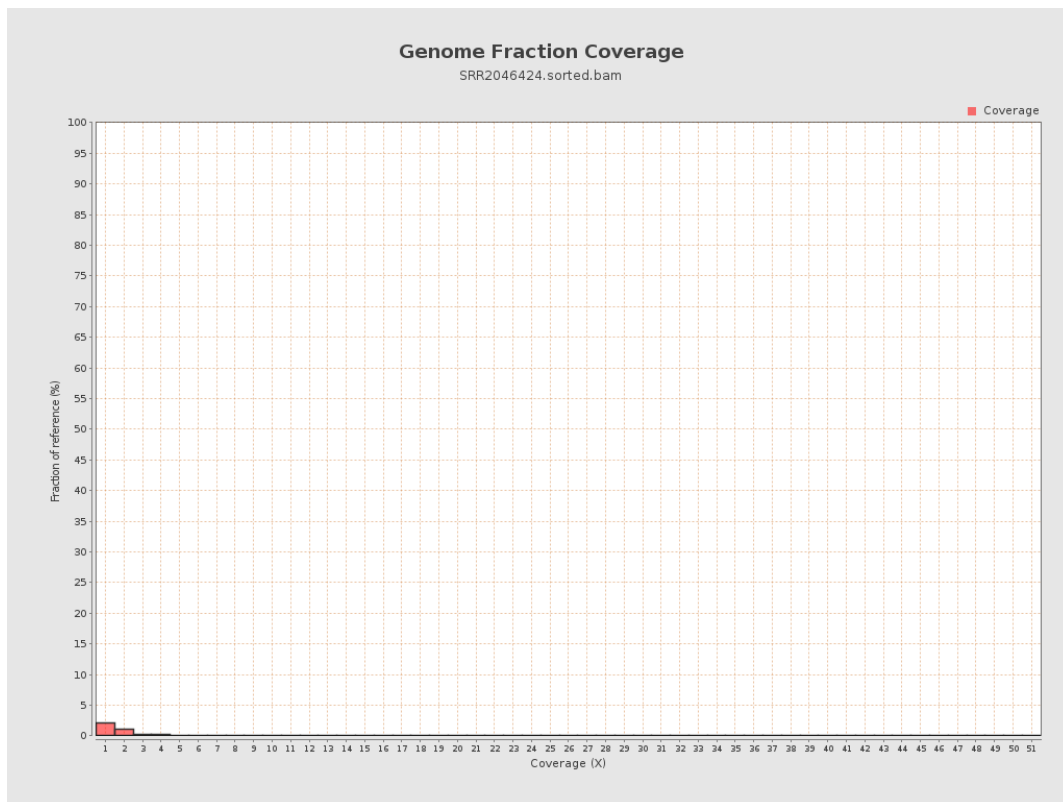
4. Results : Coverage Histogram



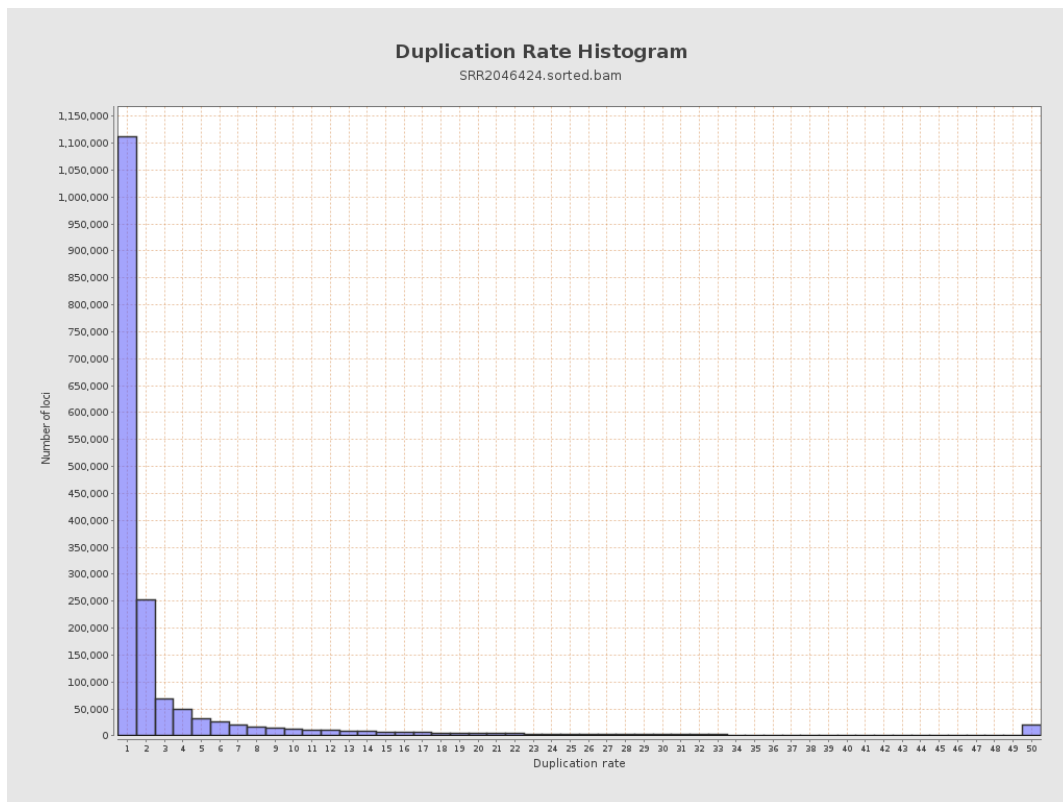
5. Results : Coverage Histogram (0-50X)



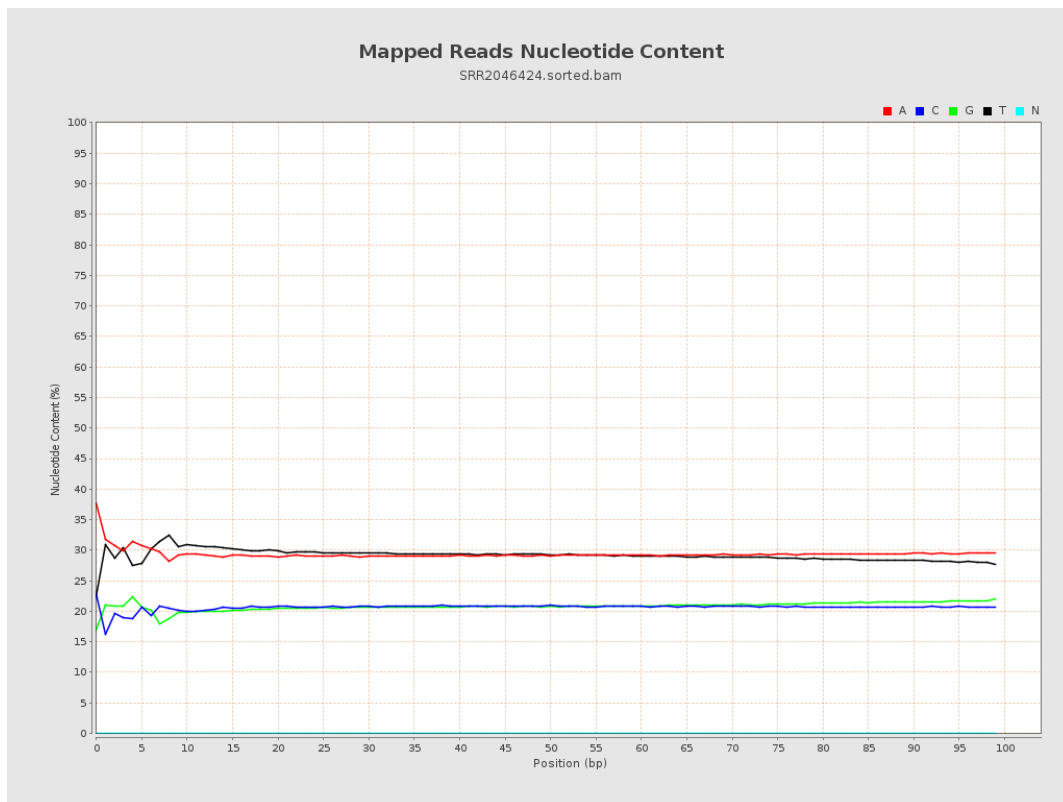
6. Results : Genome Fraction Coverage



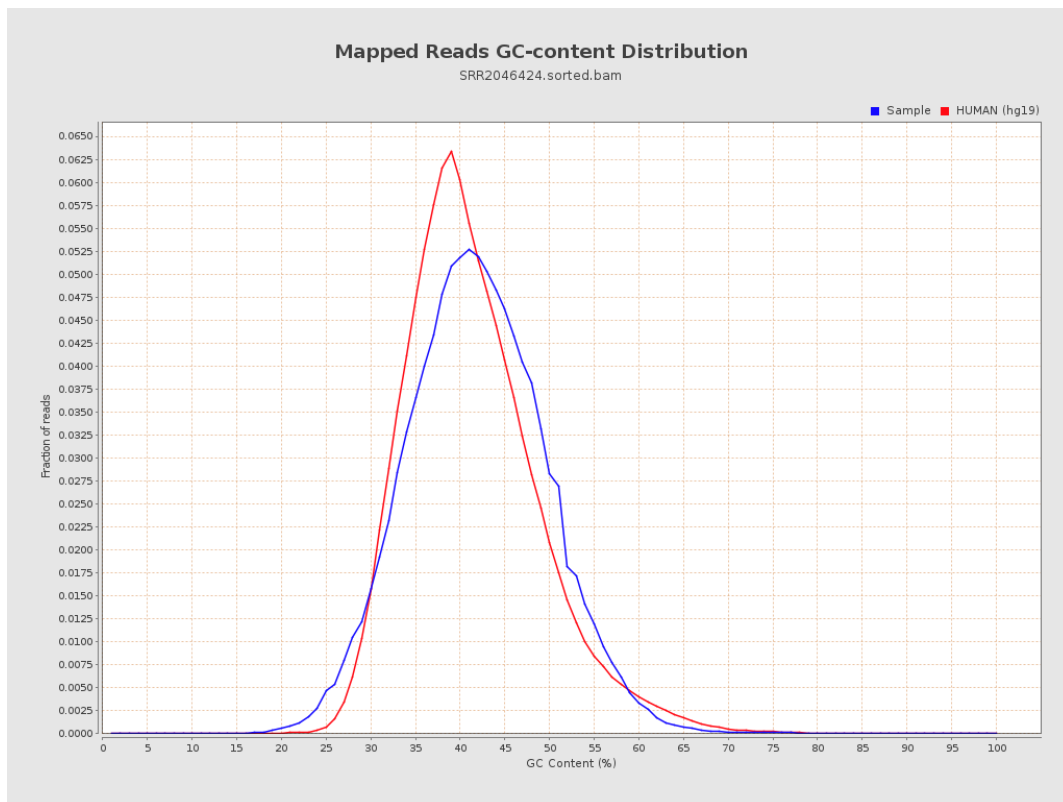
7. Results : Duplication Rate Histogram



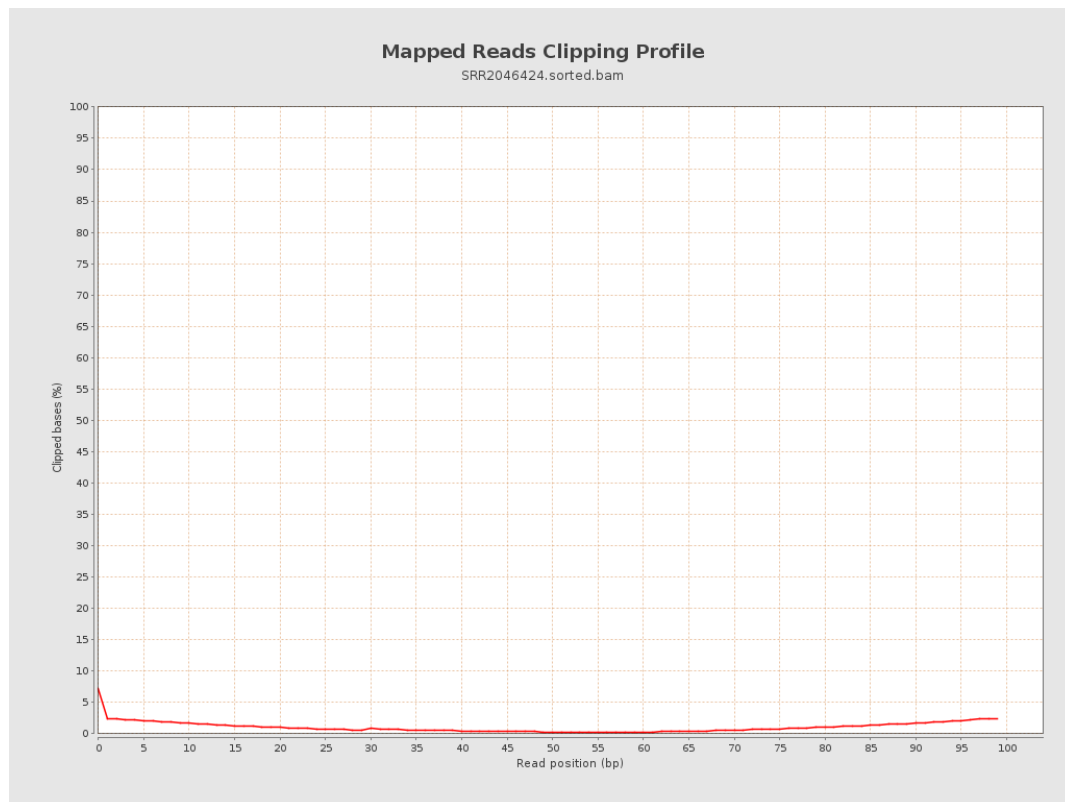
8. Results : Mapped Reads Nucleotide Content



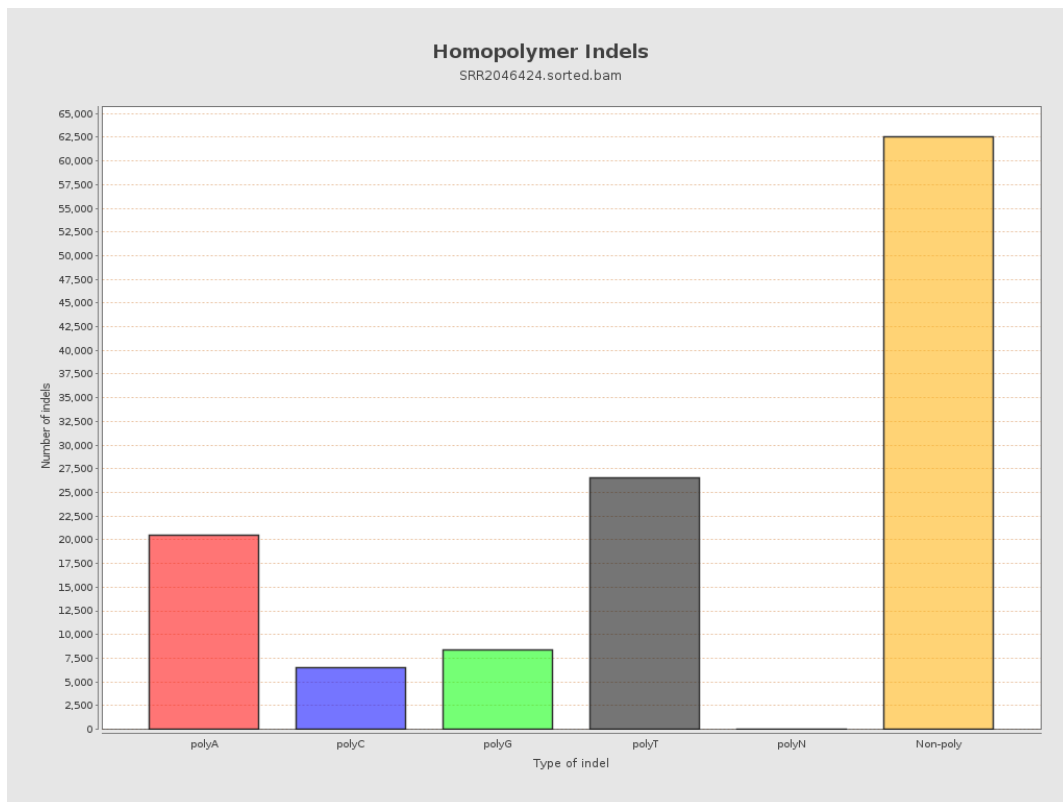
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



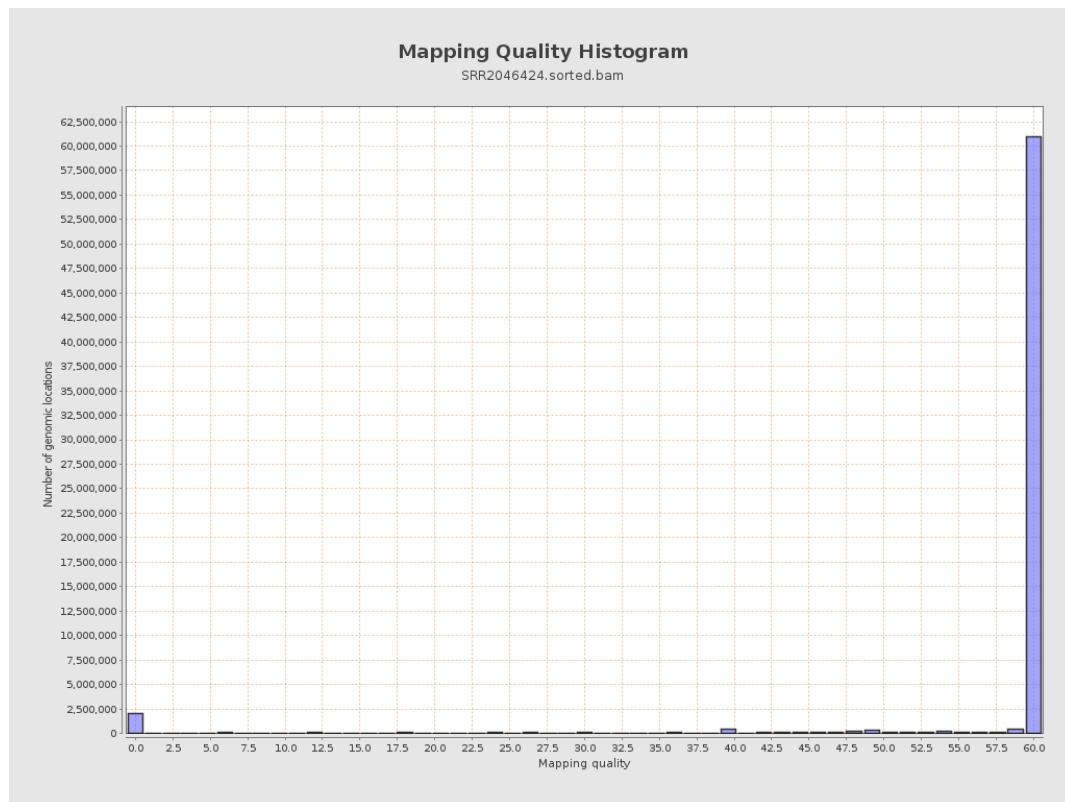
11. Results : Homopolymer Indels



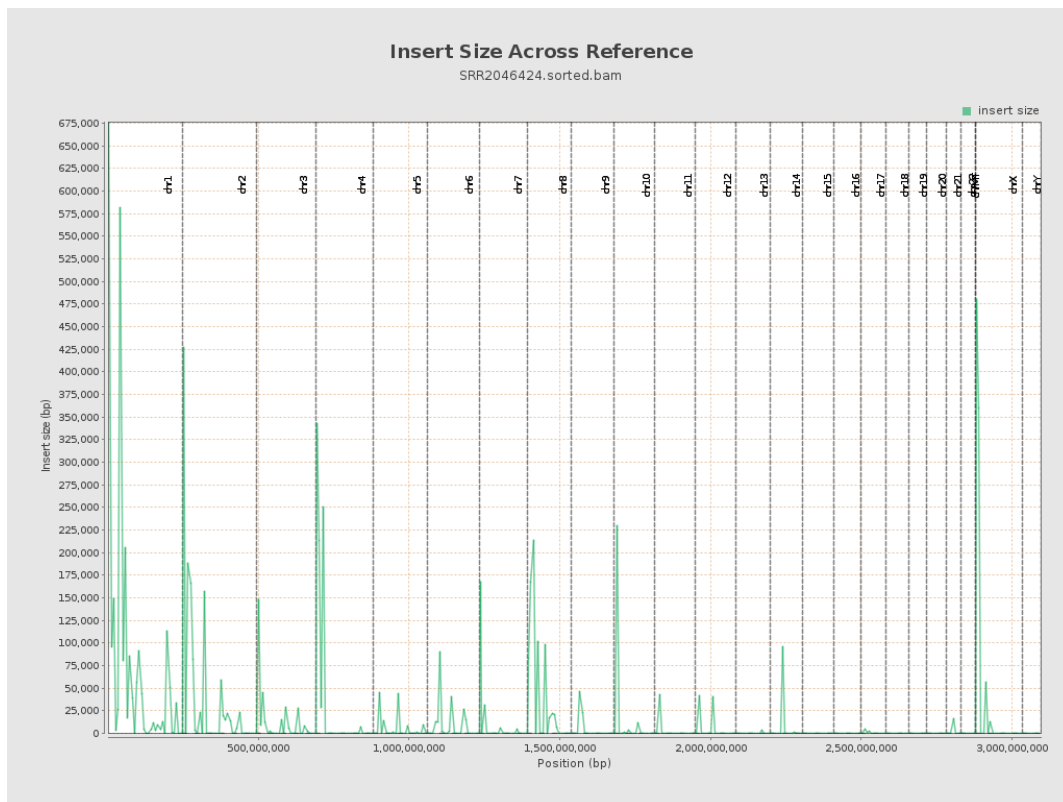
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

