

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 14:18:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046432.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_SRR2046432 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046432_1.fastq.gz SRR2046432_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 14:18:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046432.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,444,450
Mapped reads	6,410,522 / 99.47%
Unmapped reads	33,928 / 0.53%
Mapped paired reads	6,410,522 / 99.47%
Mapped reads, first in pair	3,207,182 / 49.77%
Mapped reads, second in pair	3,203,340 / 49.71%
Mapped reads, both in pair	6,387,376 / 99.11%
Mapped reads, singletons	23,146 / 0.36%
Secondary alignments	0
Supplementary alignments	53,177 / 0.83%
Read min/max/mean length	30 / 100 / 100.34
Duplicated reads (estimated)	5,073,824 / 78.73%
Duplication rate	41.19%
Clipped reads	1,544,254 / 23.96%

2.2. ACGT Content

Number/percentage of A's	181,801,351 / 29.55%
Number/percentage of C's	126,284,502 / 20.53%
Number/percentage of T's	181,607,840 / 29.52%
Number/percentage of G's	125,506,793 / 20.4%
Number/percentage of N's	55,784 / 0.01%

GC Percentage	40.92%
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2.3. Coverage

Mean	0.1988
Standard Deviation	22.0979

2.4. Mapping Quality

Mean Mapping Quality	52.19
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2.5. Insert size

Mean	15,024.64
Standard Deviation	1,200,169.05
P25/Median/P75	104 / 131 / 162

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	2,763,629
Insertions	56,548
Mapped reads with at least one insertion	0.87%
Deletions	57,316
Mapped reads with at least one deletion	0.87%
Homopolymer indels	46.38%

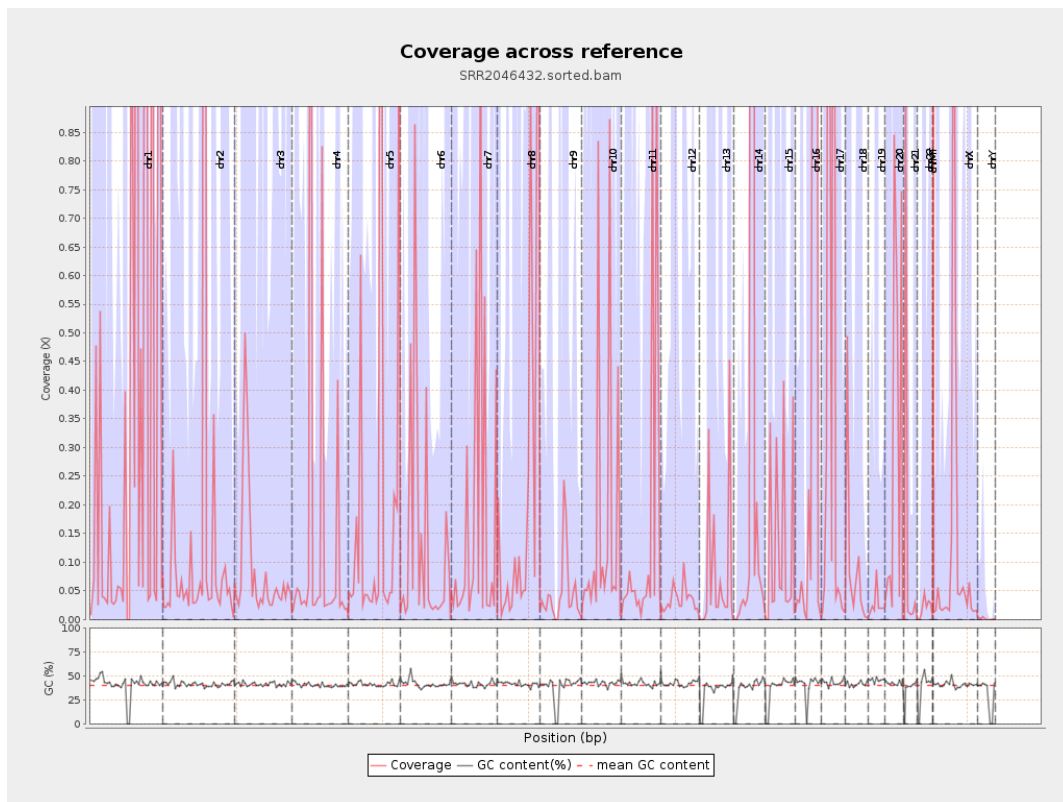
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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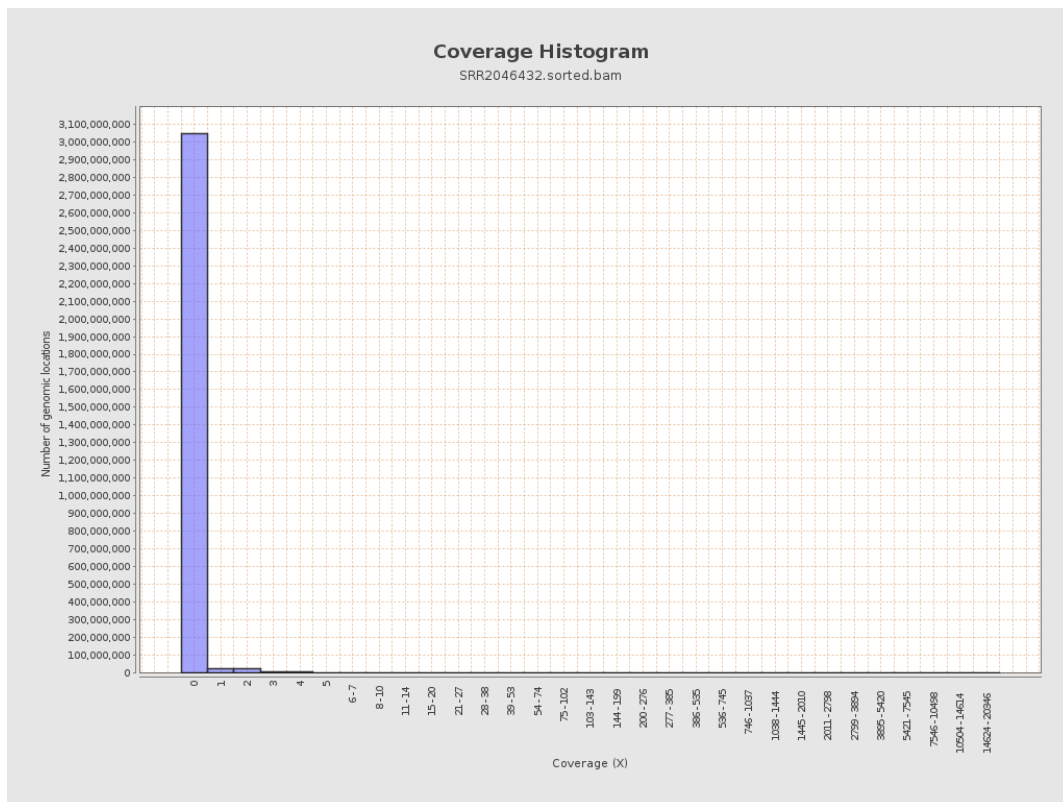
		bases	coverage	deviation
chr1	249250621	105304201	0.4225	27.6202
chr2	243199373	49010765	0.2015	21.1052
chr3	198022430	18189448	0.0919	6.2758
chr4	191154276	29578971	0.1547	20.7916
chr5	180915260	39256134	0.217	20.039
chr6	171115067	23104938	0.135	11.8695
chr7	159138663	28245414	0.1775	16.2618
chr8	146364022	34339189	0.2346	22.9777
chr9	141213431	6778293	0.048	6.257
chr10	135534747	22958348	0.1694	15.9853
chr11	135006516	19930161	0.1476	11.5848
chr12	133851895	4665020	0.0349	1.4
chr13	115169878	9397656	0.0816	7.4648
chr14	107349540	62461001	0.5818	48.1318
chr15	102531392	13479134	0.1315	13.0631
chr16	90354753	57380725	0.6351	54.6977
chr17	81195210	35686165	0.4395	31.8059
chr18	78077248	6788842	0.087	7.1868
chr19	59128983	1558242	0.0264	1.6438
chr20	63025520	18432146	0.2925	37.8844
chr21	48129895	7877808	0.1637	21.6209
chr22	51304566	1056536	0.0206	1.6873
chrMT	16571	186966	11.2827	5.6611
chrX	155270560	19654899	0.1266	26.0871

chrY	59373566	81102	0.0014	0.1118
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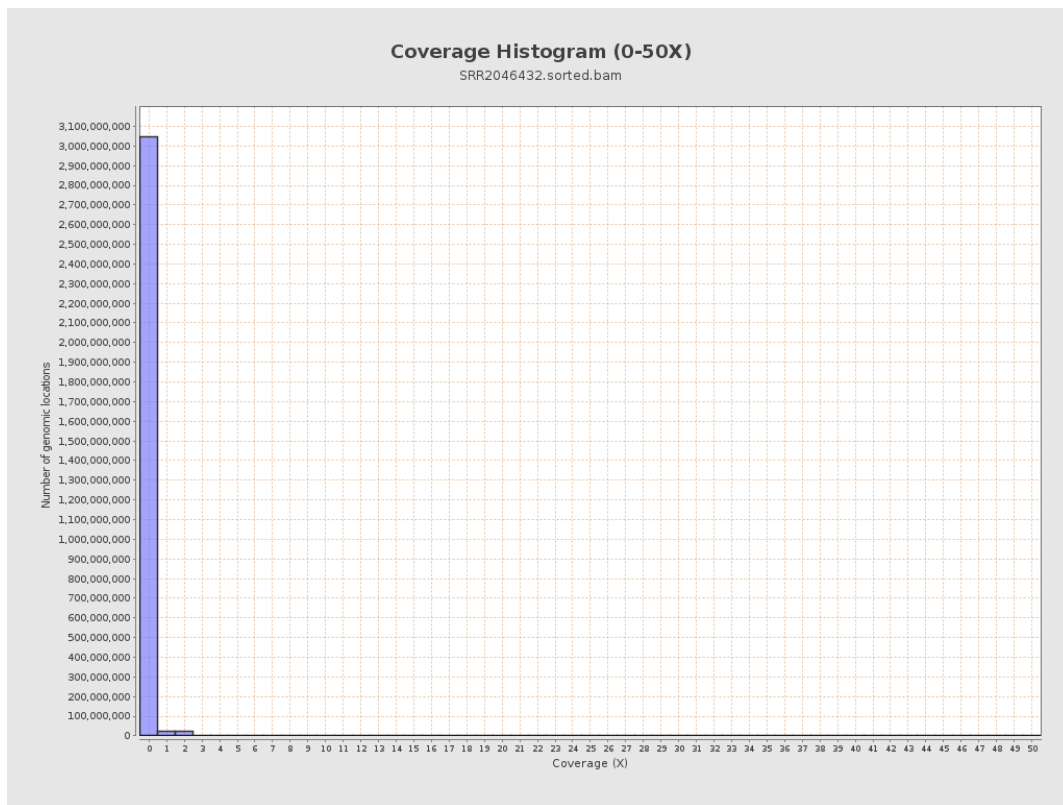
3. Results : Coverage across reference



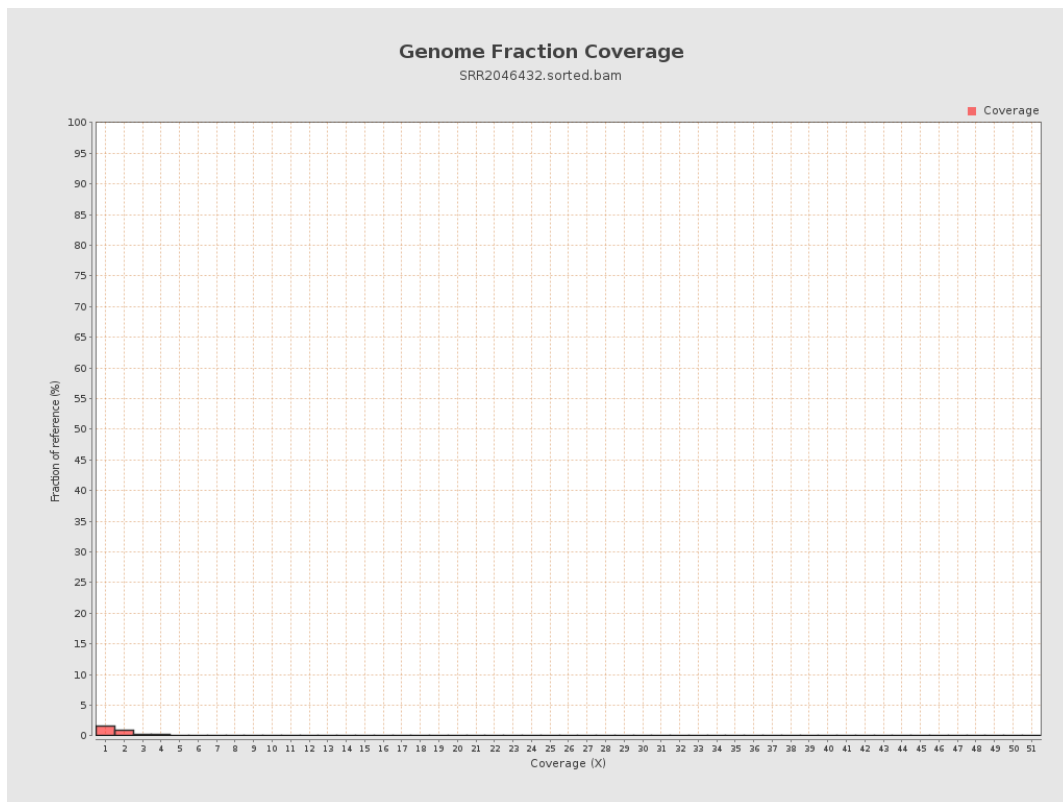
4. Results : Coverage Histogram



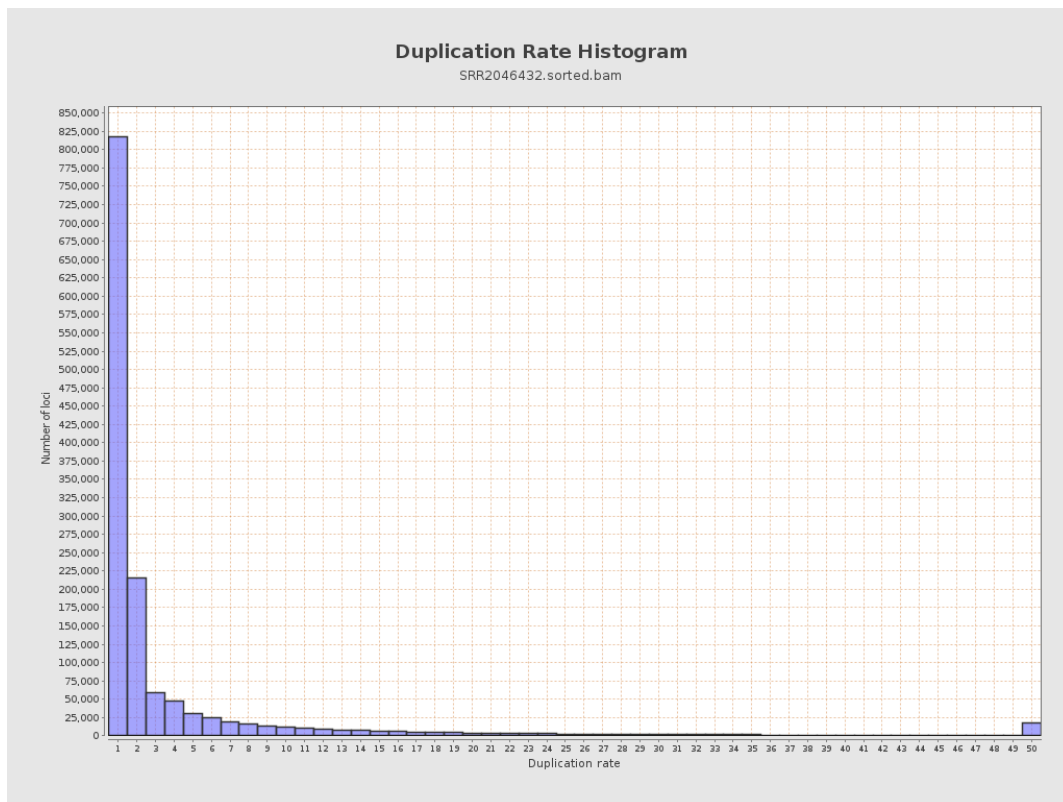
5. Results : Coverage Histogram (0-50X)



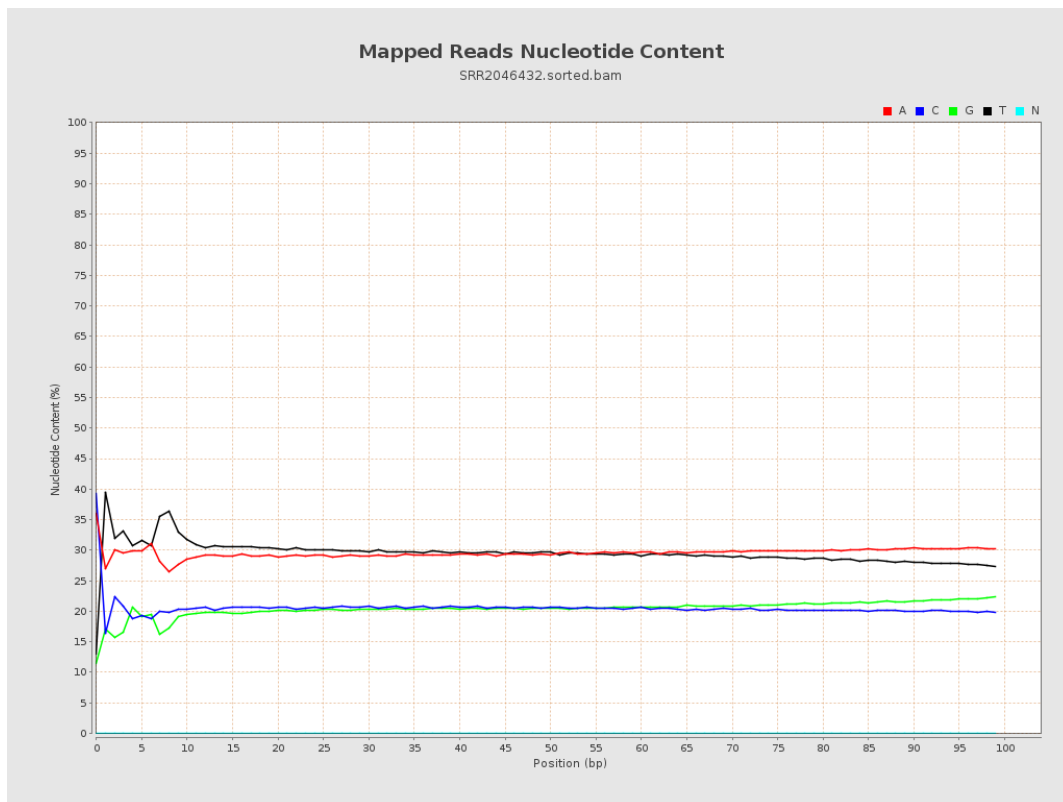
6. Results : Genome Fraction Coverage



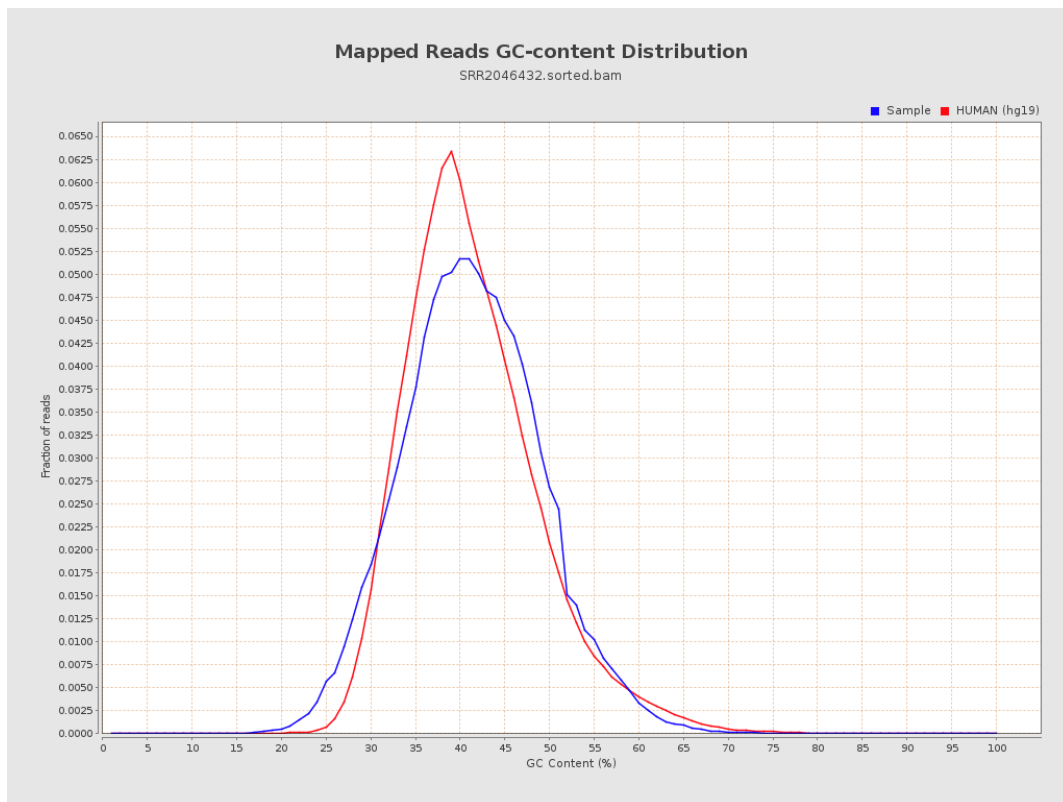
7. Results : Duplication Rate Histogram



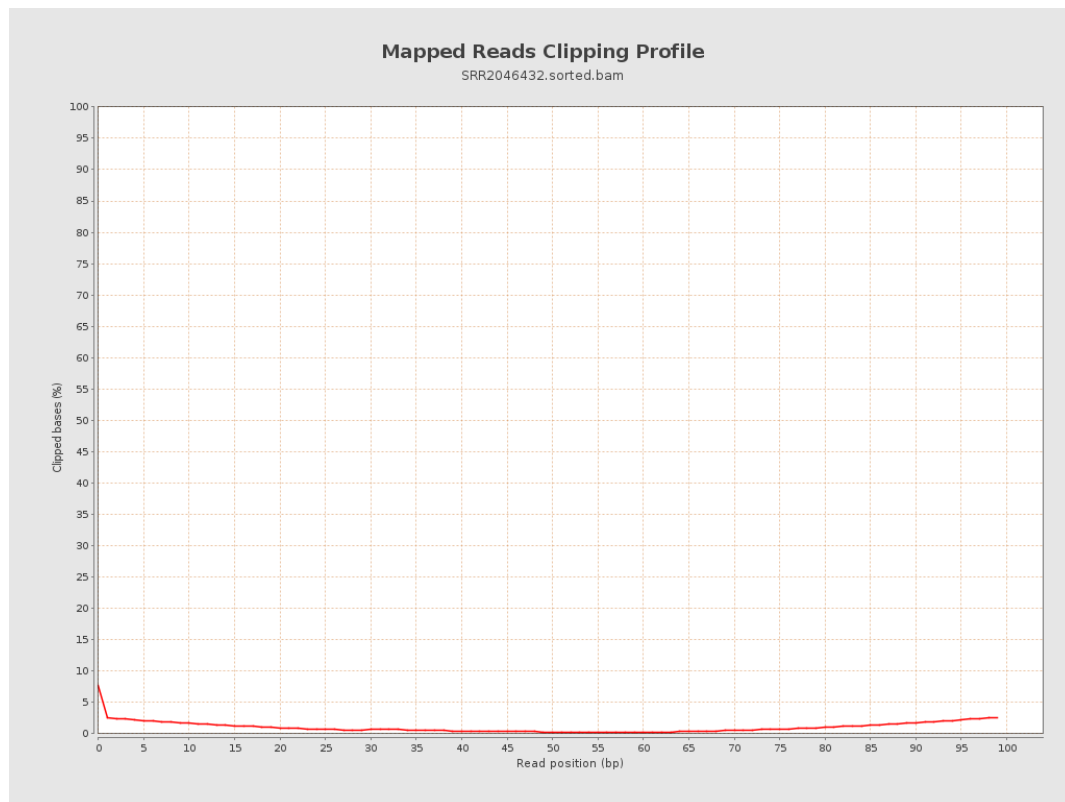
8. Results : Mapped Reads Nucleotide Content



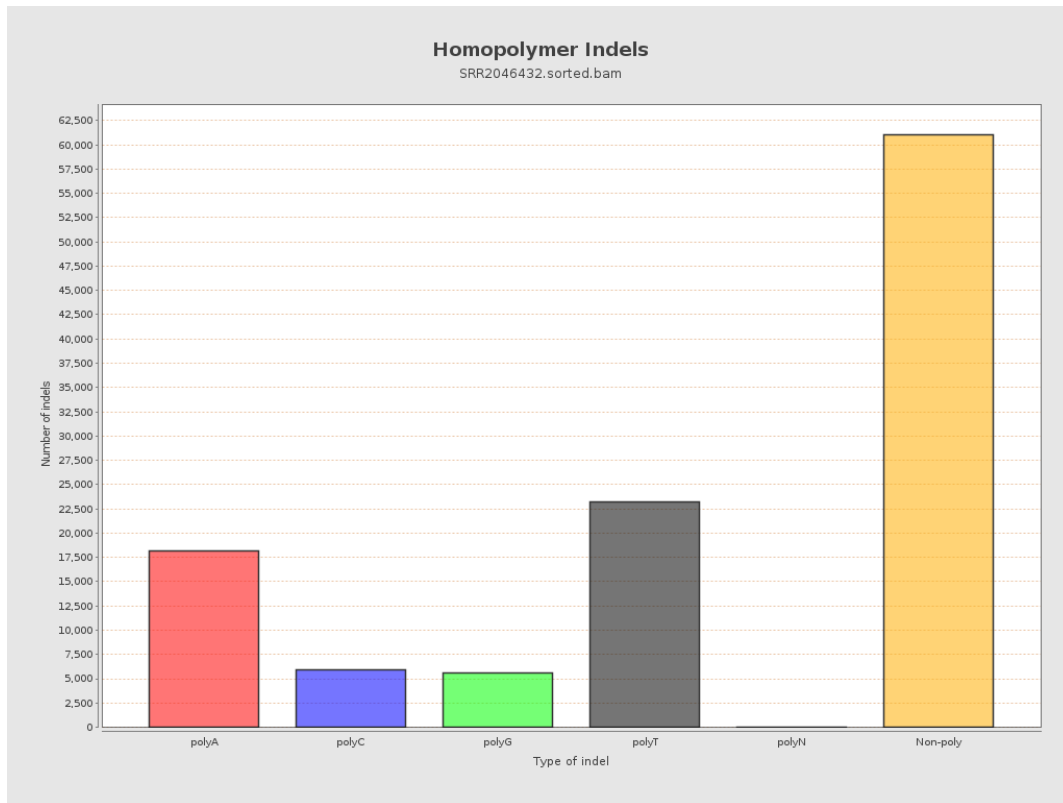
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



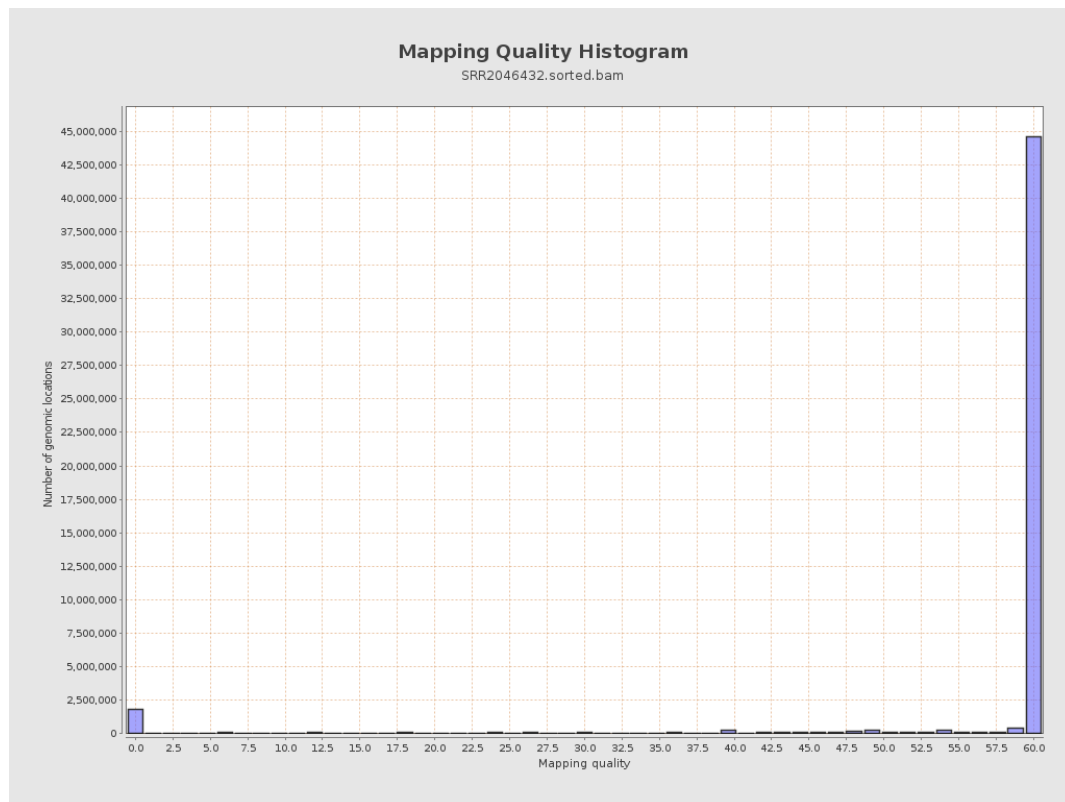
11. Results : Homopolymer Indels



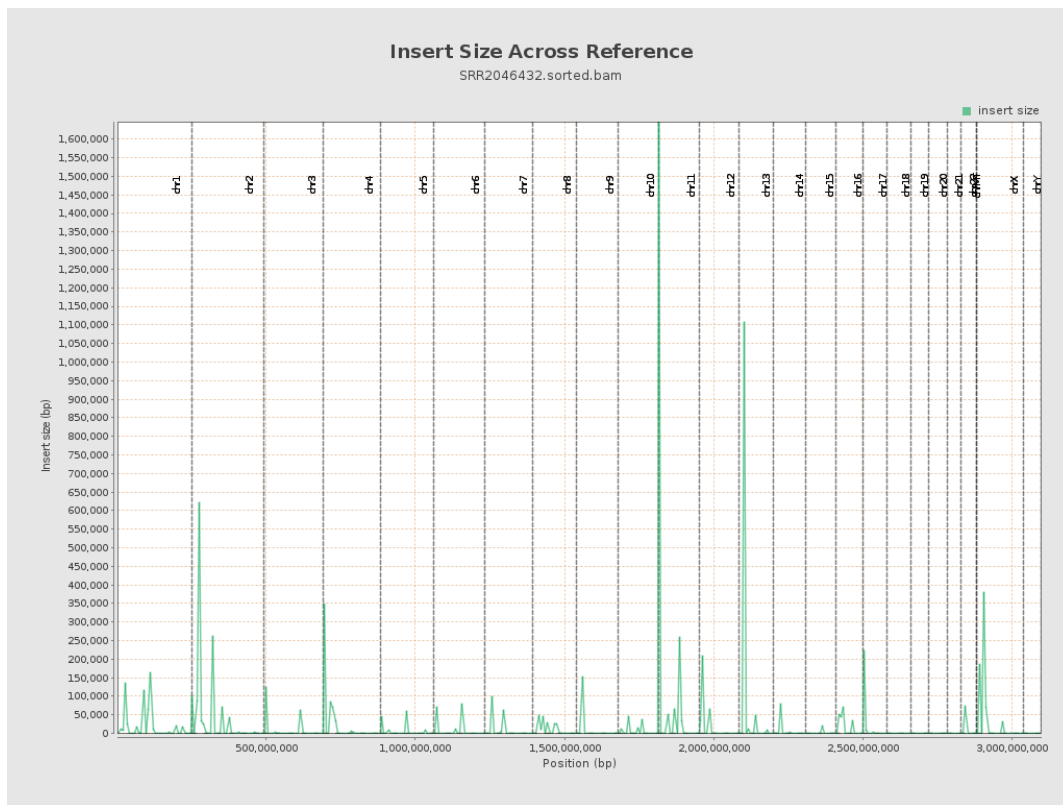
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

