

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 11:02:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124965.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_SRR3124965 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124965_1.fastq.gz SRR3124965_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 11:02:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124965.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,702,220
Mapped reads	4,469,341 / 95.05%
Unmapped reads	232,879 / 4.95%
Mapped paired reads	4,469,341 / 95.05%
Mapped reads, first in pair	2,280,464 / 48.5%
Mapped reads, second in pair	2,188,877 / 46.55%
Mapped reads, both in pair	4,344,764 / 92.4%
Mapped reads, singletons	124,577 / 2.65%
Secondary alignments	0
Supplementary alignments	14,739 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	391,214 / 8.32%
Duplication rate	4.89%
Clipped reads	2,322,838 / 49.4%

2.2. ACGT Content

Number/percentage of A's	75,479,991 / 27.73%
Number/percentage of C's	48,291,936 / 17.74%
Number/percentage of T's	82,373,902 / 30.26%
Number/percentage of G's	66,053,567 / 24.27%
Number/percentage of N's	3 / 0%

GC Percentage	42.01%
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2.3. Coverage

Mean	0.088
Standard Deviation	1.2932

2.4. Mapping Quality

Mean Mapping Quality	51.09
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2.5. Insert size

Mean	88,177.92
Standard Deviation	2,796,243.38
P25/Median/P75	130 / 178 / 247

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	2,210,342
Insertions	36,626
Mapped reads with at least one insertion	0.81%
Deletions	78,461
Mapped reads with at least one deletion	1.73%
Homopolymer indels	45.85%

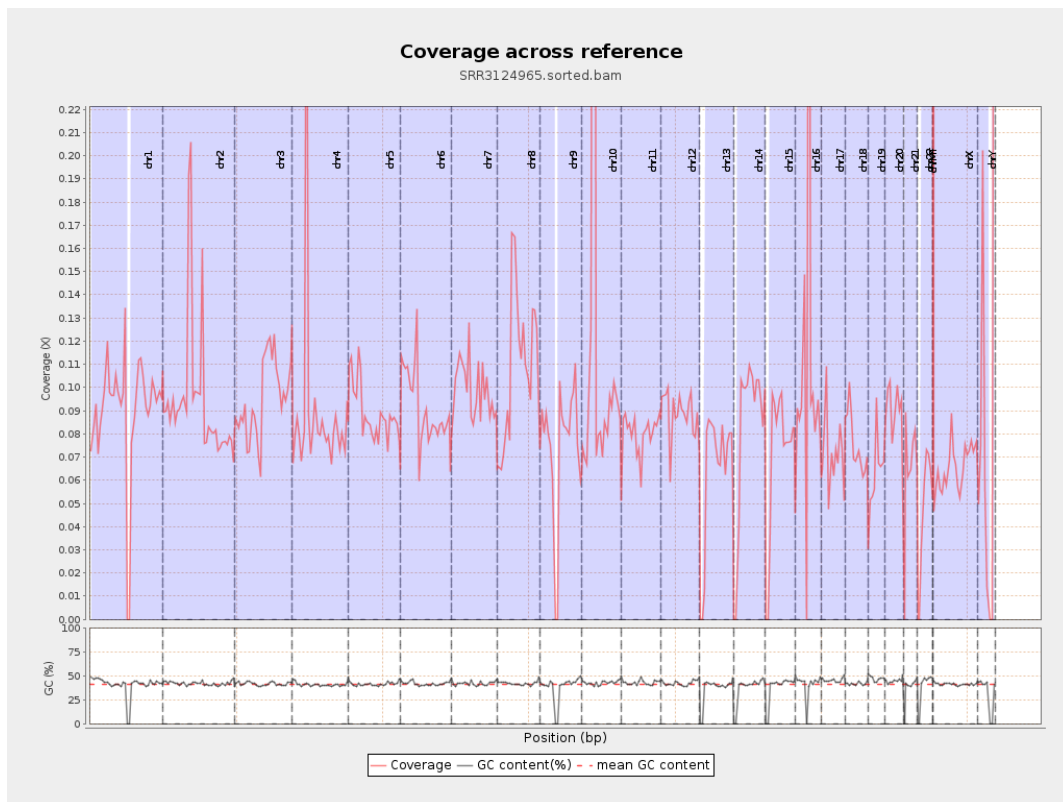
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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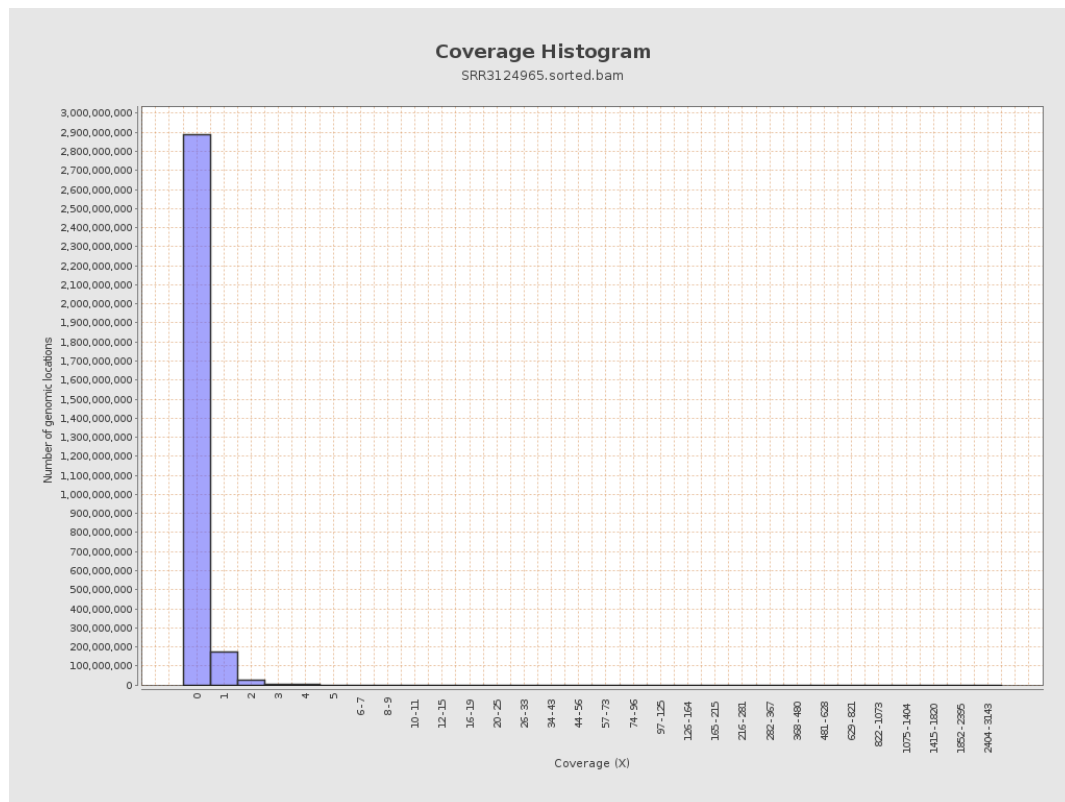
		bases	coverage	deviation
chr1	249250621	22519272	0.0903	0.7428
chr2	243199373	23054949	0.0948	1.3963
chr3	198022430	18853531	0.0952	0.4513
chr4	191154276	17233778	0.0902	1.0768
chr5	180915260	16069982	0.0888	0.3871
chr6	171115067	15593430	0.0911	0.4921
chr7	159138663	15739382	0.0989	0.732
chr8	146364022	15981130	0.1092	0.4756
chr9	141213431	10590657	0.075	0.7681
chr10	135534747	16455345	0.1214	4.5064
chr11	135006516	10810937	0.0801	0.4649
chr12	133851895	11917758	0.089	0.3673
chr13	115169878	7388462	0.0642	0.2983
chr14	107349540	8893762	0.0828	0.4197
chr15	102531392	7162900	0.0699	0.3326
chr16	90354753	10302023	0.114	2.4267
chr17	81195210	5907775	0.0728	0.7265
chr18	78077248	5930353	0.076	1.0625
chr19	59128983	3792427	0.0641	0.6208
chr20	63025520	5711037	0.0906	0.6241
chr21	48129895	3213017	0.0668	0.6059
chr22	51304566	2424809	0.0473	0.3335
chrMT	16571	91260	5.5072	4.1
chrX	155270560	10227729	0.0659	0.4603

chrY	59373566	6464535	0.1089	2.6764
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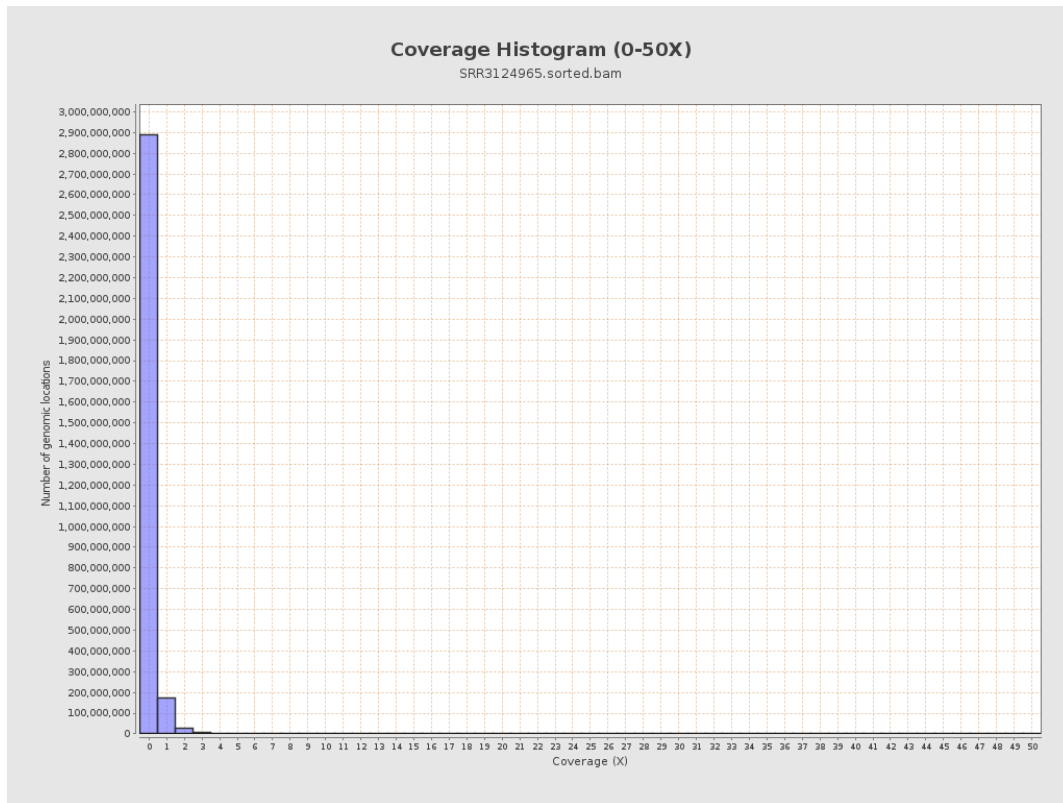
3. Results : Coverage across reference



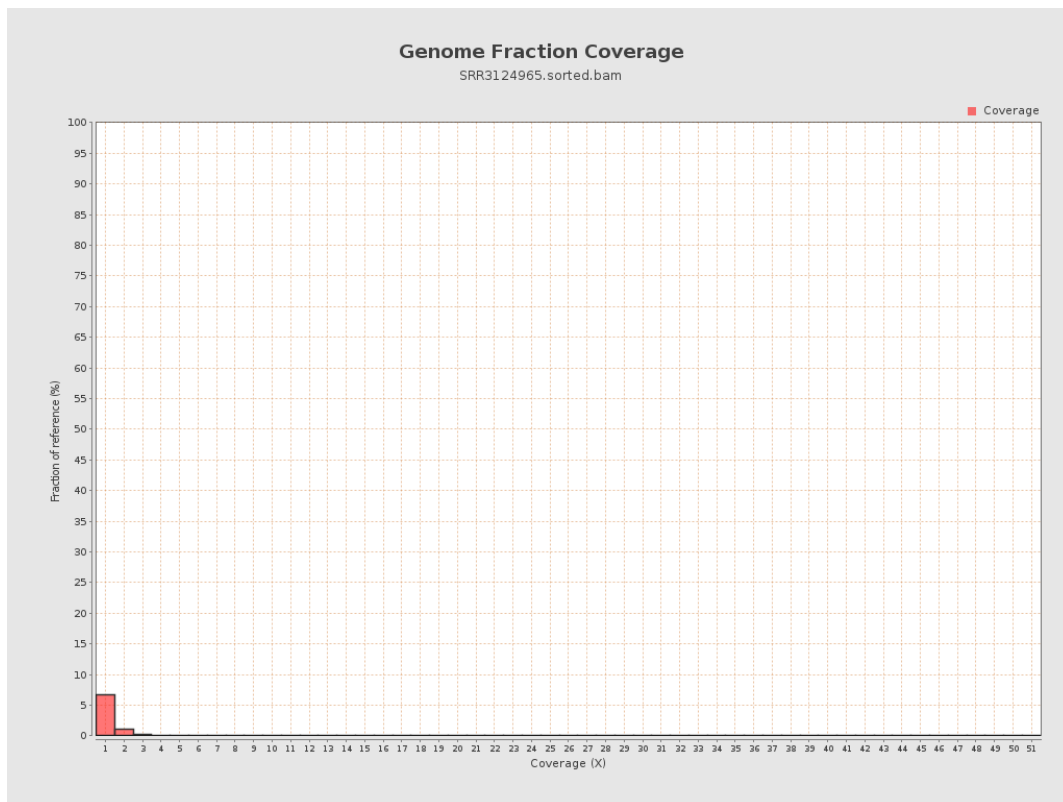
4. Results : Coverage Histogram



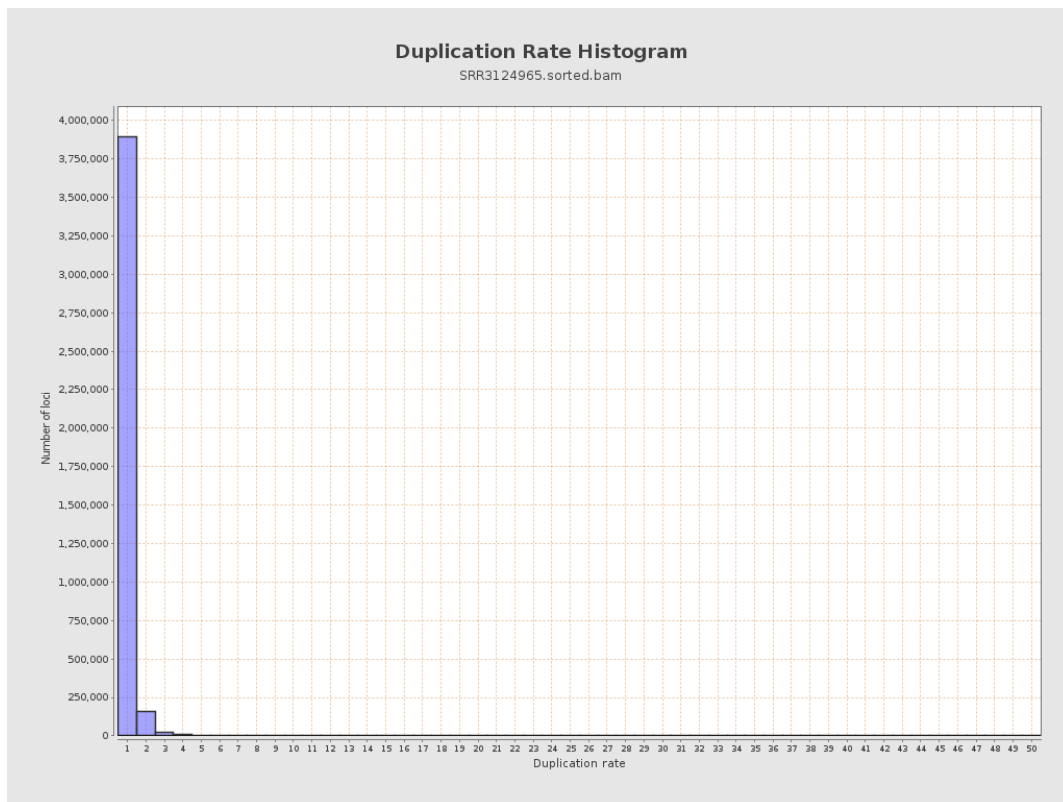
5. Results : Coverage Histogram (0-50X)



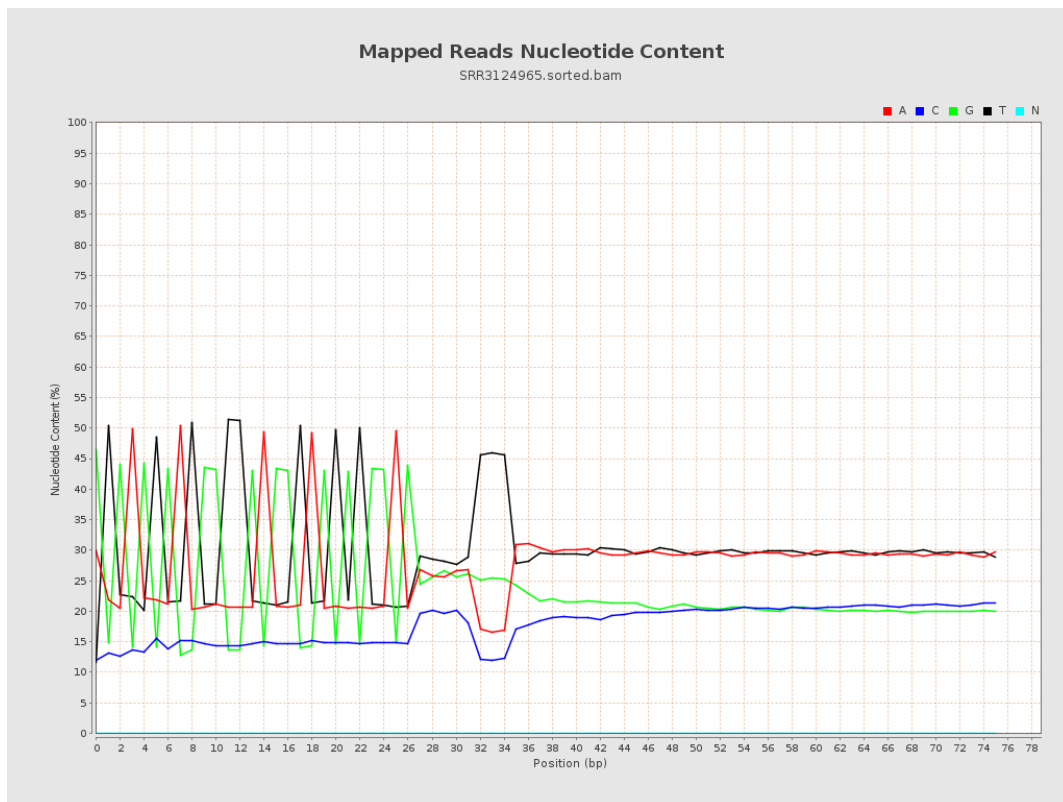
6. Results : Genome Fraction Coverage



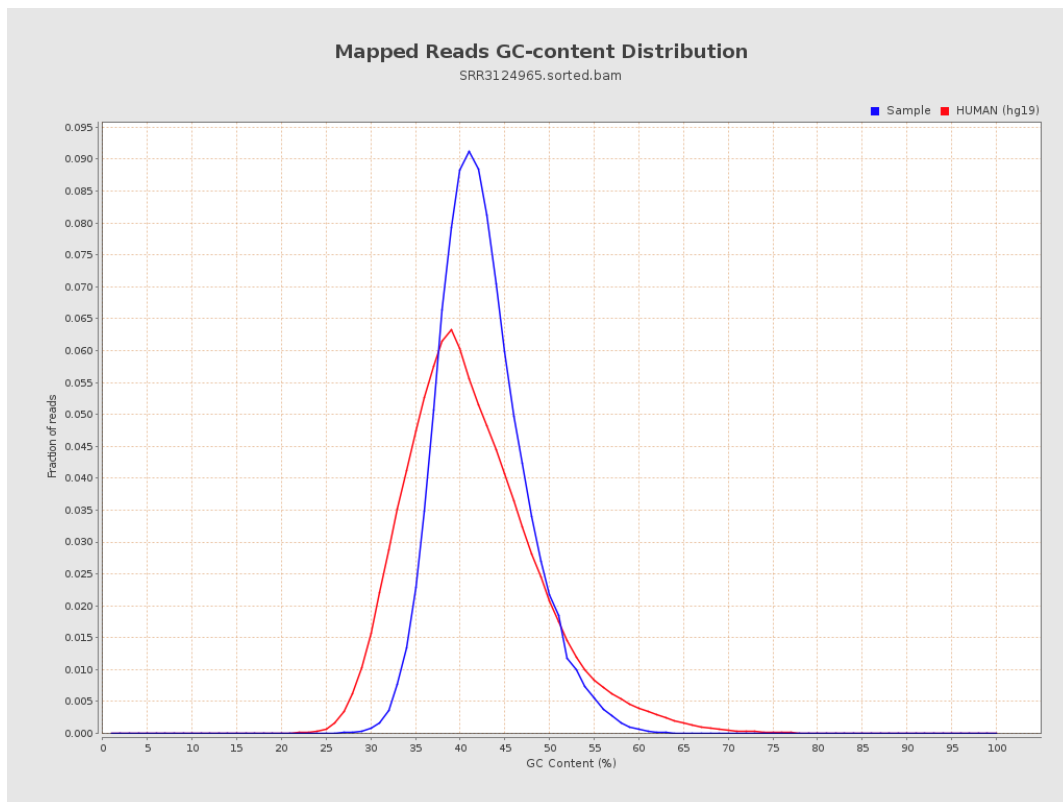
7. Results : Duplication Rate Histogram



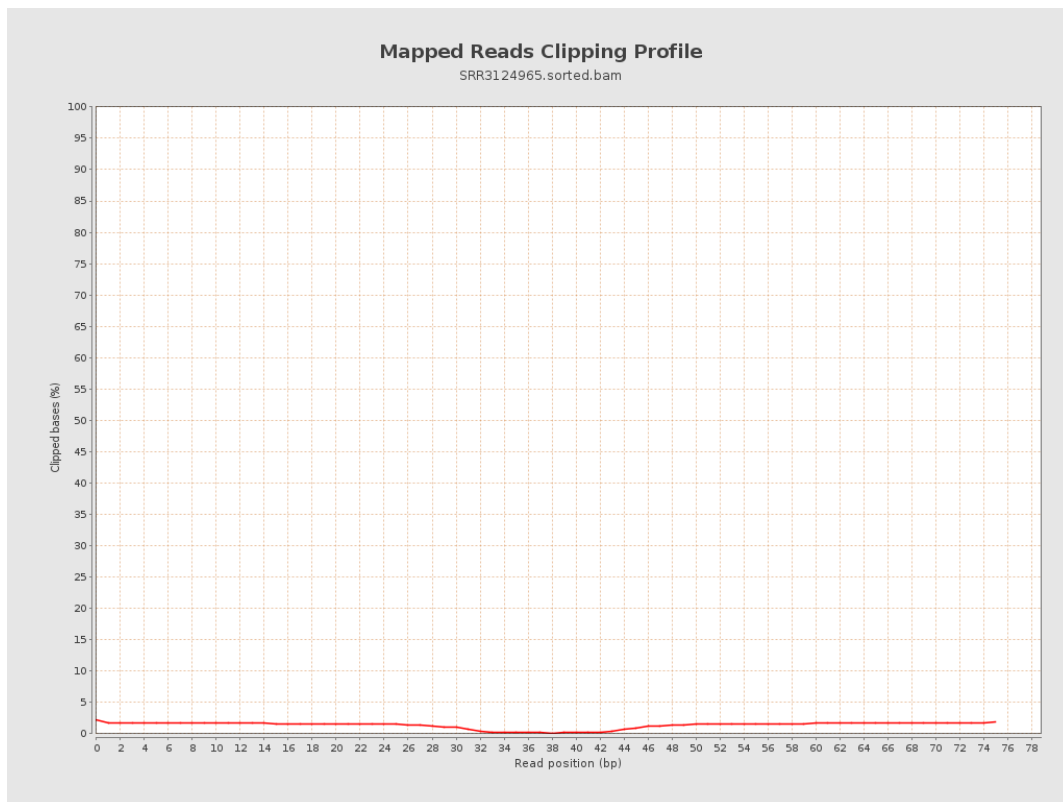
8. Results : Mapped Reads Nucleotide Content



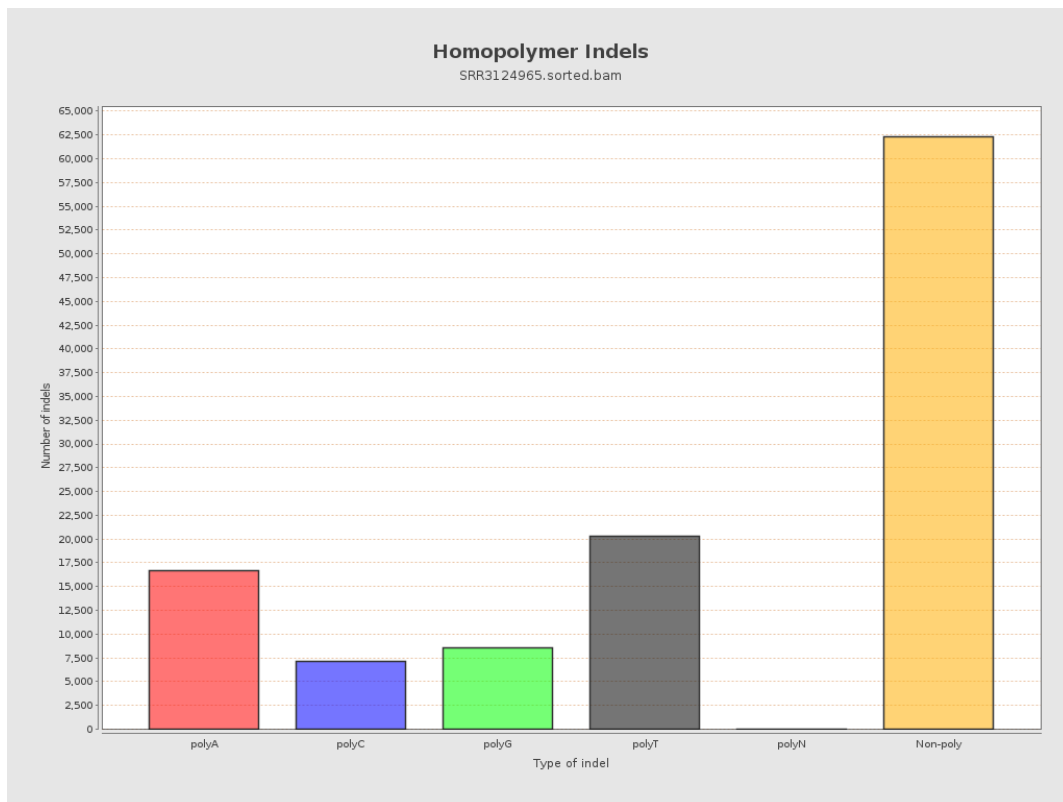
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



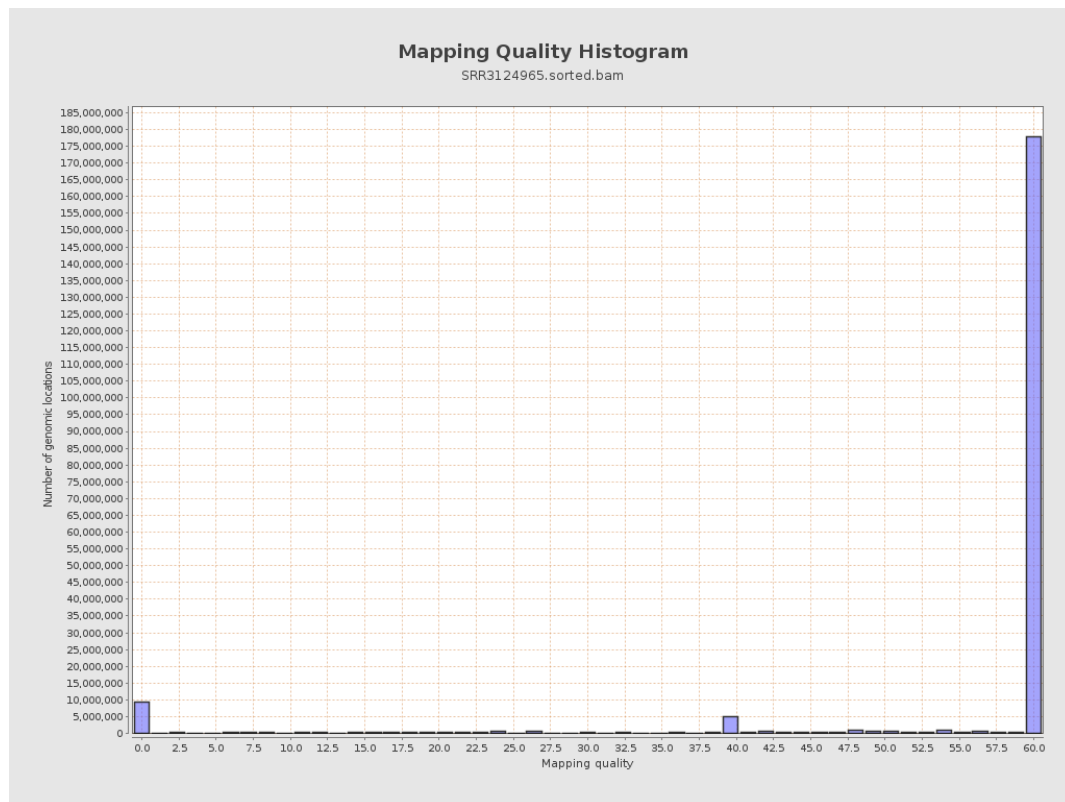
11. Results : Homopolymer Indels



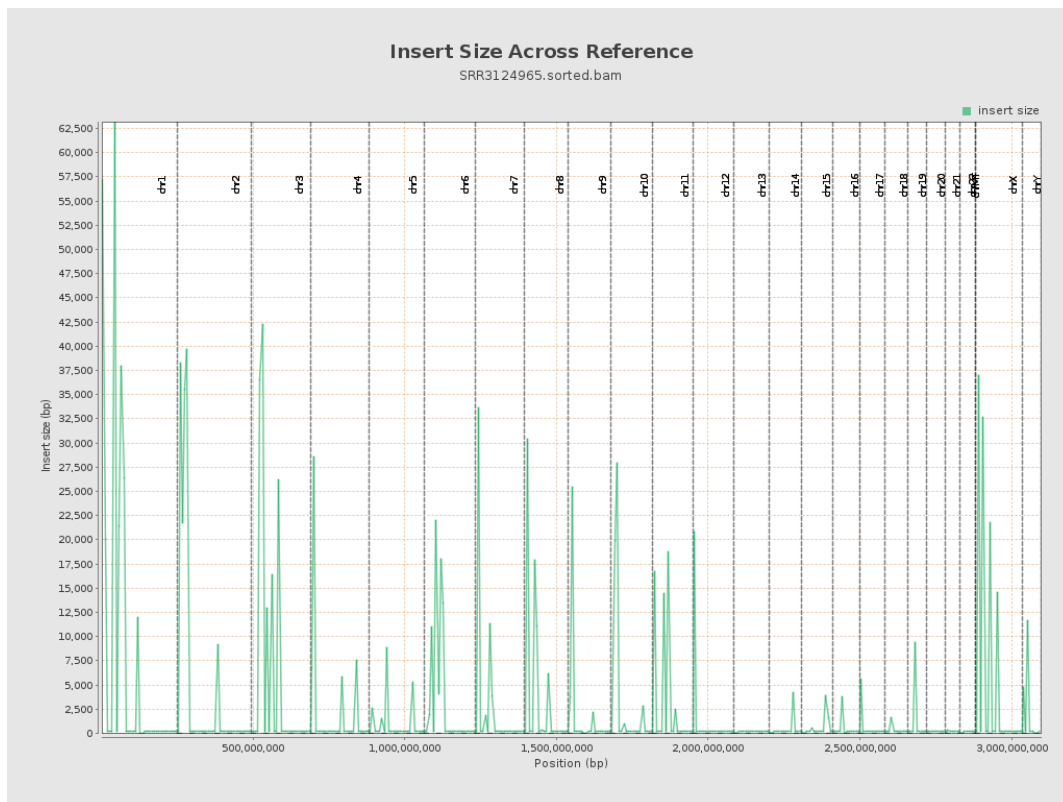
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

