

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 14:20:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173965.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_SRR10173965 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173965_1.fastq.gz SRR10173965_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 14:20:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173965.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,241,752
Mapped reads	7,093,456 / 97.95%
Unmapped reads	148,296 / 2.05%
Mapped paired reads	7,093,456 / 97.95%
Mapped reads, first in pair	3,543,554 / 48.93%
Mapped reads, second in pair	3,549,902 / 49.02%
Mapped reads, both in pair	6,995,660 / 96.6%
Mapped reads, singletons	97,796 / 1.35%
Secondary alignments	0
Supplementary alignments	1,070,671 / 14.78%
Read min/max/mean length	30 / 133 / 126.47
Duplicated reads (estimated)	5,807,694 / 80.2%
Duplication rate	65.65%
Clipped reads	3,860,239 / 53.31%

2.2. ACGT Content

Number/percentage of A's	240,610,934 / 29.85%
Number/percentage of C's	160,001,774 / 19.85%
Number/percentage of T's	238,805,623 / 29.63%
Number/percentage of G's	166,559,267 / 20.67%
Number/percentage of N's	6,053 / 0%

GC Percentage	40.52%
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2.3. Coverage

Mean	0.2606
Standard Deviation	4.557

2.4. Mapping Quality

Mean Mapping Quality	52.44
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2.5. Insert size

Mean	1,110,574.15
Standard Deviation	9,800,699.94
P25/Median/P75	105 / 155 / 241

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	6,873,849
Insertions	89,292
Mapped reads with at least one insertion	1.21%
Deletions	261,463
Mapped reads with at least one deletion	3.6%
Homopolymer indels	40.74%

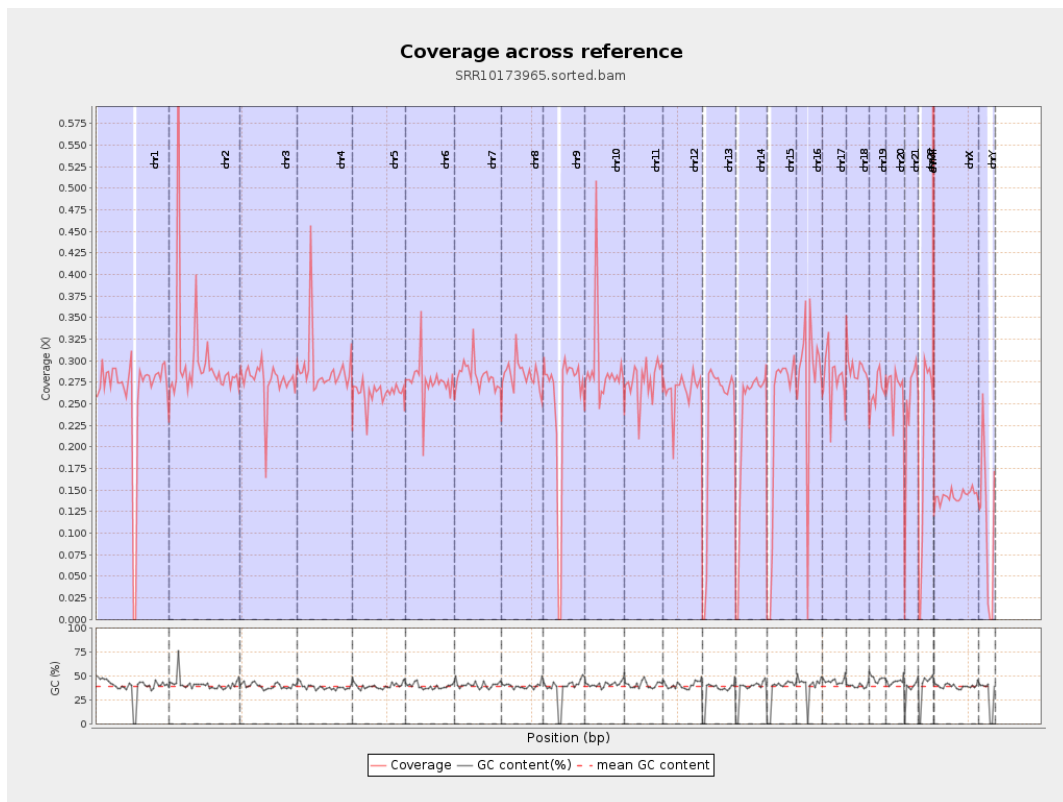
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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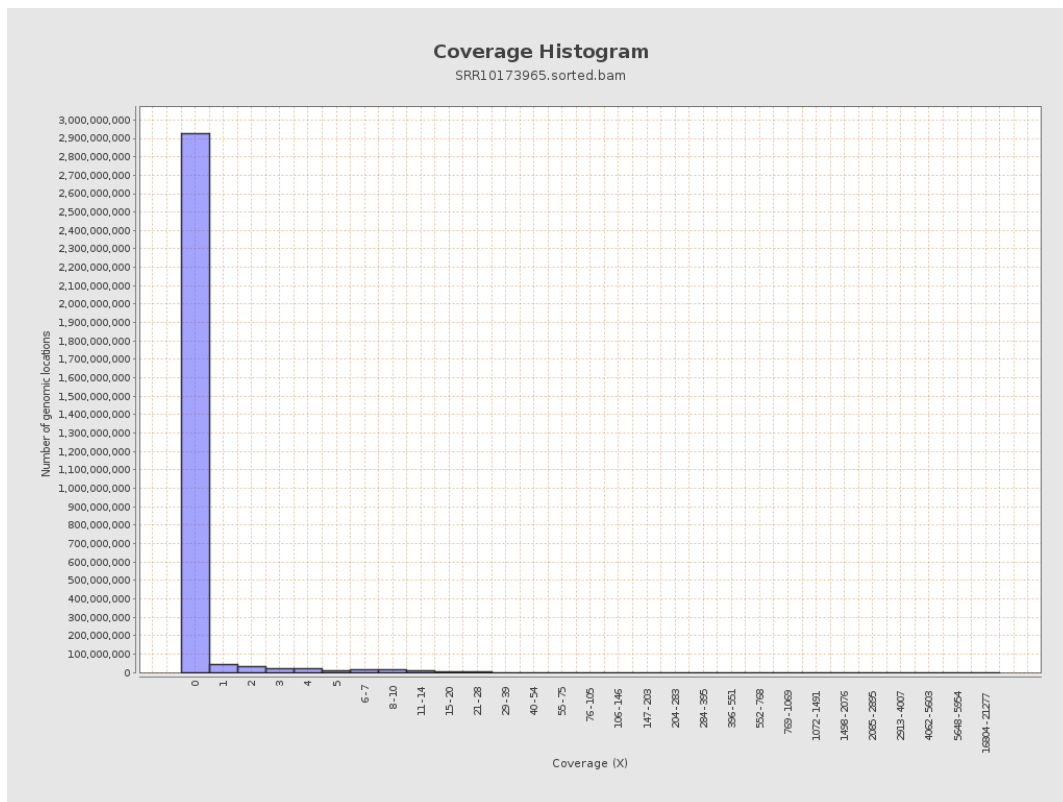
		bases	coverage	deviation
chr1	249250621	65324365	0.2621	2.1602
chr2	243199373	73088039	0.3005	14.8581
chr3	198022430	54856001	0.277	1.5827
chr4	191154276	55382744	0.2897	2.1445
chr5	180915260	47480011	0.2624	1.5268
chr6	171115067	47226238	0.276	1.8641
chr7	159138663	45088264	0.2833	2.2175
chr8	146364022	41625687	0.2844	2.5501
chr9	141213431	35210124	0.2493	2.144
chr10	135534747	39408476	0.2908	2.6654
chr11	135006516	37310078	0.2764	1.6439
chr12	133851895	35557673	0.2656	1.6038
chr13	115169878	26430247	0.2295	1.4355
chr14	107349540	24499426	0.2282	1.4477
chr15	102531392	23543256	0.2296	1.4778
chr16	90354753	25526523	0.2825	2.0375
chr17	81195210	22488460	0.277	1.7028
chr18	78077248	22809475	0.2921	2.8066
chr19	59128983	15725752	0.266	1.8901
chr20	63025520	16902797	0.2682	1.6703
chr21	48129895	11741342	0.244	1.8956
chr22	51304566	10203026	0.1989	1.5363
chrMT	16571	673352	40.6344	35.9325
chrX	155270560	22199845	0.143	1.142

chrY	59373566	6289113	0.1059	1.5275
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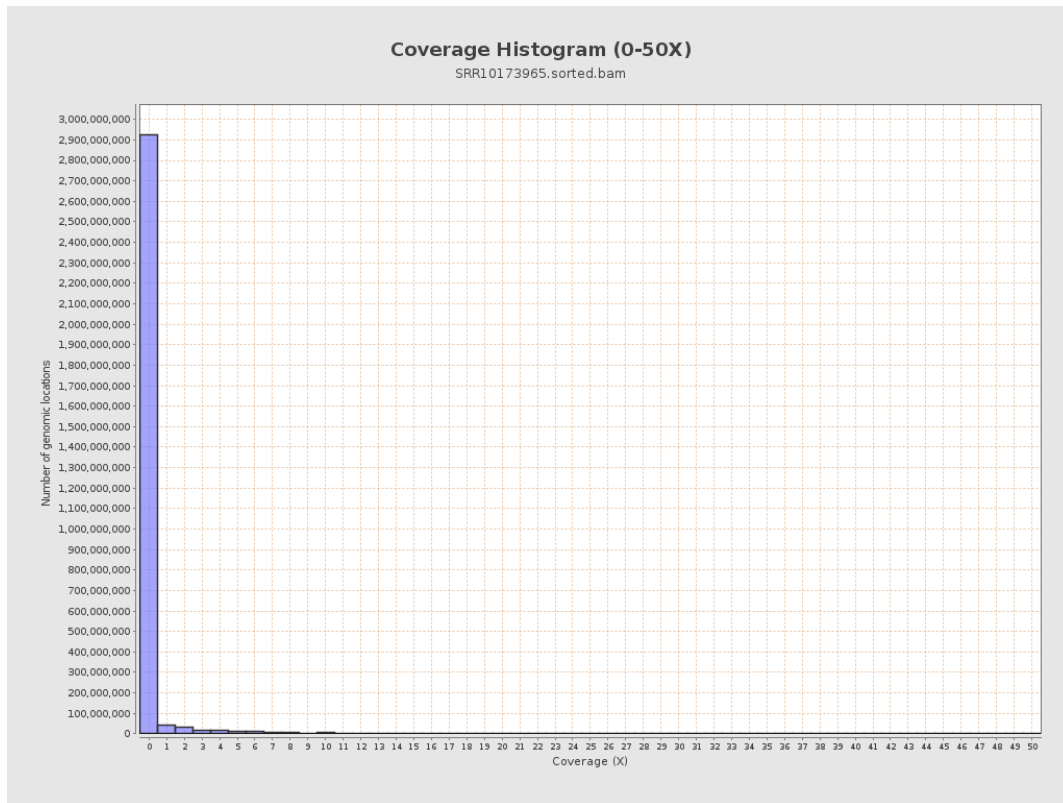
3. Results : Coverage across reference



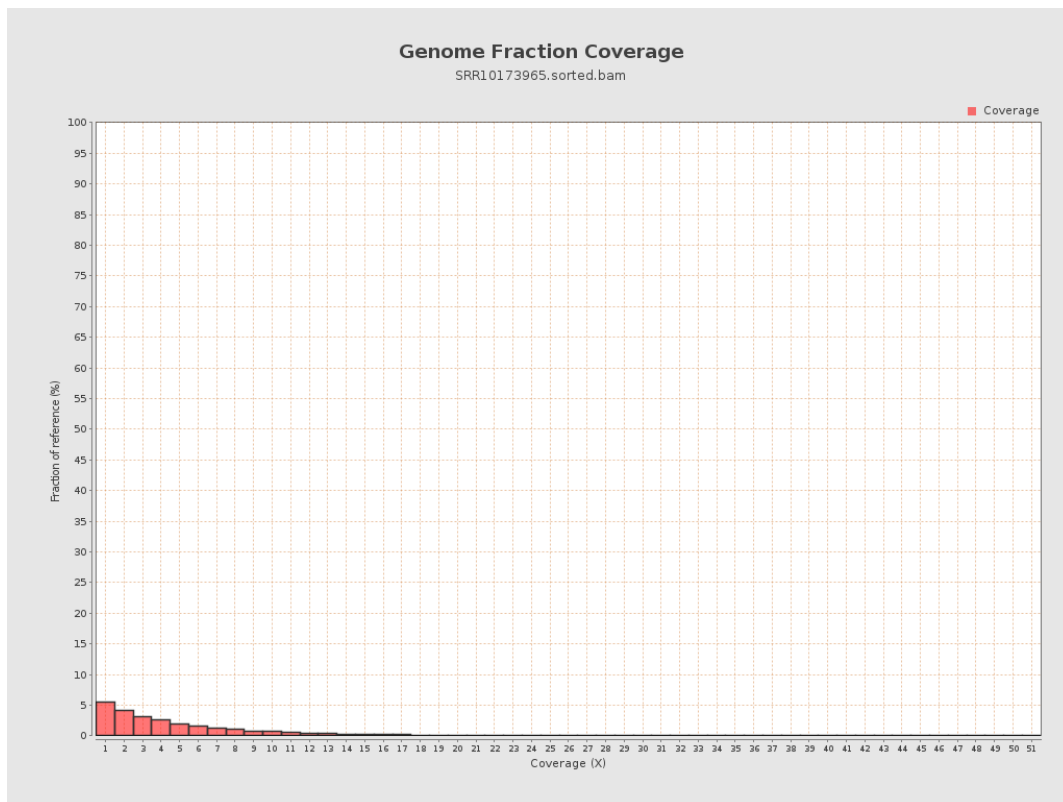
4. Results : Coverage Histogram



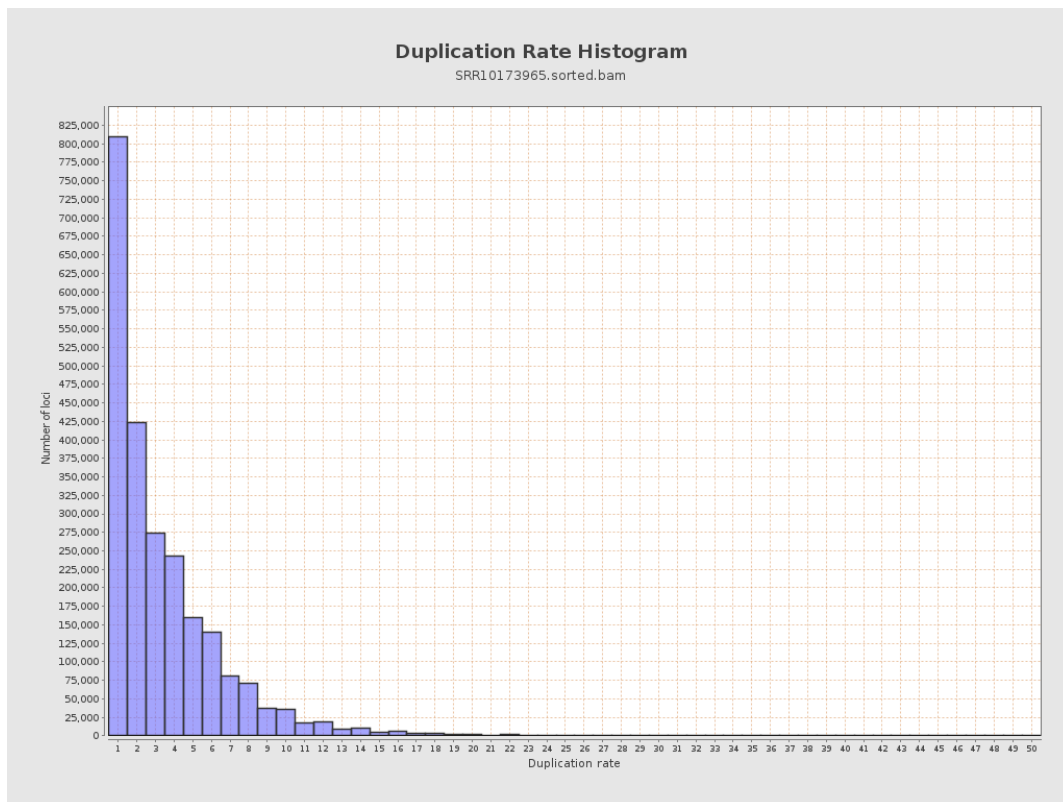
5. Results : Coverage Histogram (0-50X)



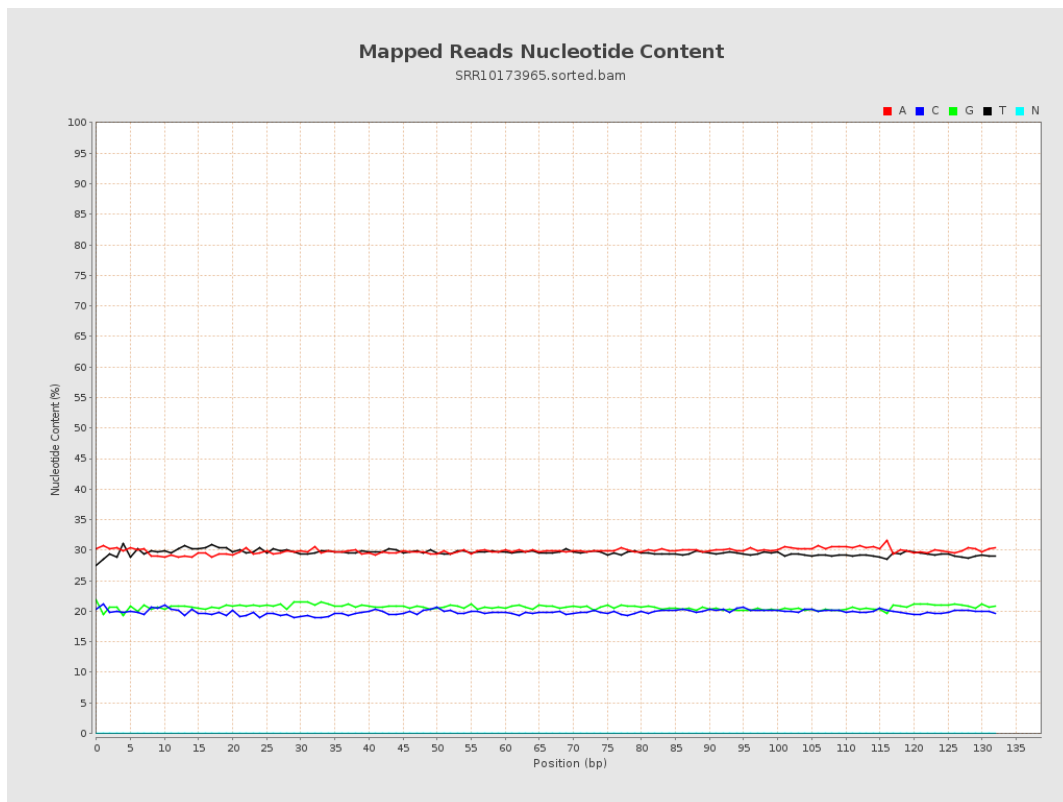
6. Results : Genome Fraction Coverage



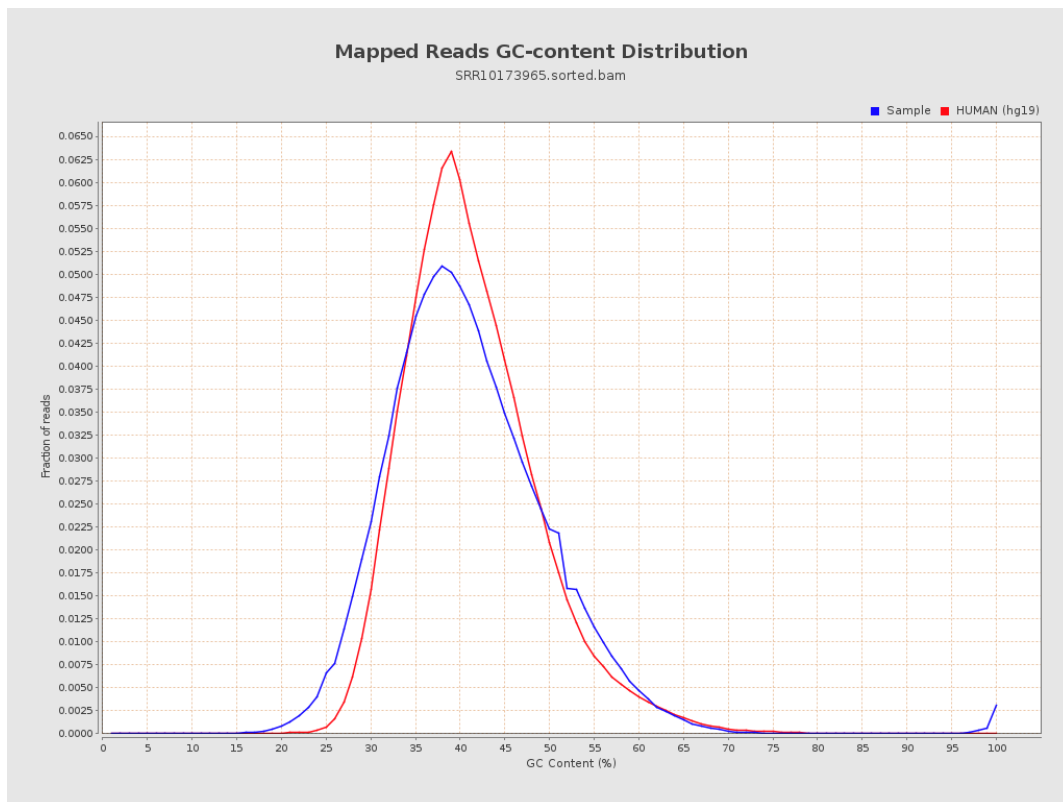
7. Results : Duplication Rate Histogram



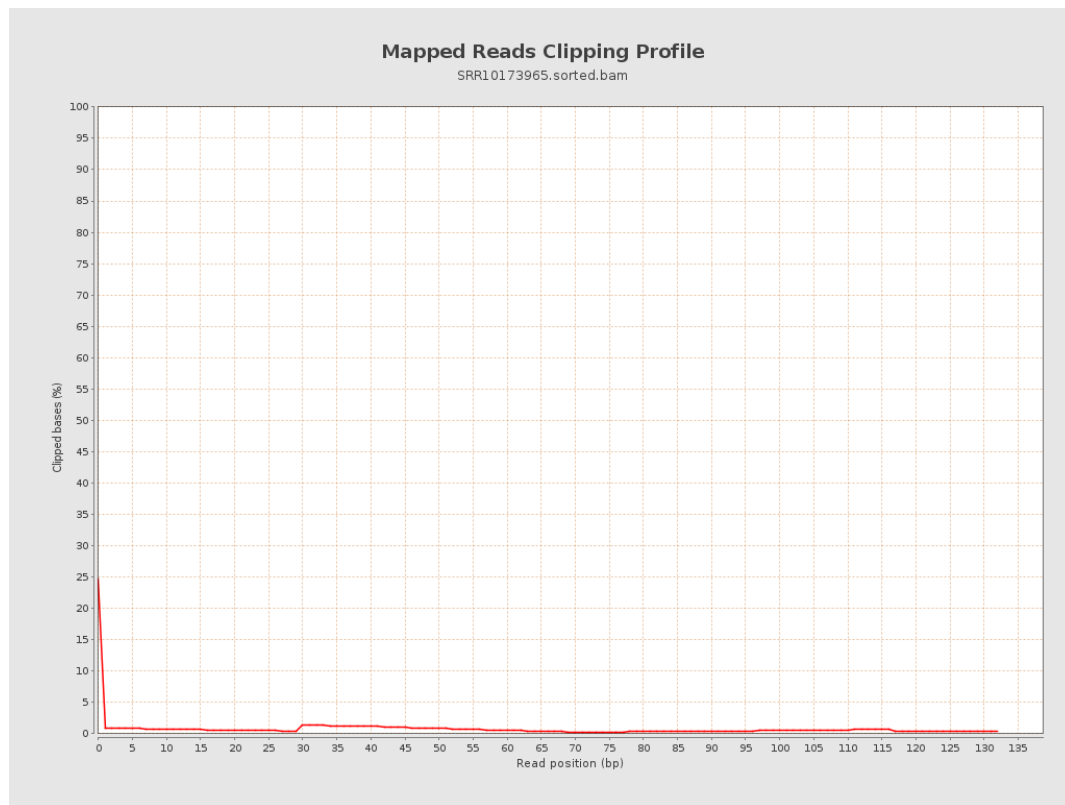
8. Results : Mapped Reads Nucleotide Content



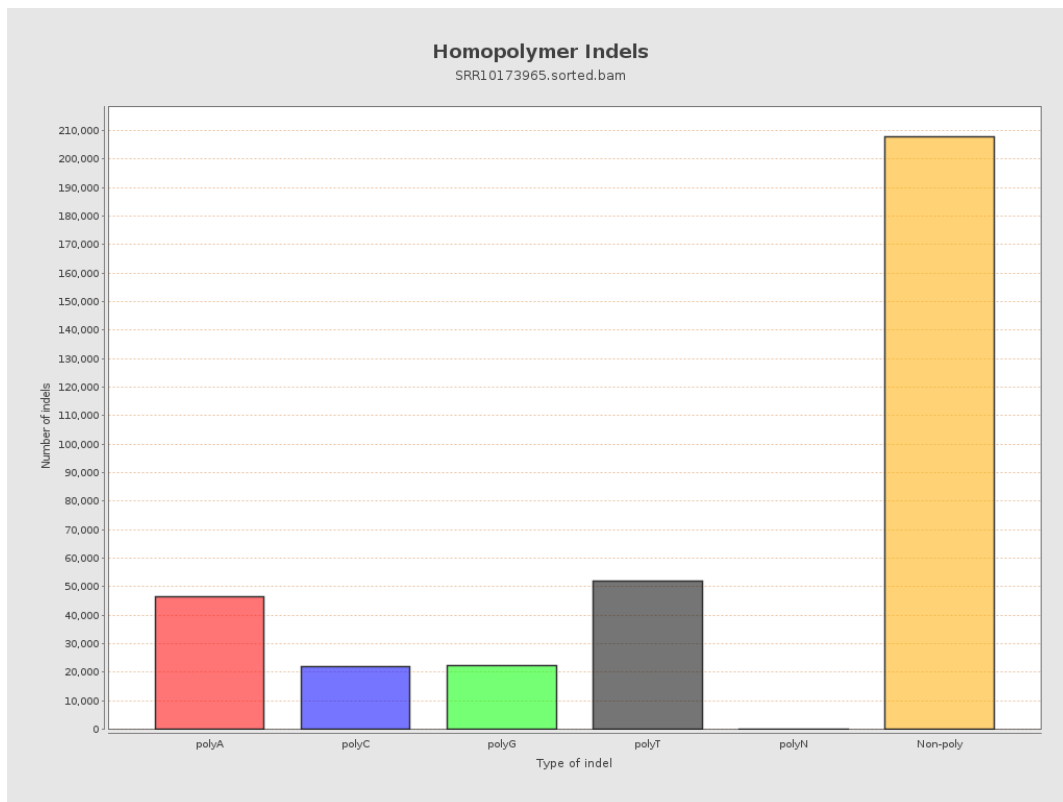
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



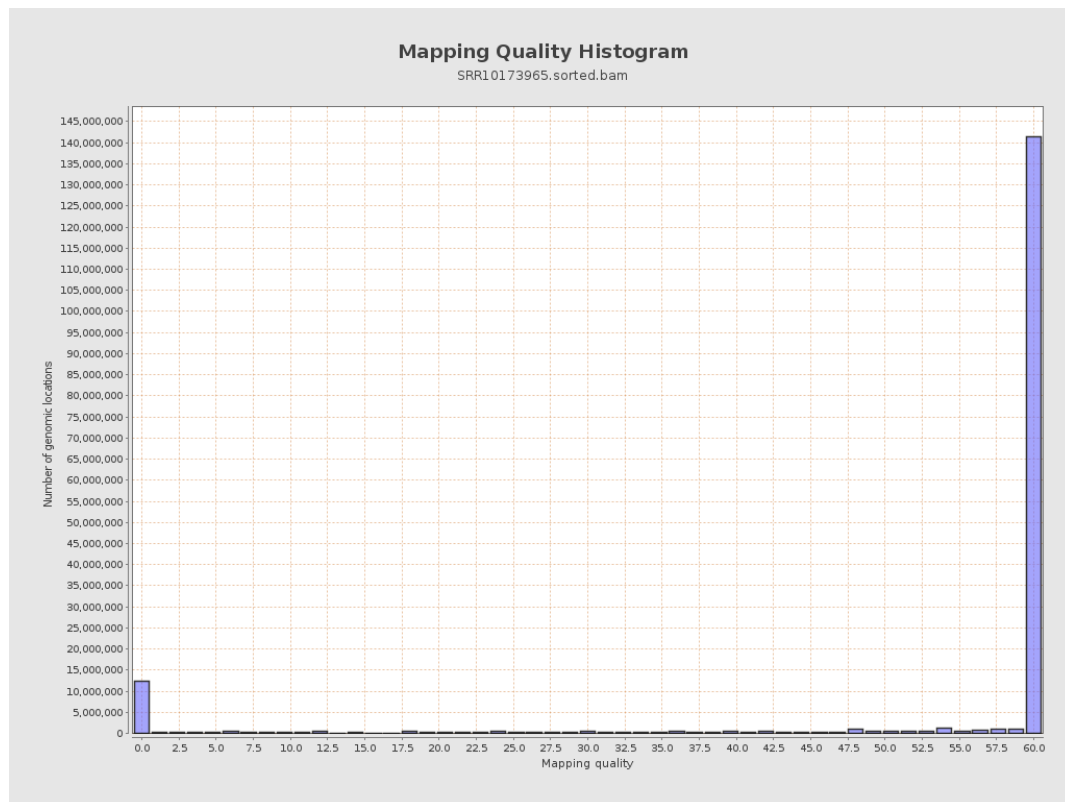
11. Results : Homopolymer Indels



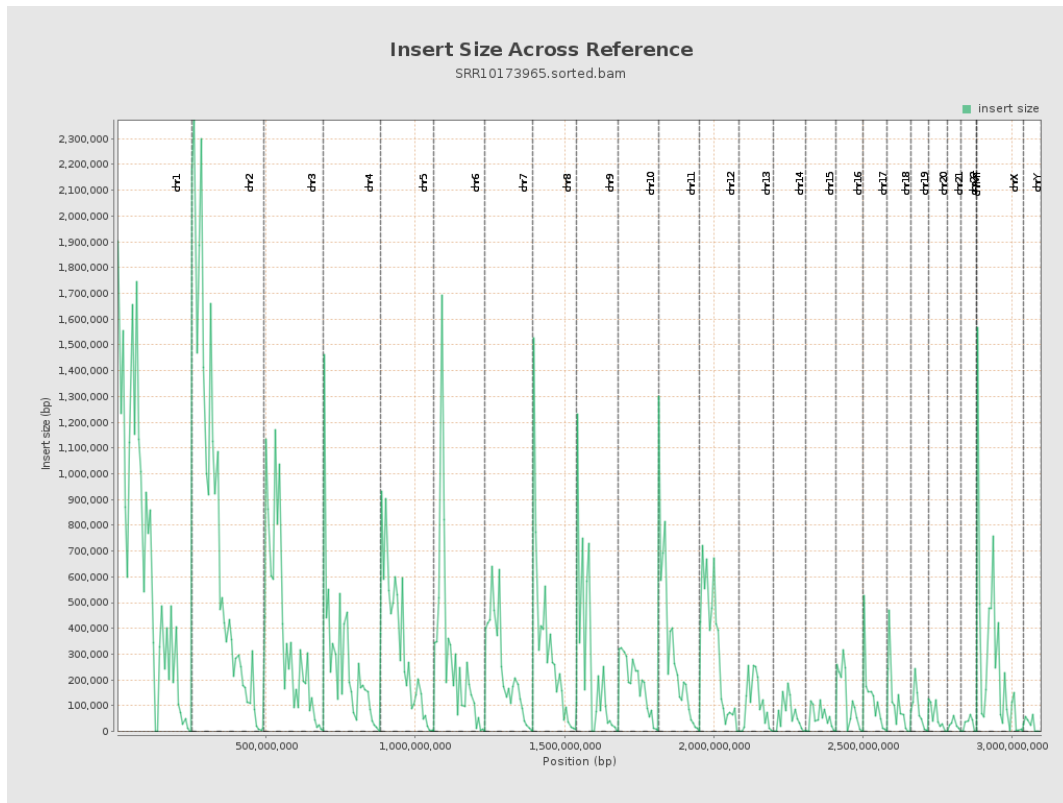
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

