

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:55:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173865.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_SRR10173865 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173865_1.fastq.gz SRR10173865_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:55:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173865.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,171,734
Mapped reads	1,146,755 / 97.87%
Unmapped reads	24,979 / 2.13%
Mapped paired reads	1,146,755 / 97.87%
Mapped reads, first in pair	573,848 / 48.97%
Mapped reads, second in pair	572,907 / 48.89%
Mapped reads, both in pair	1,131,646 / 96.58%
Mapped reads, singletons	15,109 / 1.29%
Secondary alignments	0
Supplementary alignments	103,870 / 8.86%
Read min/max/mean length	30 / 133 / 127.21
Duplicated reads (estimated)	797,817 / 68.09%
Duplication rate	60.05%
Clipped reads	426,448 / 36.39%

2.2. ACGT Content

Number/percentage of A's	41,193,807 / 30.38%
Number/percentage of C's	26,250,014 / 19.36%
Number/percentage of T's	41,019,263 / 30.25%
Number/percentage of G's	27,124,787 / 20.01%
Number/percentage of N's	1,688 / 0%

GC Percentage	39.36%
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2.3. Coverage

Mean	0.0438
Standard Deviation	0.7728

2.4. Mapping Quality

Mean Mapping Quality	53.19
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2.5. Insert size

Mean	807,409.38
Standard Deviation	8,444,334.8
P25/Median/P75	138 / 189 / 267

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	1,338,305
Insertions	14,703
Mapped reads with at least one insertion	1.24%
Deletions	29,832
Mapped reads with at least one deletion	2.54%
Homopolymer indels	42.6%

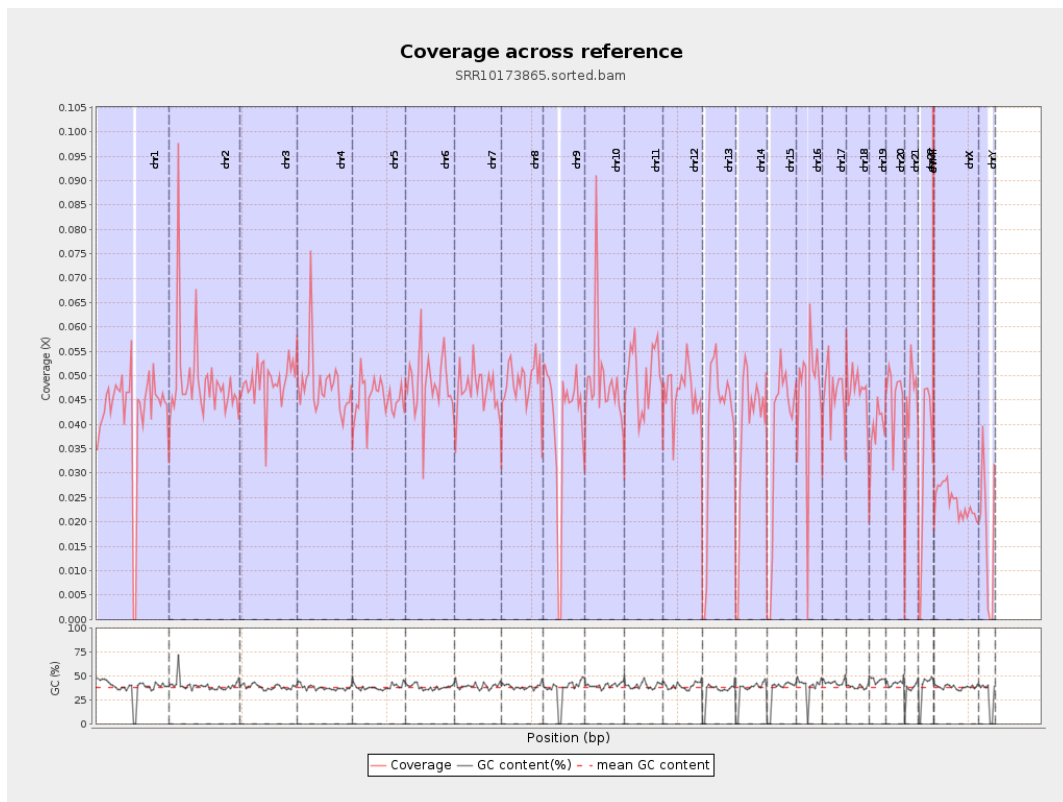
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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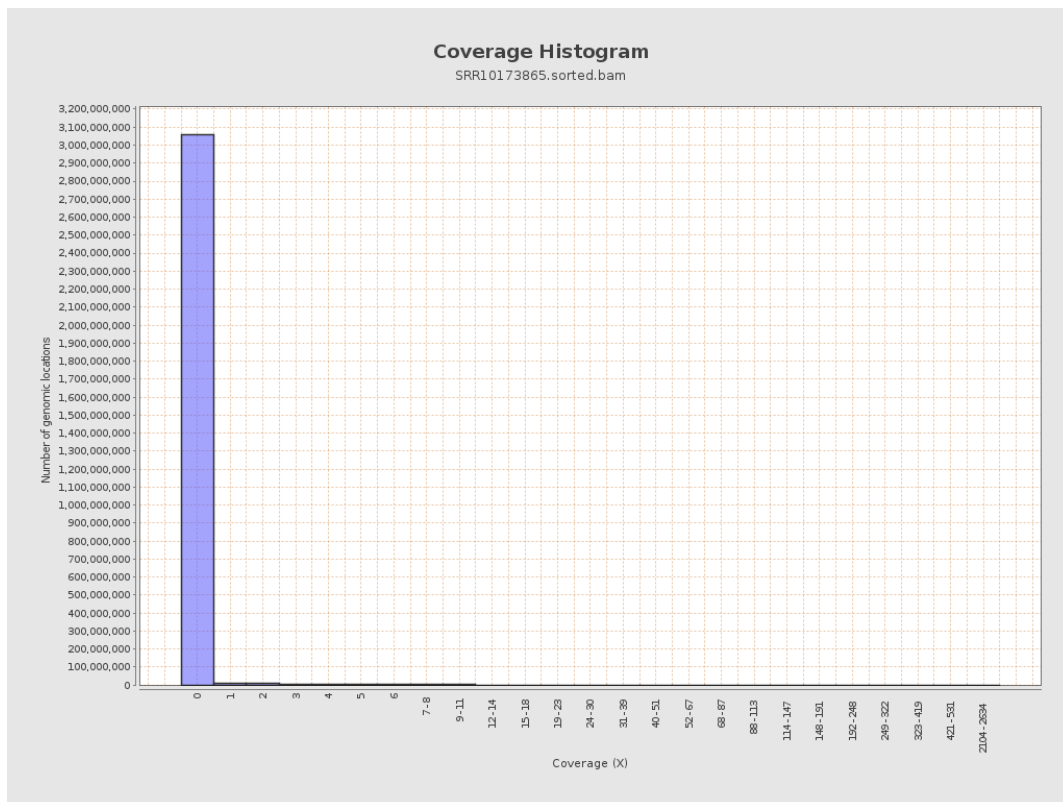
		bases	coverage	deviation
chr1	249250621	10569926	0.0424	0.5956
chr2	243199373	11921376	0.049	1.9136
chr3	198022430	9637121	0.0487	0.5786
chr4	191154276	9162361	0.0479	0.6168
chr5	180915260	8215698	0.0454	0.5558
chr6	171115067	8255484	0.0482	0.6149
chr7	159138663	7521149	0.0473	0.6227
chr8	146364022	7123850	0.0487	0.6726
chr9	141213431	5712608	0.0405	0.5855
chr10	135534747	6636519	0.049	0.6813
chr11	135006516	6694891	0.0496	0.5812
chr12	133851895	6247794	0.0467	0.5599
chr13	115169878	4497521	0.0391	0.5167
chr14	107349540	4165585	0.0388	0.5041
chr15	102531392	3842906	0.0375	0.4954
chr16	90354753	4172736	0.0462	0.5865
chr17	81195210	3747088	0.0461	0.5517
chr18	78077248	3708538	0.0475	0.7184
chr19	59128983	2330642	0.0394	0.5233
chr20	63025520	2869218	0.0455	0.5529
chr21	48129895	2021267	0.042	0.5691
chr22	51304566	1600366	0.0312	0.4725
chrMT	16571	291407	17.5854	15.6278
chrX	155270560	3703142	0.0238	0.4006

chrY	59373566	1015316	0.0171	0.3589
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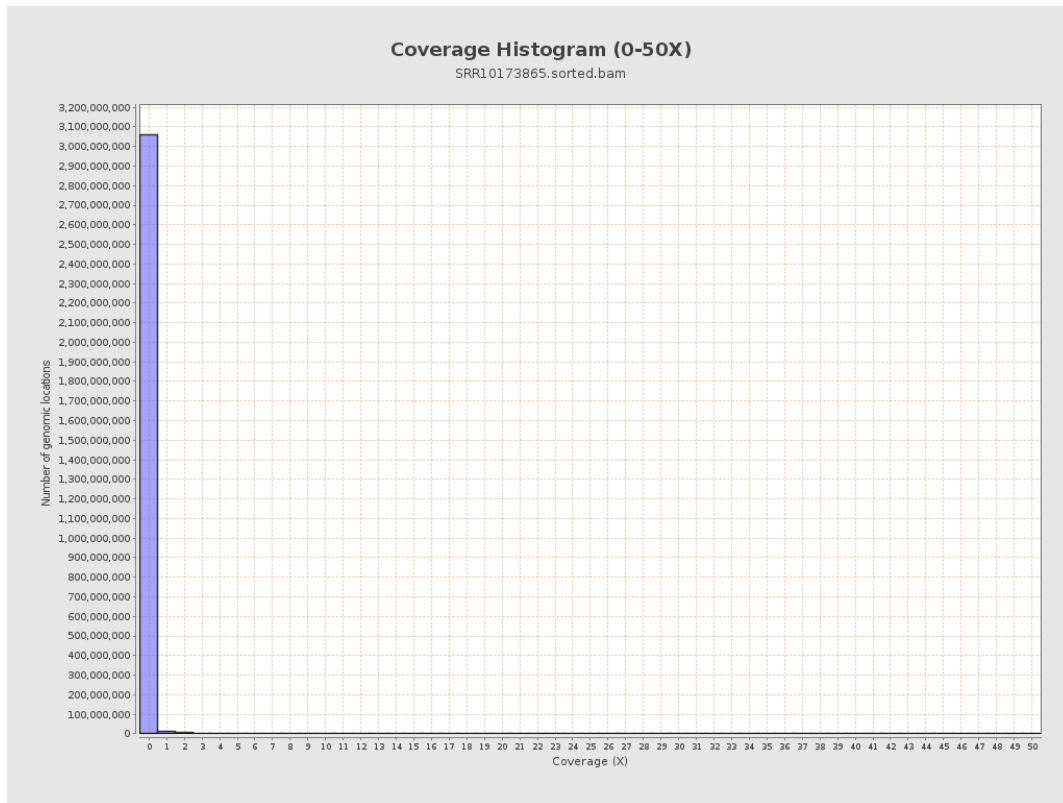
3. Results : Coverage across reference



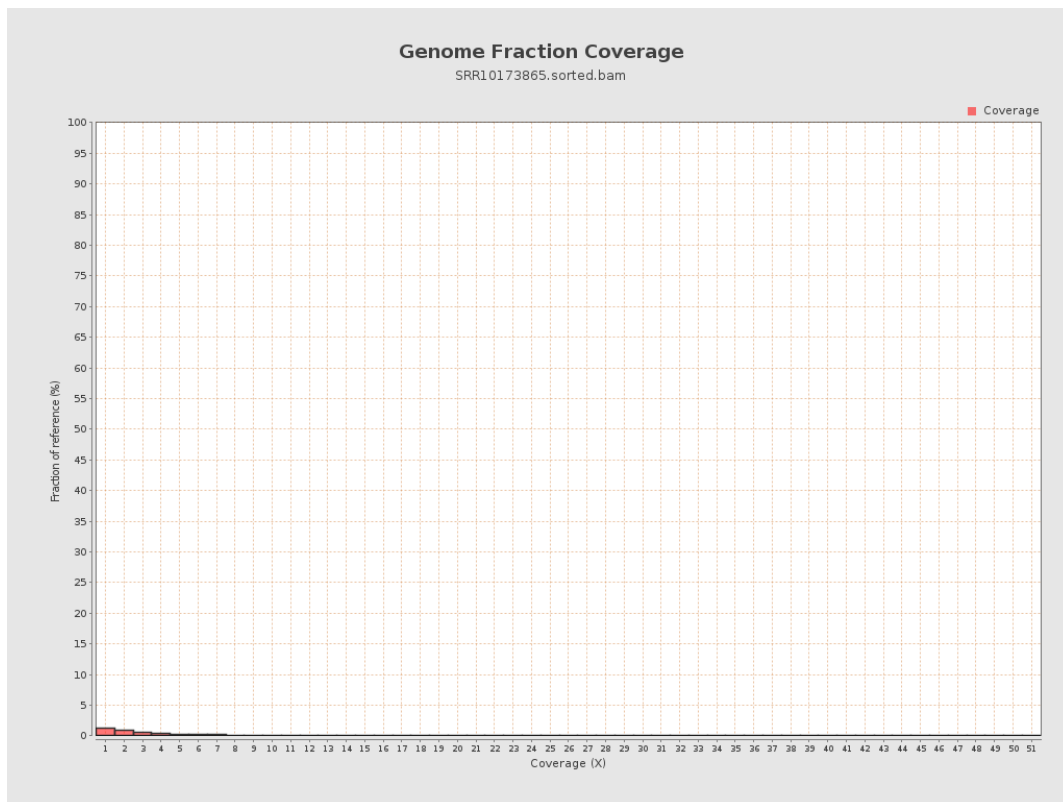
4. Results : Coverage Histogram



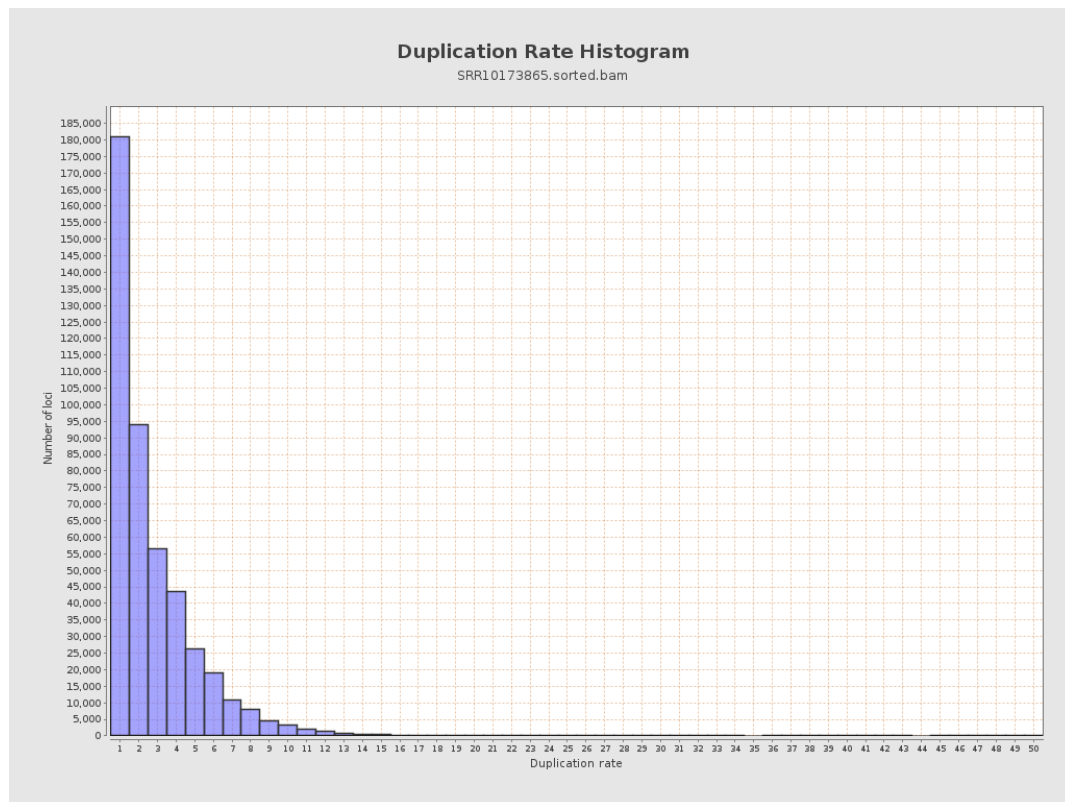
5. Results : Coverage Histogram (0-50X)



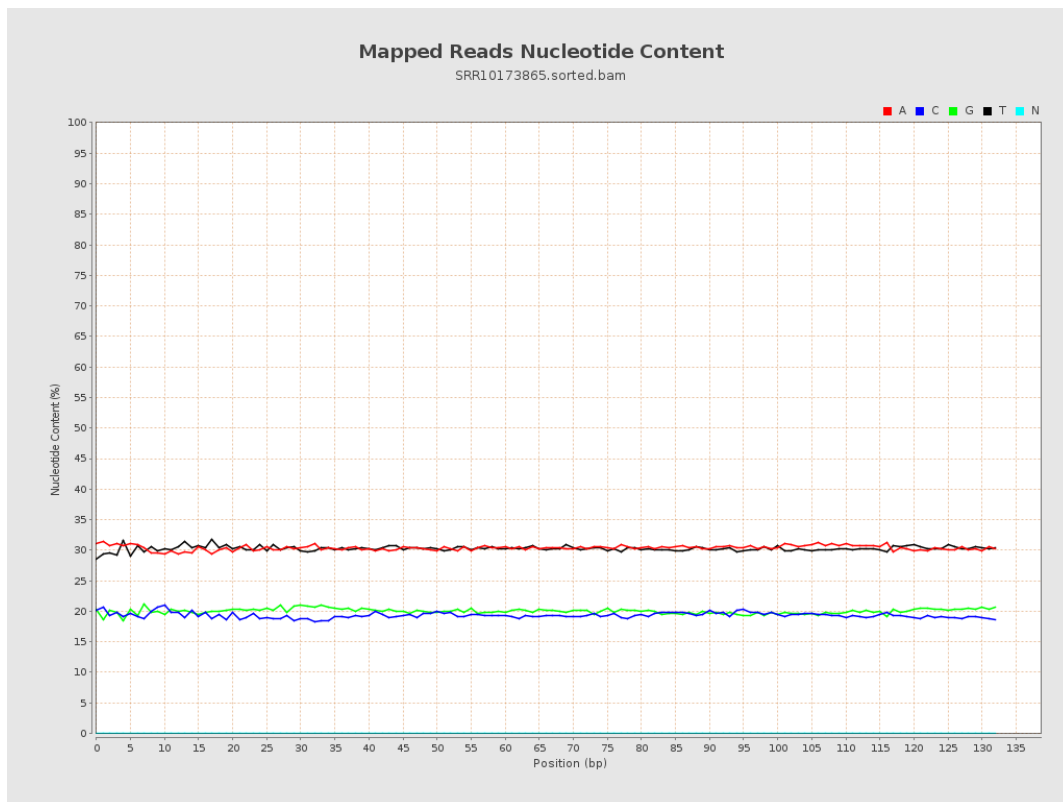
6. Results : Genome Fraction Coverage



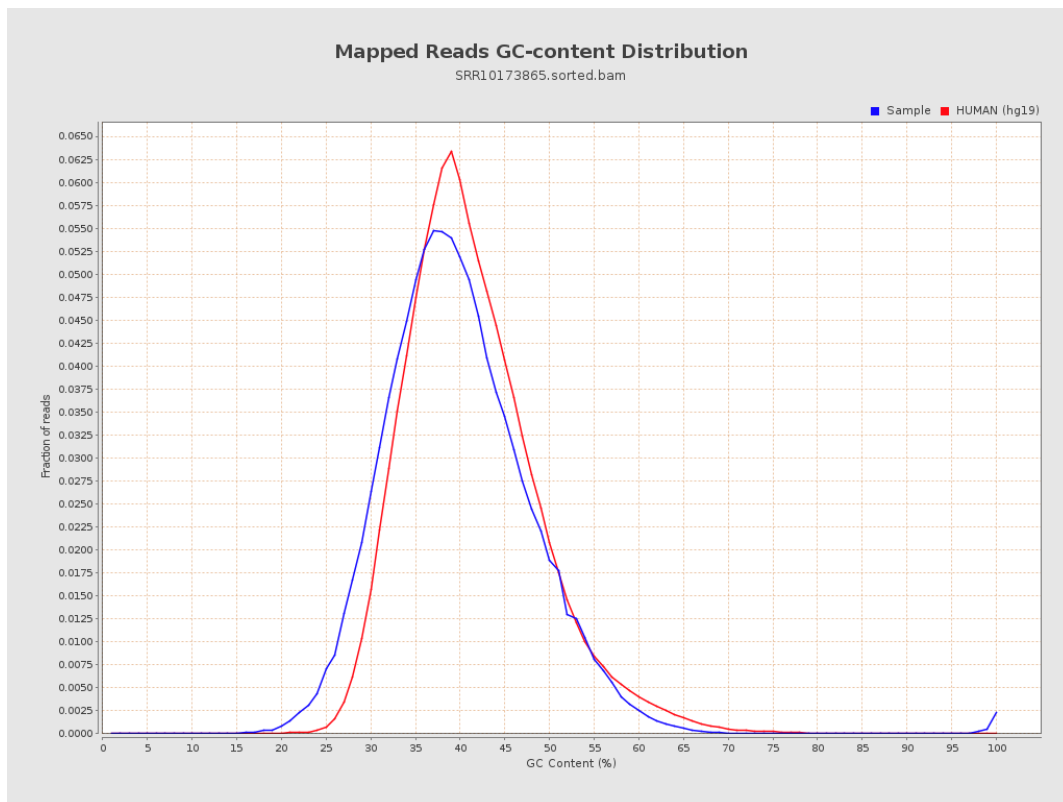
7. Results : Duplication Rate Histogram



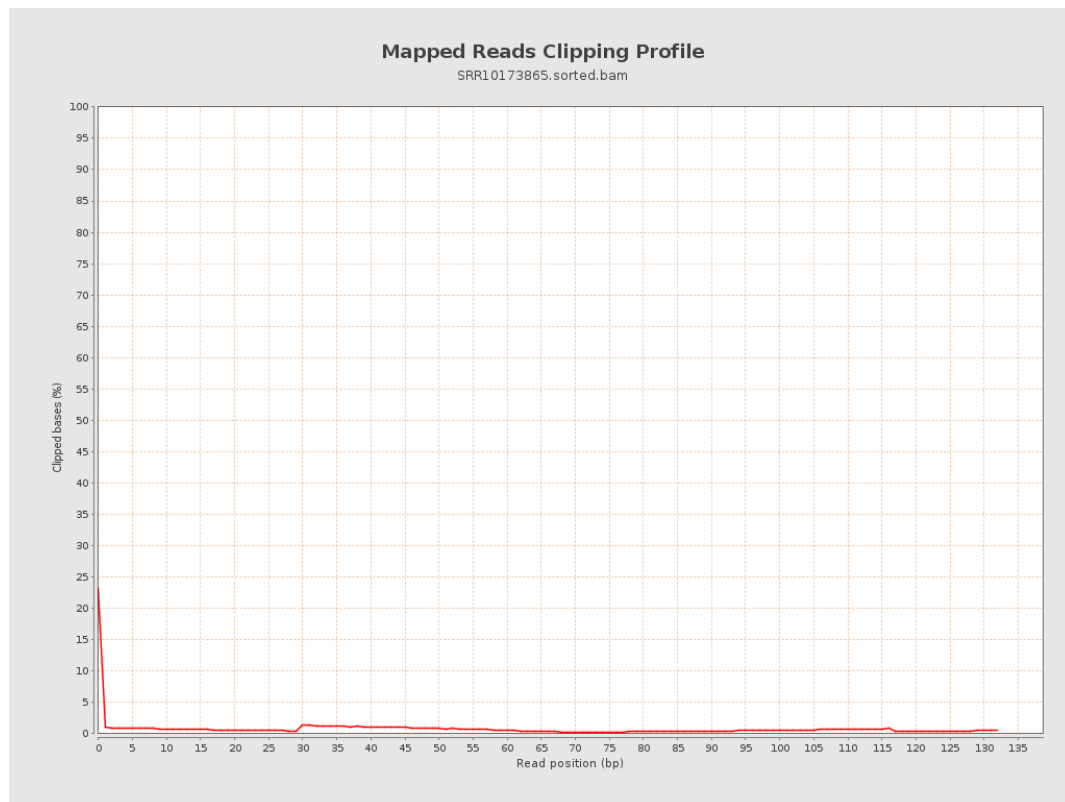
8. Results : Mapped Reads Nucleotide Content



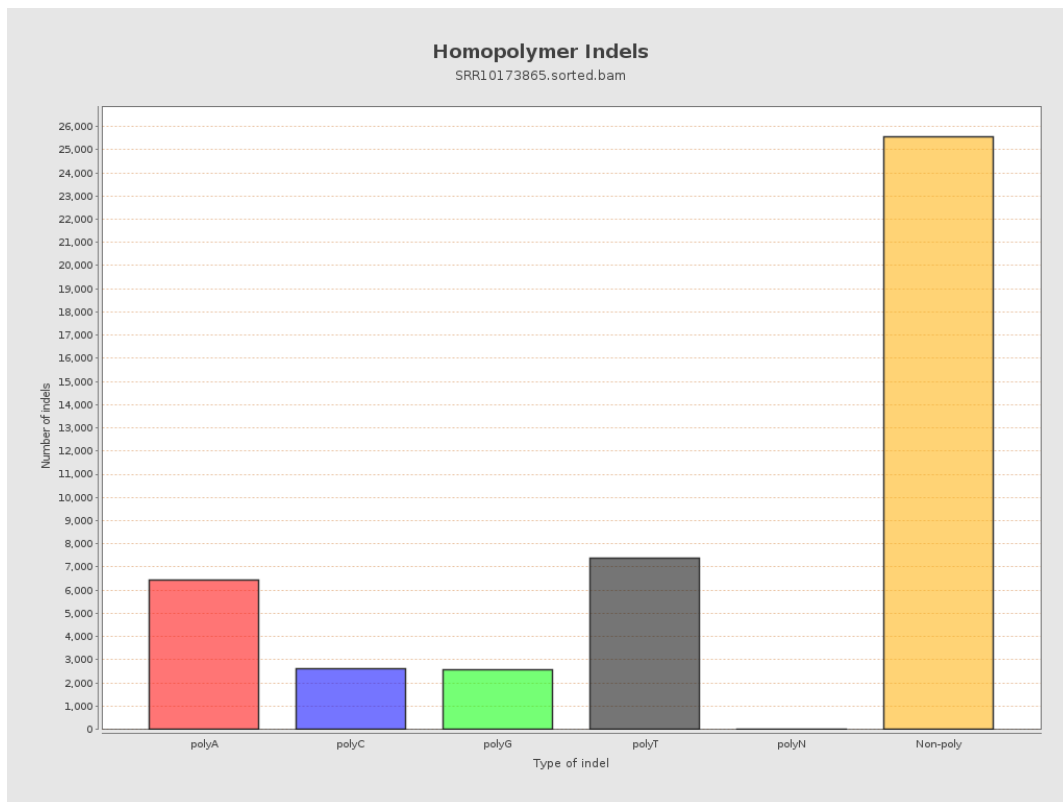
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



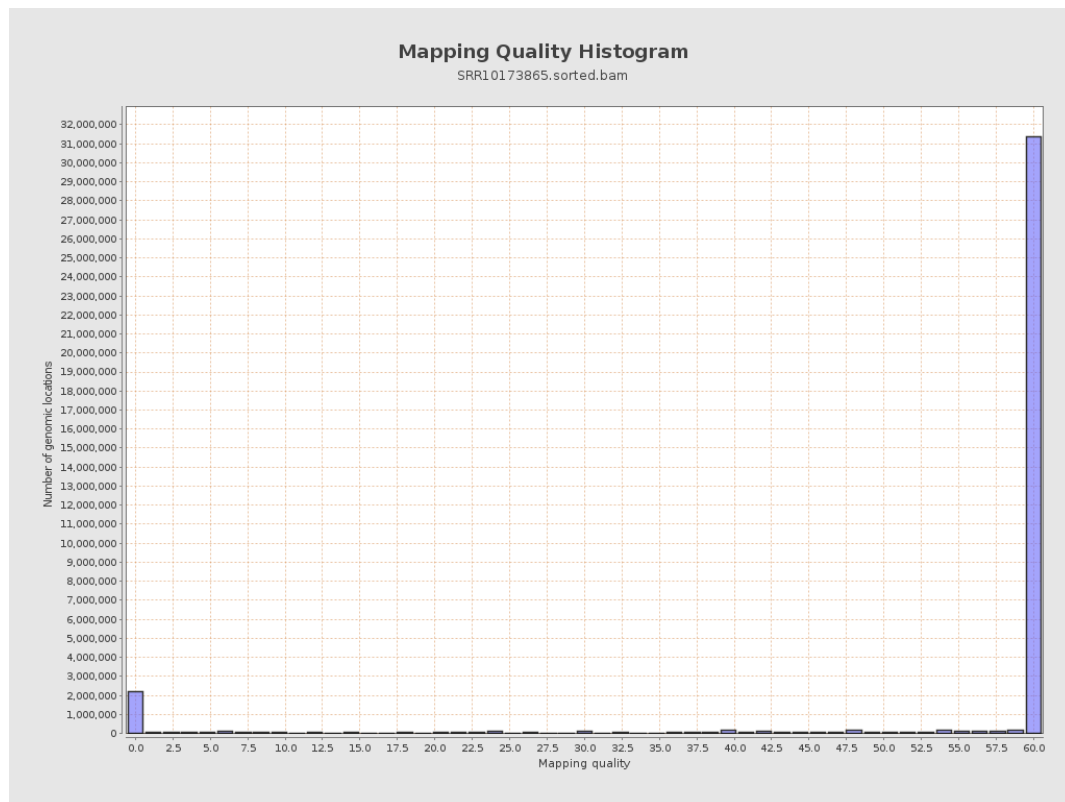
11. Results : Homopolymer Indels



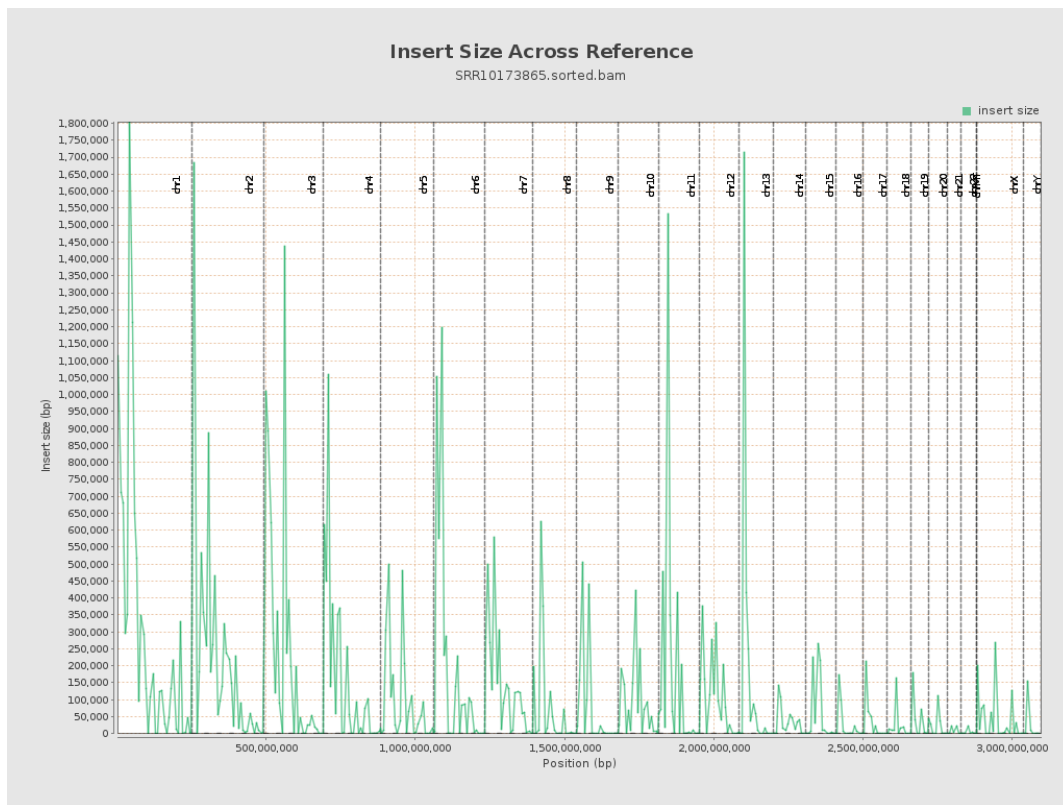
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

