

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 14:04:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173963.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_SRR10173963 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173963_1.fastq.gz SRR10173963_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 14:04:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173963.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,762,146
Mapped reads	5,617,101 / 97.48%
Unmapped reads	145,045 / 2.52%
Mapped paired reads	5,617,101 / 97.48%
Mapped reads, first in pair	2,811,365 / 48.79%
Mapped reads, second in pair	2,805,736 / 48.69%
Mapped reads, both in pair	5,516,714 / 95.74%
Mapped reads, singletons	100,387 / 1.74%
Secondary alignments	0
Supplementary alignments	543,736 / 9.44%
Read min/max/mean length	30 / 133 / 127.99
Duplicated reads (estimated)	4,402,485 / 76.4%
Duplication rate	65.73%
Clipped reads	2,218,730 / 38.51%

2.2. ACGT Content

Number/percentage of A's	200,381,026 / 30.17%
Number/percentage of C's	129,483,597 / 19.5%
Number/percentage of T's	200,065,149 / 30.13%
Number/percentage of G's	134,162,439 / 20.2%
Number/percentage of N's	8,291 / 0%

GC Percentage	39.7%
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2.3. Coverage

Mean	0.2146
Standard Deviation	3.2704

2.4. Mapping Quality

Mean Mapping Quality	52.7
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2.5. Insert size

Mean	837,677.68
Standard Deviation	8,454,032.49
P25/Median/P75	144 / 200 / 285

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	6,562,987
Insertions	68,406
Mapped reads with at least one insertion	1.18%
Deletions	146,919
Mapped reads with at least one deletion	2.55%
Homopolymer indels	43.09%

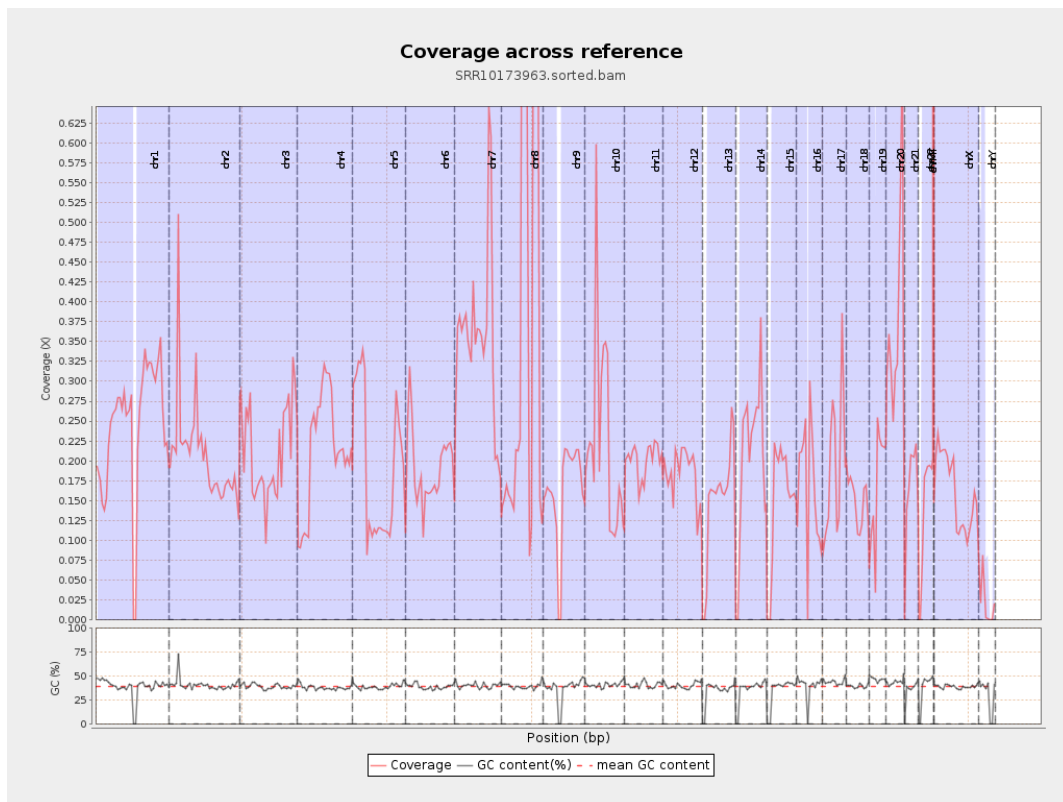
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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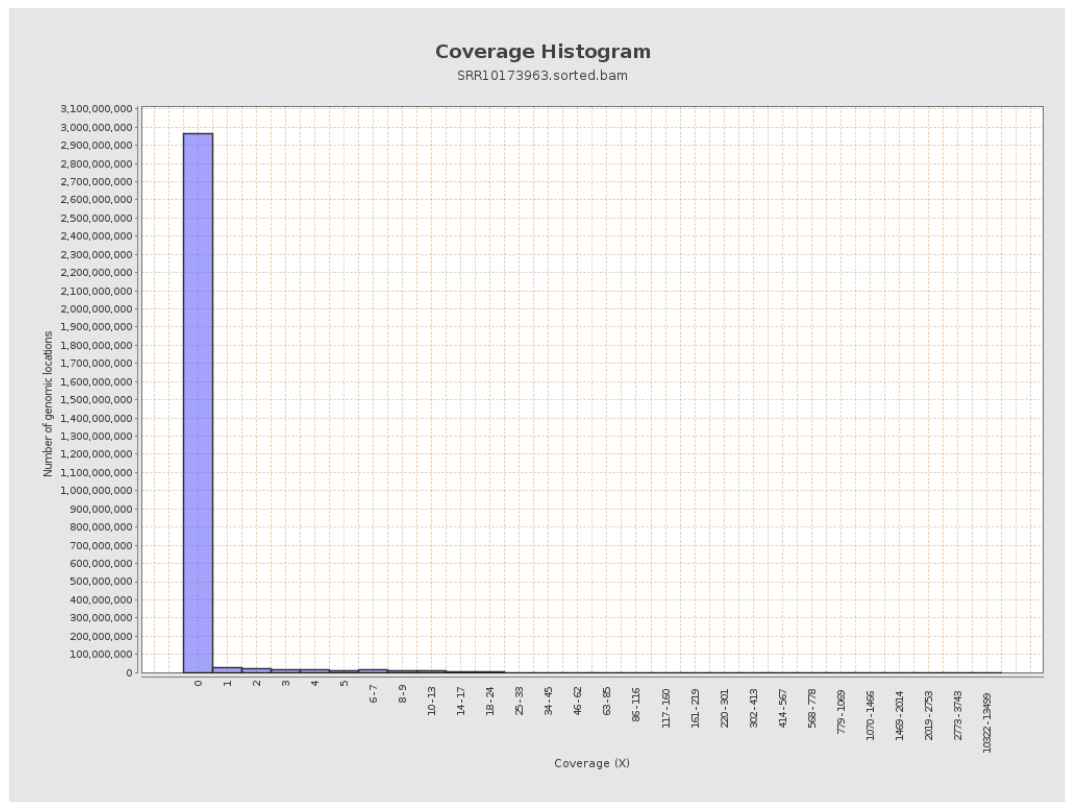
		bases	coverage	deviation
chr1	249250621	60761856	0.2438	1.8057
chr2	243199373	50470579	0.2075	9.4907
chr3	198022430	41965693	0.2119	1.3513
chr4	191154276	40564384	0.2122	1.6571
chr5	180915260	34525754	0.1908	1.2786
chr6	171115067	32254122	0.1885	1.3181
chr7	159138663	57375795	0.3605	3.4538
chr8	146364022	65772789	0.4494	2.4346
chr9	141213431	22915390	0.1623	1.5391
chr10	135534747	30591506	0.2257	4.4971
chr11	135006516	27004530	0.2	1.3441
chr12	133851895	24755013	0.1849	1.2495
chr13	115169878	17321003	0.1504	1.1395
chr14	107349540	22066167	0.2056	1.3281
chr15	102531392	15608355	0.1522	1.1261
chr16	90354753	14964474	0.1656	1.6473
chr17	81195210	15866803	0.1954	1.4281
chr18	78077248	11726845	0.1502	1.9496
chr19	59128983	9892158	0.1673	1.4834
chr20	63025520	24495910	0.3887	1.8551
chr21	48129895	7907798	0.1643	1.2908
chr22	51304566	6839633	0.1333	1.0352
chrMT	16571	2575830	155.442	129.4328
chrX	155270560	25030713	0.1612	1.1829

chrY	59373566	1211808	0.0204	0.8704
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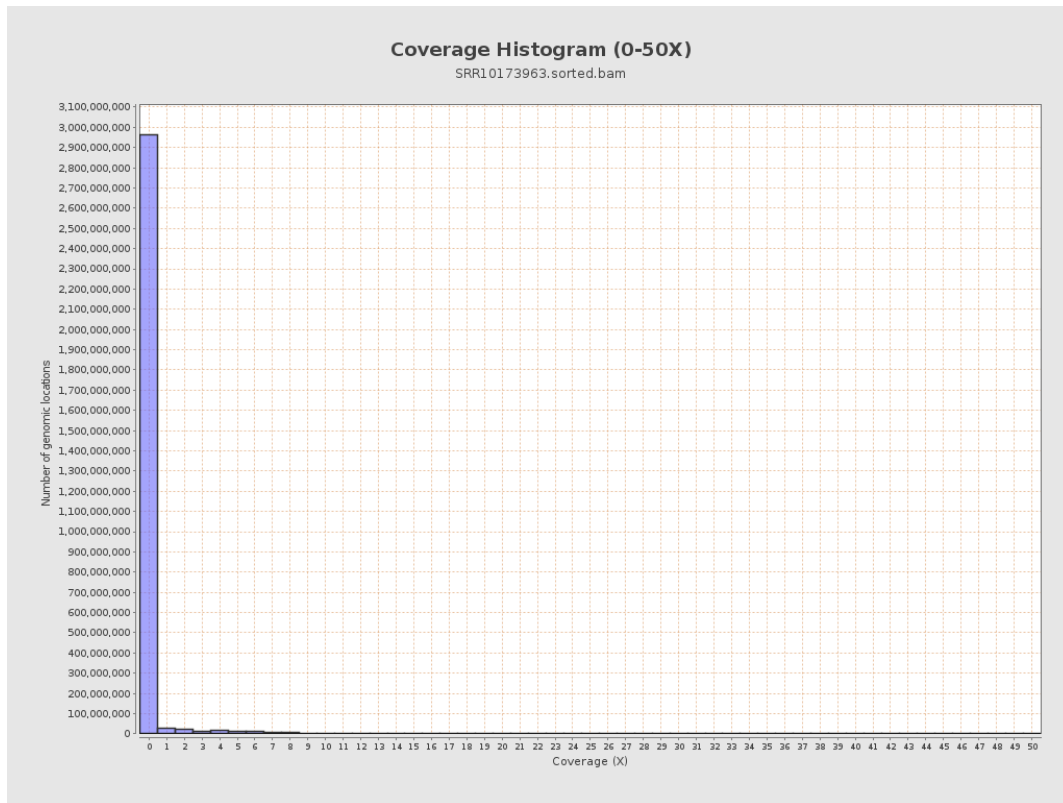
3. Results : Coverage across reference



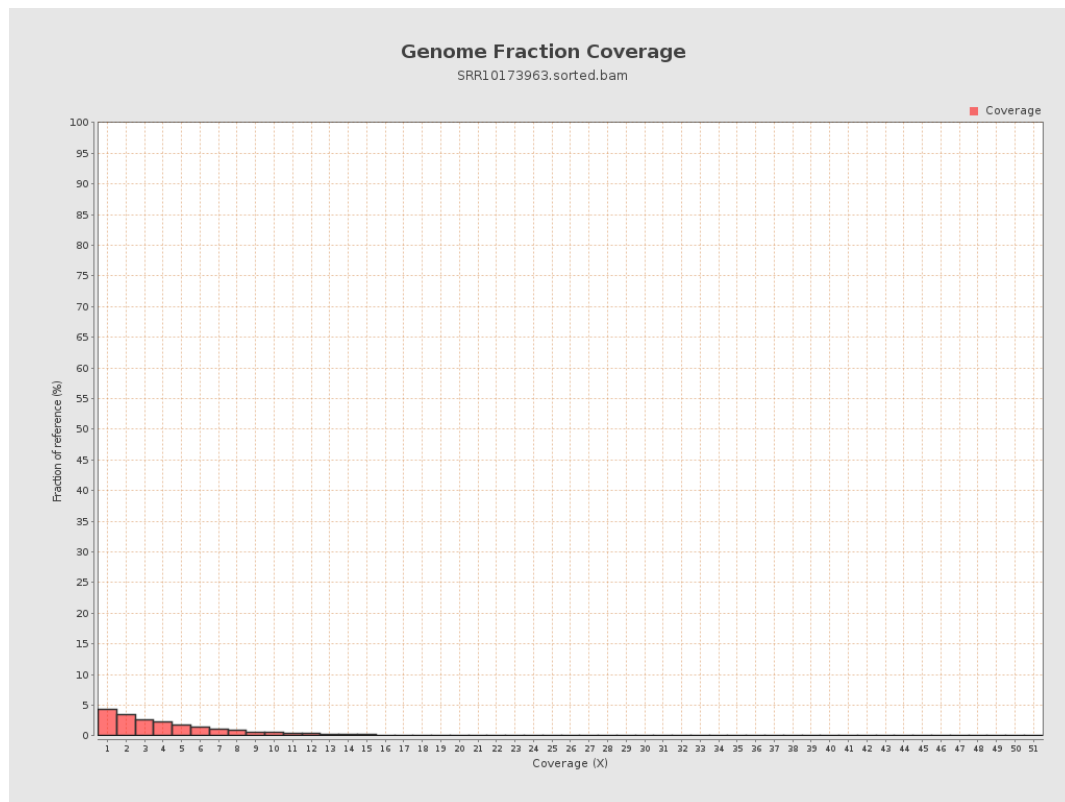
4. Results : Coverage Histogram



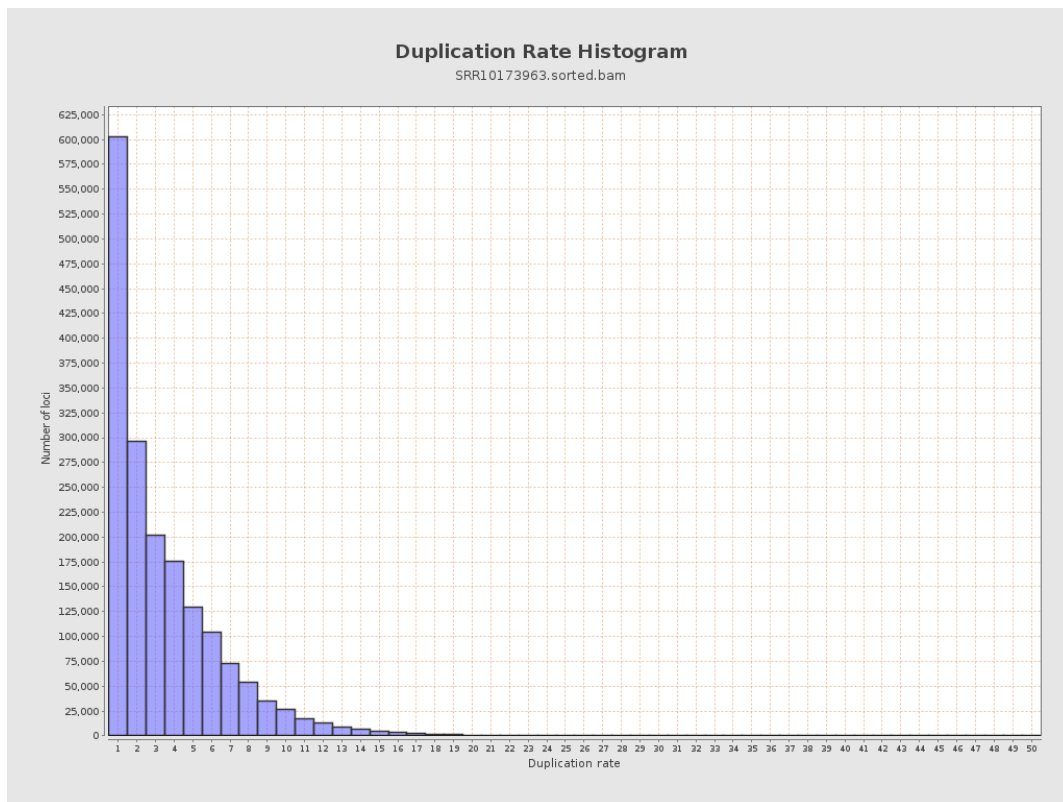
5. Results : Coverage Histogram (0-50X)



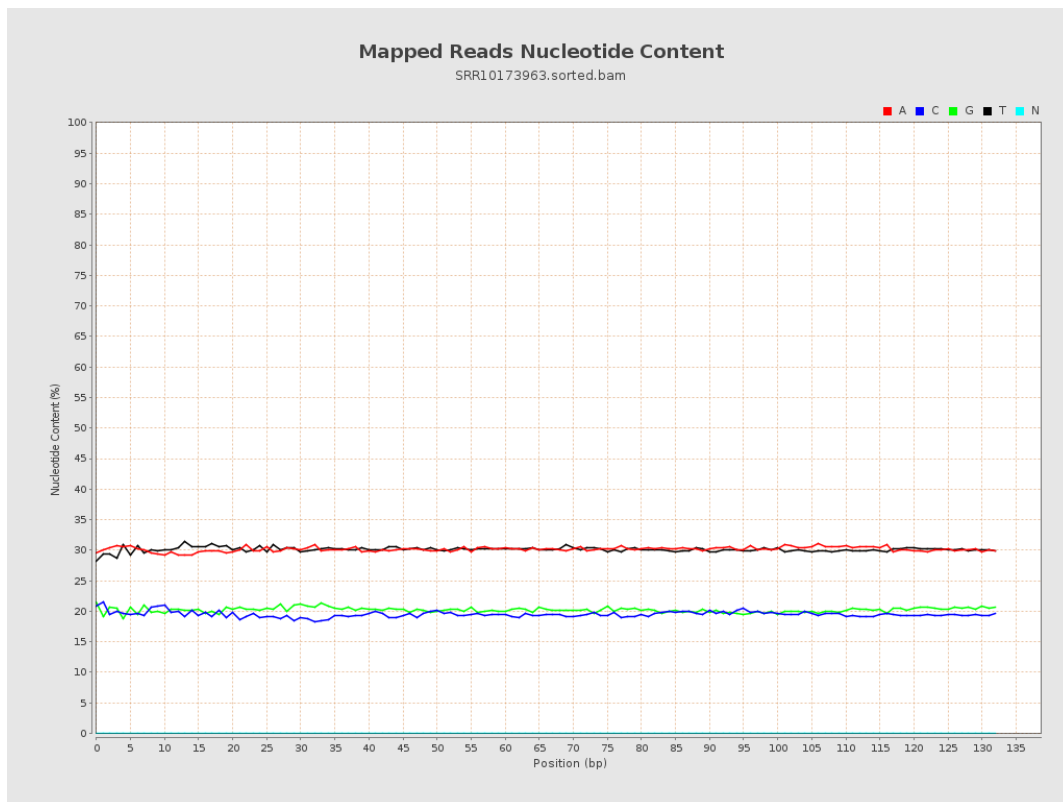
6. Results : Genome Fraction Coverage



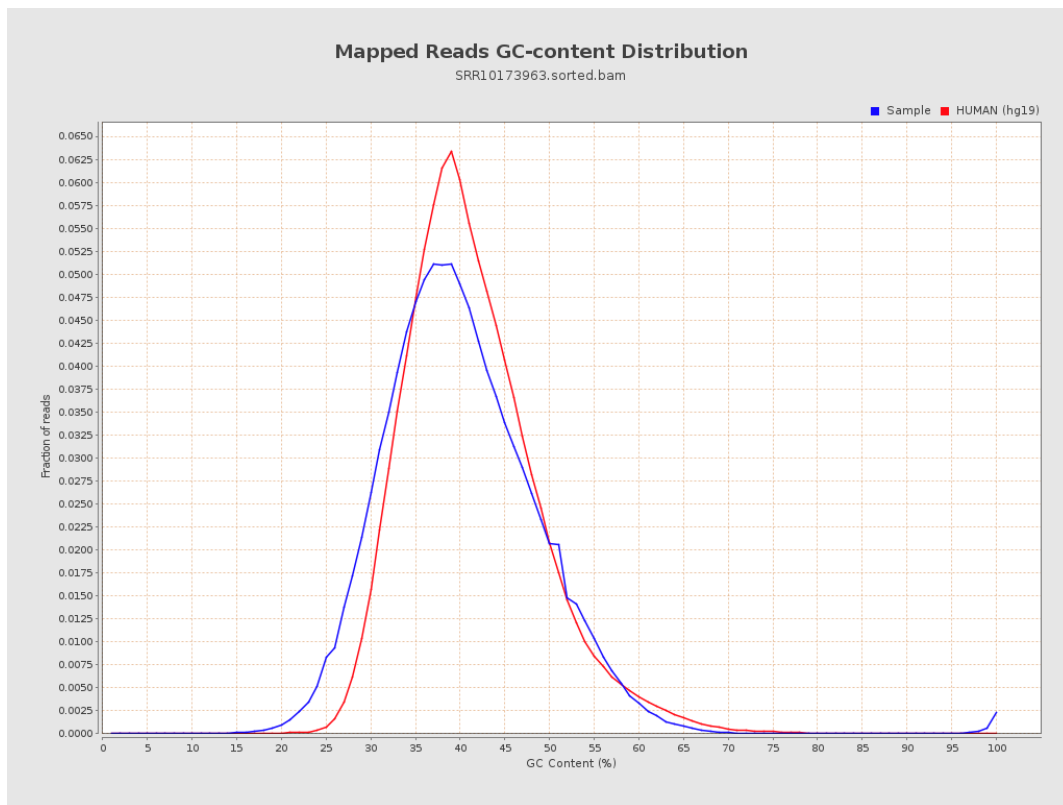
7. Results : Duplication Rate Histogram



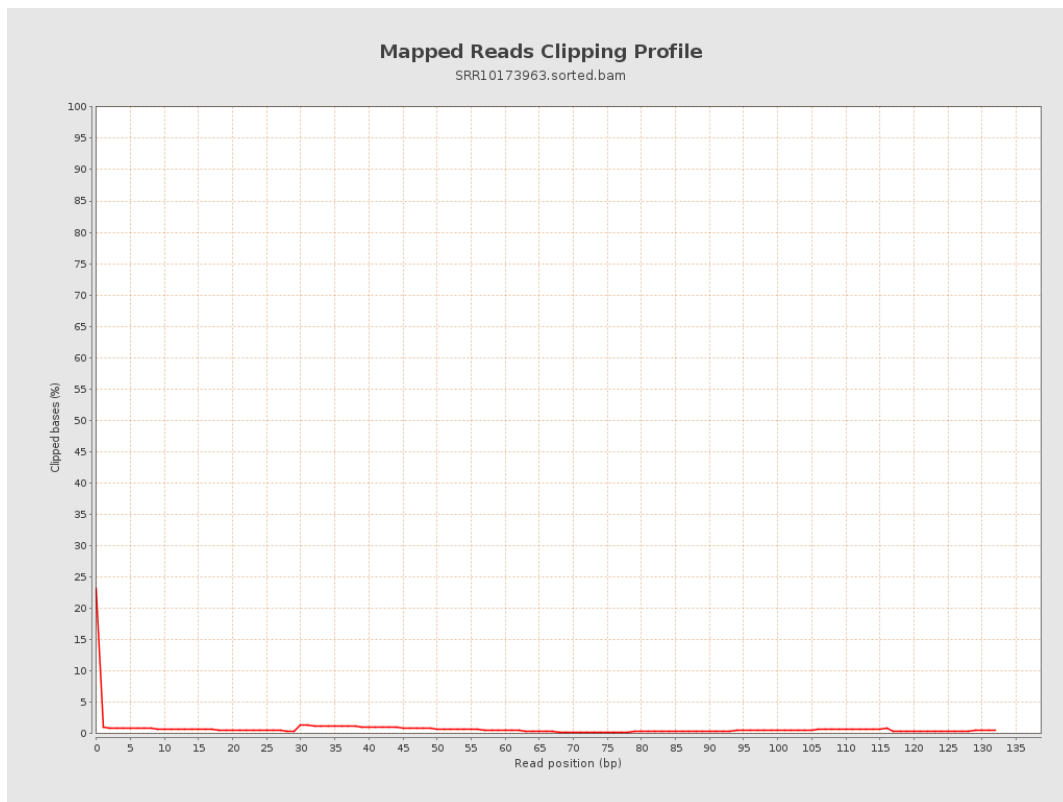
8. Results : Mapped Reads Nucleotide Content



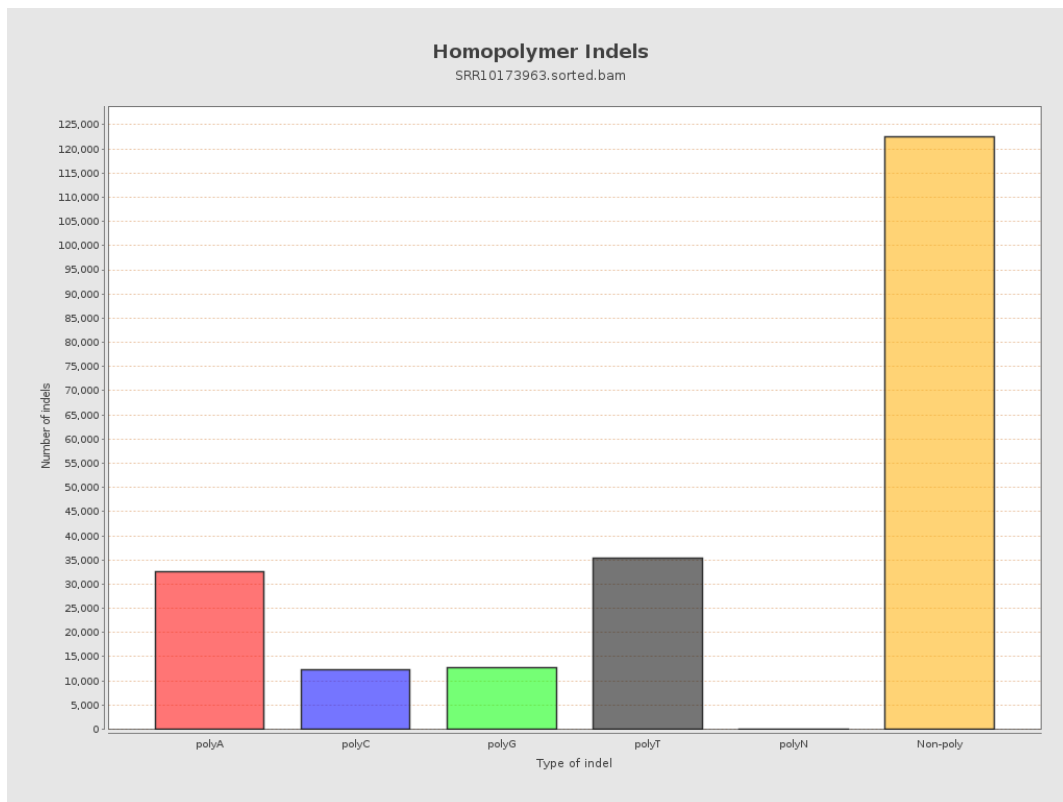
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



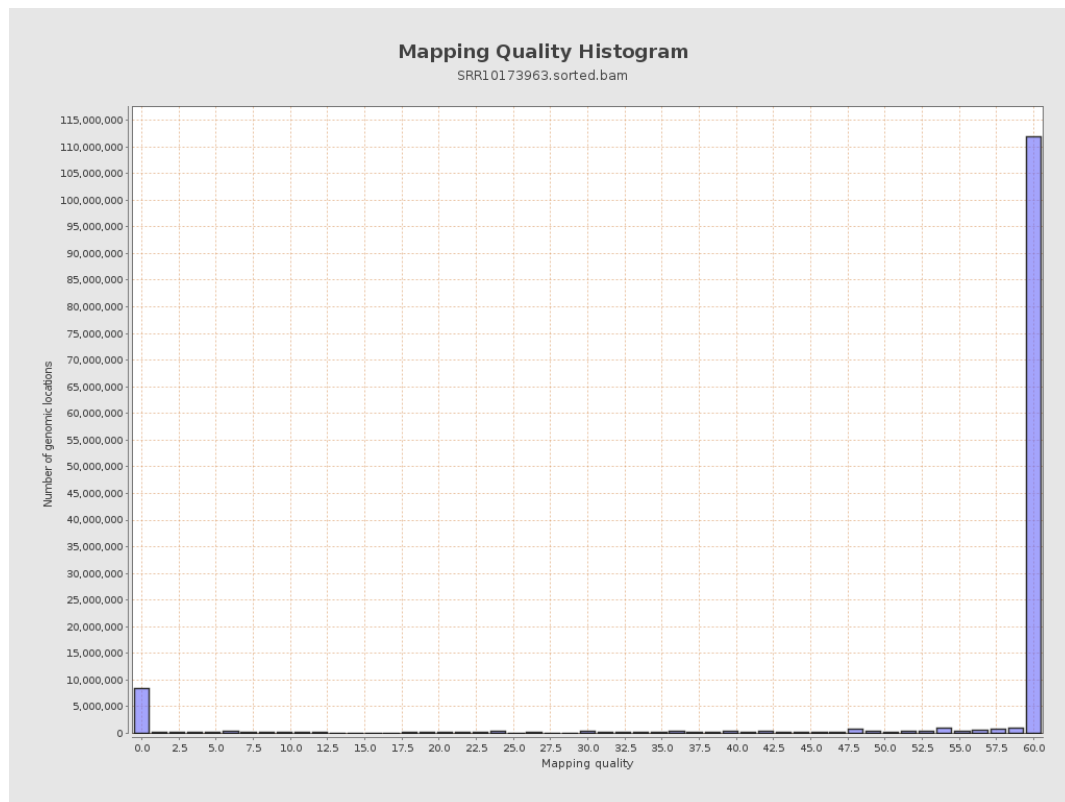
11. Results : Homopolymer Indels



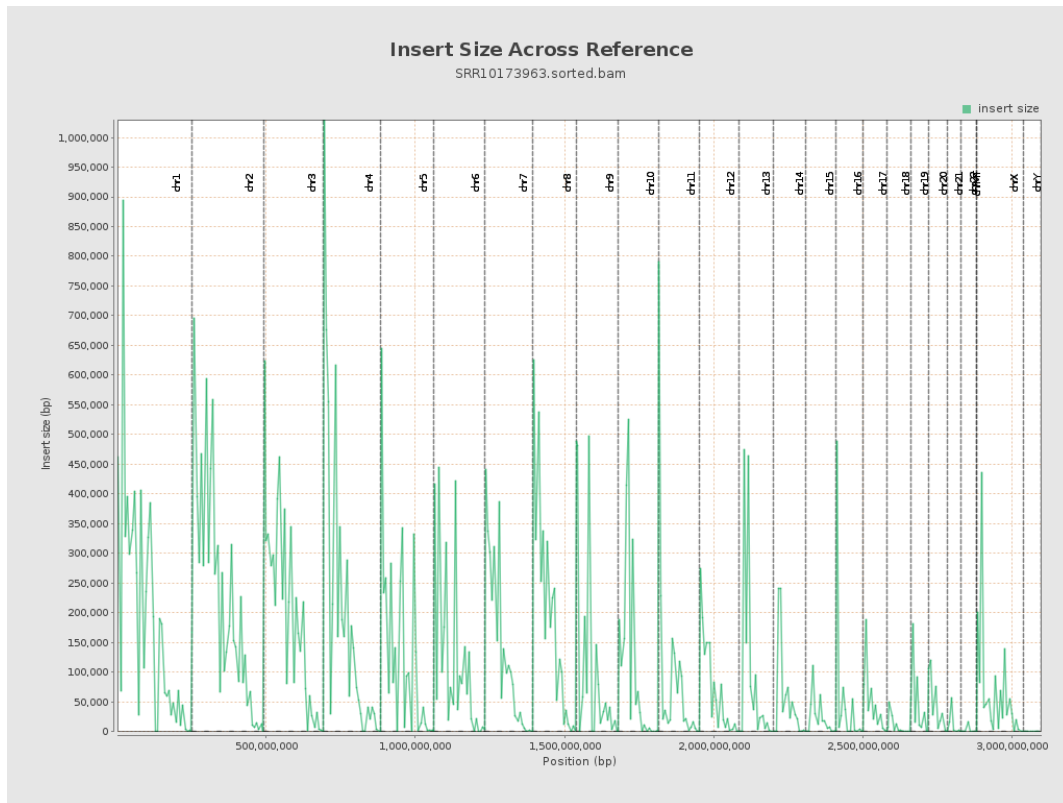
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

