

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 07:24:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173921.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_SRR10173921 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173921_1.fastq.gz SRR10173921_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 07:24:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173921.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,655,464
Mapped reads	6,473,305 / 97.26%
Unmapped reads	182,159 / 2.74%
Mapped paired reads	6,473,305 / 97.26%
Mapped reads, first in pair	3,239,455 / 48.67%
Mapped reads, second in pair	3,233,850 / 48.59%
Mapped reads, both in pair	6,354,430 / 95.48%
Mapped reads, singletons	118,875 / 1.79%
Secondary alignments	0
Supplementary alignments	614,194 / 9.23%
Read min/max/mean length	30 / 133 / 127.98
Duplicated reads (estimated)	5,085,298 / 76.41%
Duplication rate	65.46%
Clipped reads	2,522,694 / 37.9%

2.2. ACGT Content

Number/percentage of A's	230,944,496 / 30.18%
Number/percentage of C's	149,632,120 / 19.55%
Number/percentage of T's	230,239,539 / 30.08%
Number/percentage of G's	154,498,522 / 20.19%
Number/percentage of N's	9,280 / 0%

GC Percentage	39.74%
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2.3. Coverage

Mean	0.2474
Standard Deviation	3.567

2.4. Mapping Quality

Mean Mapping Quality	52.75
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2.5. Insert size

Mean	878,633.83
Standard Deviation	8,464,703.88
P25/Median/P75	145 / 200 / 285

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	7,745,325
Insertions	77,486
Mapped reads with at least one insertion	1.15%
Deletions	158,308
Mapped reads with at least one deletion	2.38%
Homopolymer indels	43.44%

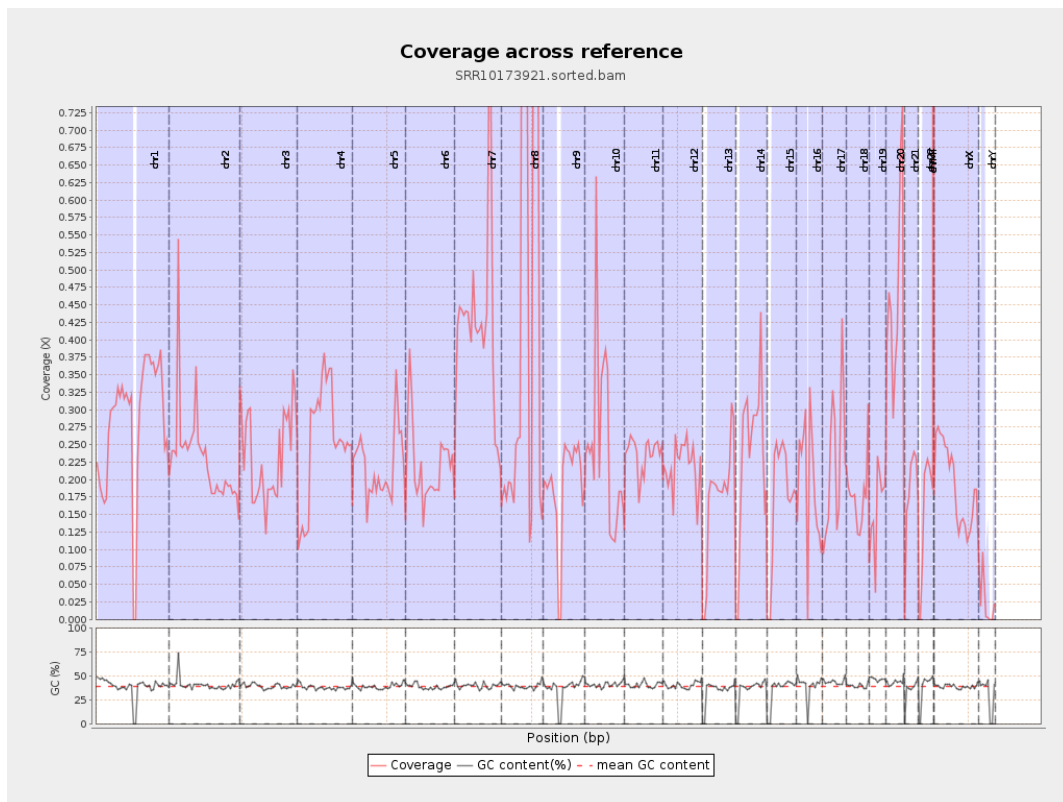
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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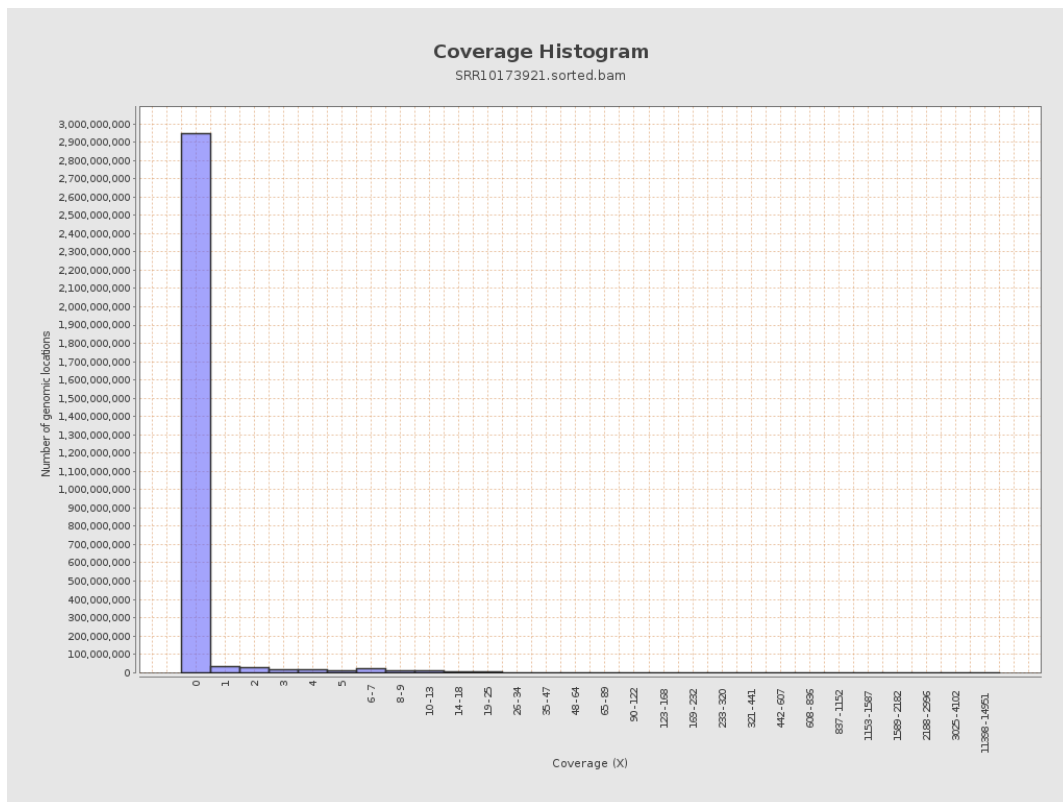
		bases	coverage	deviation
chr1	249250621	70318310	0.2821	1.8987
chr2	243199373	56261665	0.2313	10.4907
chr3	198022430	46517798	0.2349	1.4363
chr4	191154276	48311061	0.2527	1.9527
chr5	180915260	39616243	0.219	1.3812
chr6	171115067	37394029	0.2185	1.4463
chr7	159138663	67709011	0.4255	4.0397
chr8	146364022	76865131	0.5252	2.7804
chr9	141213431	26828622	0.19	1.6086
chr10	135534747	34060488	0.2513	4.4017
chr11	135006516	31793945	0.2355	1.4679
chr12	133851895	29421235	0.2198	1.3942
chr13	115169878	19987814	0.1736	1.2388
chr14	107349540	25433304	0.2369	1.4505
chr15	102531392	17879444	0.1744	1.2099
chr16	90354753	17280097	0.1912	1.7382
chr17	81195210	18313777	0.2256	1.5563
chr18	78077248	13614407	0.1744	2.0322
chr19	59128983	9458970	0.16	1.3625
chr20	63025520	29066905	0.4612	2.0588
chr21	48129895	8739594	0.1816	1.423
chr22	51304566	7607524	0.1483	1.0947
chrMT	16571	1991839	120.2003	88.3225
chrX	155270560	29869117	0.1924	1.3128

chrY	59373566	1390061	0.0234	1.095
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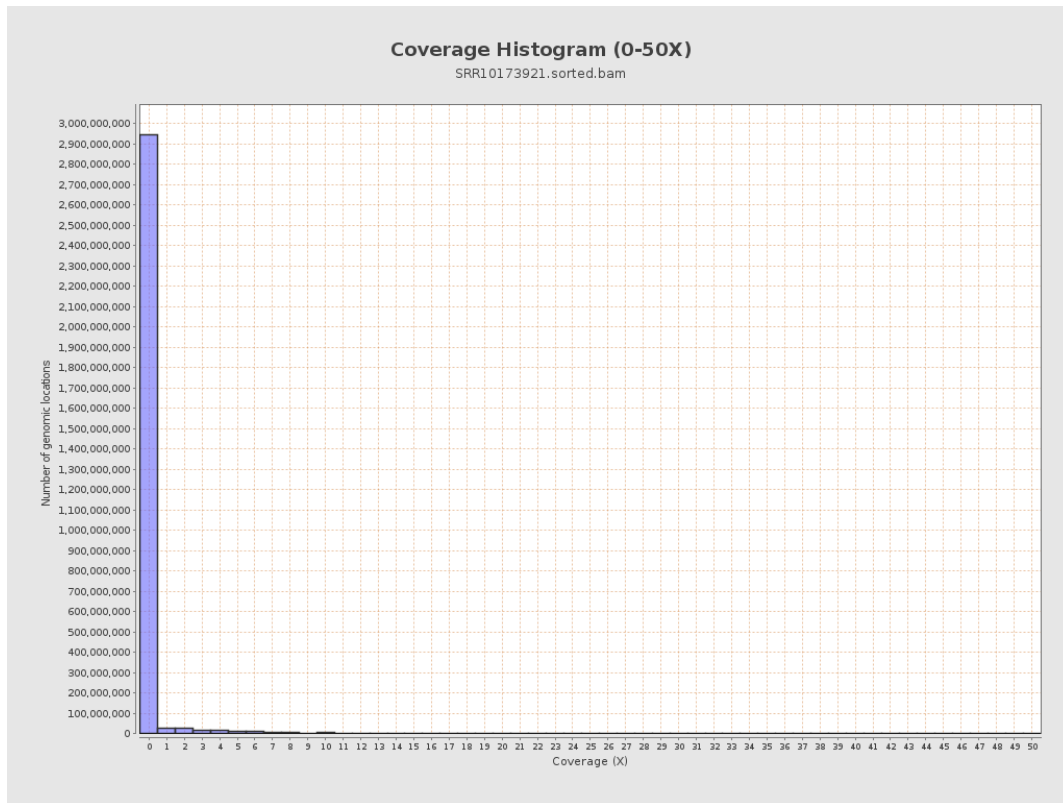
3. Results : Coverage across reference



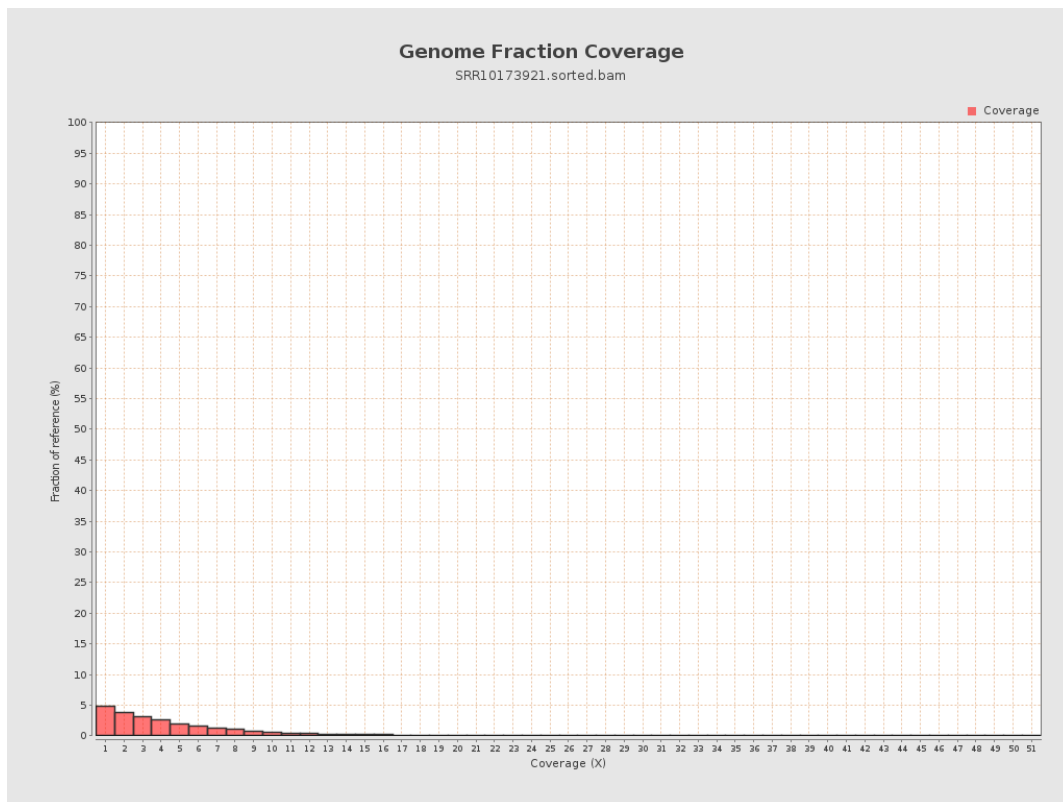
4. Results : Coverage Histogram



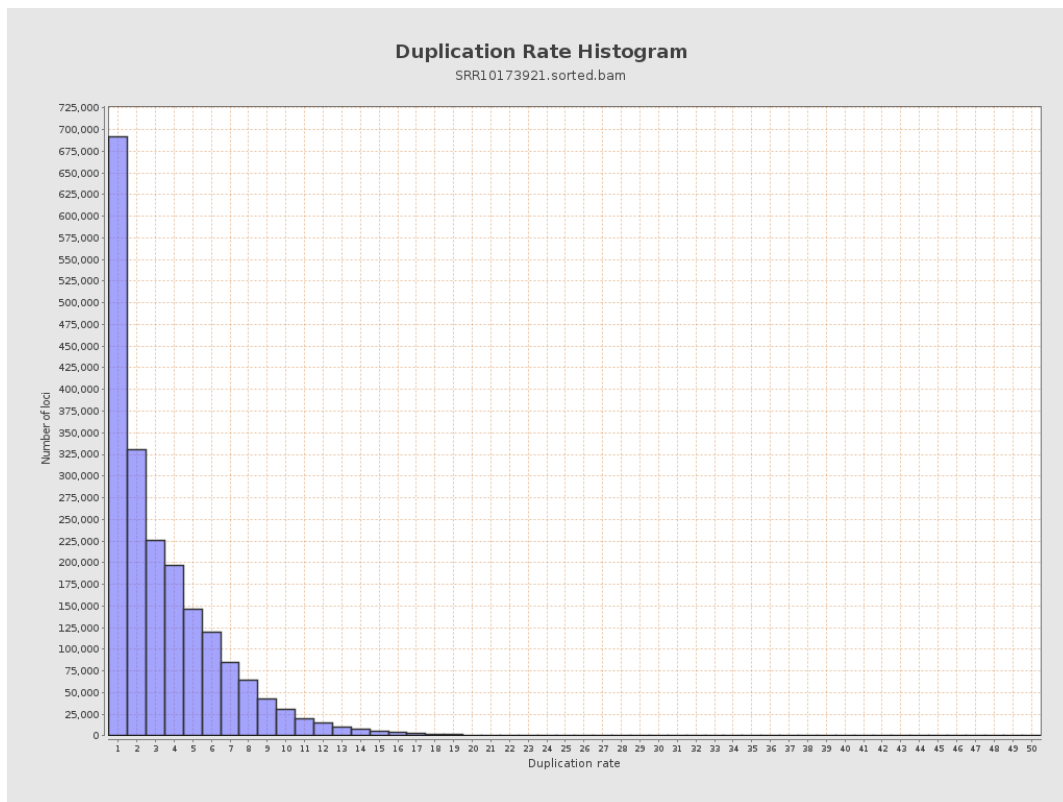
5. Results : Coverage Histogram (0-50X)



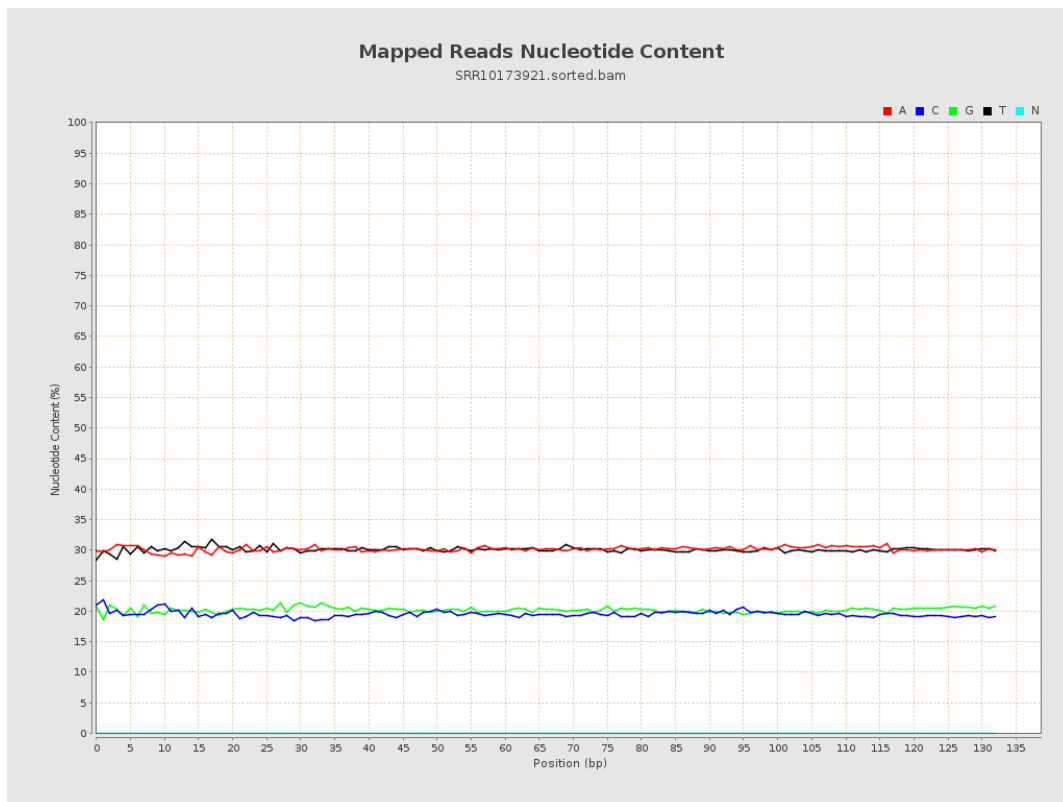
6. Results : Genome Fraction Coverage



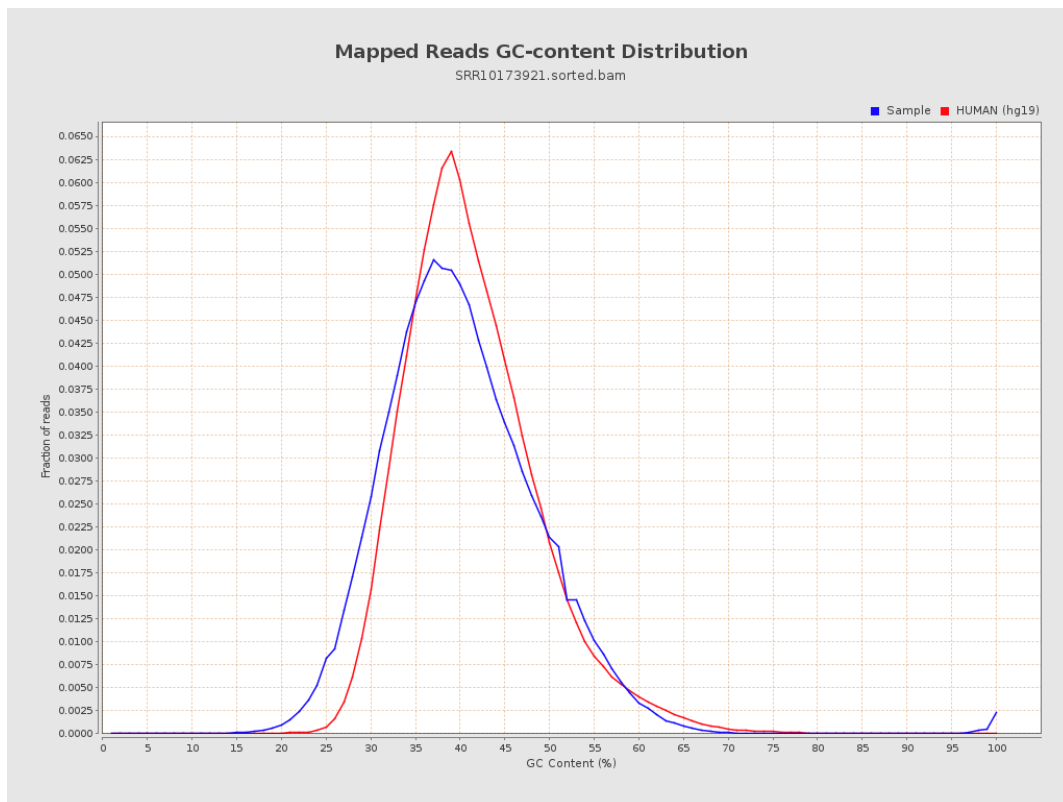
7. Results : Duplication Rate Histogram



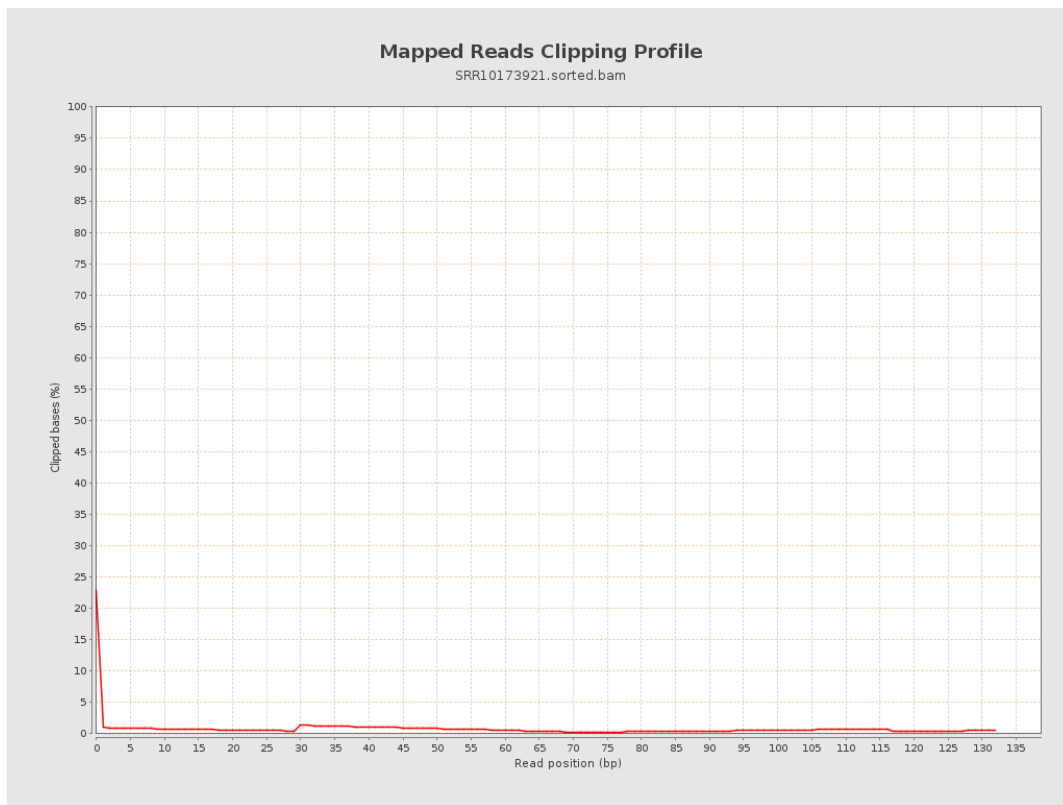
8. Results : Mapped Reads Nucleotide Content



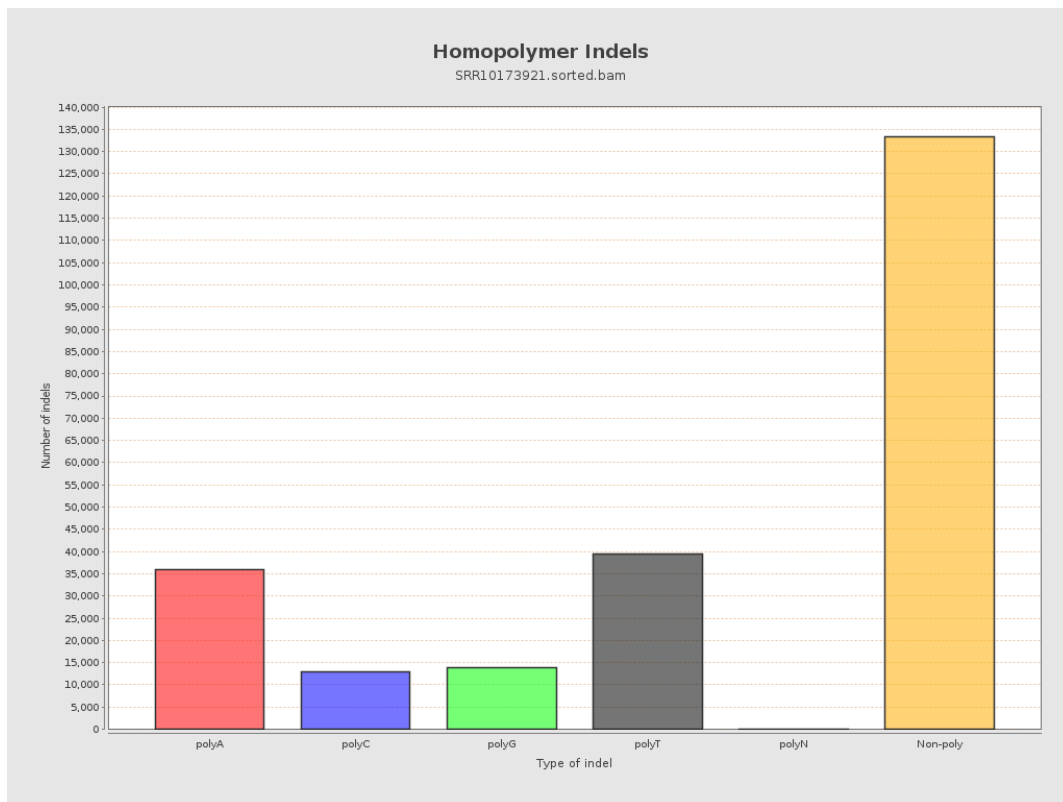
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



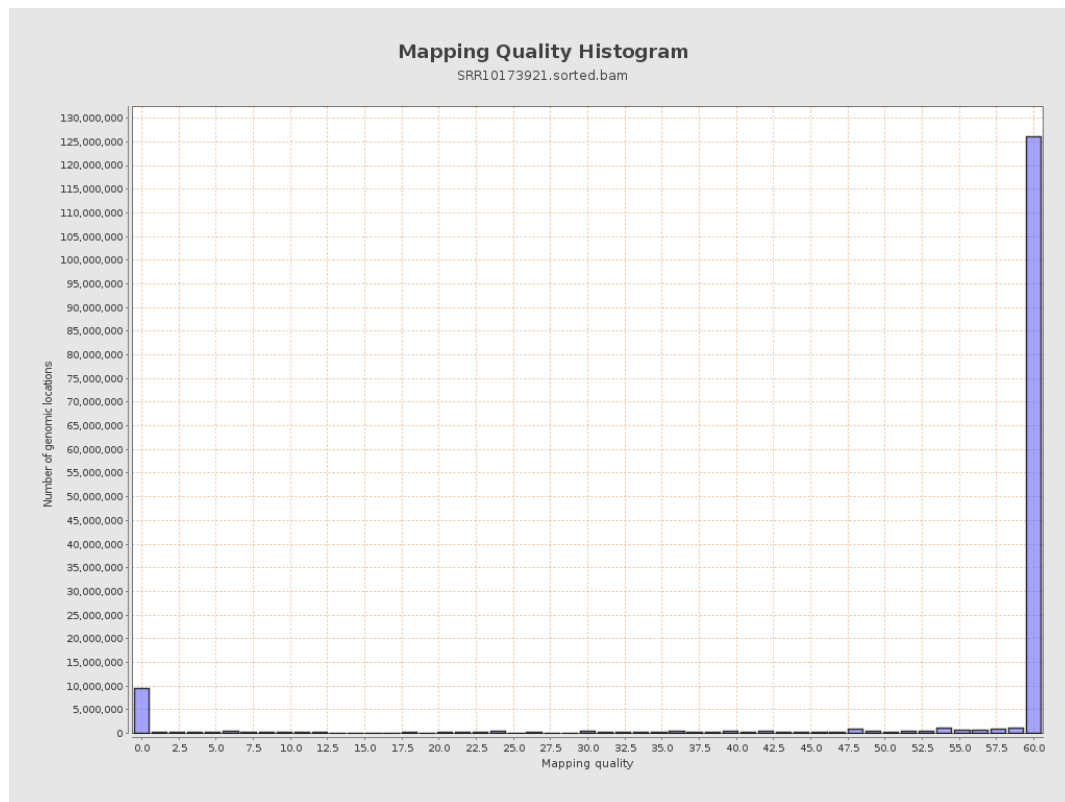
11. Results : Homopolymer Indels



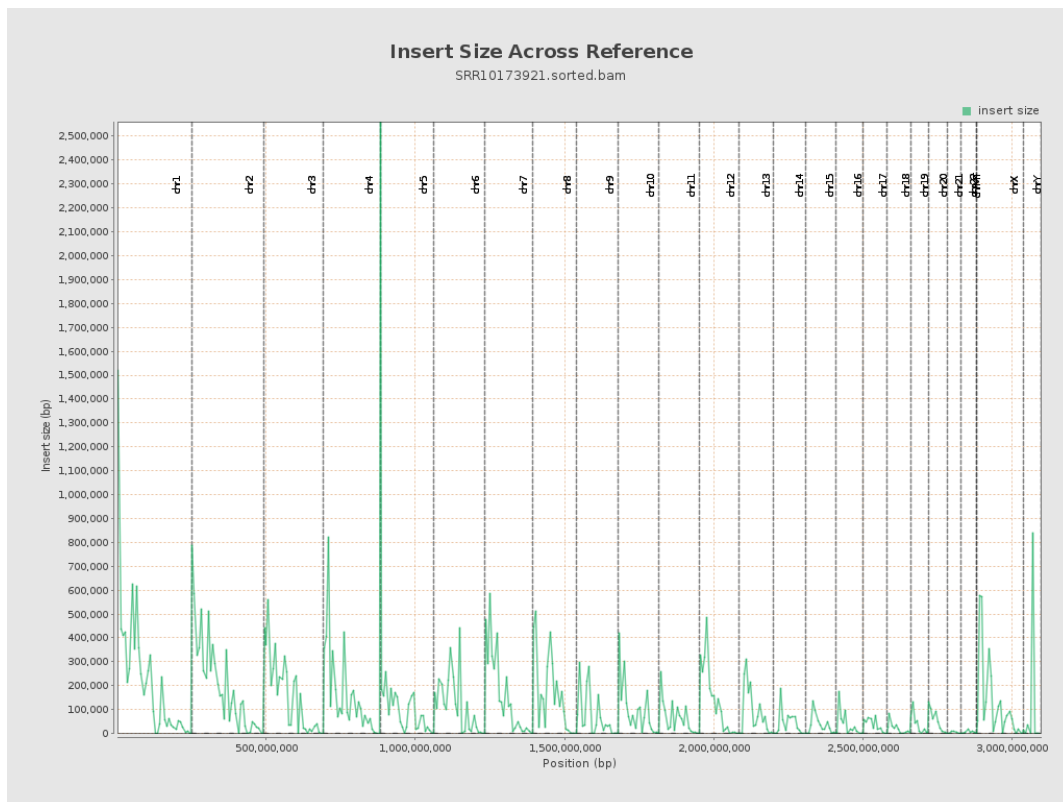
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

