

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 07:38:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173924.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_SRR10173924 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173924_1.fastq.gz SRR10173924_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 07:38:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173924.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,461,872
Mapped reads	1,427,275 / 97.63%
Unmapped reads	34,597 / 2.37%
Mapped paired reads	1,427,275 / 97.63%
Mapped reads, first in pair	711,079 / 48.64%
Mapped reads, second in pair	716,196 / 48.99%
Mapped reads, both in pair	1,403,554 / 96.01%
Mapped reads, singletons	23,721 / 1.62%
Secondary alignments	0
Supplementary alignments	127,173 / 8.7%
Read min/max/mean length	30 / 133 / 127.4
Duplicated reads (estimated)	1,089,850 / 74.55%
Duplication rate	65.56%
Clipped reads	565,923 / 38.71%

2.2. ACGT Content

Number/percentage of A's	50,339,959 / 29.79%
Number/percentage of C's	33,707,390 / 19.95%
Number/percentage of T's	50,225,785 / 29.72%
Number/percentage of G's	34,695,922 / 20.53%
Number/percentage of N's	1,967 / 0%

GC Percentage	40.48%
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2.3. Coverage

Mean	0.0546
Standard Deviation	0.9791

2.4. Mapping Quality

Mean Mapping Quality	53
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2.5. Insert size

Mean	670,623.46
Standard Deviation	7,696,304.19
P25/Median/P75	139 / 192 / 270

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	1,599,680
Insertions	16,869
Mapped reads with at least one insertion	1.15%
Deletions	29,208
Mapped reads with at least one deletion	1.99%
Homopolymer indels	45.27%

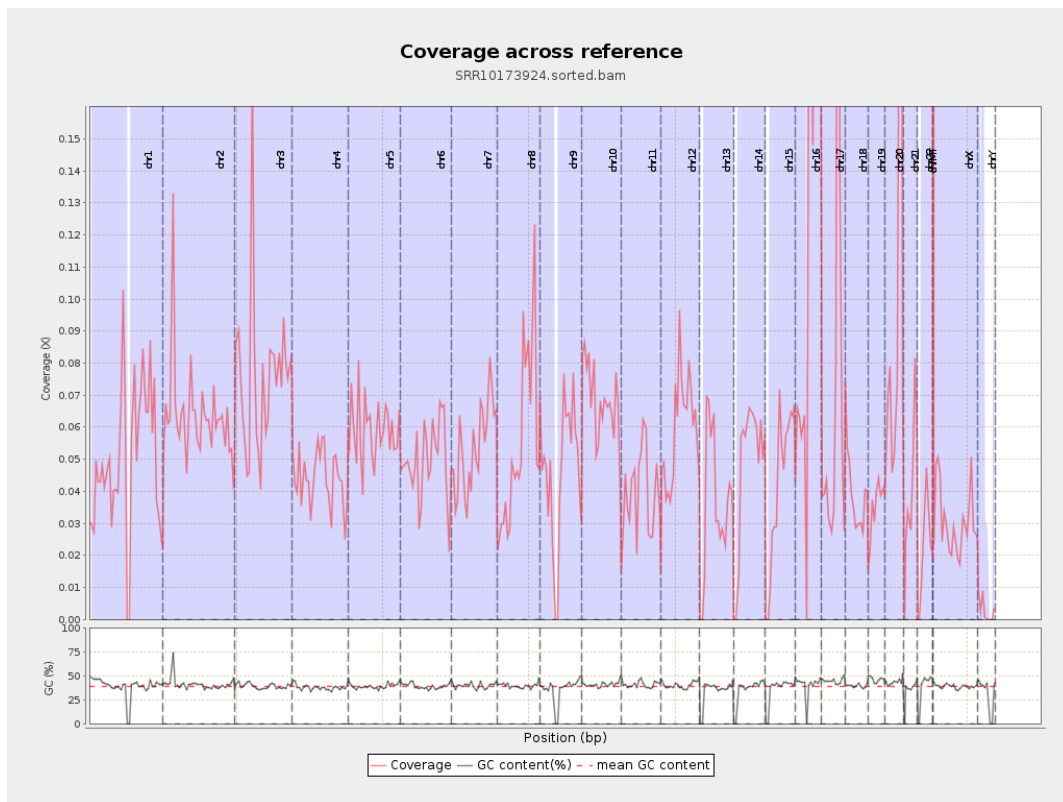
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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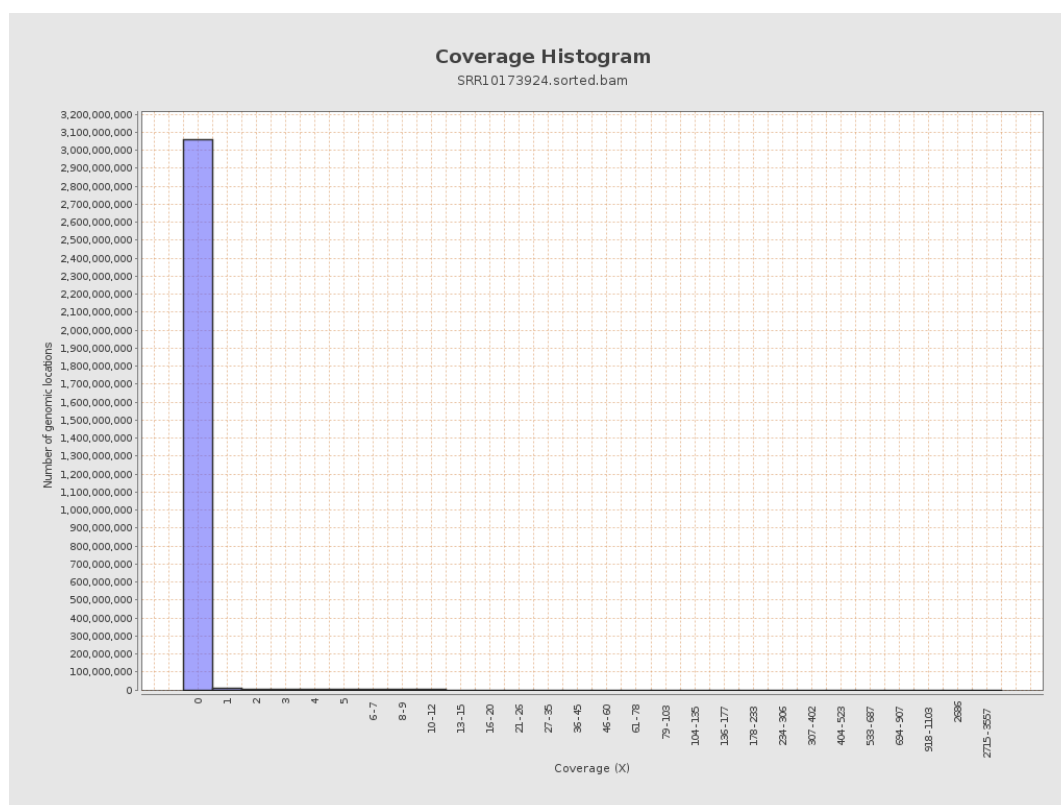
		bases	coverage	deviation
chr1	249250621	12527794	0.0503	0.7169
chr2	243199373	15474872	0.0636	2.5625
chr3	198022430	14818540	0.0748	0.7865
chr4	191154276	8436865	0.0441	0.6085
chr5	180915260	10679760	0.059	0.6974
chr6	171115067	8453787	0.0494	0.657
chr7	159138663	8519458	0.0535	0.6842
chr8	146364022	8075735	0.0552	0.685
chr9	141213431	6464338	0.0458	0.6373
chr10	135534747	9267958	0.0684	0.8018
chr11	135006516	5241056	0.0388	0.5609
chr12	133851895	8060703	0.0602	0.6953
chr13	115169878	4170502	0.0362	0.5482
chr14	107349540	5190758	0.0484	0.6165
chr15	102531392	4161651	0.0406	0.5718
chr16	90354753	11641979	0.1288	1.0975
chr17	81195210	6749719	0.0831	0.8395
chr18	78077248	3036204	0.0389	0.6319
chr19	59128983	2099685	0.0355	0.5761
chr20	63025520	7316777	0.1161	0.9935
chr21	48129895	1952040	0.0406	0.5716
chr22	51304566	1188353	0.0232	0.4104
chrMT	16571	567319	34.2357	35.3593
chrX	155270560	4778620	0.0308	0.4937

chrY	59373566	170523	0.0029	0.1415
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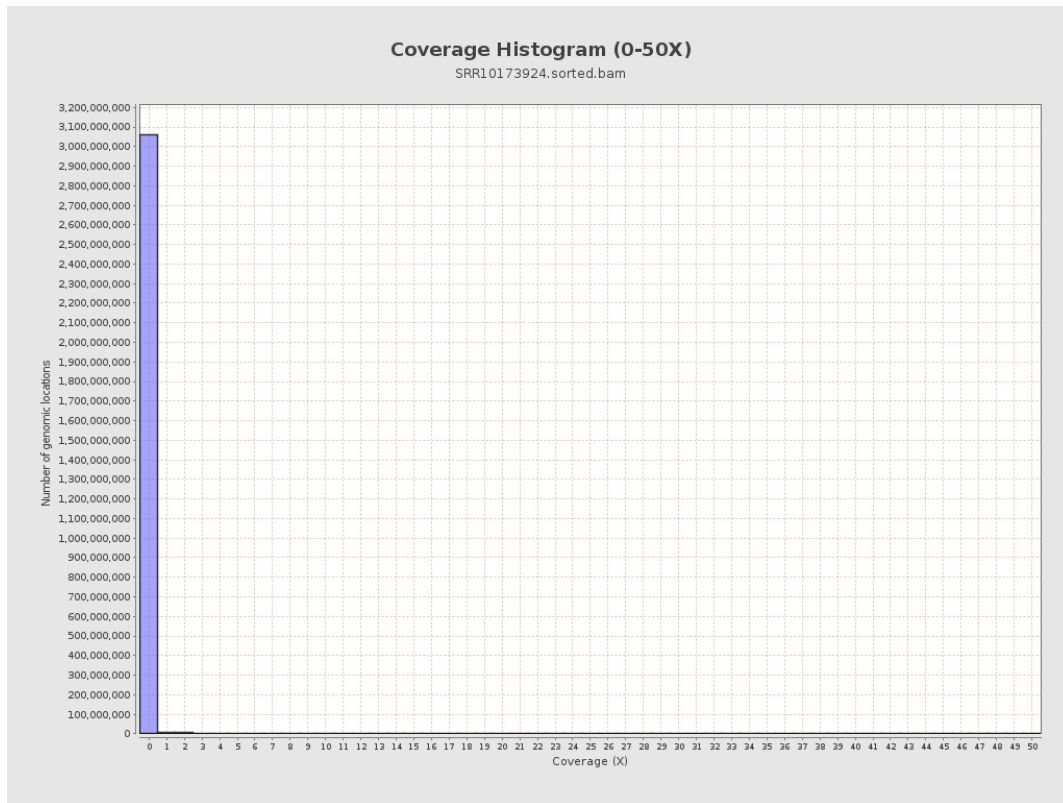
3. Results : Coverage across reference



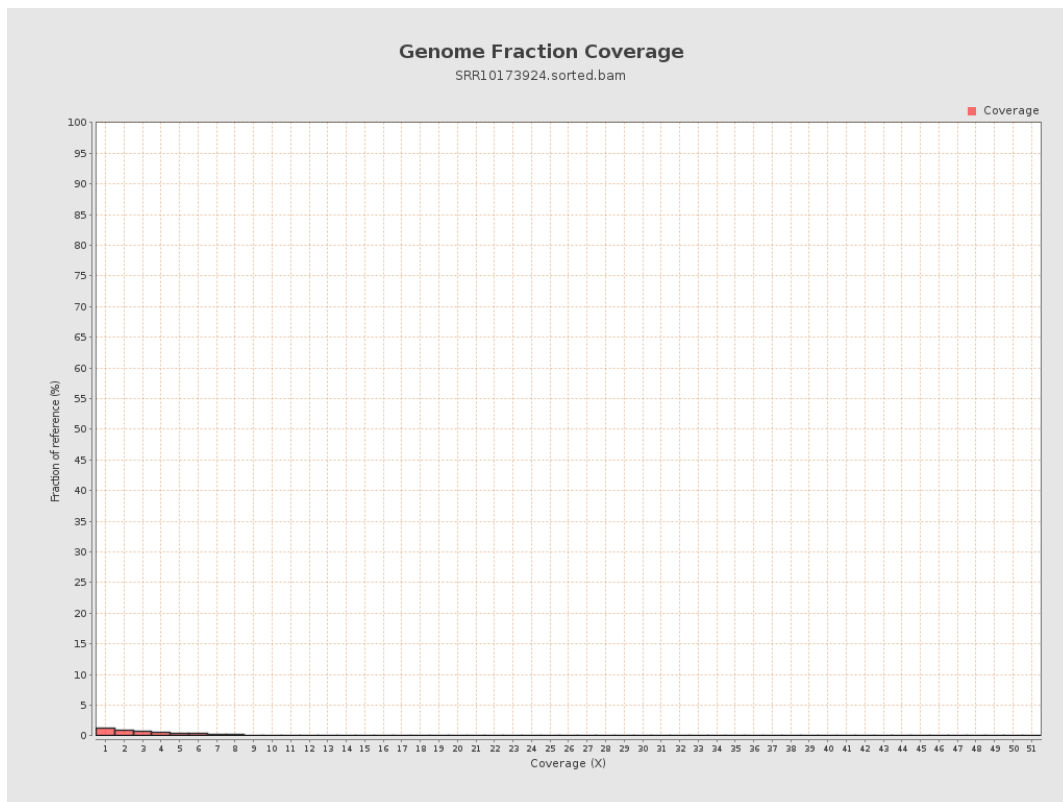
4. Results : Coverage Histogram



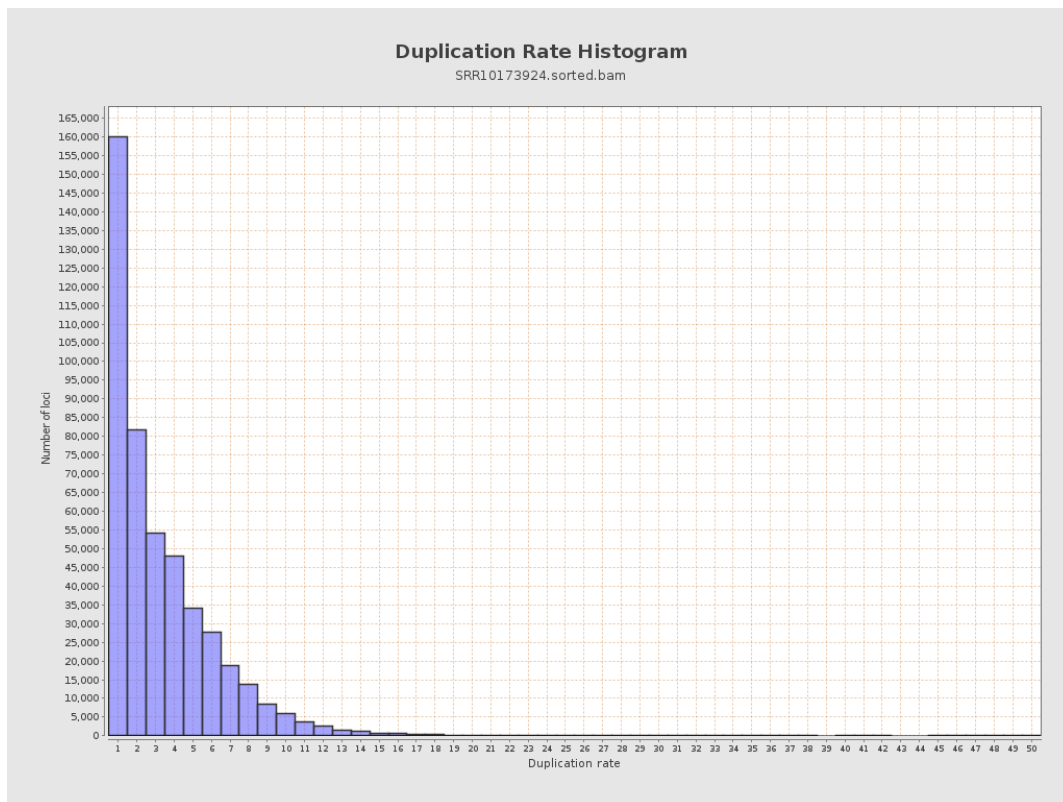
5. Results : Coverage Histogram (0-50X)



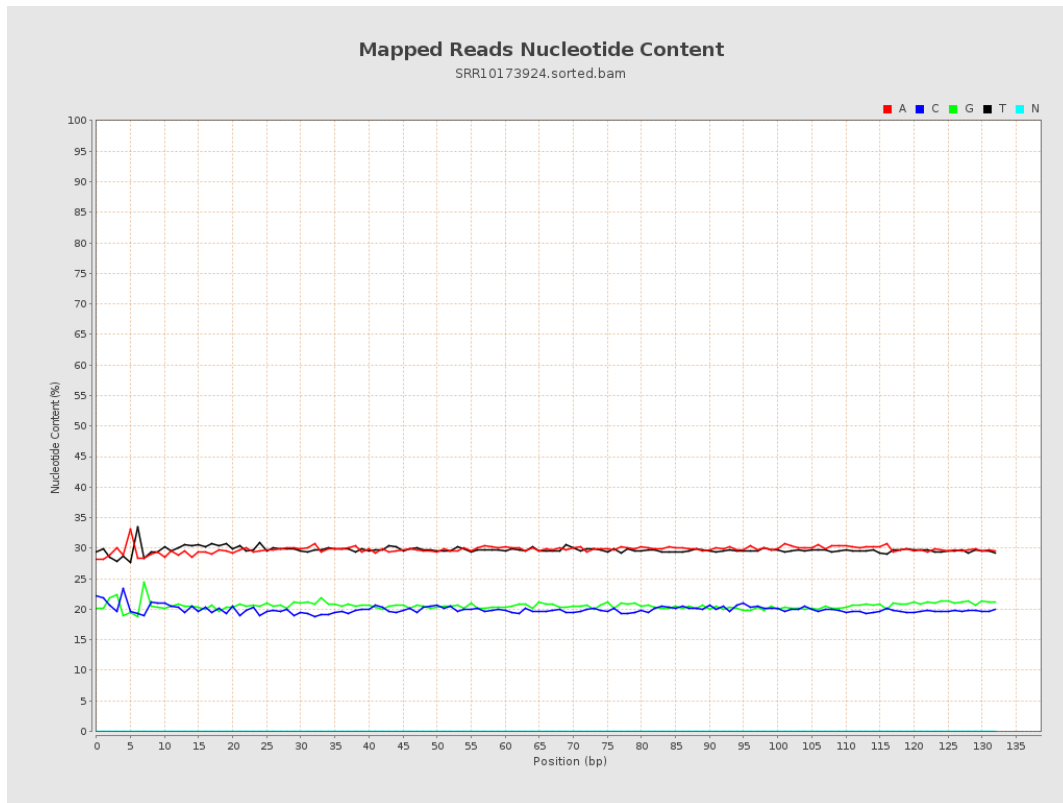
6. Results : Genome Fraction Coverage



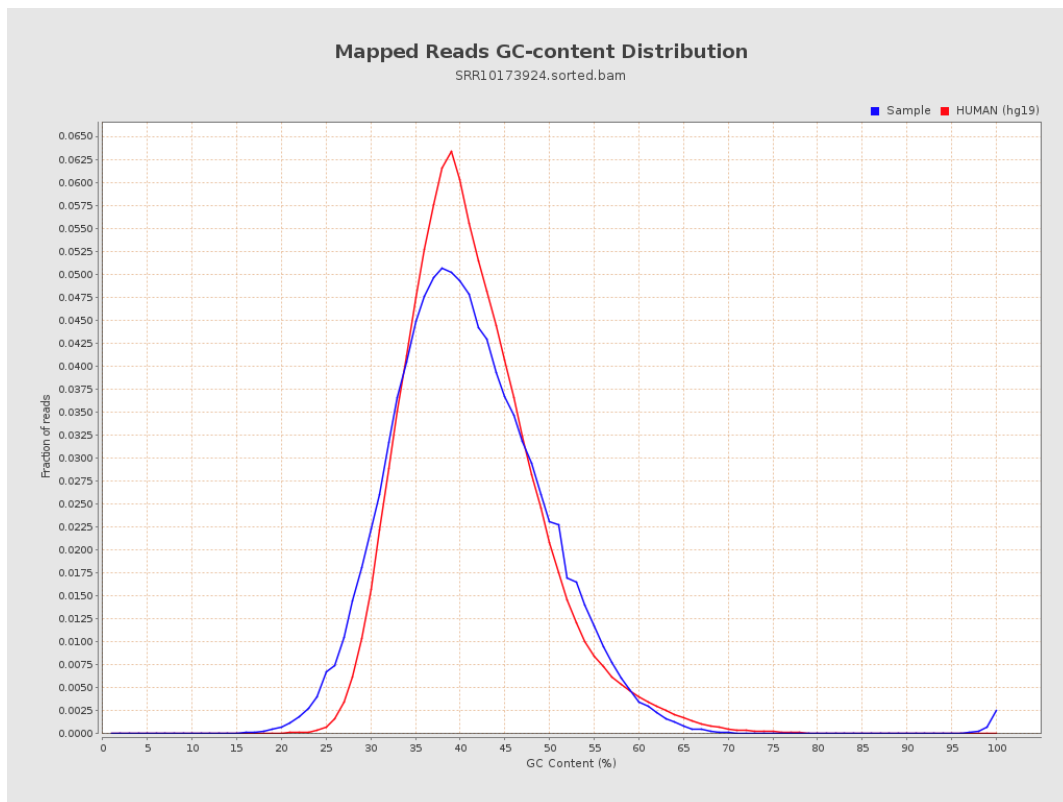
7. Results : Duplication Rate Histogram



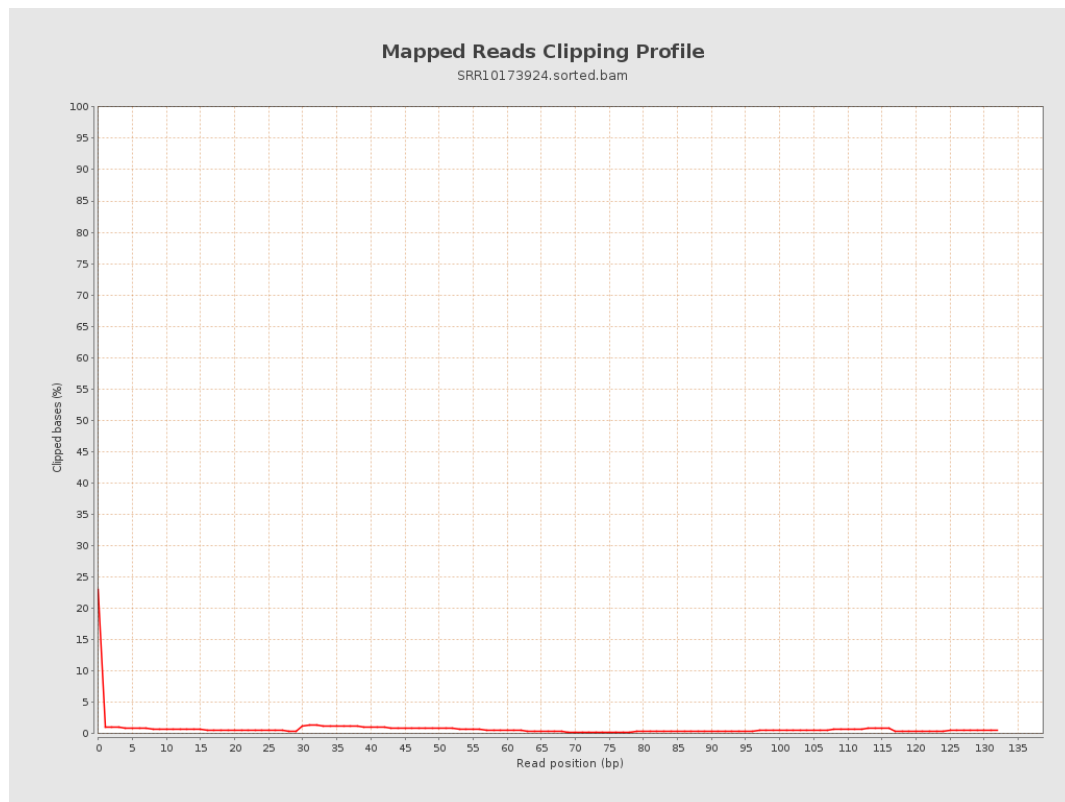
8. Results : Mapped Reads Nucleotide Content



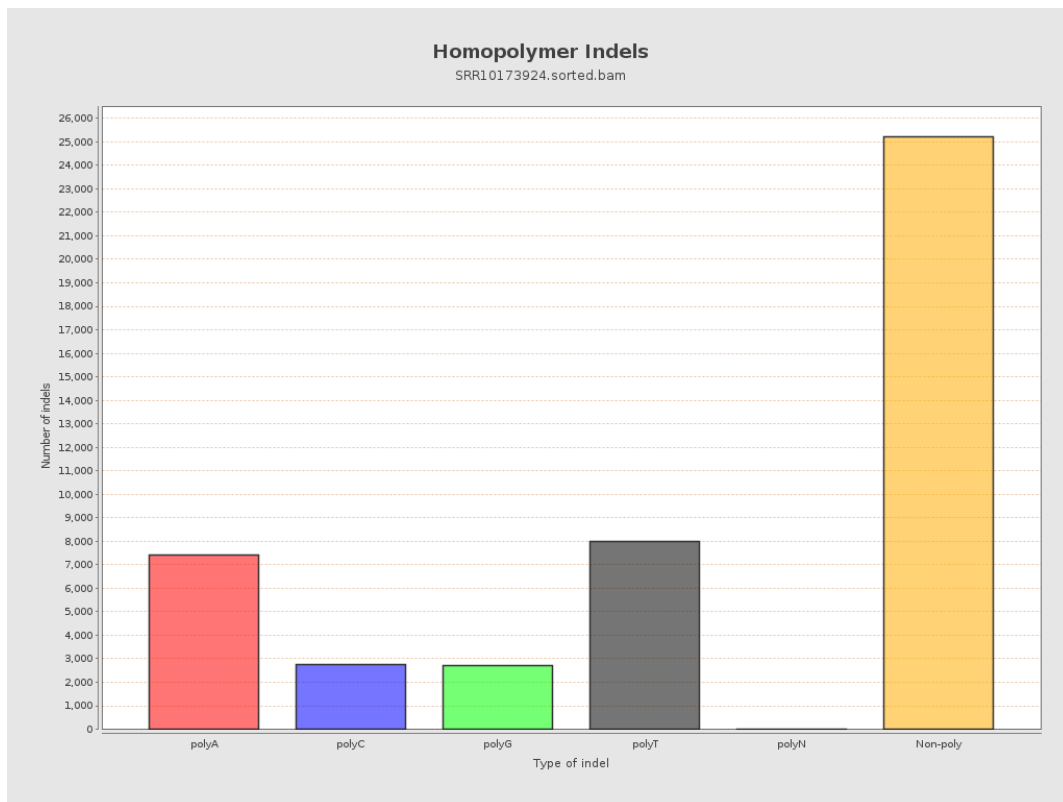
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



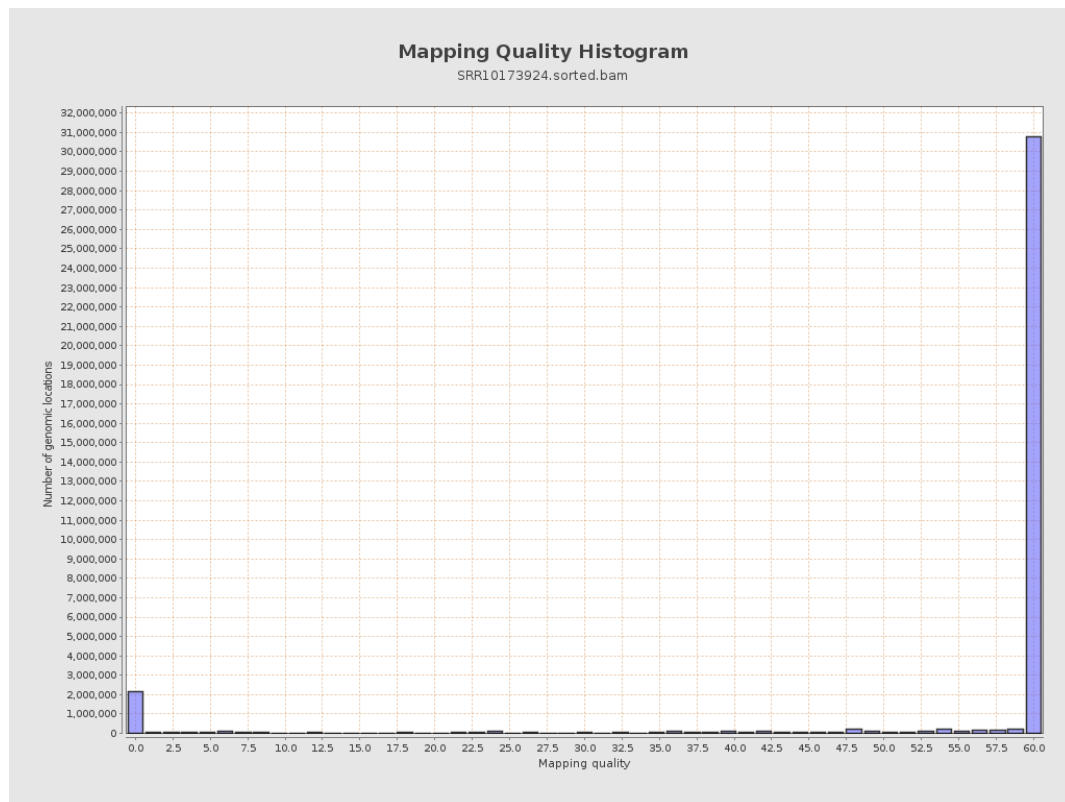
11. Results : Homopolymer Indels



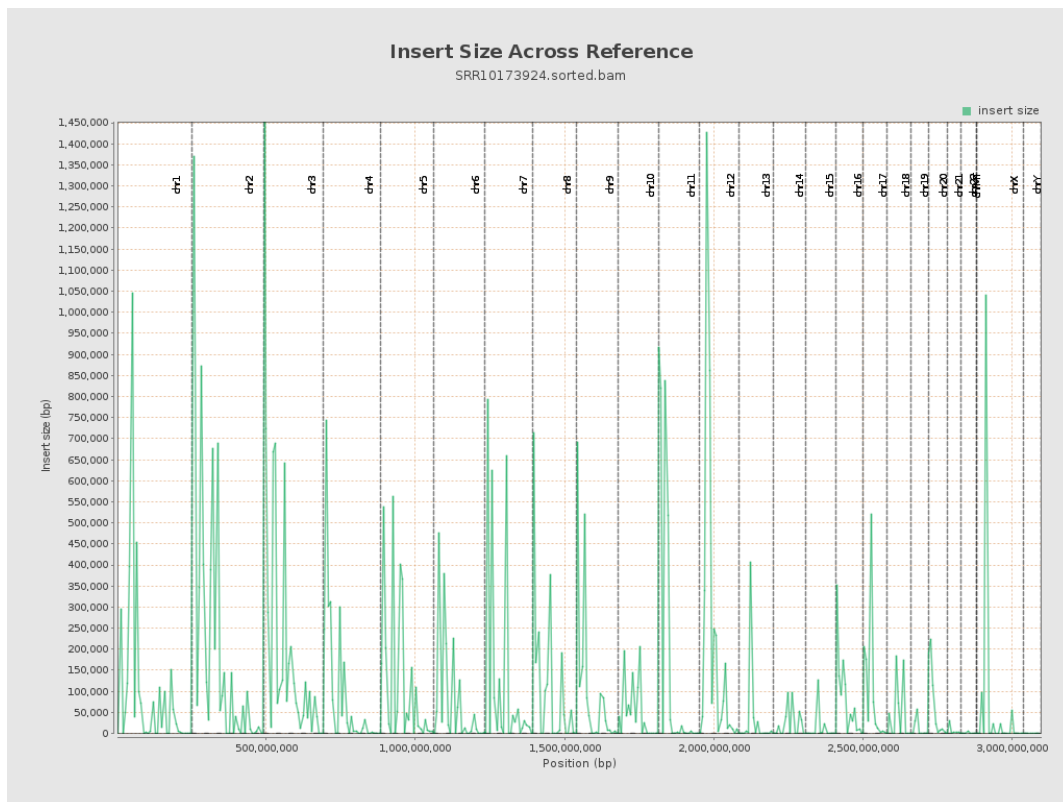
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

