

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 09:45:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173940.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_SRR10173940 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173940_1.fastq.gz SRR10173940_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 09:45:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173940.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,660,348
Mapped reads	3,563,702 / 97.36%
Unmapped reads	96,646 / 2.64%
Mapped paired reads	3,563,702 / 97.36%
Mapped reads, first in pair	1,787,020 / 48.82%
Mapped reads, second in pair	1,776,682 / 48.54%
Mapped reads, both in pair	3,500,514 / 95.63%
Mapped reads, singletons	63,188 / 1.73%
Secondary alignments	0
Supplementary alignments	346,462 / 9.47%
Read min/max/mean length	30 / 133 / 127.52
Duplicated reads (estimated)	2,695,881 / 73.65%
Duplication rate	63.39%
Clipped reads	1,469,844 / 40.16%

2.2. ACGT Content

Number/percentage of A's	126,563,264 / 30.24%
Number/percentage of C's	81,594,617 / 19.49%
Number/percentage of T's	126,141,262 / 30.14%
Number/percentage of G's	84,256,955 / 20.13%
Number/percentage of N's	5,279 / 0%

GC Percentage	39.62%
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2.3. Coverage

Mean	0.1353
Standard Deviation	2.1031

2.4. Mapping Quality

Mean Mapping Quality	52.78
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2.5. Insert size

Mean	850,999.75
Standard Deviation	8,757,395.92
P25/Median/P75	137 / 190 / 270

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	4,332,527
Insertions	42,083
Mapped reads with at least one insertion	1.15%
Deletions	103,982
Mapped reads with at least one deletion	2.85%
Homopolymer indels	42.24%

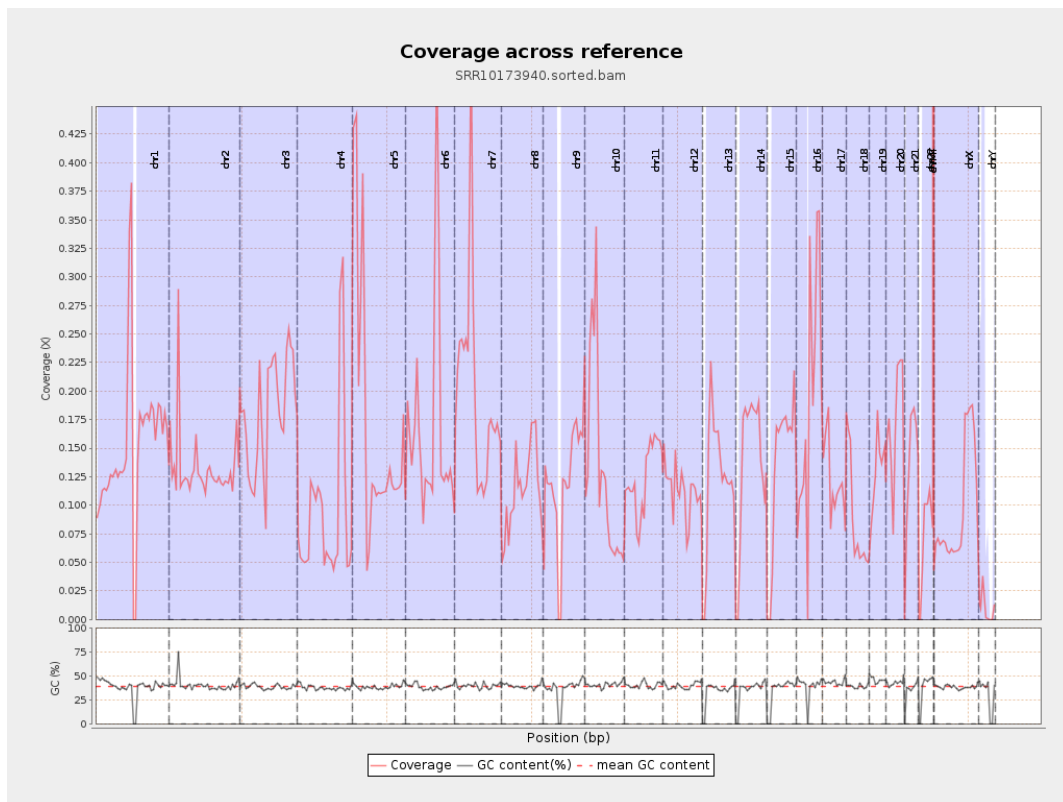
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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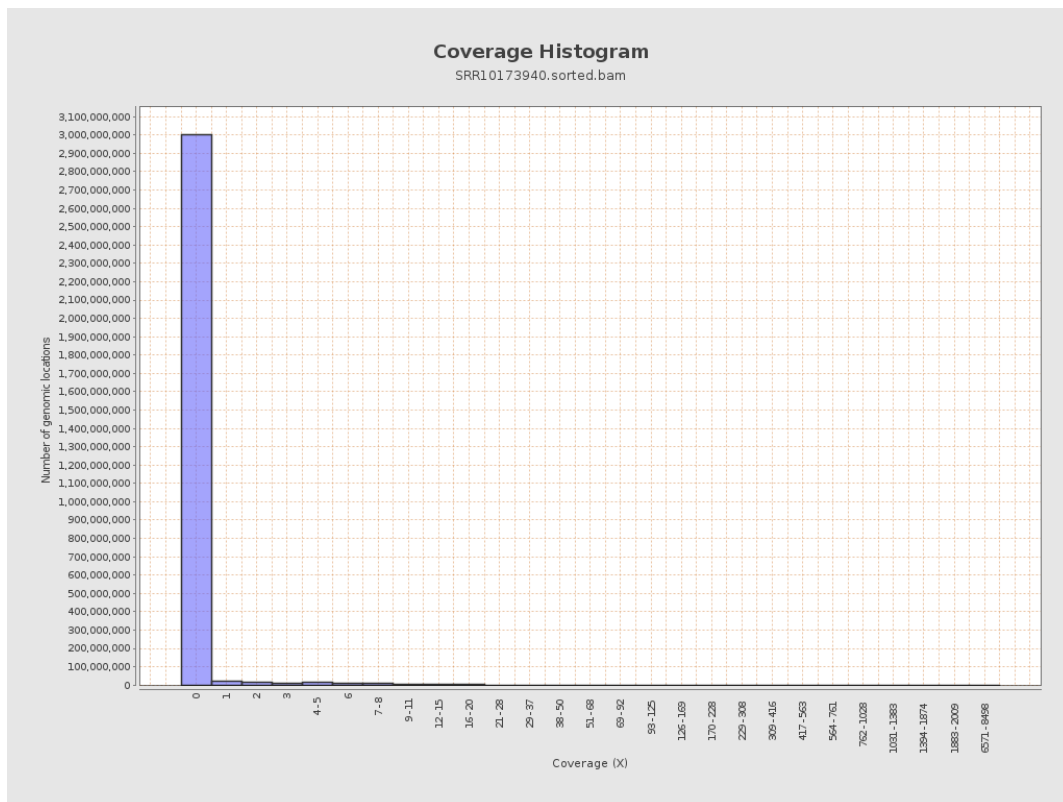
		bases	coverage	deviation
chr1	249250621	37738087	0.1514	1.6546
chr2	243199373	32277606	0.1327	5.9636
chr3	198022430	35861933	0.1811	1.2185
chr4	191154276	17260626	0.0903	0.9858
chr5	180915260	30504138	0.1686	1.1889
chr6	171115067	29003917	0.1695	1.2164
chr7	159138663	31448723	0.1976	2.1495
chr8	146364022	16742351	0.1144	1.1129
chr9	141213431	16947950	0.12	1.128
chr10	135534747	17756389	0.131	2.0639
chr11	135006516	16753442	0.1241	1.0198
chr12	133851895	15025925	0.1123	0.9507
chr13	115169878	13921883	0.1209	0.9991
chr14	107349540	14758351	0.1375	1.059
chr15	102531392	13806399	0.1347	1.0356
chr16	90354753	17285103	0.1913	1.5785
chr17	81195210	9699332	0.1195	1.0797
chr18	78077248	6722765	0.0861	1.4269
chr19	59128983	7619938	0.1289	1.6235
chr20	63025520	10832208	0.1719	1.1639
chr21	48129895	6479375	0.1346	1.0728
chr22	51304566	3656866	0.0713	0.7105
chrMT	16571	1243111	75.0173	61.0772
chrX	155270560	14912567	0.096	0.8886

chrY	59373566	554657	0.0093	0.3939
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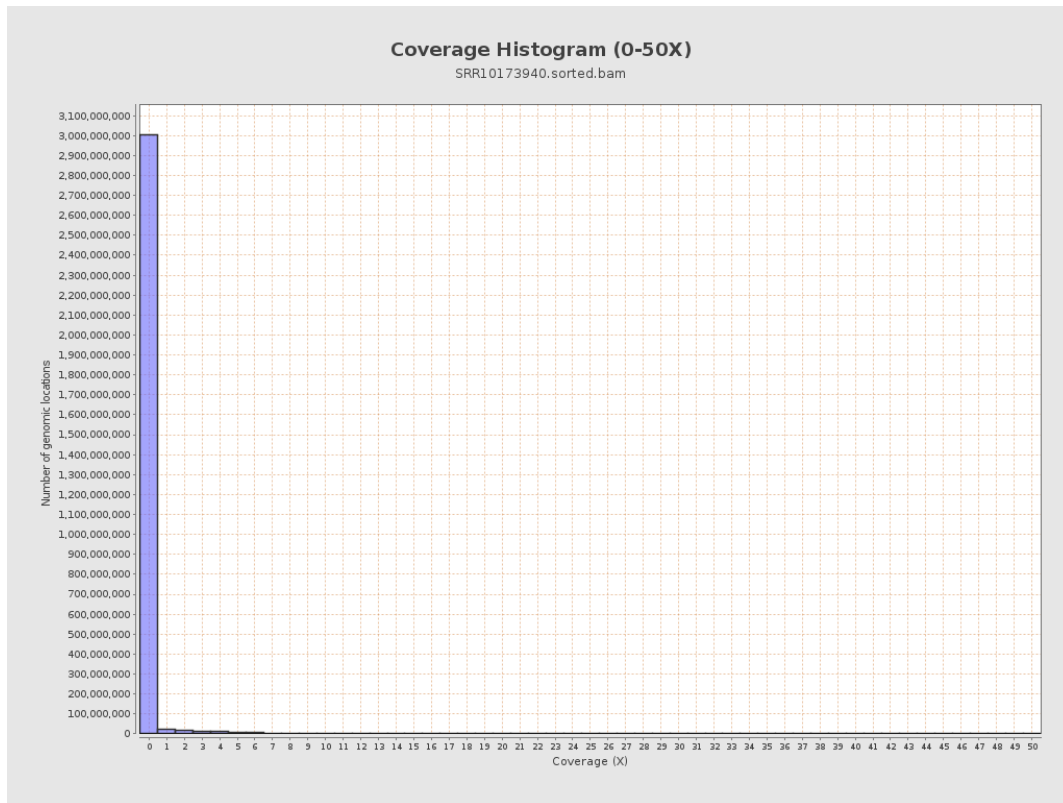
3. Results : Coverage across reference



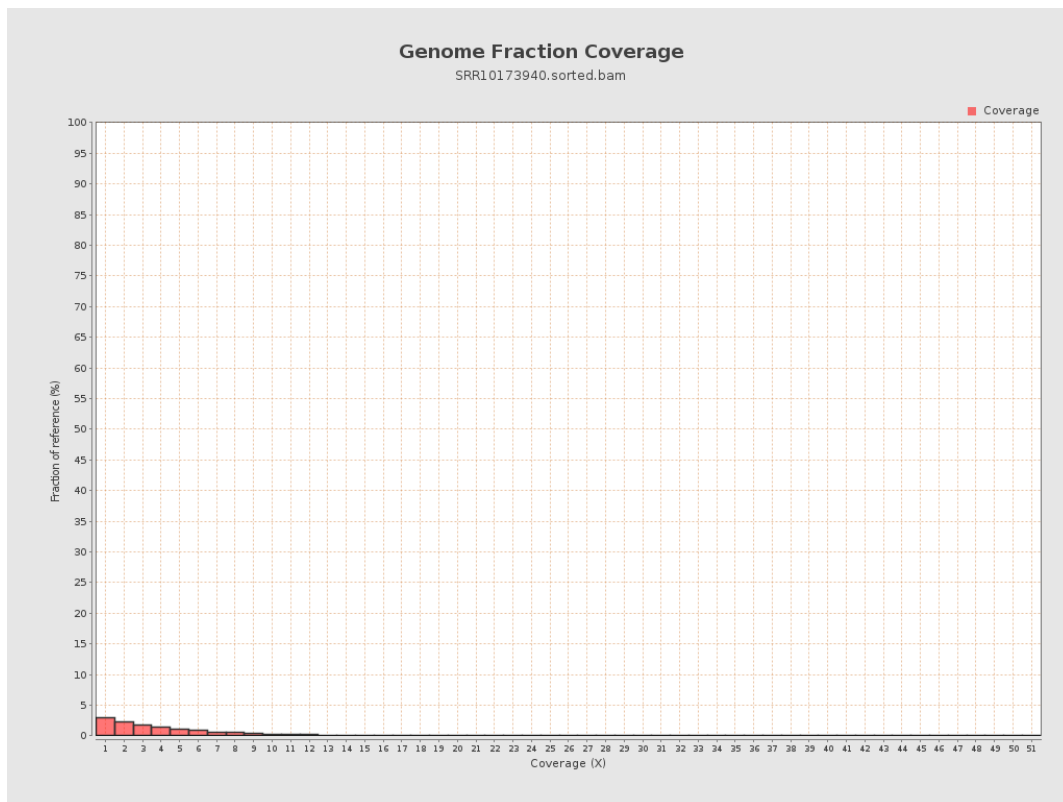
4. Results : Coverage Histogram



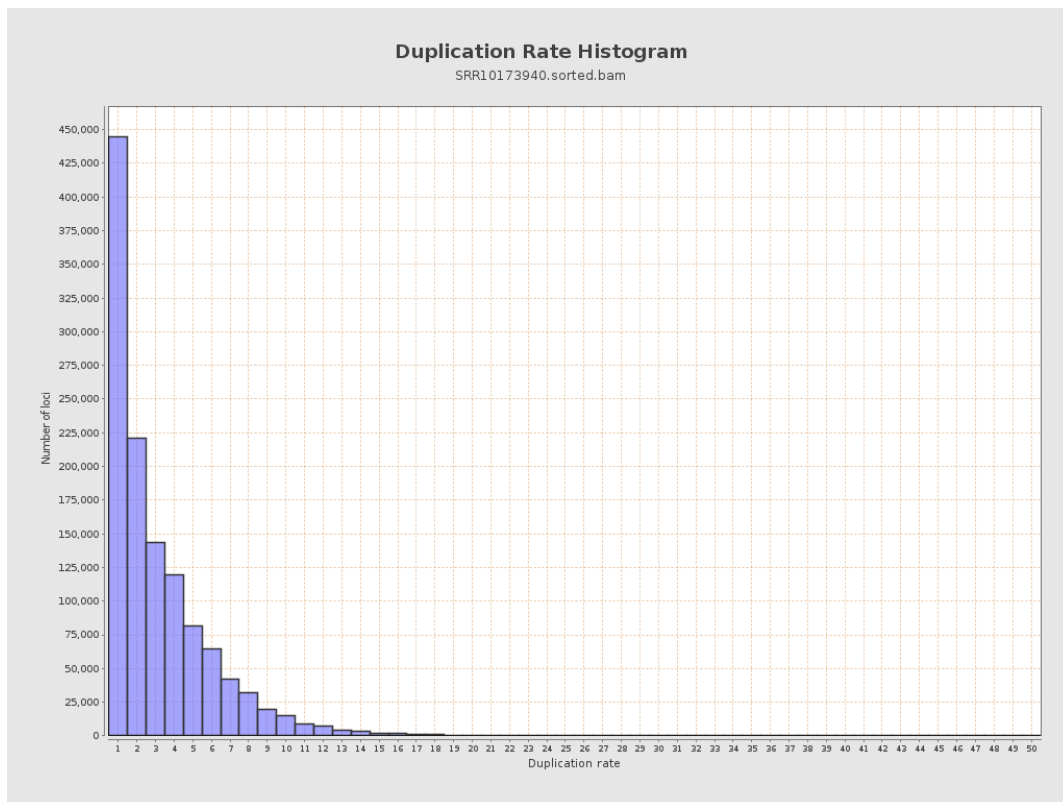
5. Results : Coverage Histogram (0-50X)



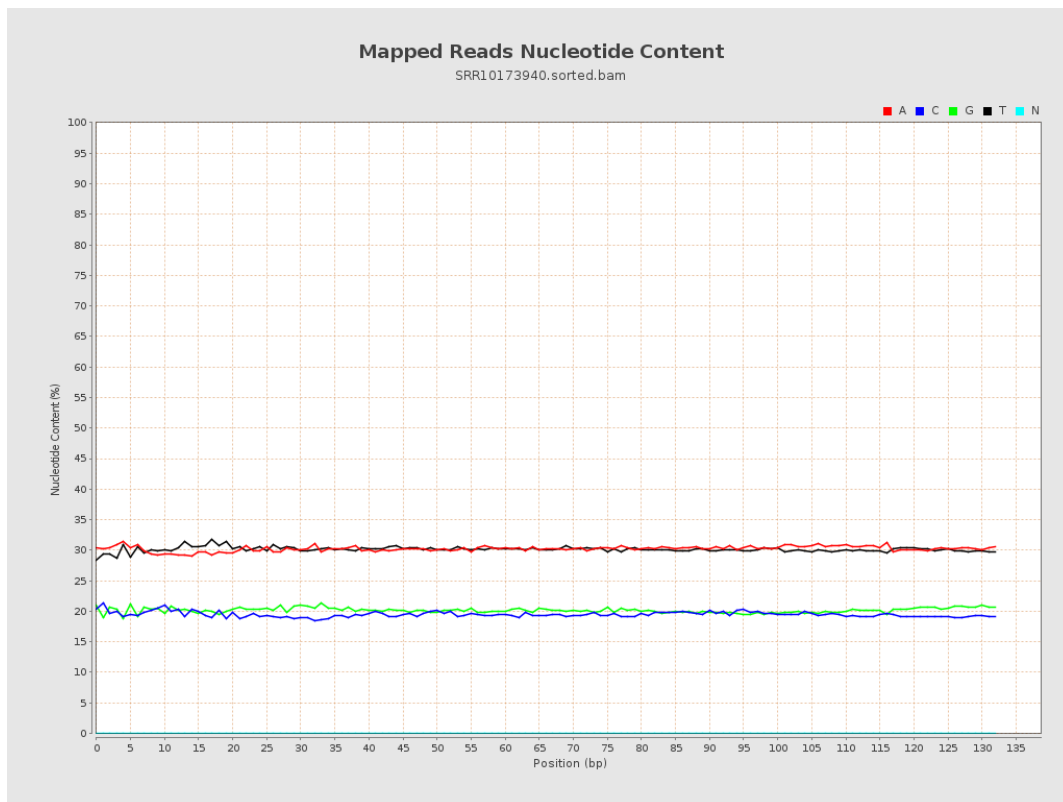
6. Results : Genome Fraction Coverage



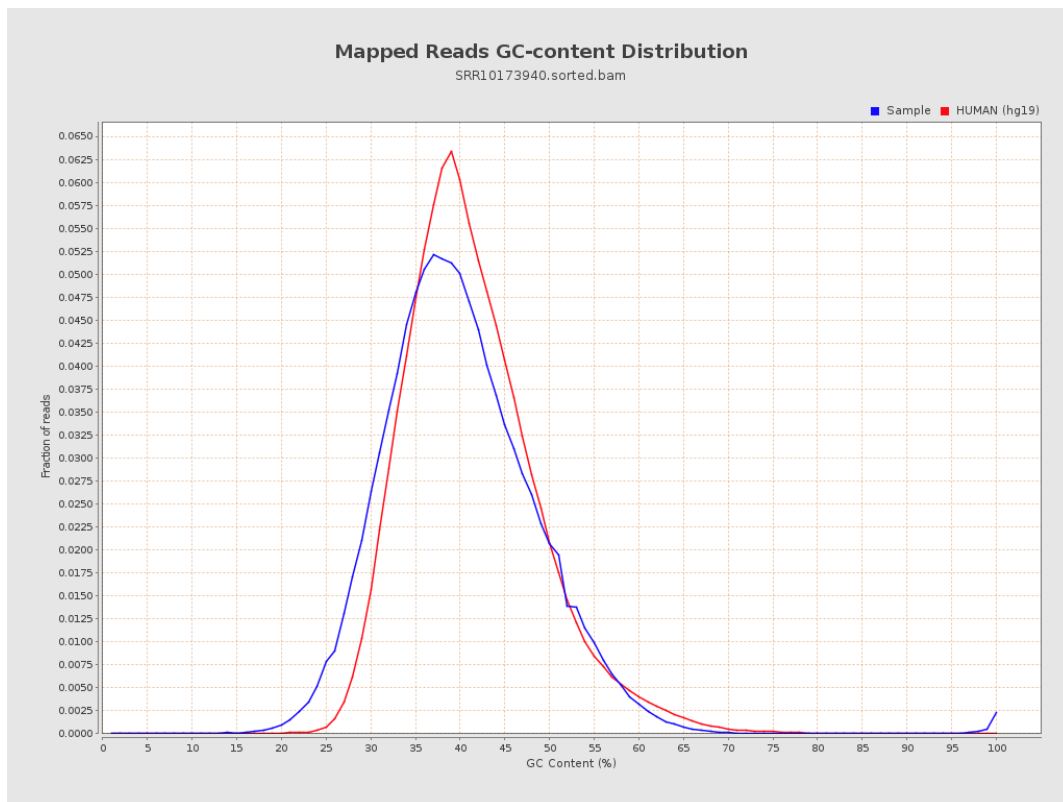
7. Results : Duplication Rate Histogram



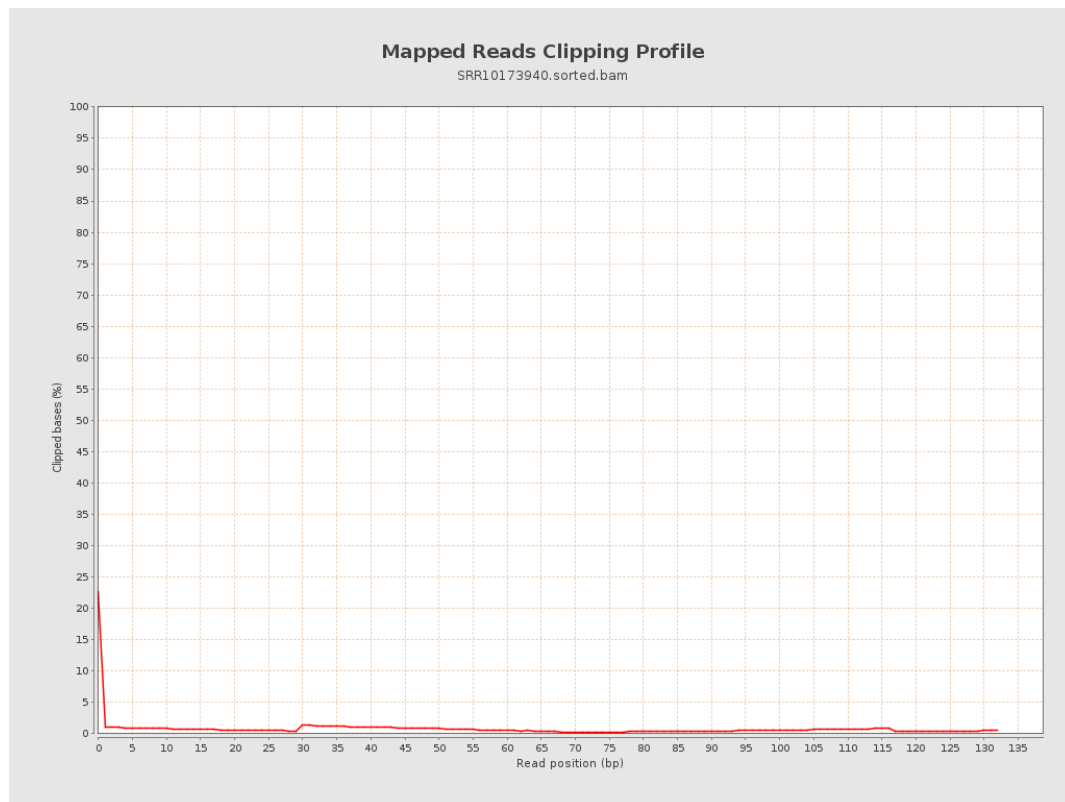
8. Results : Mapped Reads Nucleotide Content



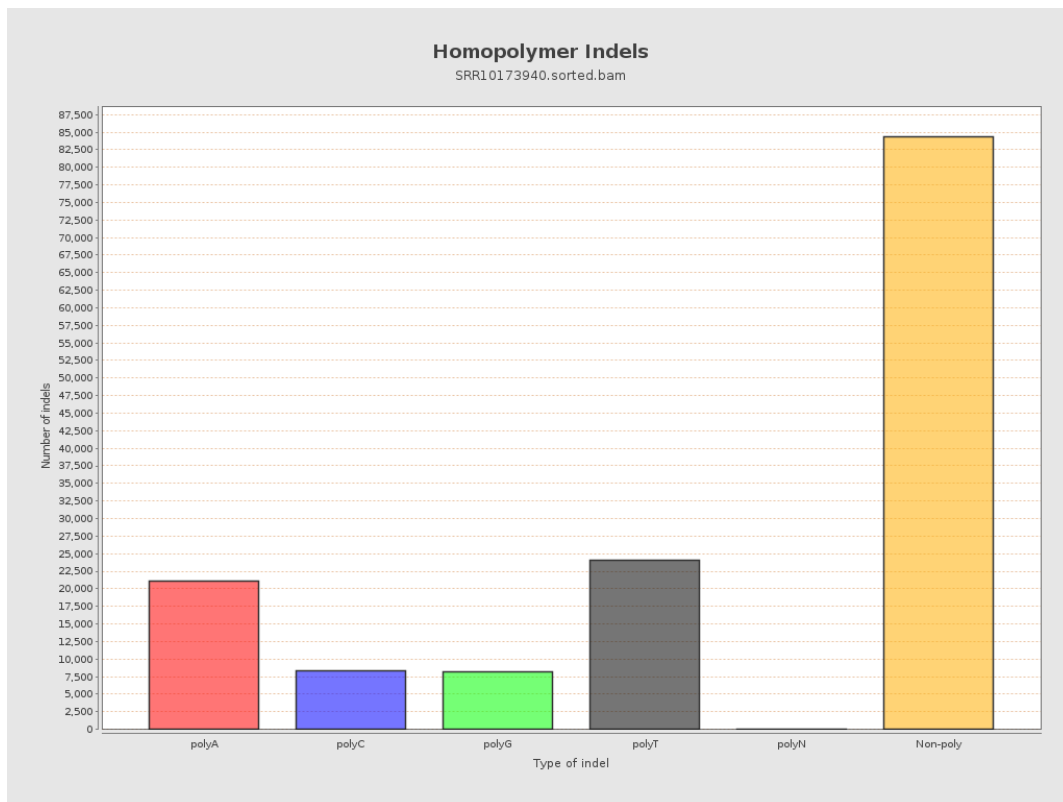
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



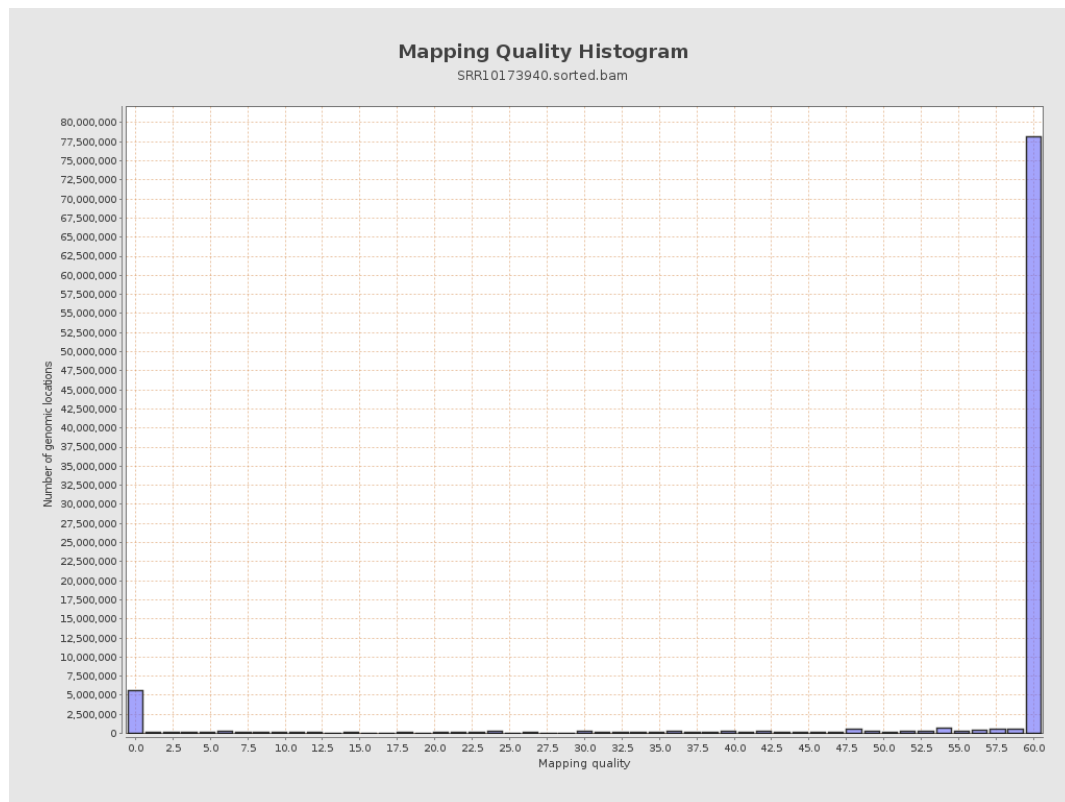
11. Results : Homopolymer Indels



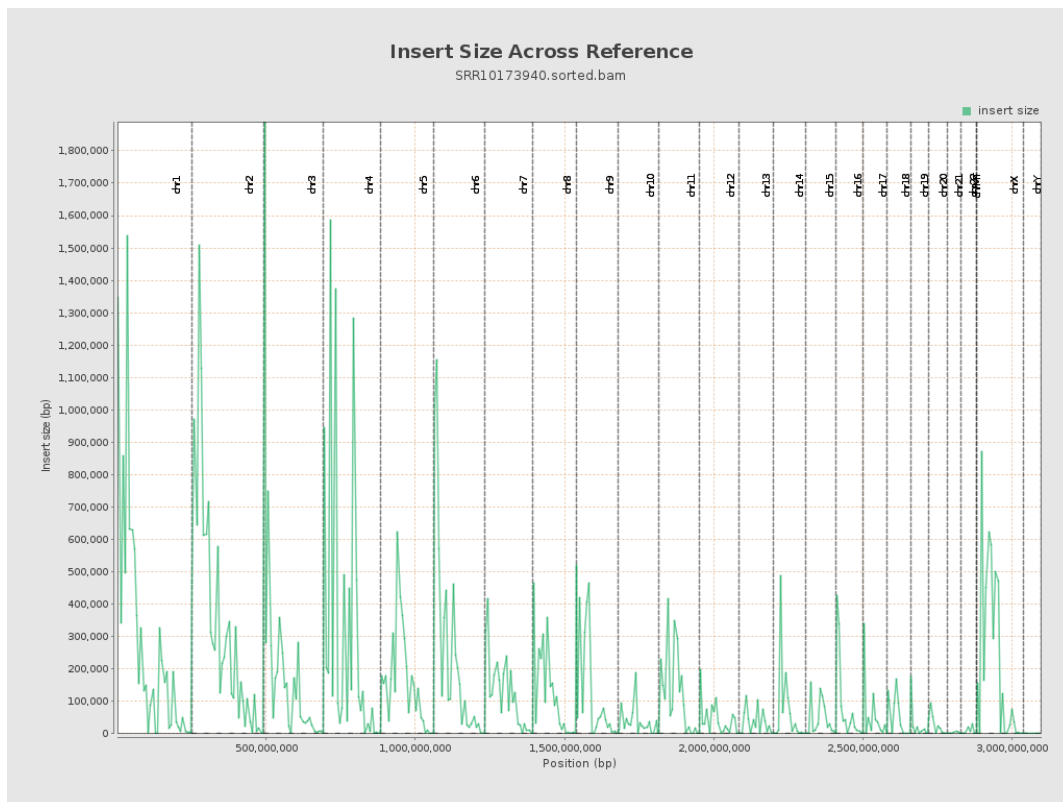
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

