

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:18:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173880.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_SRR10173880 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173880_1.fastq.gz SRR10173880_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:18:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173880.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,298,102
Mapped reads	5,161,542 / 97.42%
Unmapped reads	136,560 / 2.58%
Mapped paired reads	5,161,542 / 97.42%
Mapped reads, first in pair	2,581,188 / 48.72%
Mapped reads, second in pair	2,580,354 / 48.7%
Mapped reads, both in pair	5,068,522 / 95.67%
Mapped reads, singletons	93,020 / 1.76%
Secondary alignments	0
Supplementary alignments	533,780 / 10.07%
Read min/max/mean length	30 / 133 / 128.36
Duplicated reads (estimated)	4,065,401 / 76.73%
Duplication rate	65.16%
Clipped reads	2,114,798 / 39.92%

2.2. ACGT Content

Number/percentage of A's	184,287,087 / 30.2%
Number/percentage of C's	118,828,376 / 19.47%
Number/percentage of T's	183,975,478 / 30.15%
Number/percentage of G's	123,104,473 / 20.17%
Number/percentage of N's	6,904 / 0%

GC Percentage	39.65%
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2.3. Coverage

Mean	0.1972
Standard Deviation	2.9949

2.4. Mapping Quality

Mean Mapping Quality	52.67
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2.5. Insert size

Mean	951,286.68
Standard Deviation	8,766,194.98
P25/Median/P75	144 / 199 / 285

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	6,091,573
Insertions	62,647
Mapped reads with at least one insertion	1.18%
Deletions	142,006
Mapped reads with at least one deletion	2.68%
Homopolymer indels	42.64%

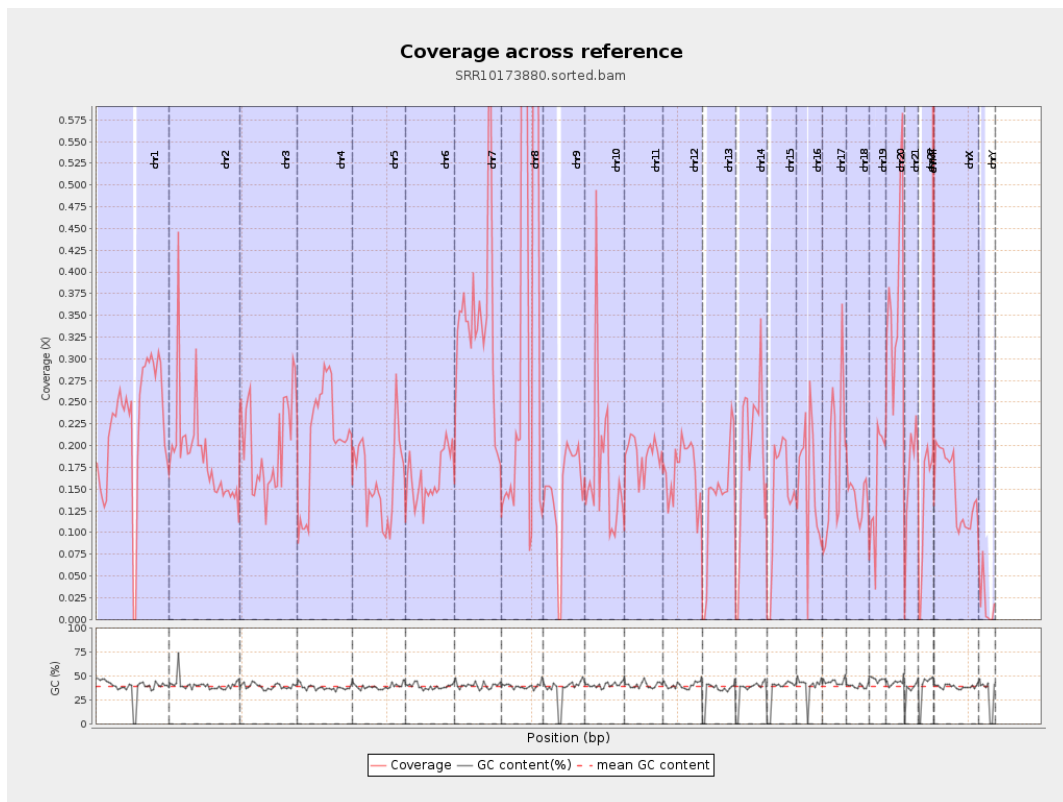
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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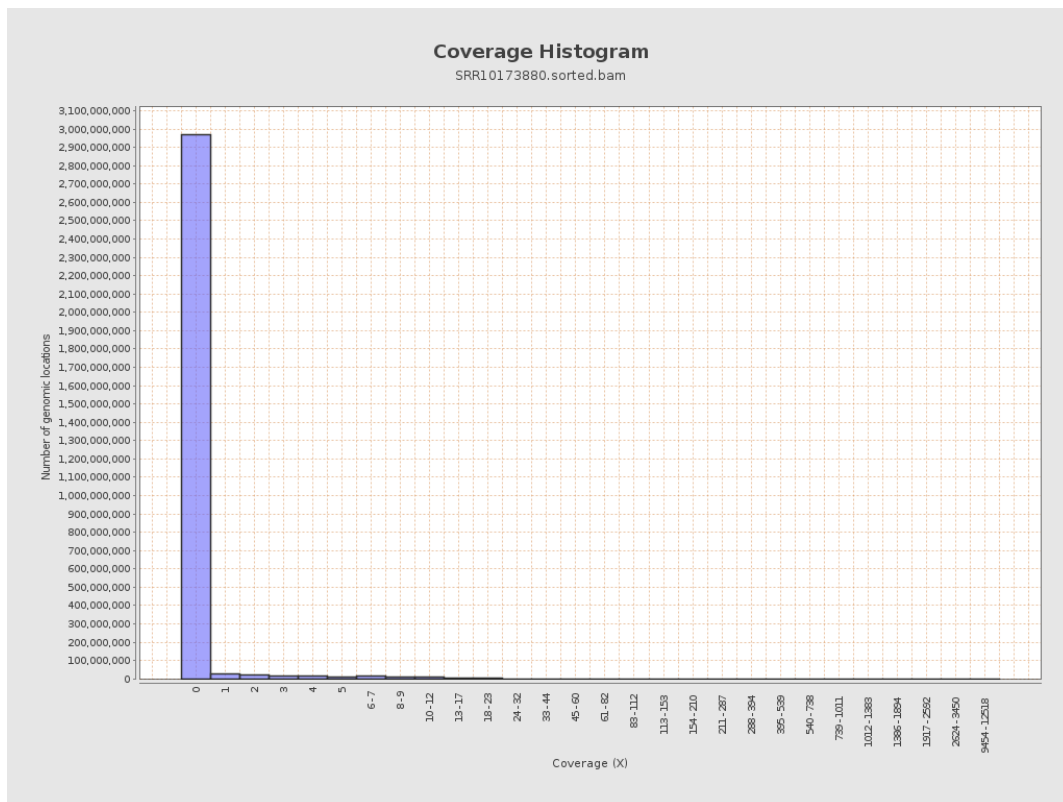
		bases	coverage	deviation
chr1	249250621	55472742	0.2226	1.7602
chr2	243199373	45484689	0.187	8.7763
chr3	198022430	39837949	0.2012	1.34
chr4	191154276	39404460	0.2061	1.6142
chr5	180915260	29404658	0.1625	1.1831
chr6	171115067	27786843	0.1624	1.2313
chr7	159138663	54552337	0.3428	3.283
chr8	146364022	62053416	0.424	2.2932
chr9	141213431	21041699	0.149	1.4222
chr10	135534747	23184205	0.1711	3.6651
chr11	135006516	25605359	0.1897	1.3002
chr12	133851895	22901535	0.1711	1.2187
chr13	115169878	16015487	0.1391	1.0968
chr14	107349540	20353056	0.1896	1.2869
chr15	102531392	14459704	0.141	1.0823
chr16	90354753	14005285	0.155	1.4697
chr17	81195210	14943902	0.184	1.3344
chr18	78077248	11123694	0.1425	1.7563
chr19	59128983	9287901	0.1571	1.4188
chr20	63025520	23459714	0.3722	1.8202
chr21	48129895	8075353	0.1678	1.2781
chr22	51304566	6615454	0.1289	1.0076
chrMT	16571	1106999	66.8034	60.9333
chrX	155270560	23264889	0.1498	1.1523

chrY	59373566	1113991	0.0188	0.8525
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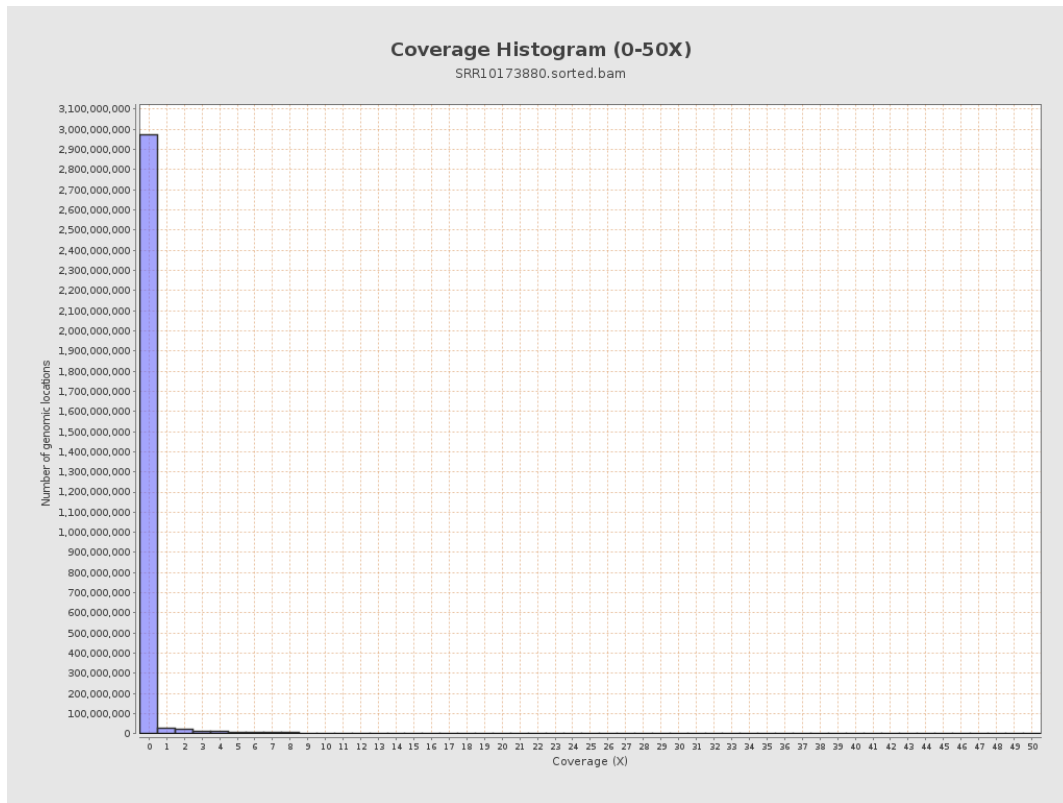
3. Results : Coverage across reference



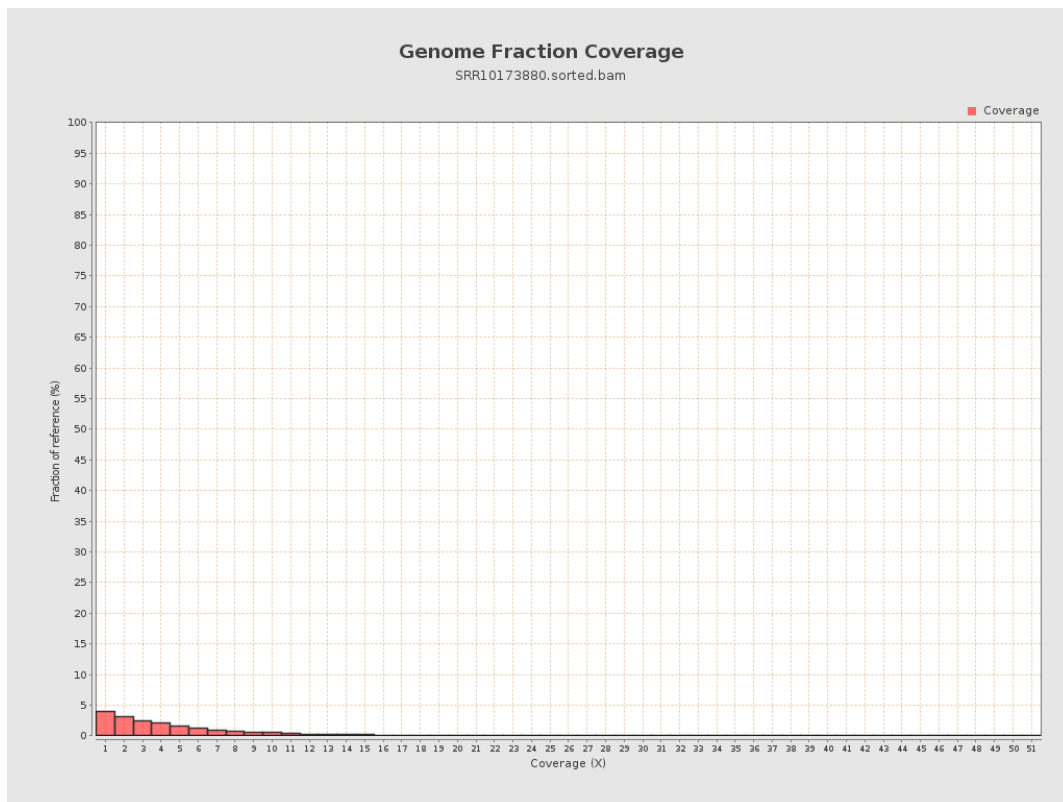
4. Results : Coverage Histogram



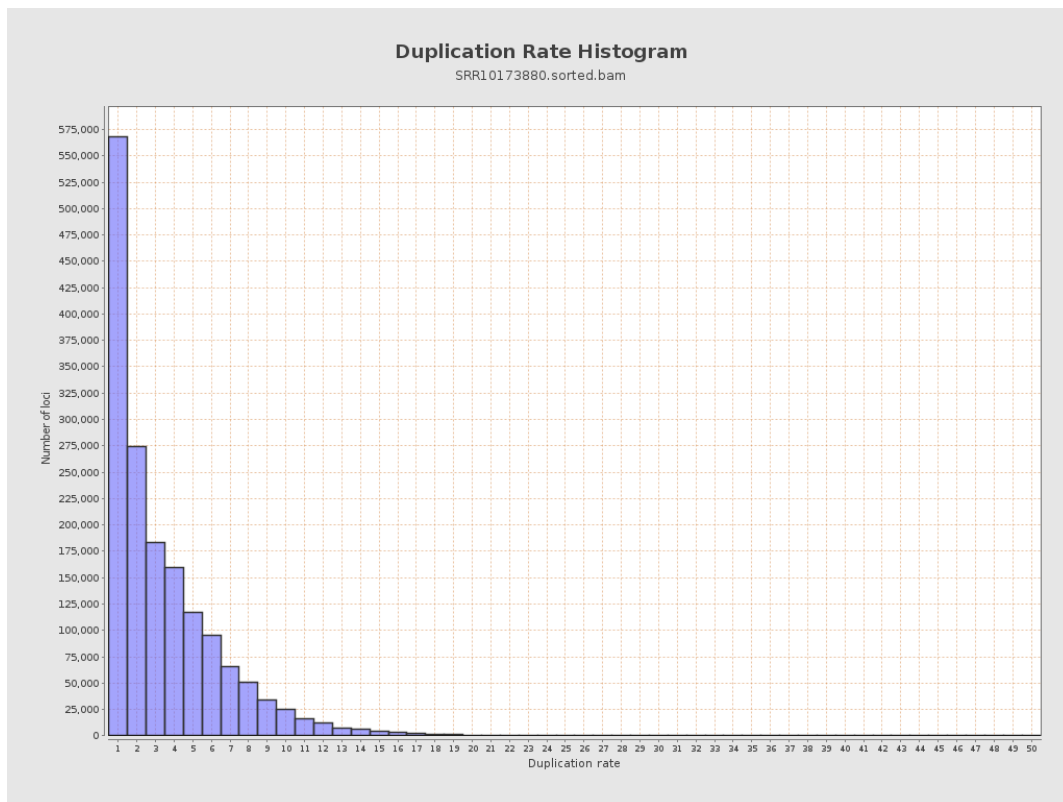
5. Results : Coverage Histogram (0-50X)



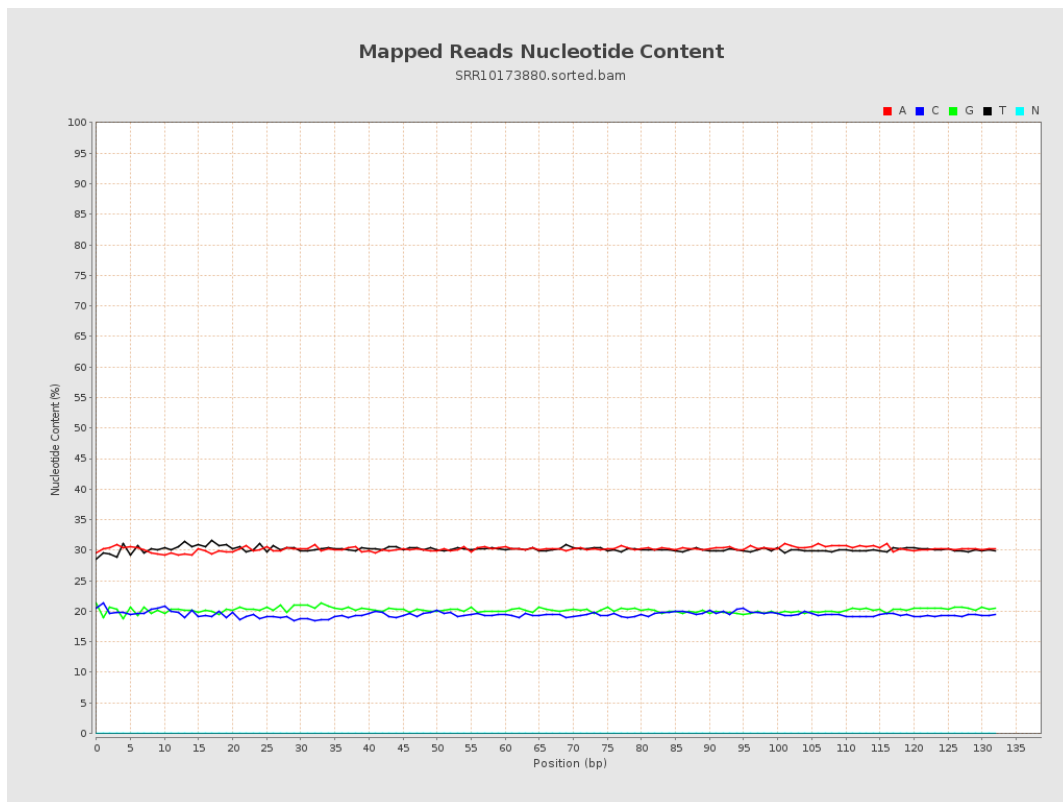
6. Results : Genome Fraction Coverage



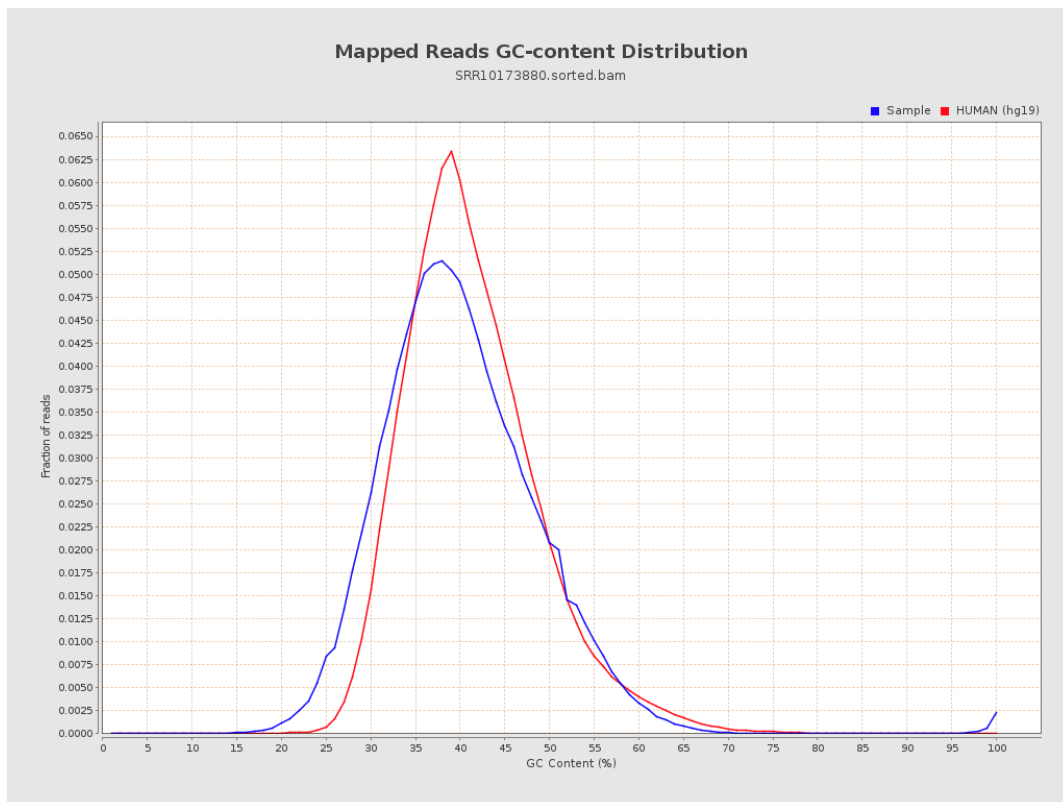
7. Results : Duplication Rate Histogram



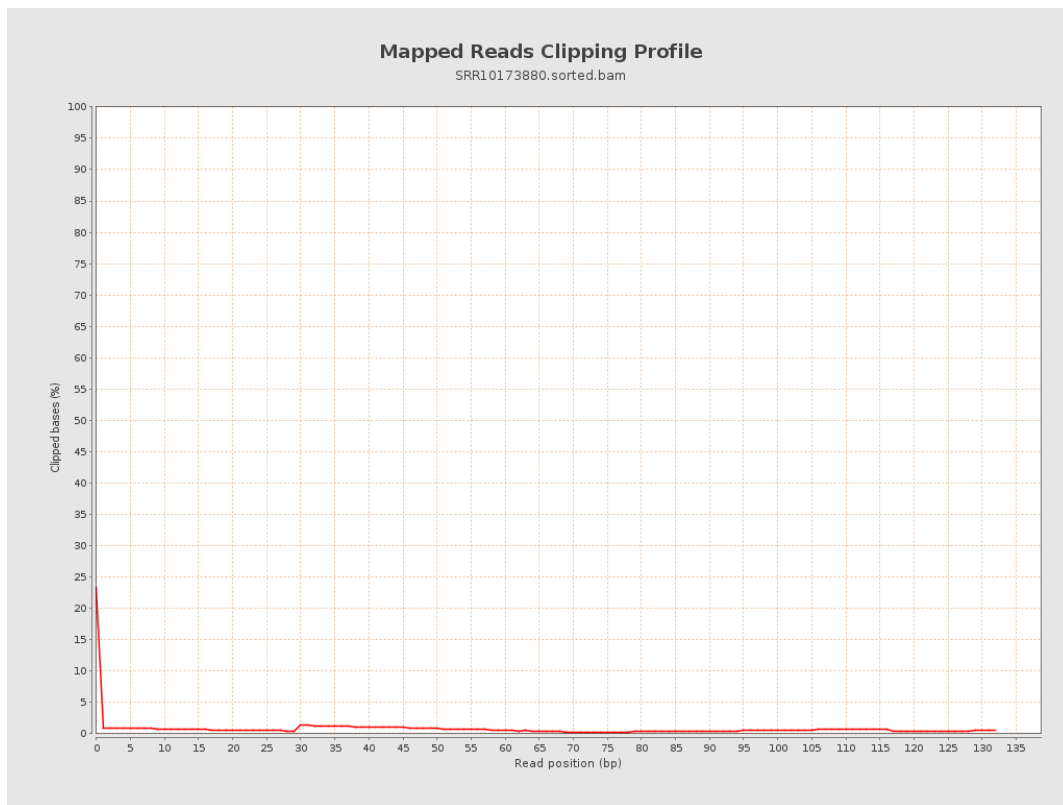
8. Results : Mapped Reads Nucleotide Content



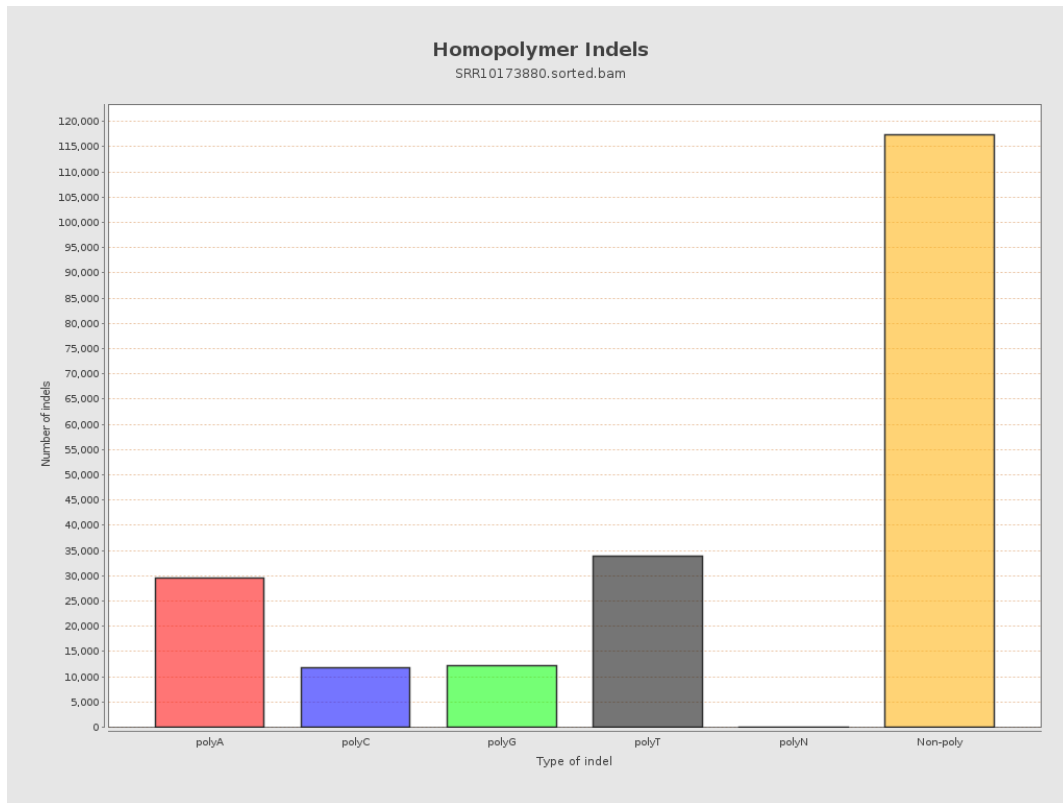
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



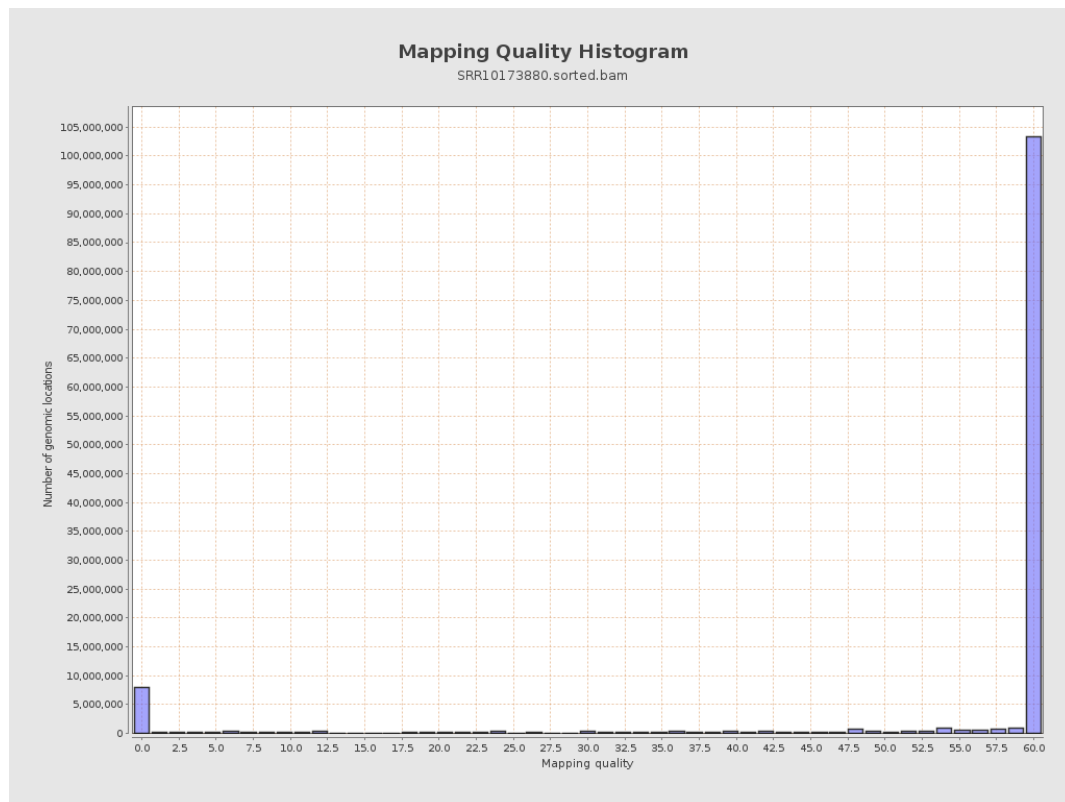
11. Results : Homopolymer Indels



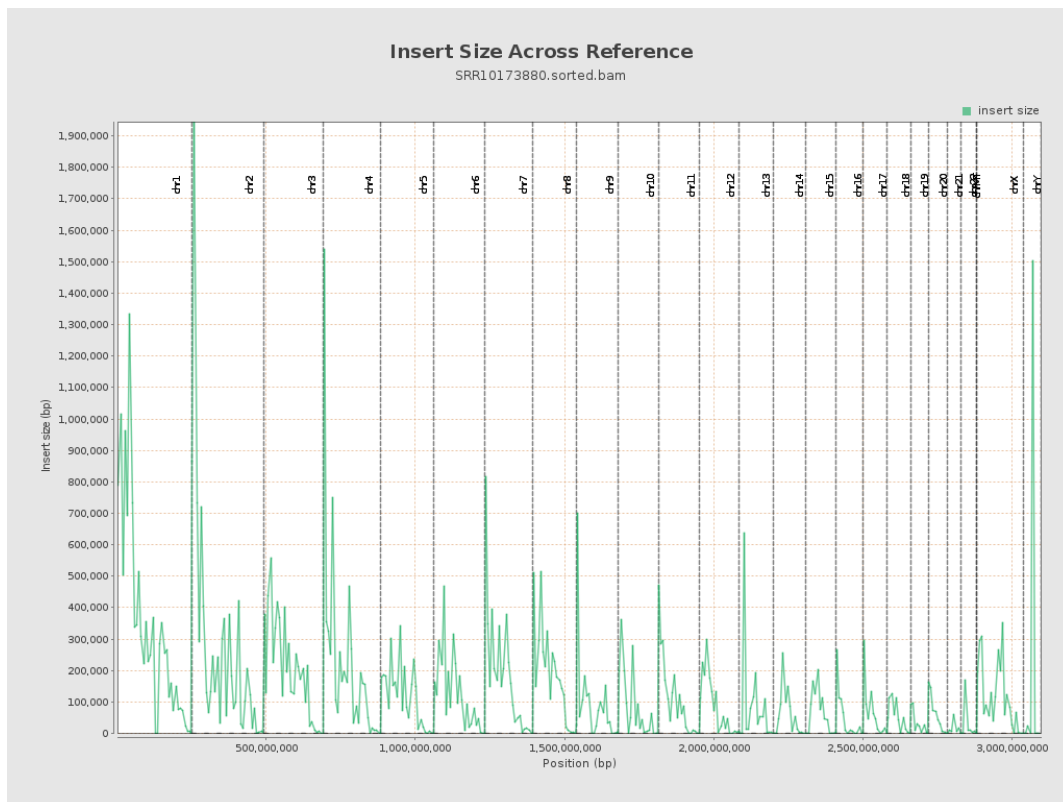
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

