

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:52:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173886.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_SRR10173886 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173886_1.fastq.gz SRR10173886_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:52:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173886.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,761,680
Mapped reads	4,630,995 / 97.26%
Unmapped reads	130,685 / 2.74%
Mapped paired reads	4,630,995 / 97.26%
Mapped reads, first in pair	2,319,281 / 48.71%
Mapped reads, second in pair	2,311,714 / 48.55%
Mapped reads, both in pair	4,543,690 / 95.42%
Mapped reads, singletons	87,305 / 1.83%
Secondary alignments	0
Supplementary alignments	464,835 / 9.76%
Read min/max/mean length	30 / 133 / 128.18
Duplicated reads (estimated)	3,502,968 / 73.57%
Duplication rate	63.89%
Clipped reads	2,104,715 / 44.2%

2.2. ACGT Content

Number/percentage of A's	164,492,357 / 30.3%
Number/percentage of C's	105,039,511 / 19.35%
Number/percentage of T's	164,208,404 / 30.25%
Number/percentage of G's	109,089,620 / 20.1%
Number/percentage of N's	5,877 / 0%

GC Percentage	39.45%
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2.3. Coverage

Mean	0.1755
Standard Deviation	2.6534

2.4. Mapping Quality

Mean Mapping Quality	52.69
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2.5. Insert size

Mean	935,632.52
Standard Deviation	8,533,611.66
P25/Median/P75	142 / 197 / 283

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	5,515,035
Insertions	56,741
Mapped reads with at least one insertion	1.18%
Deletions	125,824
Mapped reads with at least one deletion	2.64%
Homopolymer indels	43.05%

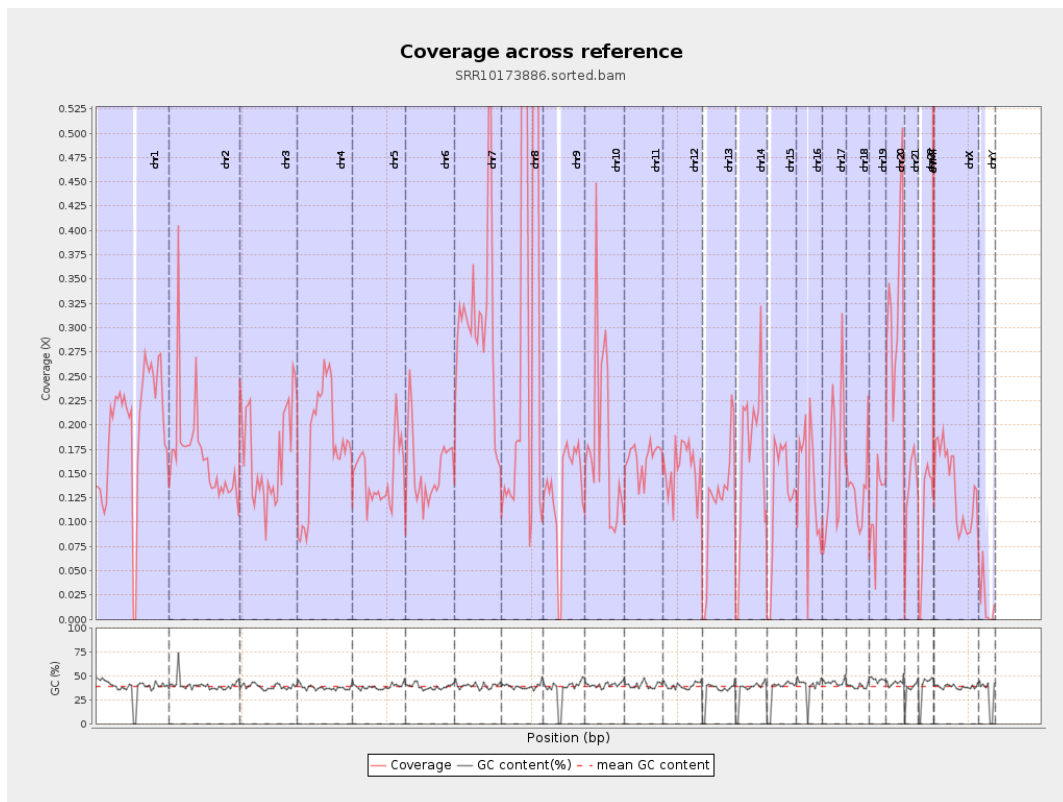
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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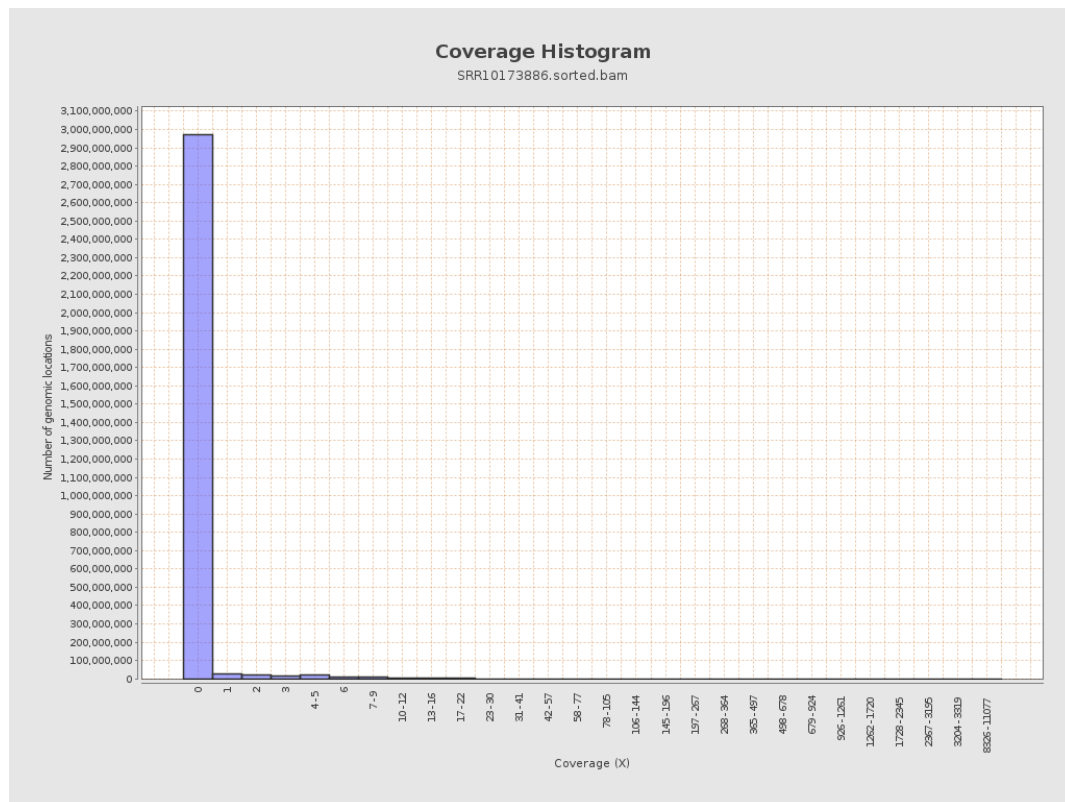
		bases	coverage	deviation
chr1	249250621	48799181	0.1958	1.5317
chr2	243199373	40793362	0.1677	7.7843
chr3	198022430	34040992	0.1719	1.1541
chr4	191154276	34230751	0.1791	1.4102
chr5	180915260	26833144	0.1483	1.0647
chr6	171115067	26269264	0.1535	1.1257
chr7	159138663	48729125	0.3062	3.0034
chr8	146364022	53579341	0.3661	2.0745
chr9	141213431	18983620	0.1344	1.3105
chr10	135534747	24741437	0.1825	3.0466
chr11	135006516	22270470	0.165	1.1739
chr12	133851895	20867756	0.1559	1.1066
chr13	115169878	14121567	0.1226	0.9795
chr14	107349540	18079478	0.1684	1.1539
chr15	102531392	13065185	0.1274	0.9797
chr16	90354753	12265843	0.1358	1.2605
chr17	81195210	13097000	0.1613	1.2012
chr18	78077248	10263168	0.1314	1.6163
chr19	59128983	6817487	0.1153	1.1822
chr20	63025520	20469478	0.3248	1.6028
chr21	48129895	6388234	0.1327	1.0848
chr22	51304566	5340797	0.1041	0.8582
chrMT	16571	1164253	70.2585	54.9567
chrX	155270560	20920821	0.1347	1.018

chrY	59373566	1013763	0.0171	0.716
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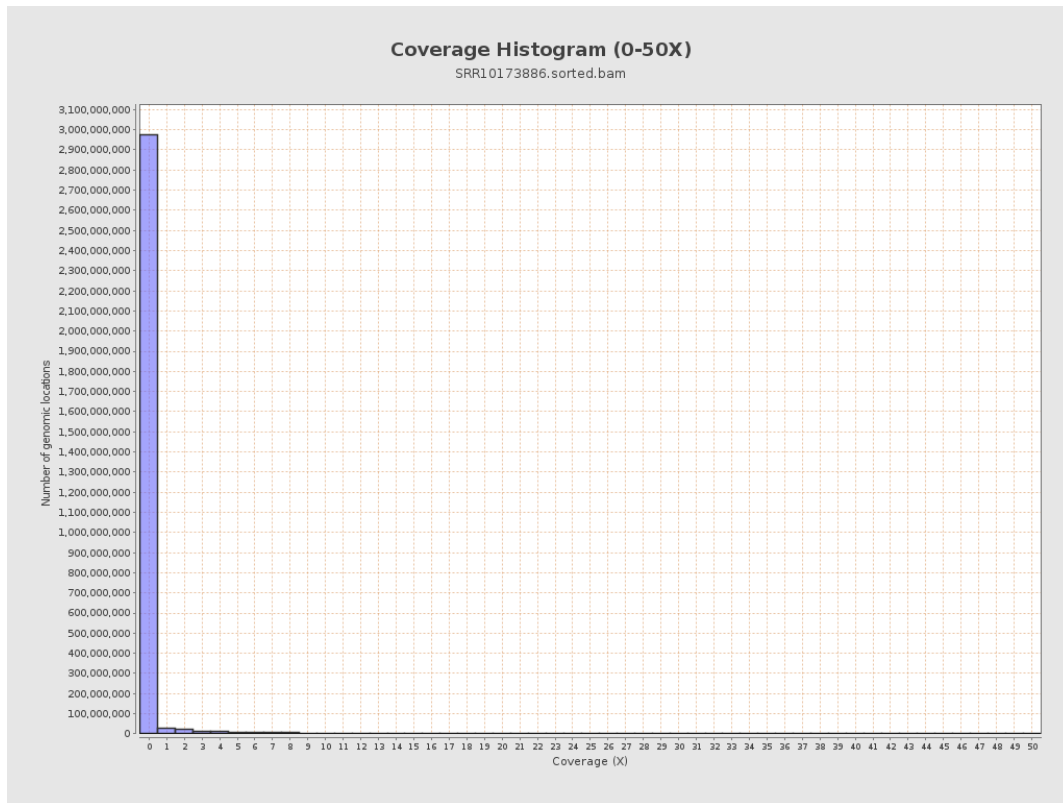
3. Results : Coverage across reference



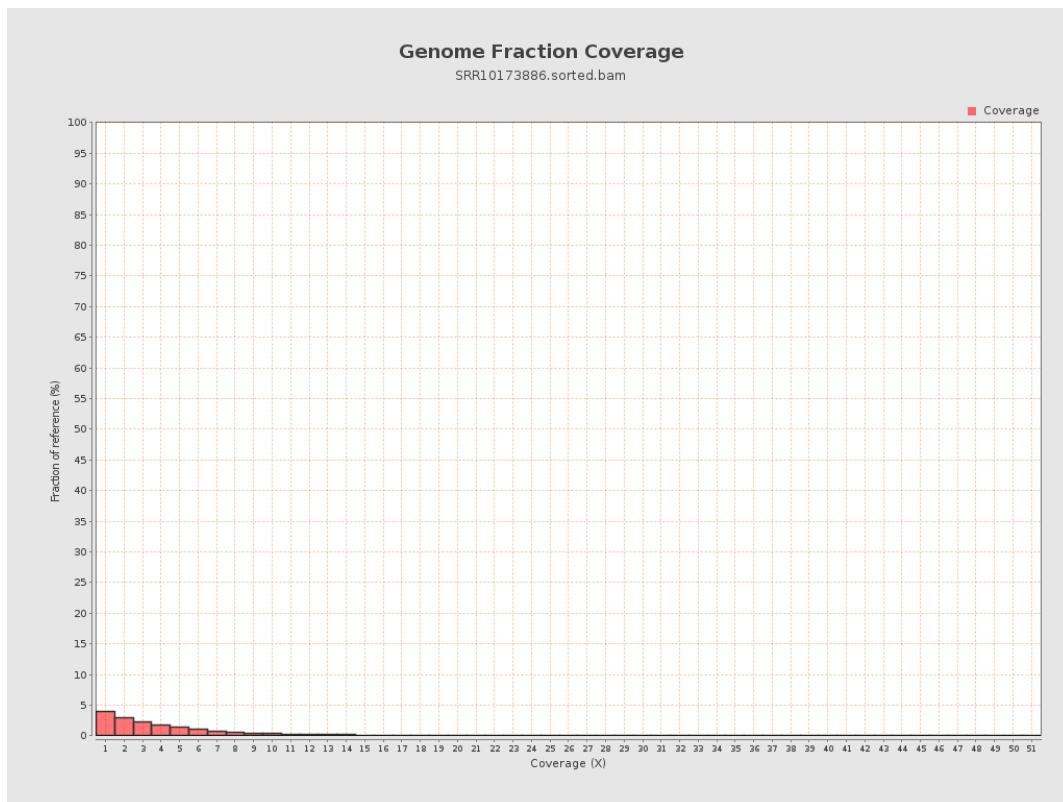
4. Results : Coverage Histogram



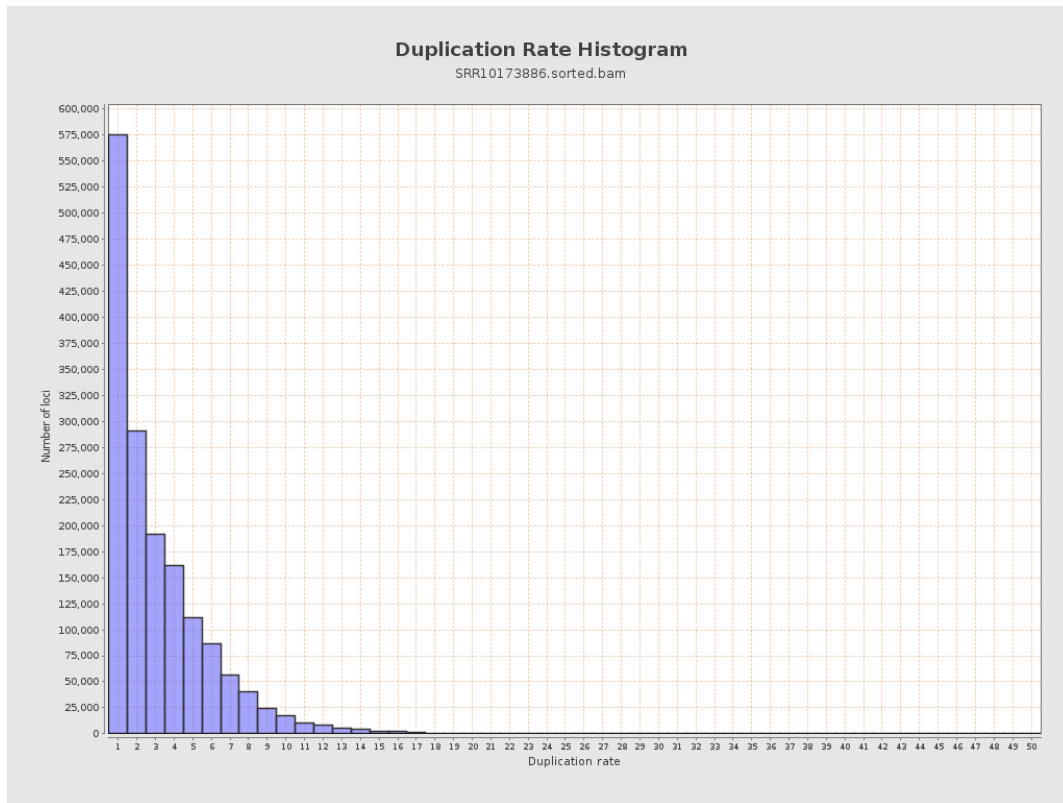
5. Results : Coverage Histogram (0-50X)



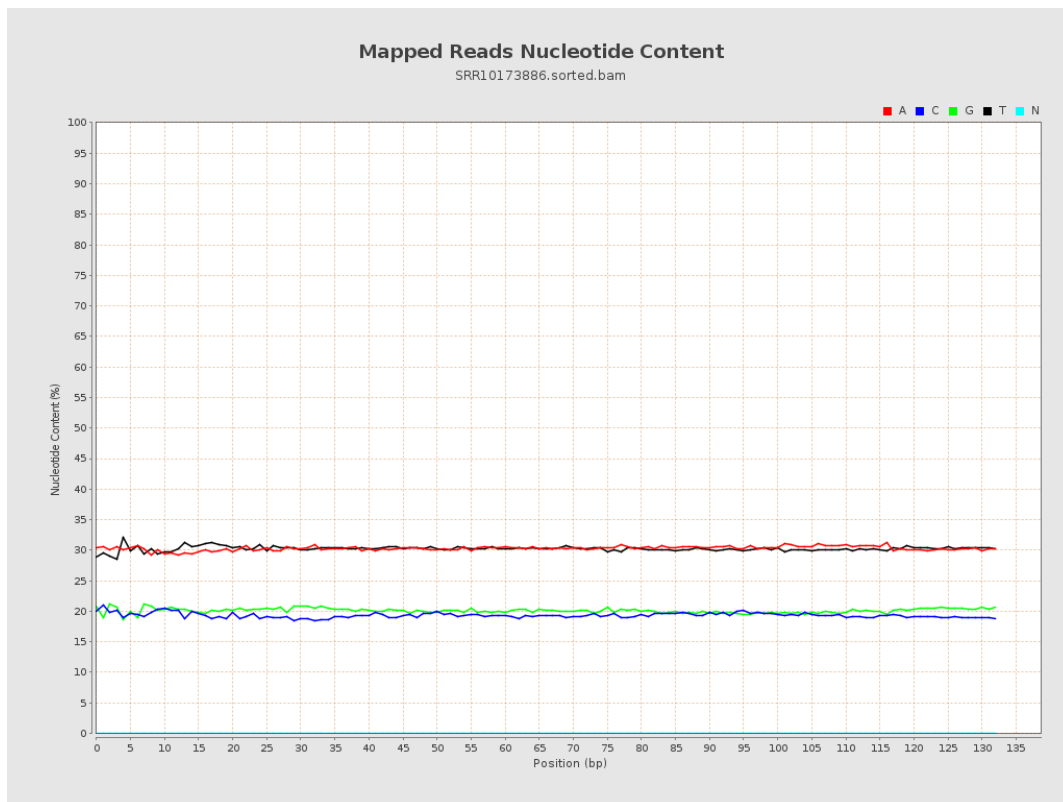
6. Results : Genome Fraction Coverage



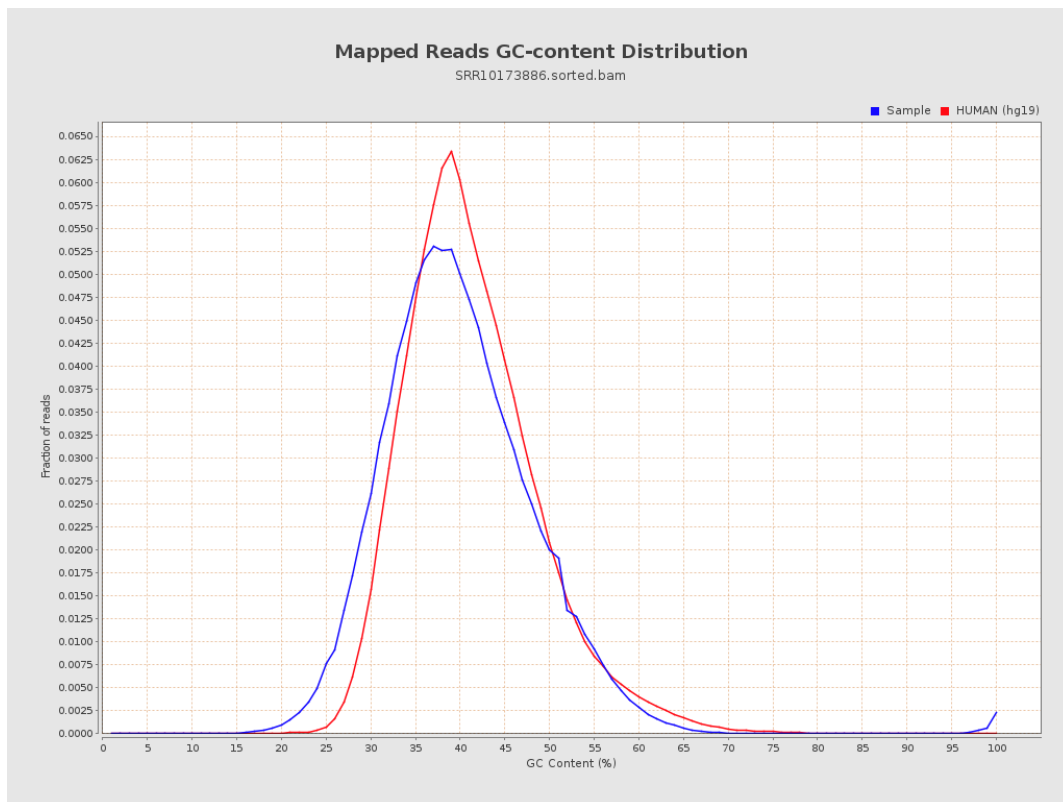
7. Results : Duplication Rate Histogram



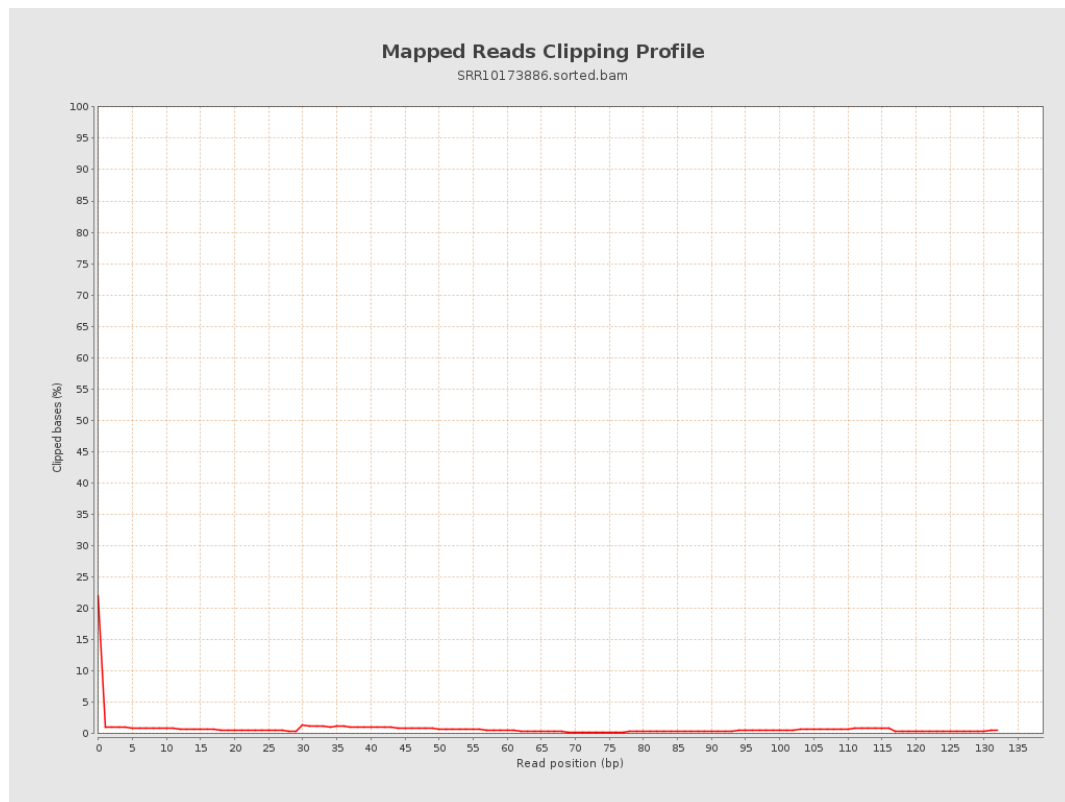
8. Results : Mapped Reads Nucleotide Content



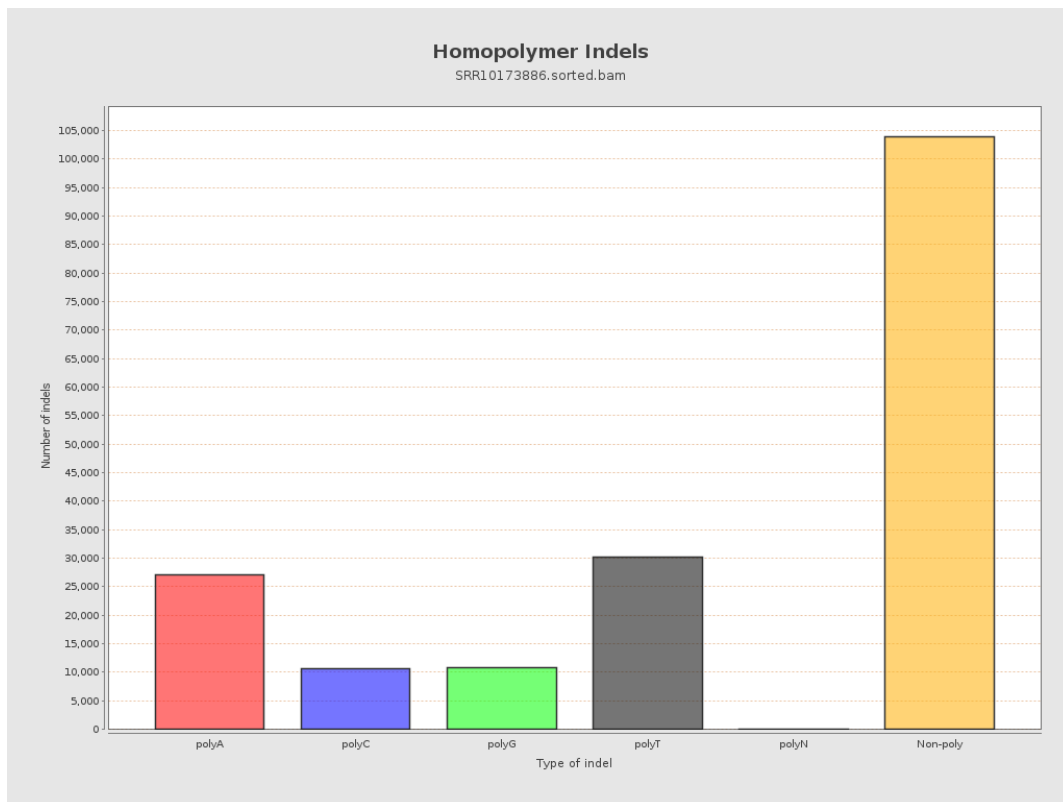
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



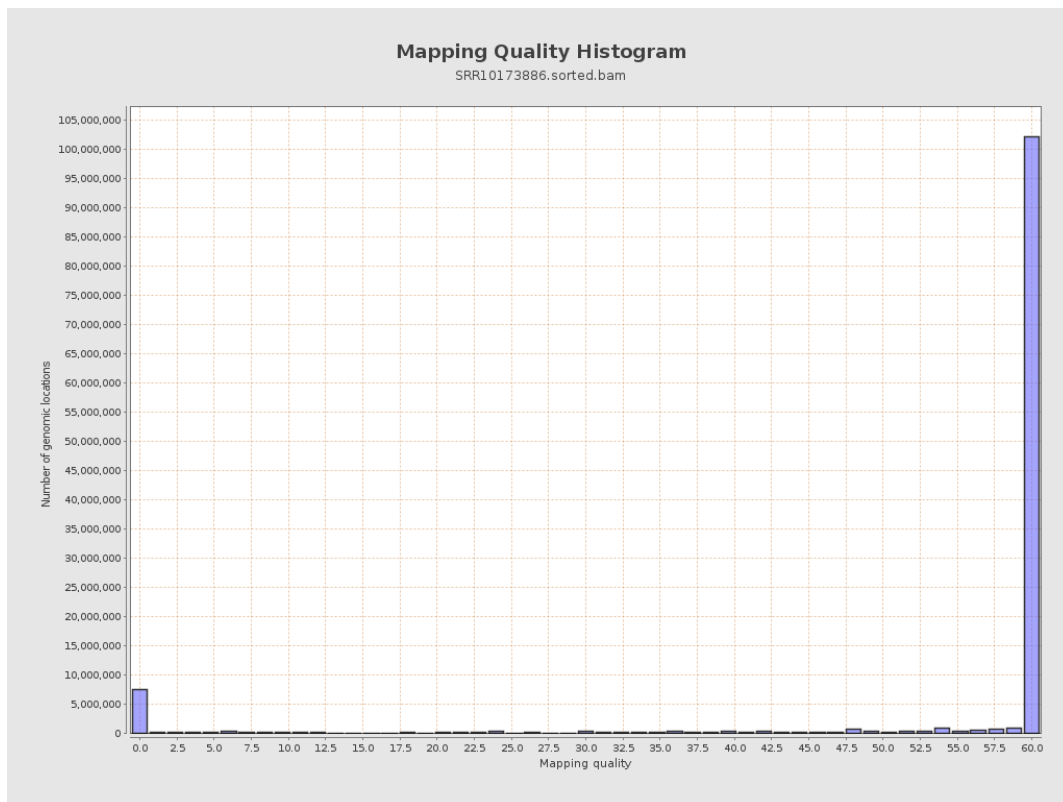
11. Results : Homopolymer Indels



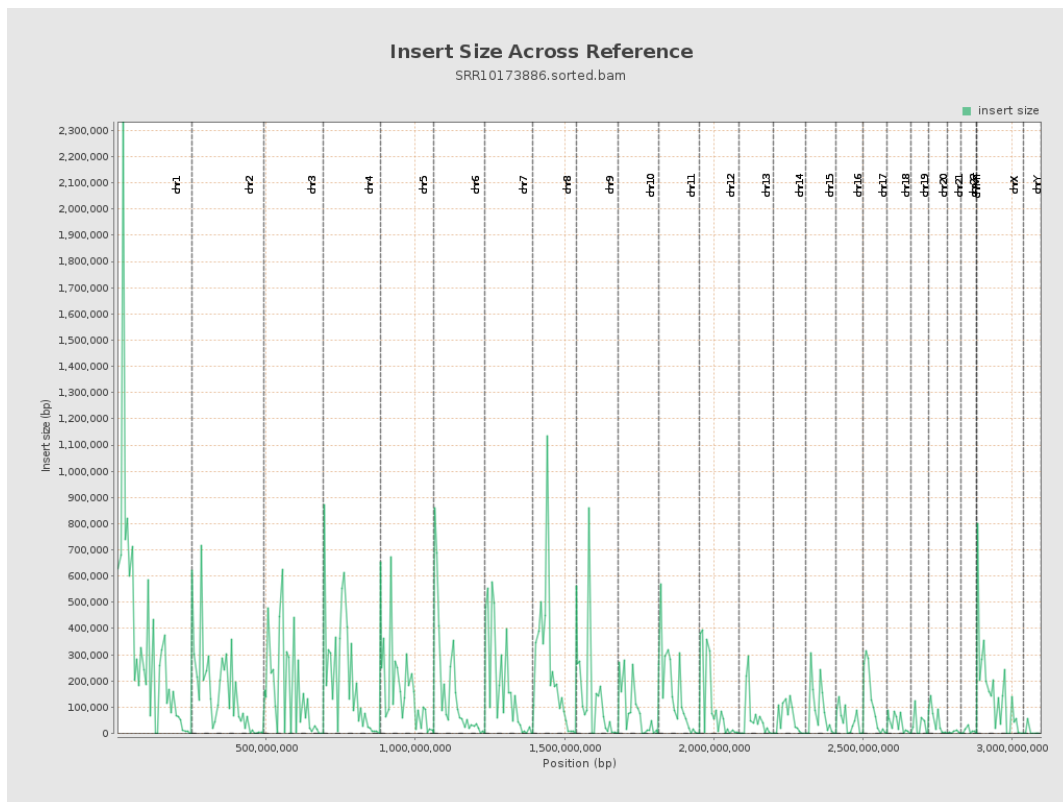
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

