

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:18:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173869.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_SRR10173869 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173869_1.fastq.gz SRR10173869_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:18:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173869.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,529,804
Mapped reads	3,442,828 / 97.54%
Unmapped reads	86,976 / 2.46%
Mapped paired reads	3,442,828 / 97.54%
Mapped reads, first in pair	1,724,461 / 48.85%
Mapped reads, second in pair	1,718,367 / 48.68%
Mapped reads, both in pair	3,385,942 / 95.92%
Mapped reads, singletons	56,886 / 1.61%
Secondary alignments	0
Supplementary alignments	343,564 / 9.73%
Read min/max/mean length	30 / 133 / 127.73
Duplicated reads (estimated)	2,642,661 / 74.87%
Duplication rate	63.69%
Clipped reads	1,406,580 / 39.85%

2.2. ACGT Content

Number/percentage of A's	121,172,865 / 29.91%
Number/percentage of C's	80,387,594 / 19.84%
Number/percentage of T's	120,634,275 / 29.78%
Number/percentage of G's	82,922,268 / 20.47%
Number/percentage of N's	4,832 / 0%

GC Percentage	40.31%
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2.3. Coverage

Mean	0.1309
Standard Deviation	1.988

2.4. Mapping Quality

Mean Mapping Quality	52.71
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2.5. Insert size

Mean	844,566.74
Standard Deviation	8,826,288.75
P25/Median/P75	139 / 195 / 279

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	4,151,040
Insertions	41,938
Mapped reads with at least one insertion	1.18%
Deletions	94,382
Mapped reads with at least one deletion	2.67%
Homopolymer indels	43.28%

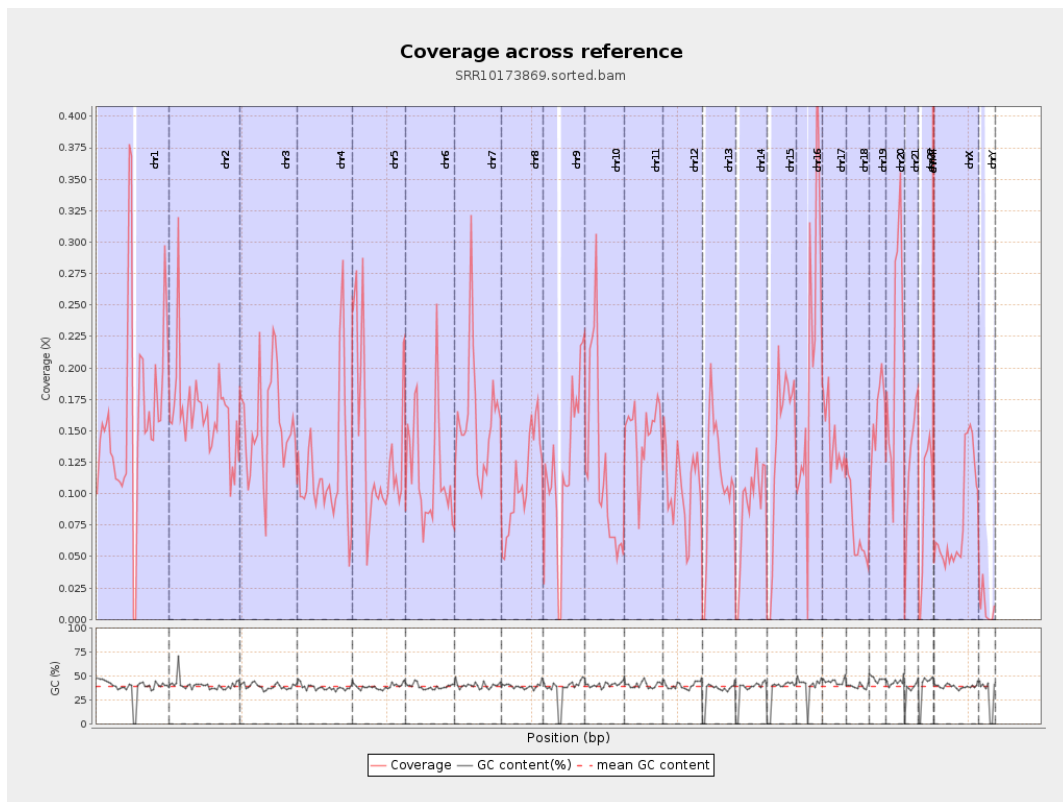
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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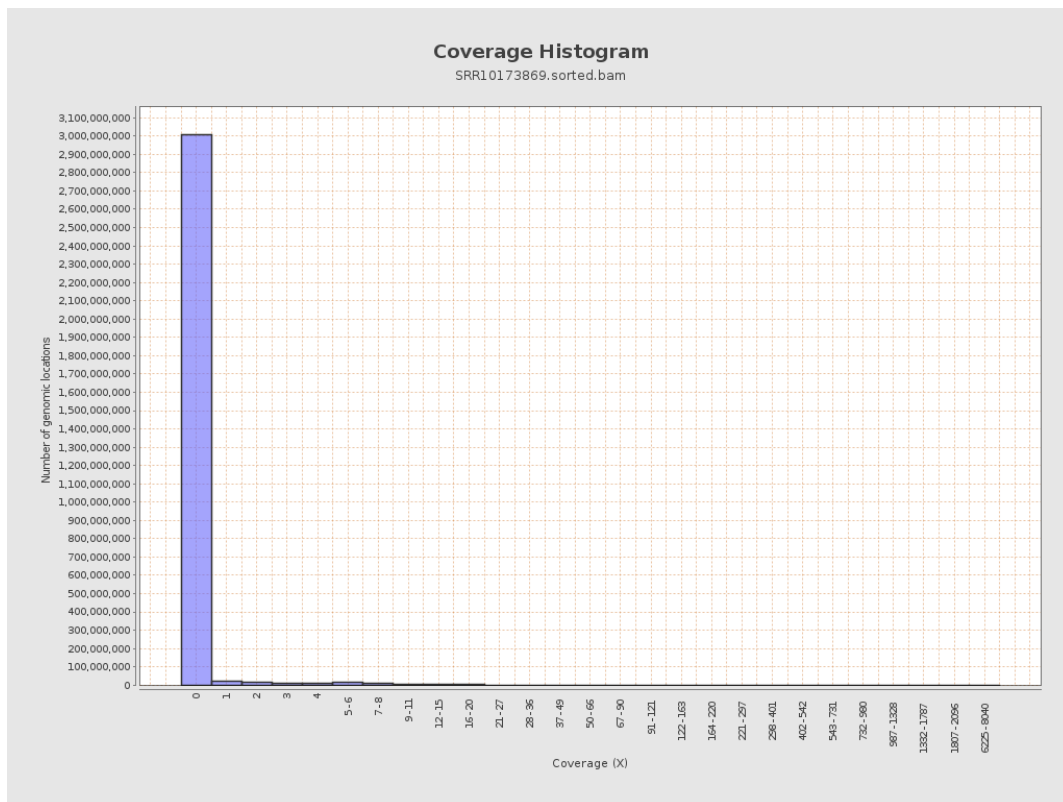
		bases	coverage	deviation
chr1	249250621	39802414	0.1597	1.5183
chr2	243199373	39907685	0.1641	5.6894
chr3	198022430	30668781	0.1549	1.15
chr4	191154276	22121565	0.1157	1.1122
chr5	180915260	24963644	0.138	1.0851
chr6	171115067	20052003	0.1172	1.0082
chr7	159138663	25202207	0.1584	1.6128
chr8	146364022	16005664	0.1094	1.0597
chr9	141213431	17523140	0.1241	1.1273
chr10	135534747	16185706	0.1194	1.8359
chr11	135006516	20043095	0.1485	1.1262
chr12	133851895	14086953	0.1052	0.9371
chr13	115169878	12500193	0.1085	0.9706
chr14	107349540	9474117	0.0883	0.8581
chr15	102531392	13996692	0.1365	1.0569
chr16	90354753	18221337	0.2017	1.6672
chr17	81195210	11452076	0.141	1.0941
chr18	78077248	5505228	0.0705	1.244
chr19	59128983	9370587	0.1585	1.4807
chr20	63025520	13491564	0.2141	1.3363
chr21	48129895	6006711	0.1248	1.0589
chr22	51304566	4622606	0.0901	0.8153
chrMT	16571	1368358	82.5755	65.7554
chrX	155270560	12256816	0.0789	0.7977

chrY	59373566	528723	0.0089	0.4238
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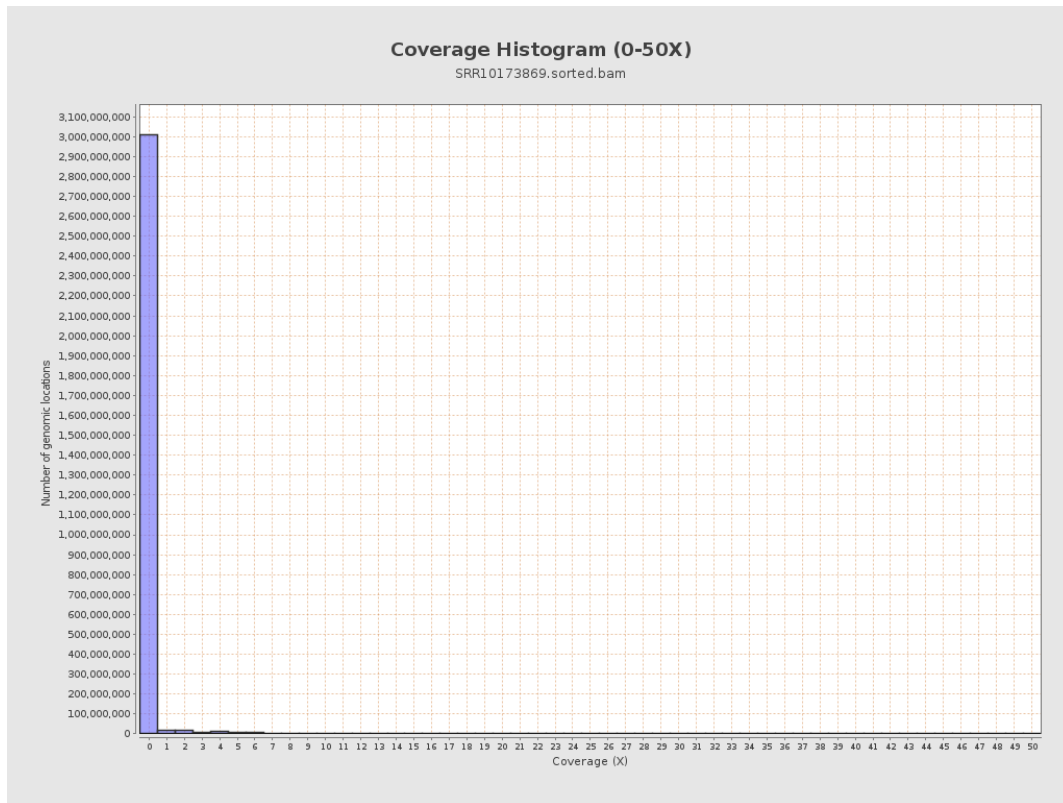
3. Results : Coverage across reference



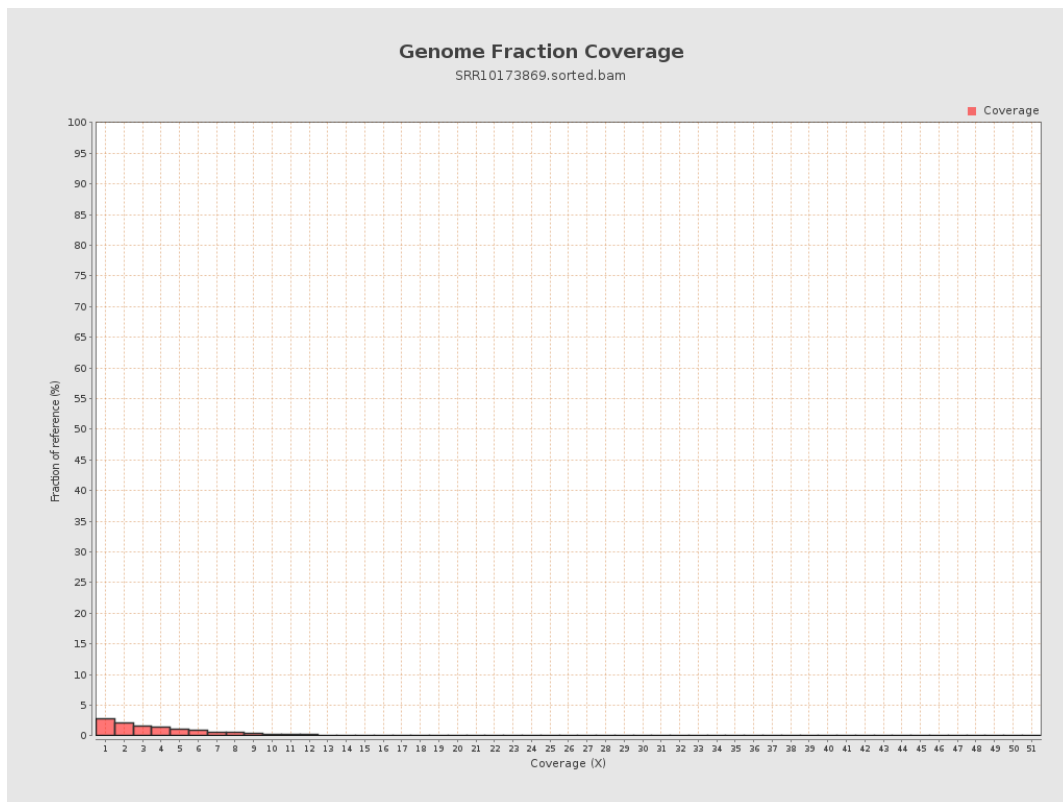
4. Results : Coverage Histogram



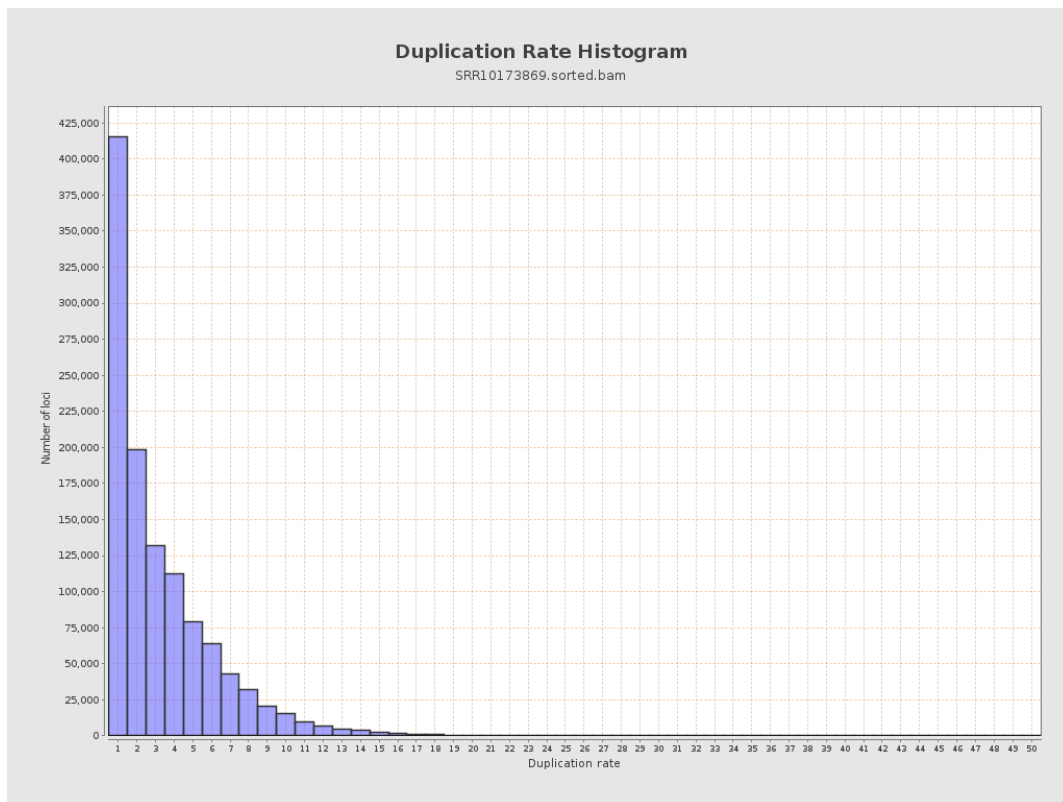
5. Results : Coverage Histogram (0-50X)



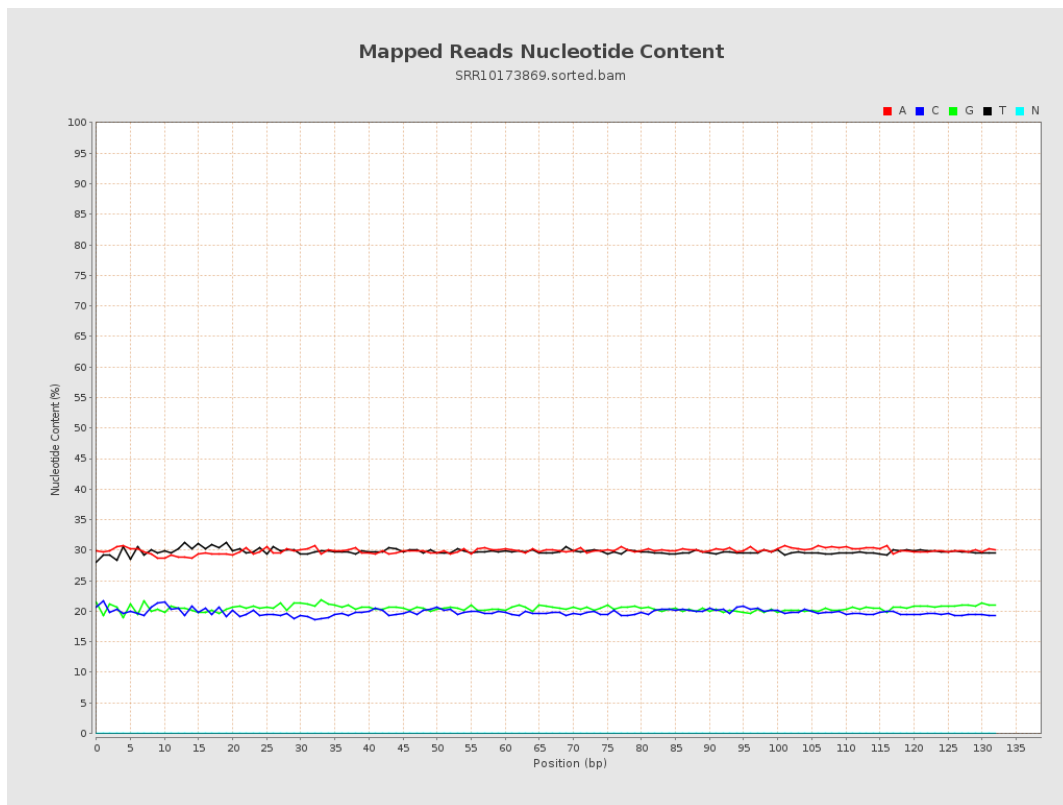
6. Results : Genome Fraction Coverage



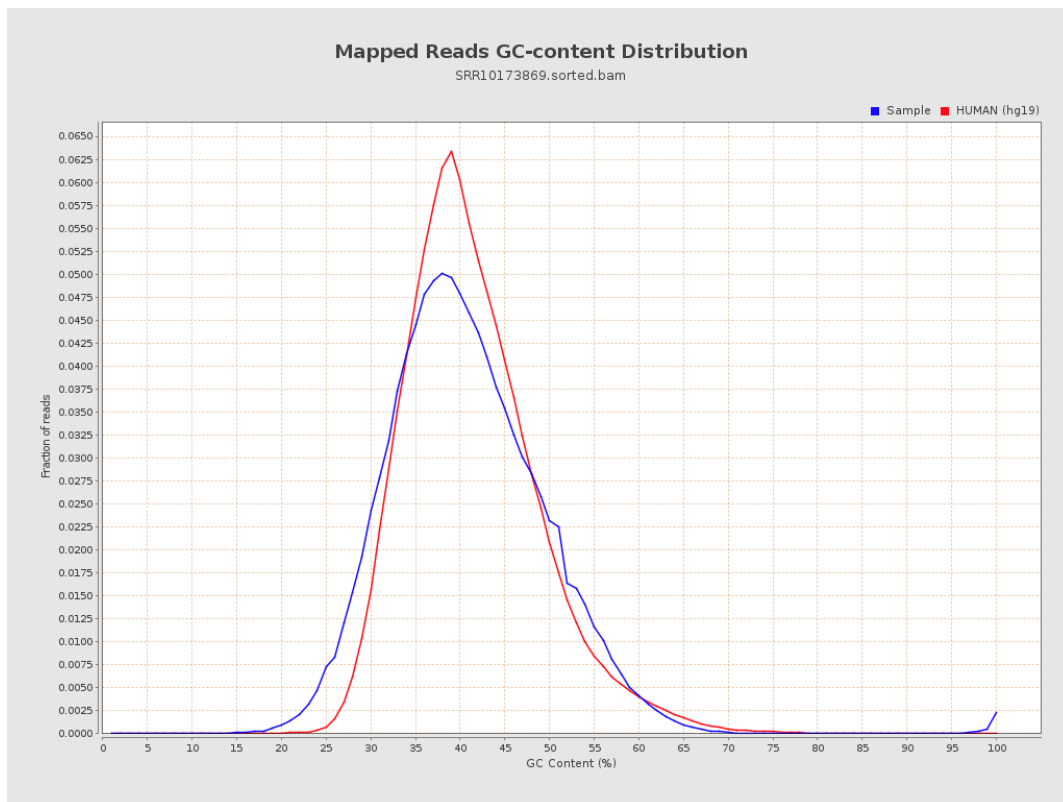
7. Results : Duplication Rate Histogram



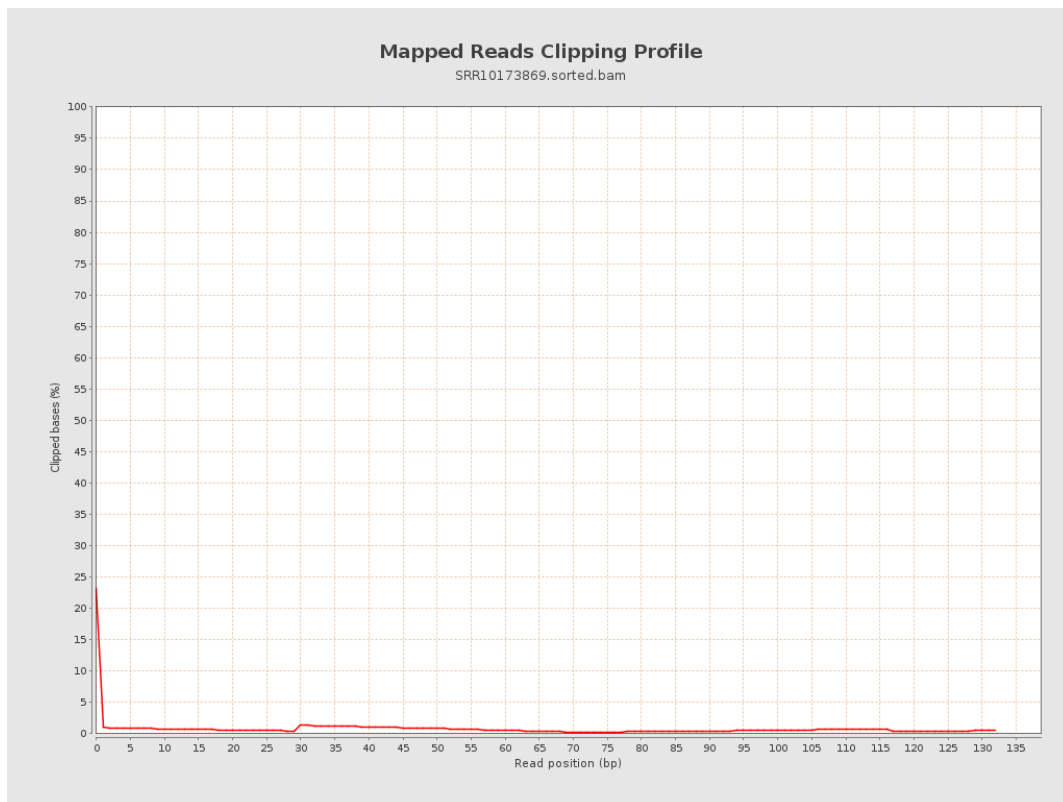
8. Results : Mapped Reads Nucleotide Content



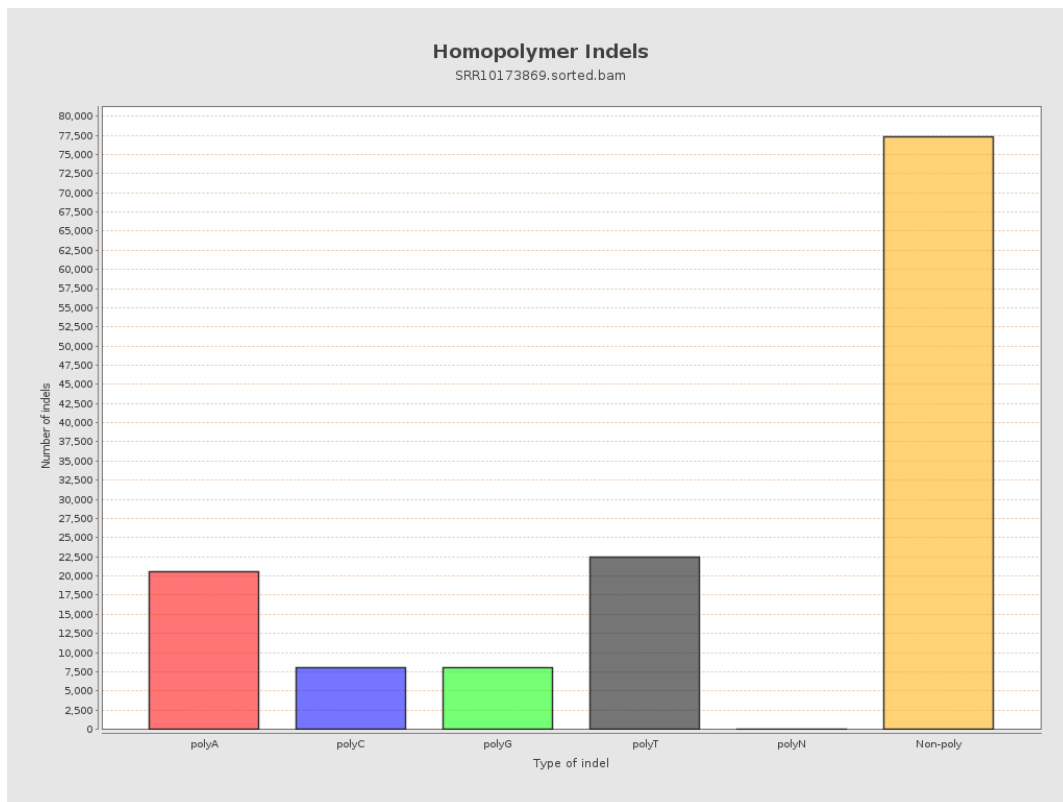
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



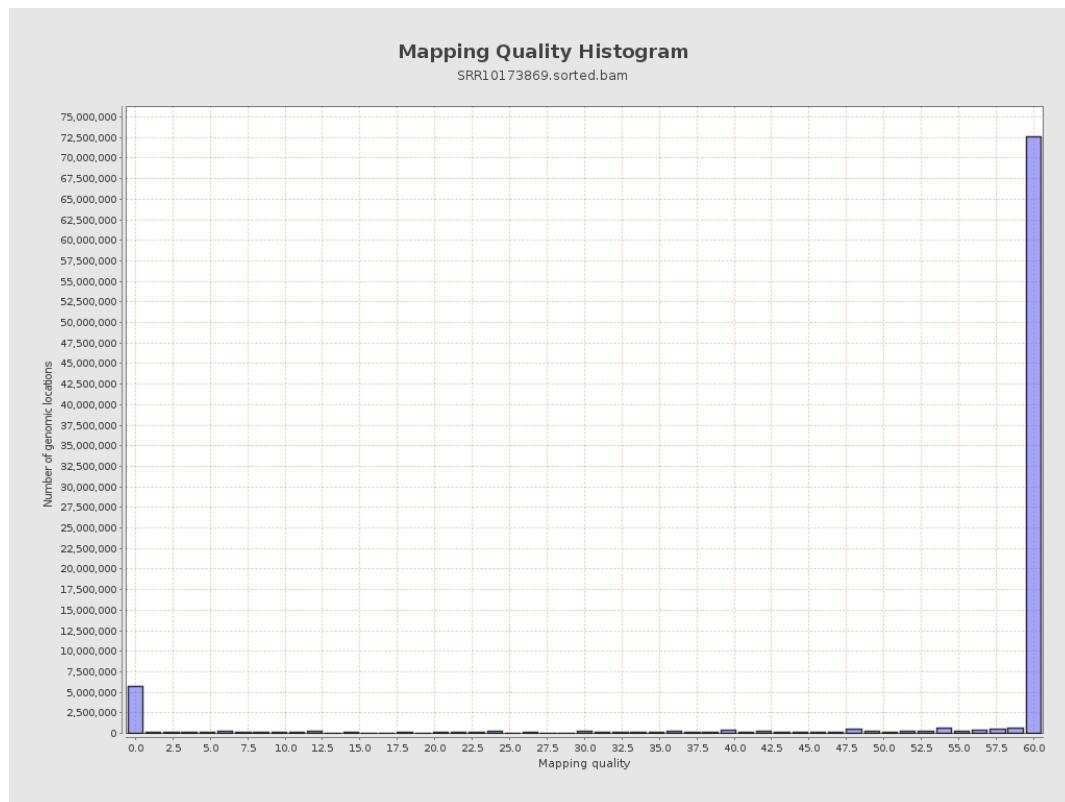
11. Results : Homopolymer Indels



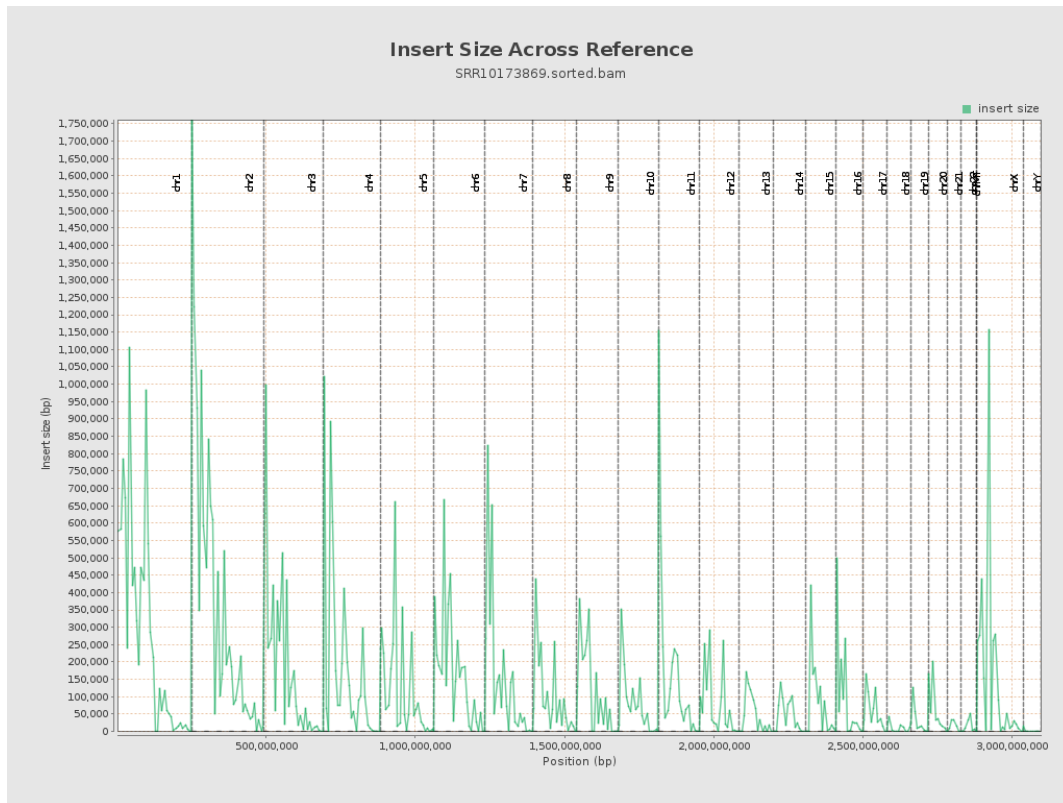
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

