

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 18:17:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173993.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_SRR10173993 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173993_1.fastq.gz SRR10173993_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 18:17:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173993.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,838,304
Mapped reads	10,608,223 / 97.88%
Unmapped reads	230,081 / 2.12%
Mapped paired reads	10,608,223 / 97.88%
Mapped reads, first in pair	5,301,912 / 48.92%
Mapped reads, second in pair	5,306,311 / 48.96%
Mapped reads, both in pair	10,455,310 / 96.47%
Mapped reads, singletons	152,913 / 1.41%
Secondary alignments	0
Supplementary alignments	1,490,850 / 13.76%
Read min/max/mean length	30 / 133 / 126.2
Duplicated reads (estimated)	8,659,007 / 79.89%
Duplication rate	65.62%
Clipped reads	5,472,100 / 50.49%

2.2. ACGT Content

Number/percentage of A's	360,651,376 / 29.85%
Number/percentage of C's	240,066,174 / 19.87%
Number/percentage of T's	357,844,945 / 29.62%
Number/percentage of G's	249,450,420 / 20.65%
Number/percentage of N's	8,773 / 0%

GC Percentage	40.52%
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2.3. Coverage

Mean	0.3905
Standard Deviation	6.7093

2.4. Mapping Quality

Mean Mapping Quality	52.47
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2.5. Insert size

Mean	1,081,021.45
Standard Deviation	9,567,418.32
P25/Median/P75	107 / 159 / 248

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	10,194,113
Insertions	133,946
Mapped reads with at least one insertion	1.21%
Deletions	342,966
Mapped reads with at least one deletion	3.15%
Homopolymer indels	41.2%

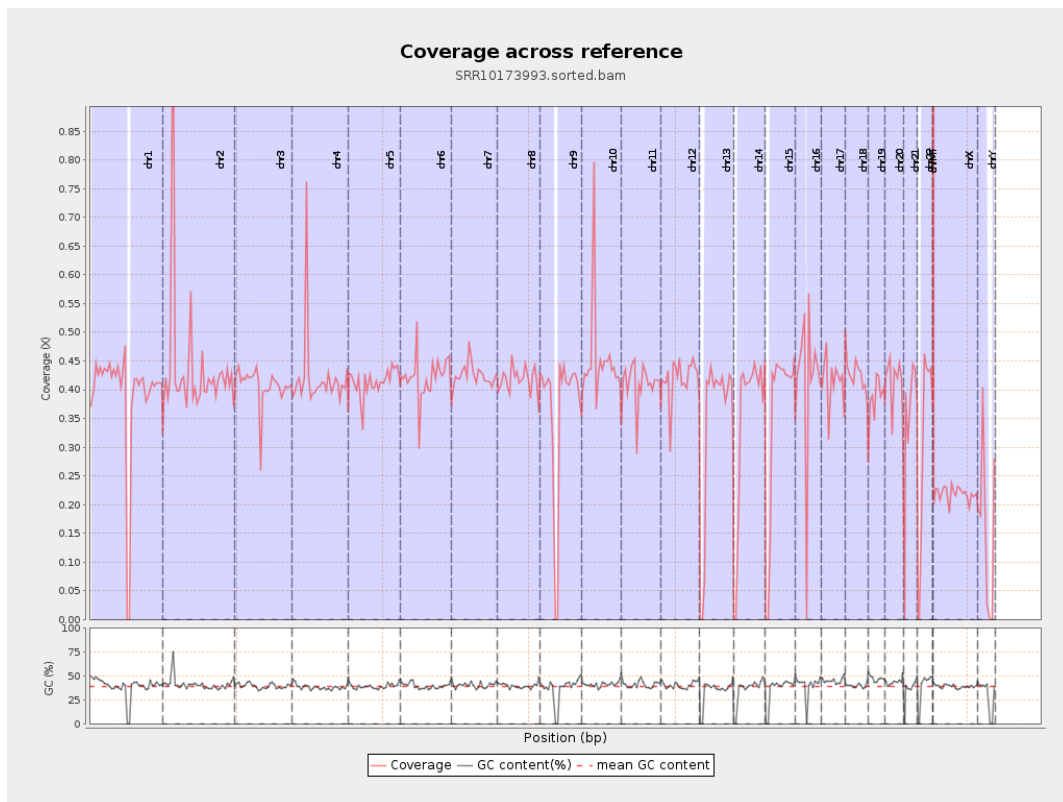
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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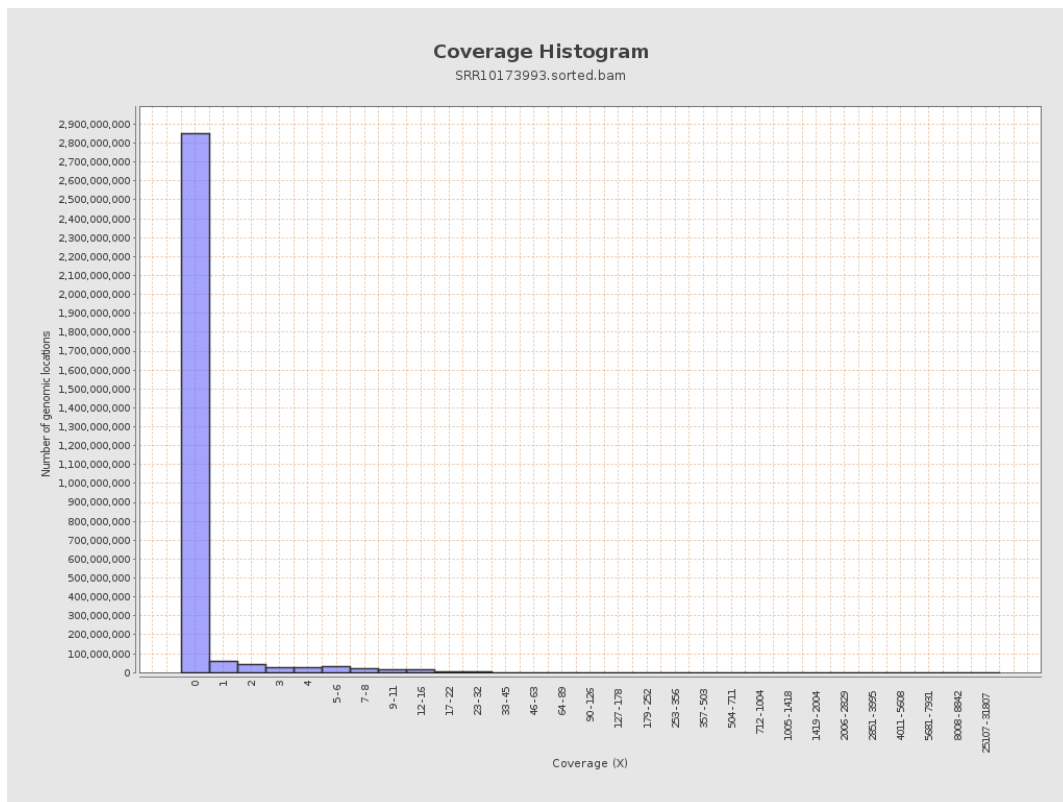
		bases	coverage	deviation
chr1	249250621	97625082	0.3917	3.0138
chr2	243199373	106020210	0.4359	22.1287
chr3	198022430	80515486	0.4066	1.9369
chr4	191154276	80520528	0.4212	3.2464
chr5	180915260	74792337	0.4134	1.9718
chr6	171115067	72291445	0.4225	2.44
chr7	159138663	67653309	0.4251	3.11
chr8	146364022	61006212	0.4168	3.5451
chr9	141213431	51605743	0.3654	2.8997
chr10	135534747	61053519	0.4505	3.9502
chr11	135006516	55366396	0.4101	2.0519
chr12	133851895	56330491	0.4208	2.099
chr13	115169878	39526580	0.3432	1.7874
chr14	107349540	37762155	0.3518	1.863
chr15	102531392	35660652	0.3478	1.8794
chr16	90354753	37483008	0.4148	2.7435
chr17	81195210	33798738	0.4163	2.2989
chr18	78077248	33258470	0.426	4.1651
chr19	59128983	22928226	0.3878	2.4881
chr20	63025520	26301697	0.4173	2.1558
chr21	48129895	17180941	0.357	2.7279
chr22	51304566	15631493	0.3047	2.3477
chrMT	16571	1074313	64.8309	56.7935
chrX	155270560	33950420	0.2187	1.4442

chrY	59373566	9514737	0.1603	2.4525
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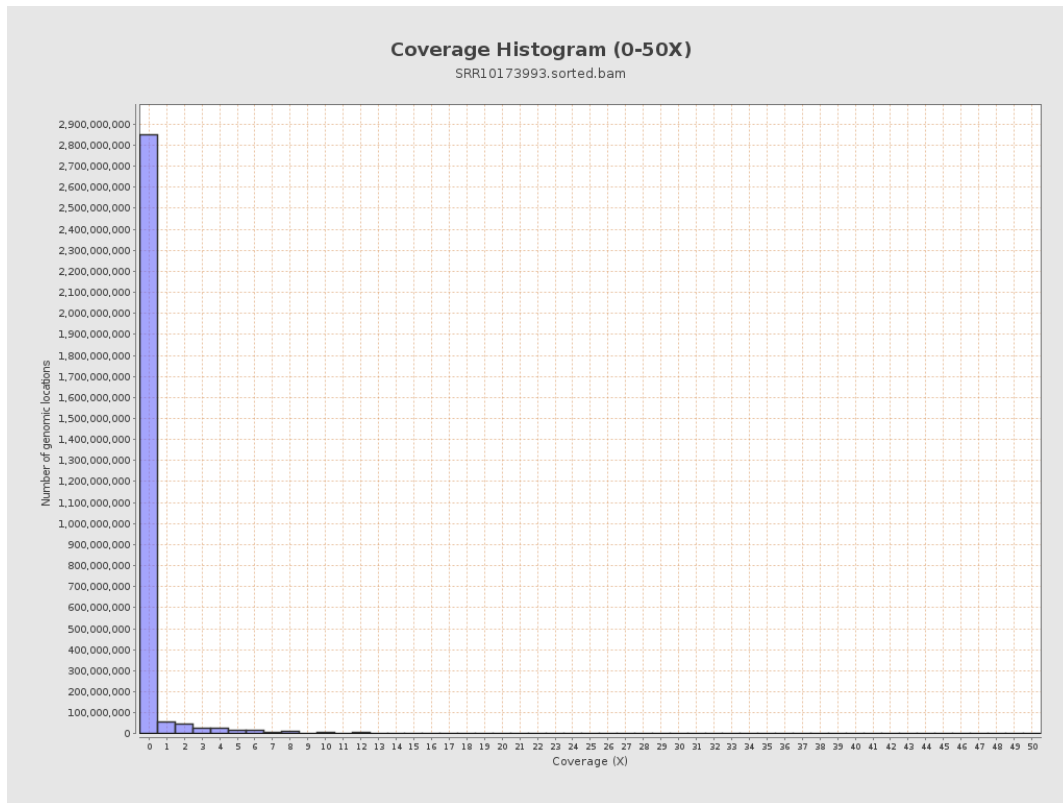
3. Results : Coverage across reference



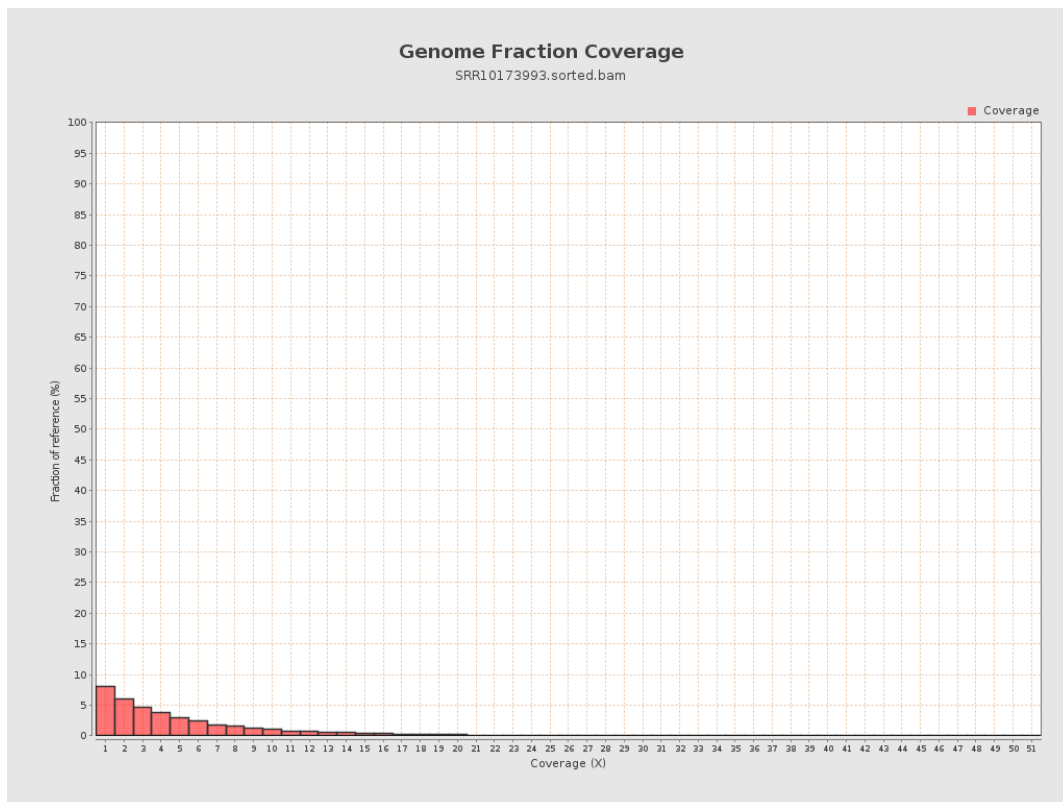
4. Results : Coverage Histogram



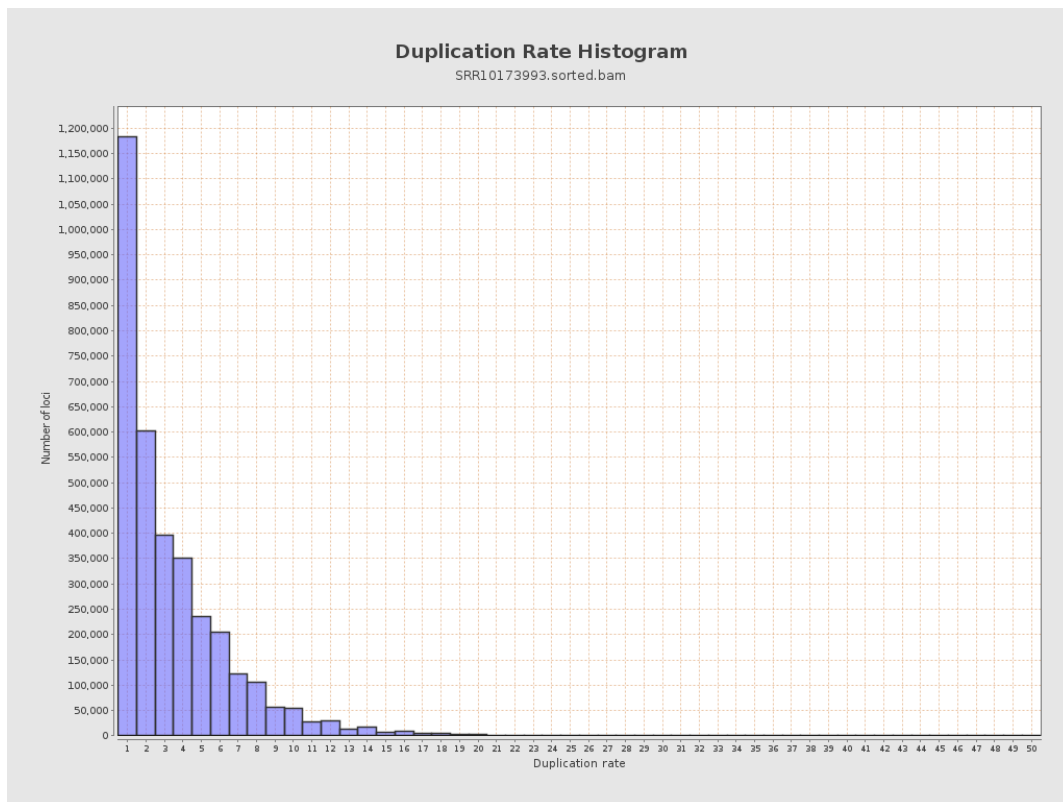
5. Results : Coverage Histogram (0-50X)



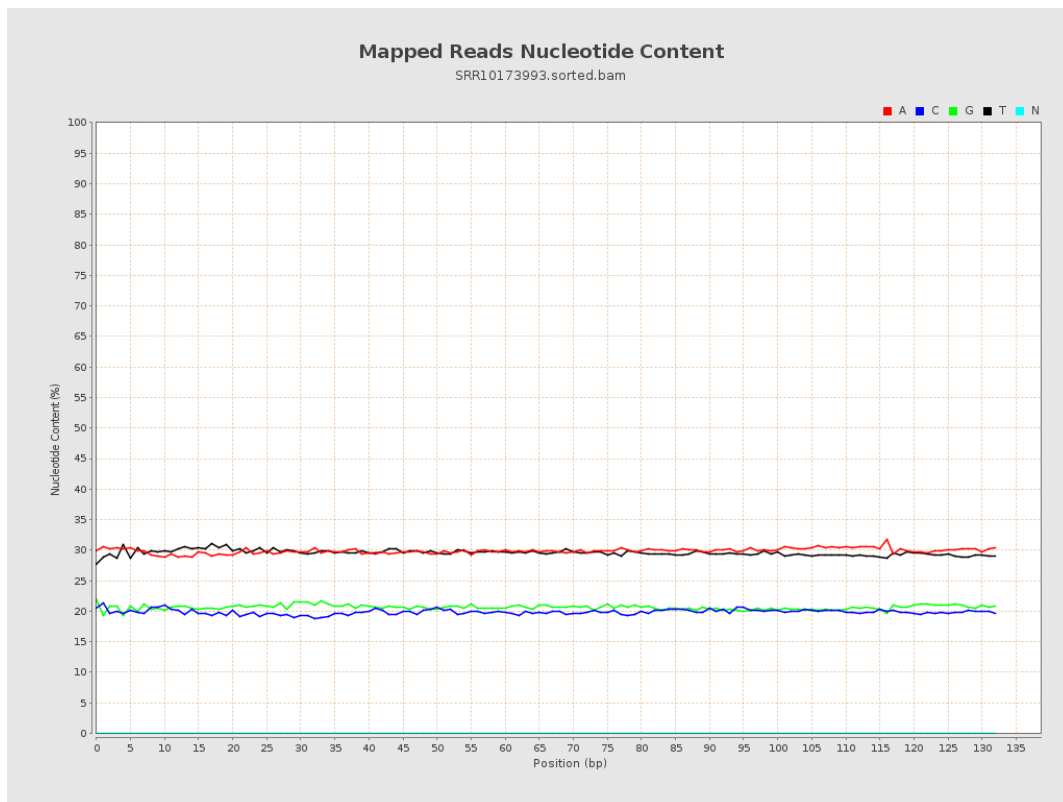
6. Results : Genome Fraction Coverage



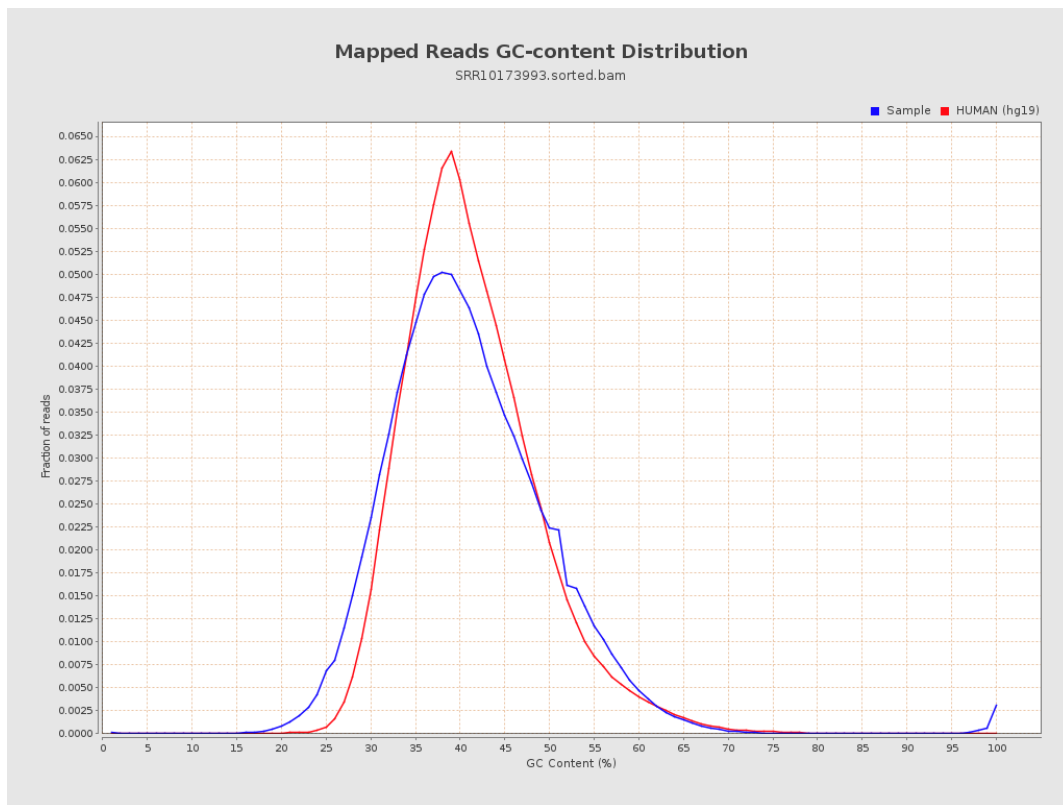
7. Results : Duplication Rate Histogram



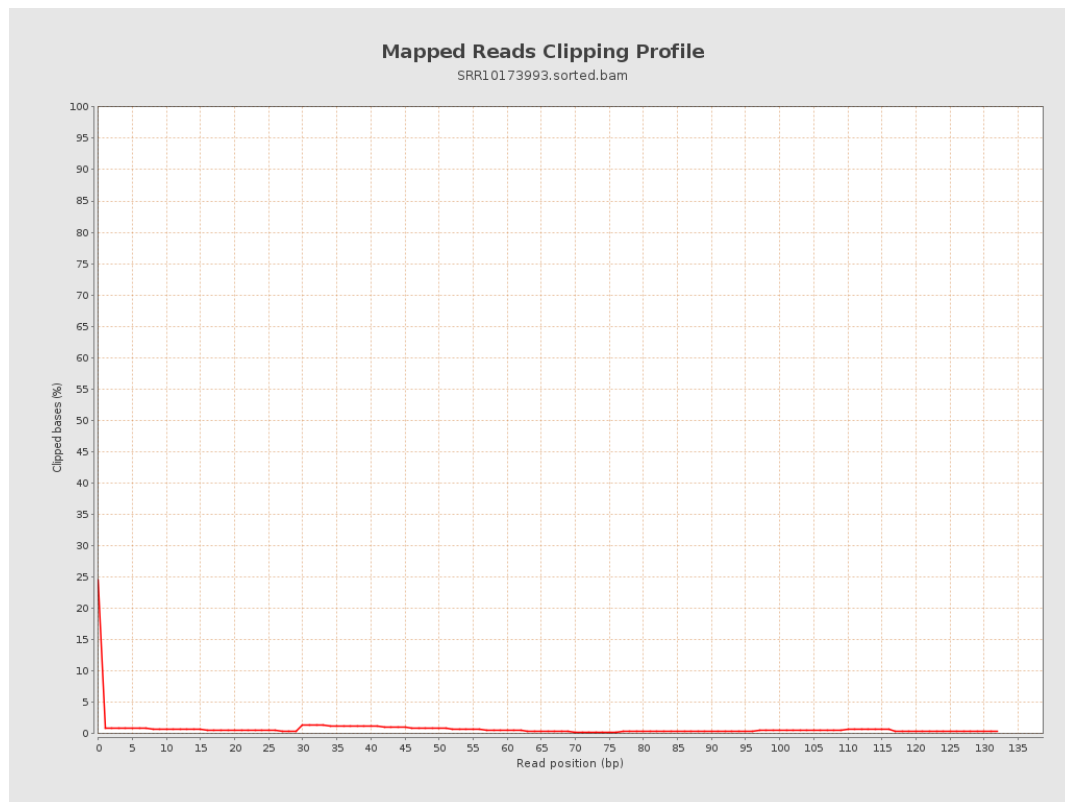
8. Results : Mapped Reads Nucleotide Content



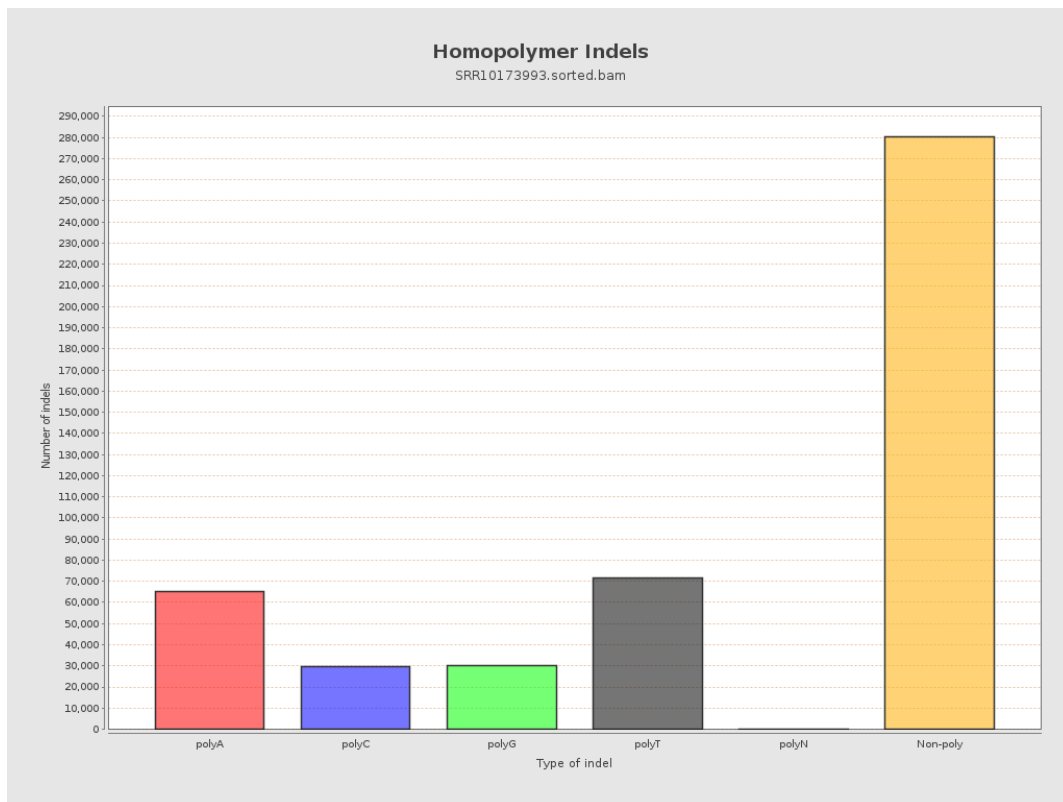
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



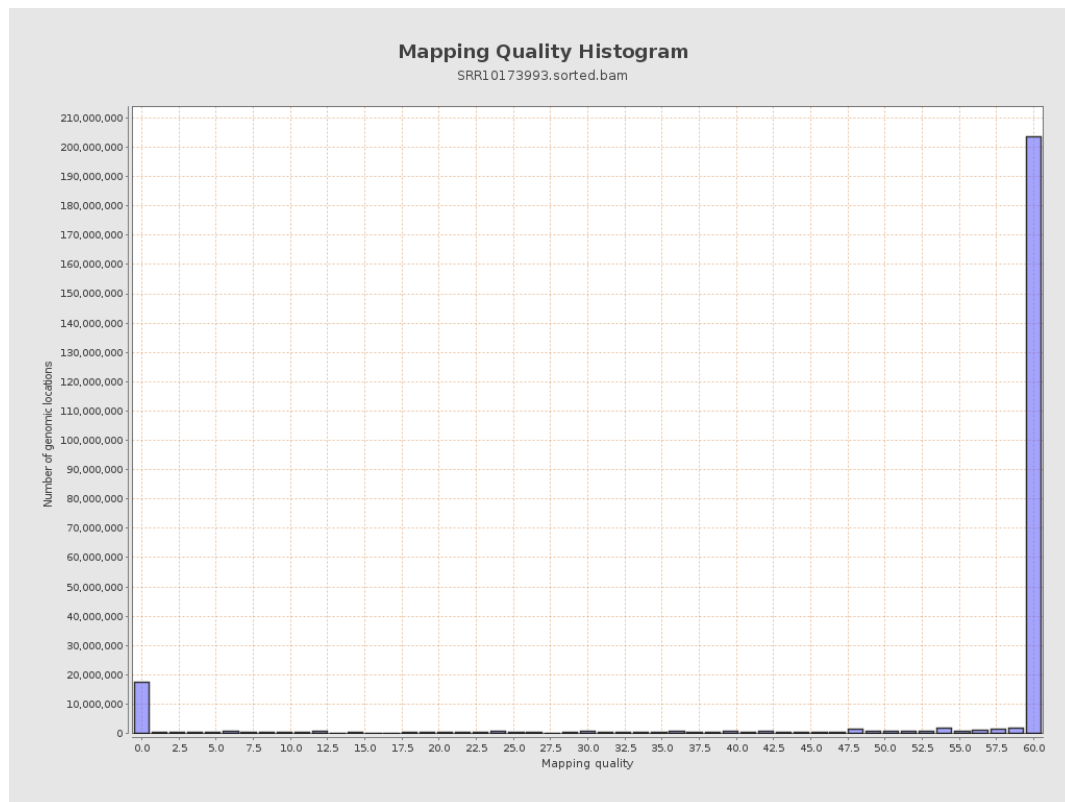
11. Results : Homopolymer Indels



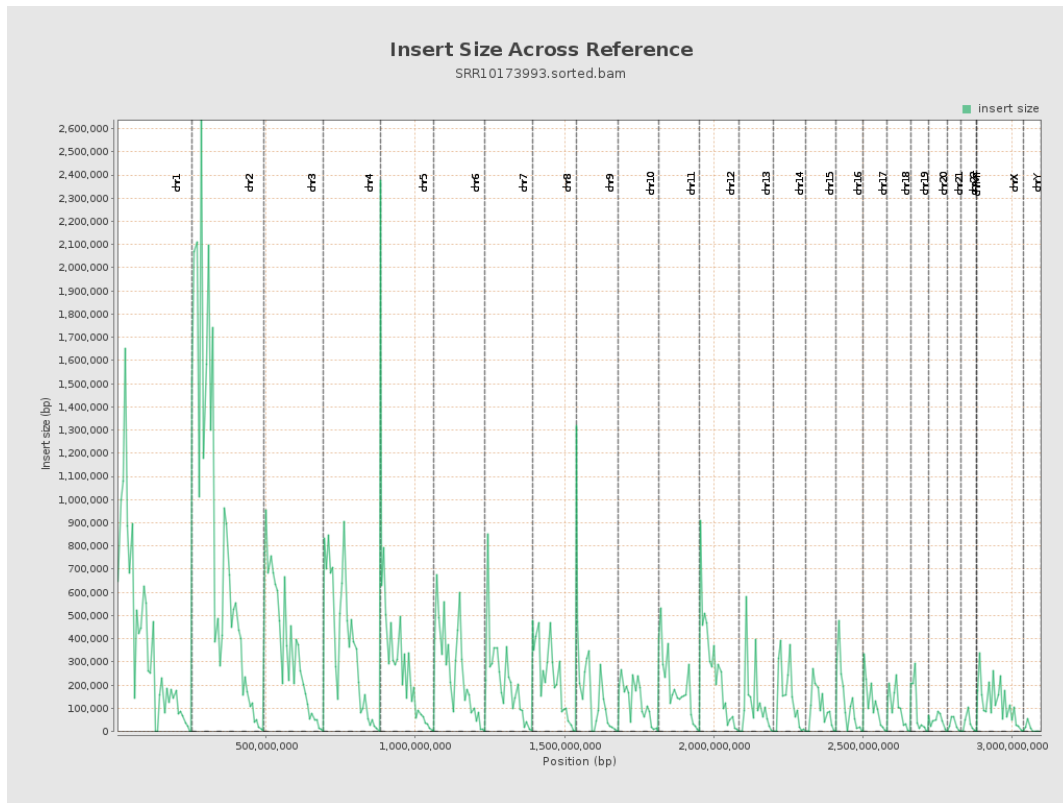
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

