

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 10:04:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173942.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_SRR10173942 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173942_1.fastq.gz SRR10173942_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 10:04:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173942.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,836,836
Mapped reads	14,497,856 / 97.72%
Unmapped reads	338,980 / 2.28%
Mapped paired reads	14,497,856 / 97.72%
Mapped reads, first in pair	7,245,421 / 48.83%
Mapped reads, second in pair	7,252,435 / 48.88%
Mapped reads, both in pair	14,285,256 / 96.28%
Mapped reads, singletons	212,600 / 1.43%
Secondary alignments	0
Supplementary alignments	2,018,201 / 13.6%
Read min/max/mean length	30 / 133 / 126.52
Duplicated reads (estimated)	11,649,195 / 78.52%
Duplication rate	65.36%
Clipped reads	8,003,516 / 53.94%

2.2. ACGT Content

Number/percentage of A's	495,916,650 / 30.02%
Number/percentage of C's	324,887,377 / 19.67%
Number/percentage of T's	492,084,479 / 29.79%
Number/percentage of G's	339,040,071 / 20.52%
Number/percentage of N's	11,619 / 0%

GC Percentage	40.19%
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2.3. Coverage

Mean	0.534
Standard Deviation	9.6455

2.4. Mapping Quality

Mean Mapping Quality	52.4
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2.5. Insert size

Mean	958,679.23
Standard Deviation	9,211,524.53
P25/Median/P75	108 / 161 / 250

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	14,924,425
Insertions	192,530
Mapped reads with at least one insertion	1.27%
Deletions	494,482
Mapped reads with at least one deletion	3.32%
Homopolymer indels	41.07%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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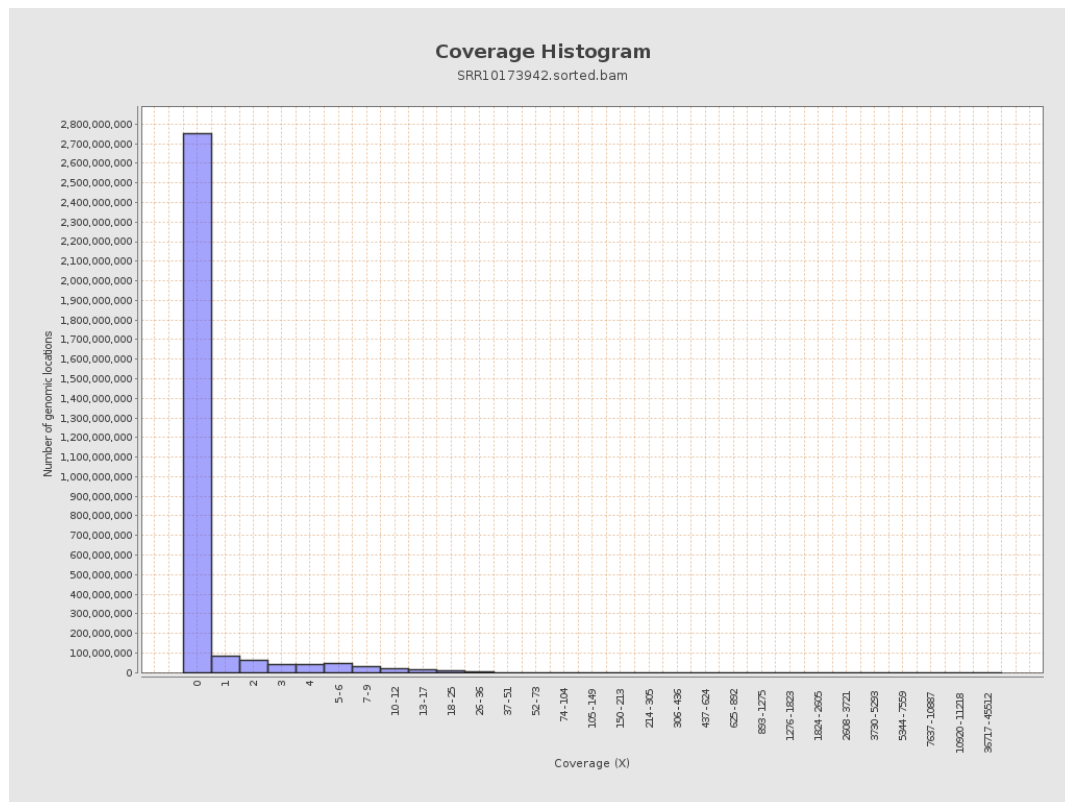
		bases	coverage	deviation
chr1	249250621	134159566	0.5383	4.8462
chr2	243199373	149822591	0.616	31.7692
chr3	198022430	111679156	0.564	2.2215
chr4	191154276	112760735	0.5899	4.5176
chr5	180915260	102730710	0.5678	2.2482
chr6	171115067	98356993	0.5748	3.3483
chr7	159138663	90492114	0.5686	4.5289
chr8	146364022	84570038	0.5778	5.3565
chr9	141213431	70938470	0.5023	4.4702
chr10	135534747	81816954	0.6037	6.603
chr11	135006516	73158977	0.5419	2.4338
chr12	133851895	74920237	0.5597	2.4873
chr13	115169878	54866049	0.4764	2.0512
chr14	107349540	51933816	0.4838	2.1669
chr15	102531392	47515719	0.4634	2.1942
chr16	90354753	51333493	0.5681	4.0673
chr17	81195210	44474964	0.5478	3.0013
chr18	78077248	46151609	0.5911	6.3704
chr19	59128983	31064995	0.5254	3.8022
chr20	63025520	34630899	0.5495	2.6472
chr21	48129895	23799109	0.4945	3.4934
chr22	51304566	19905533	0.388	2.7249
chrMT	16571	2780721	167.8065	134.5025
chrX	155270560	45925589	0.2958	1.7001

chrY	59373566	13318456	0.2243	3.6456
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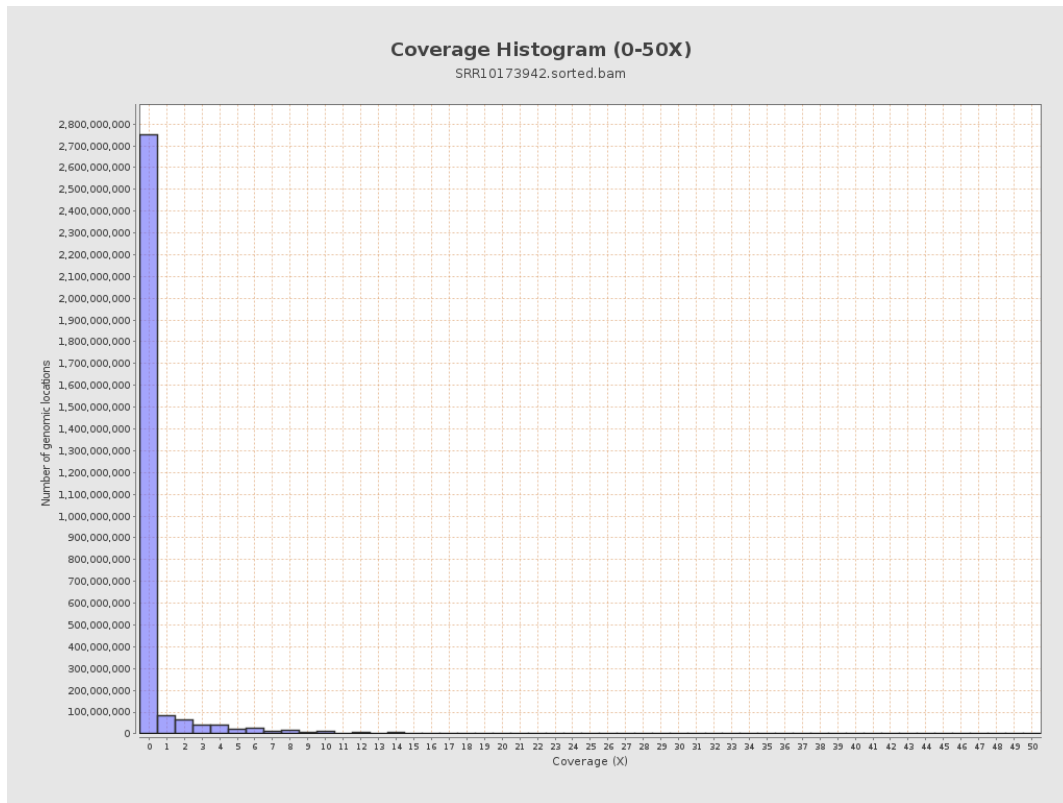
3. Results : Coverage across reference



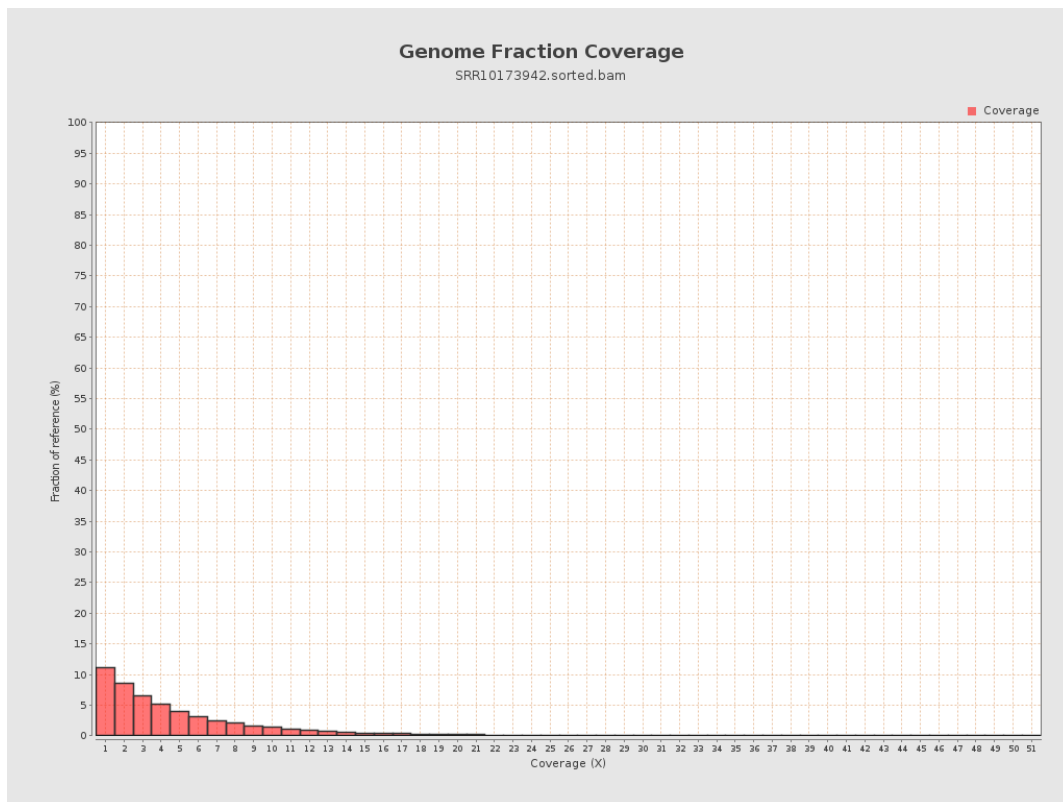
4. Results : Coverage Histogram



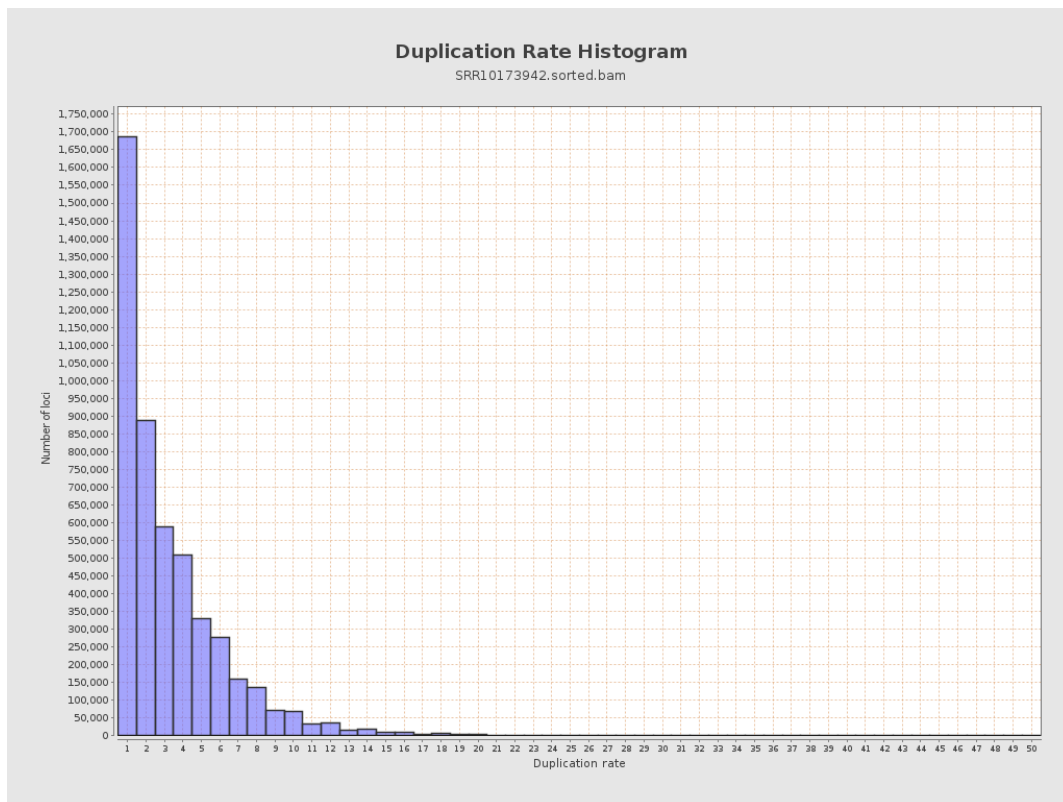
5. Results : Coverage Histogram (0-50X)



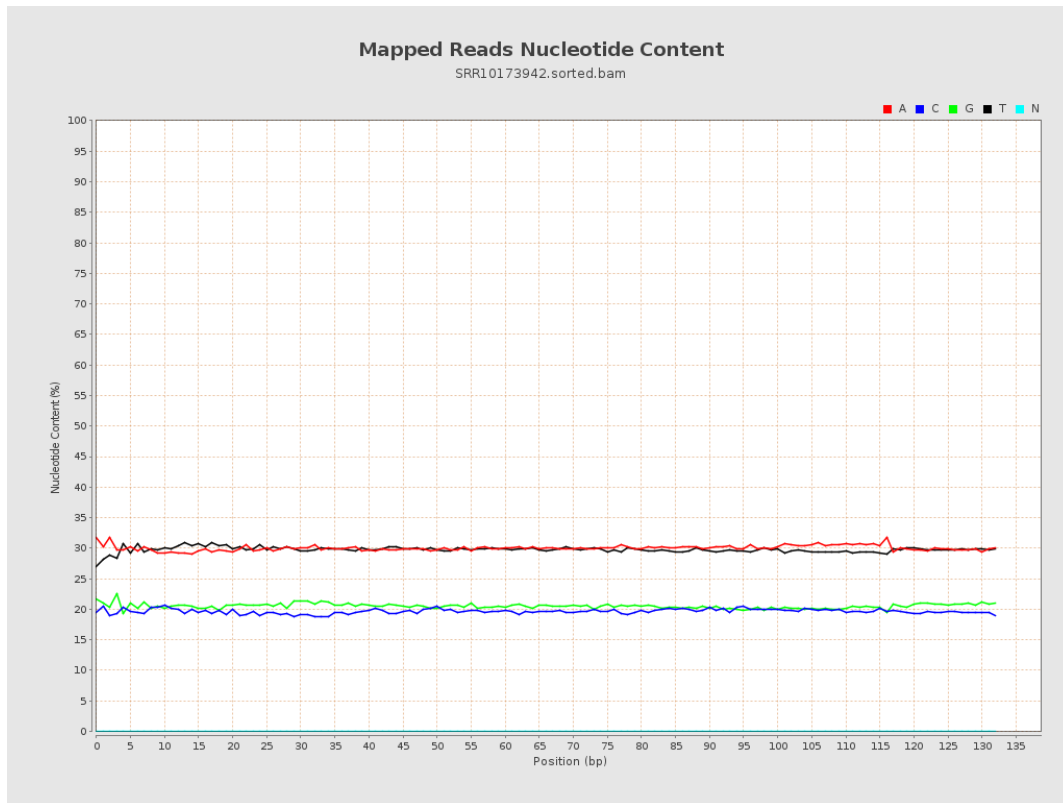
6. Results : Genome Fraction Coverage



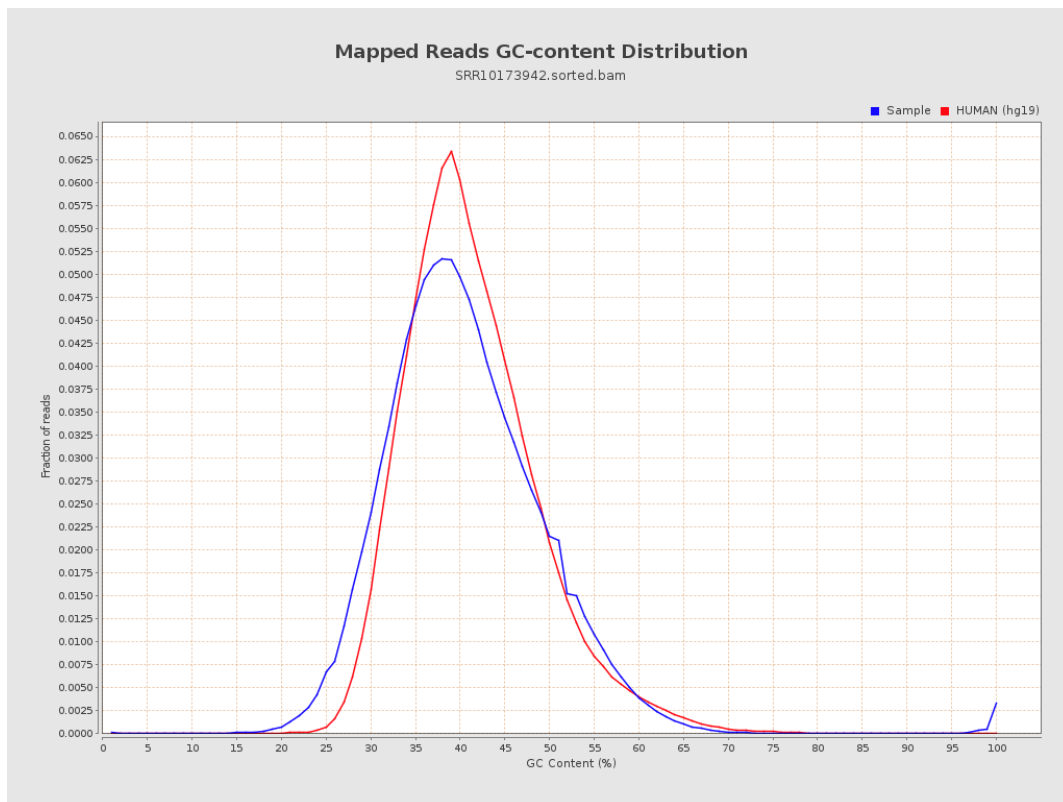
7. Results : Duplication Rate Histogram



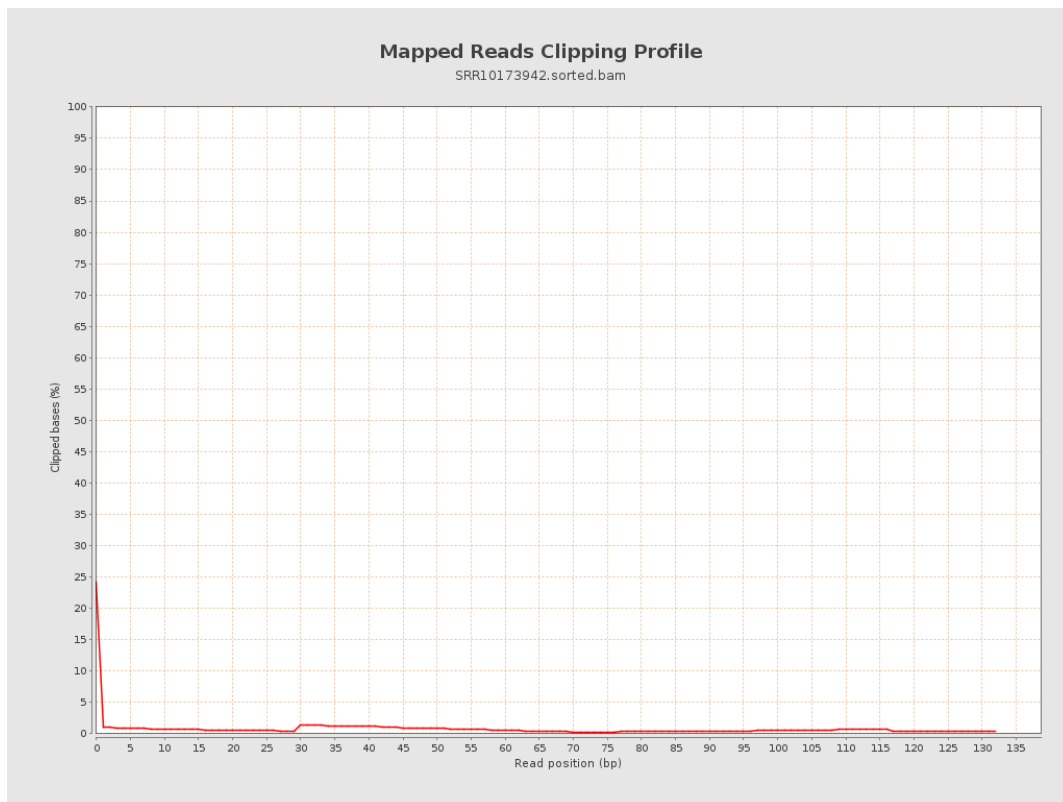
8. Results : Mapped Reads Nucleotide Content



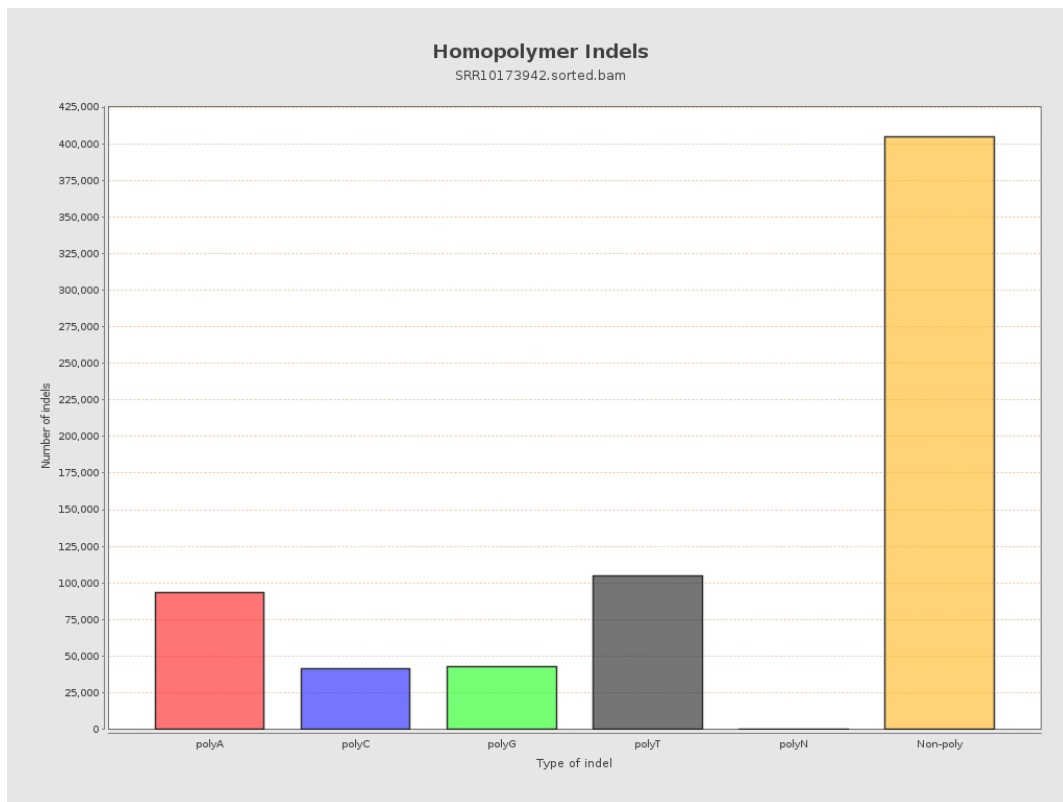
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



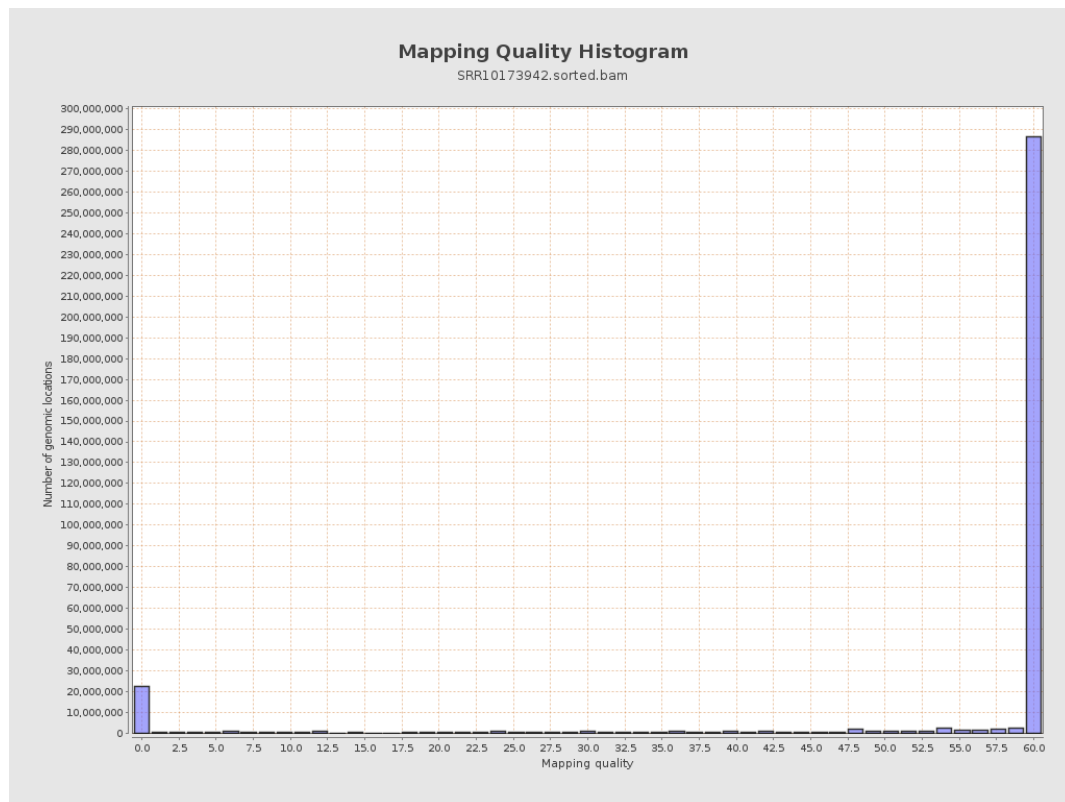
11. Results : Homopolymer Indels



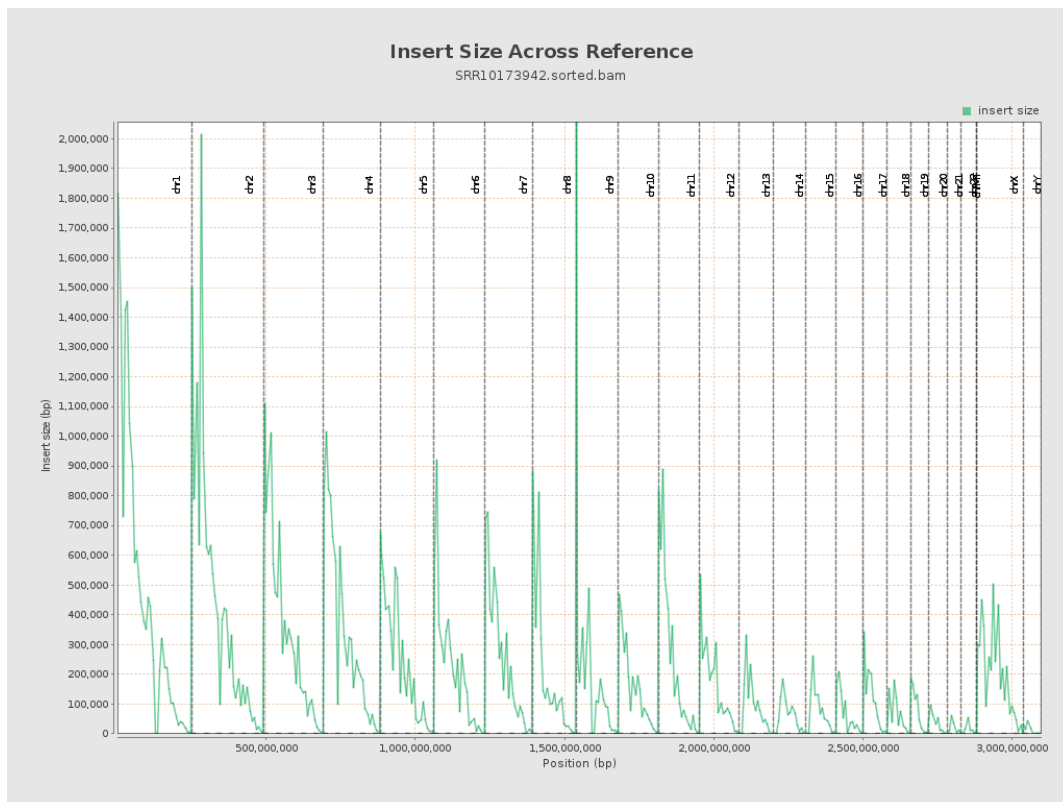
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

