

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:56:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173912.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_SRR10173912 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173912_1.fastq.gz SRR10173912_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:56:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173912.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,617,794
Mapped reads	1,578,122 / 97.55%
Unmapped reads	39,672 / 2.45%
Mapped paired reads	1,578,122 / 97.55%
Mapped reads, first in pair	790,704 / 48.88%
Mapped reads, second in pair	787,418 / 48.67%
Mapped reads, both in pair	1,552,846 / 95.99%
Mapped reads, singletons	25,276 / 1.56%
Secondary alignments	0
Supplementary alignments	161,868 / 10.01%
Read min/max/mean length	30 / 133 / 128.57
Duplicated reads (estimated)	1,205,513 / 74.52%
Duplication rate	62.81%
Clipped reads	639,141 / 39.51%

2.2. ACGT Content

Number/percentage of A's	56,395,187 / 30.11%
Number/percentage of C's	36,667,086 / 19.58%
Number/percentage of T's	56,259,140 / 30.04%
Number/percentage of G's	37,974,946 / 20.28%
Number/percentage of N's	2,540 / 0%

GC Percentage	39.85%
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2.3. Coverage

Mean	0.0605
Standard Deviation	1.0045

2.4. Mapping Quality

Mean Mapping Quality	52.94
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2.5. Insert size

Mean	1,196,190.51
Standard Deviation	10,109,181.55
P25/Median/P75	150 / 208 / 297

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	1,971,874
Insertions	21,750
Mapped reads with at least one insertion	1.32%
Deletions	44,960
Mapped reads with at least one deletion	2.78%
Homopolymer indels	42.67%

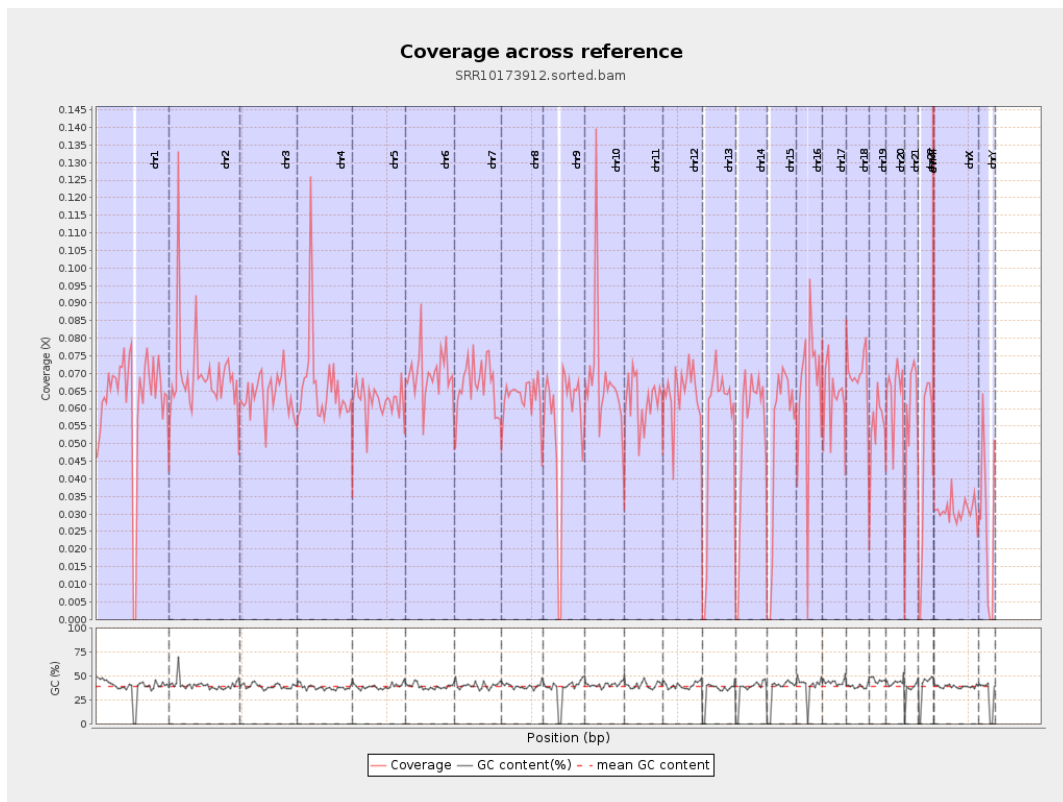
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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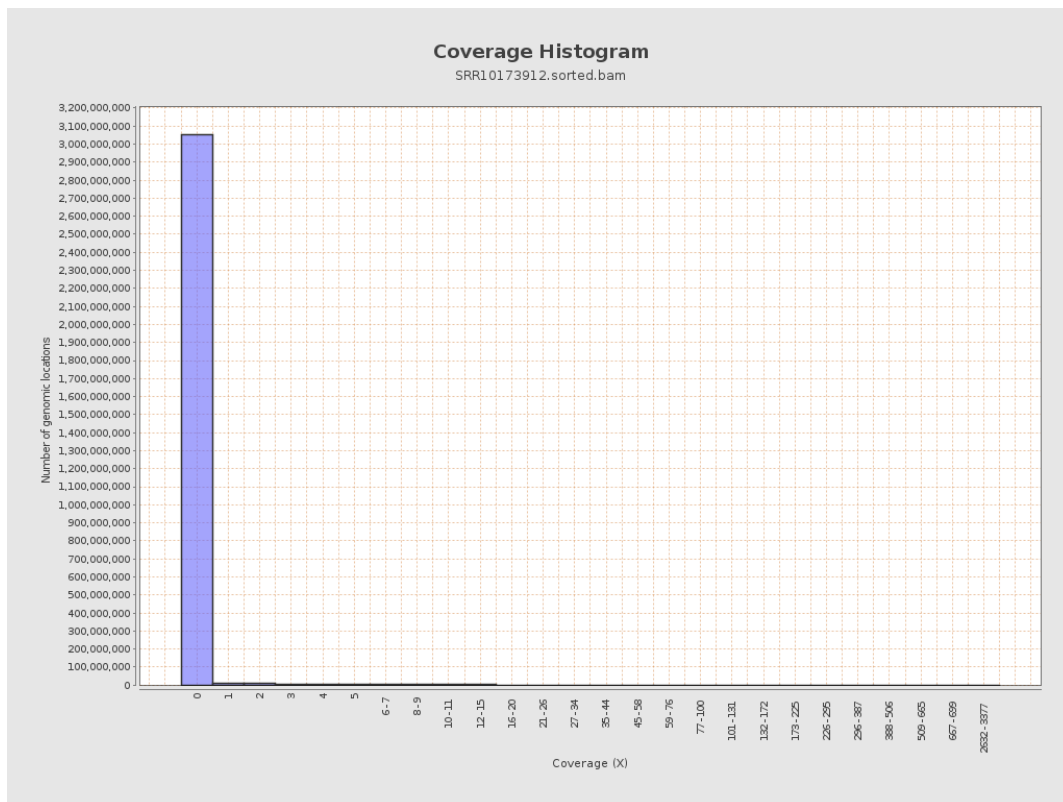
		bases	coverage	deviation
chr1	249250621	15531287	0.0623	0.8242
chr2	243199373	16923685	0.0696	2.4509
chr3	198022430	12635949	0.0638	0.7099
chr4	191154276	12665287	0.0663	0.837
chr5	180915260	11252298	0.0622	0.6994
chr6	171115067	11932599	0.0697	0.7902
chr7	159138663	10659639	0.067	0.8451
chr8	146364022	9207385	0.0629	0.8555
chr9	141213431	7870008	0.0557	0.7899
chr10	135534747	9255417	0.0683	0.9877
chr11	135006516	8335207	0.0617	0.6977
chr12	133851895	8629767	0.0645	0.7191
chr13	115169878	6224058	0.054	0.6601
chr14	107349540	5691371	0.053	0.6438
chr15	102531392	5309570	0.0518	0.6207
chr16	90354753	5836894	0.0646	0.7891
chr17	81195210	5037560	0.062	0.7379
chr18	78077248	5492726	0.0703	1.0371
chr19	59128983	3264037	0.0552	0.6923
chr20	63025520	4014613	0.0637	0.7089
chr21	48129895	2734544	0.0568	0.7824
chr22	51304566	2250839	0.0439	0.5785
chrMT	16571	258505	15.5998	15.9597
chrX	155270560	4837198	0.0312	0.4918

chrY	59373566	1563236	0.0263	0.5399
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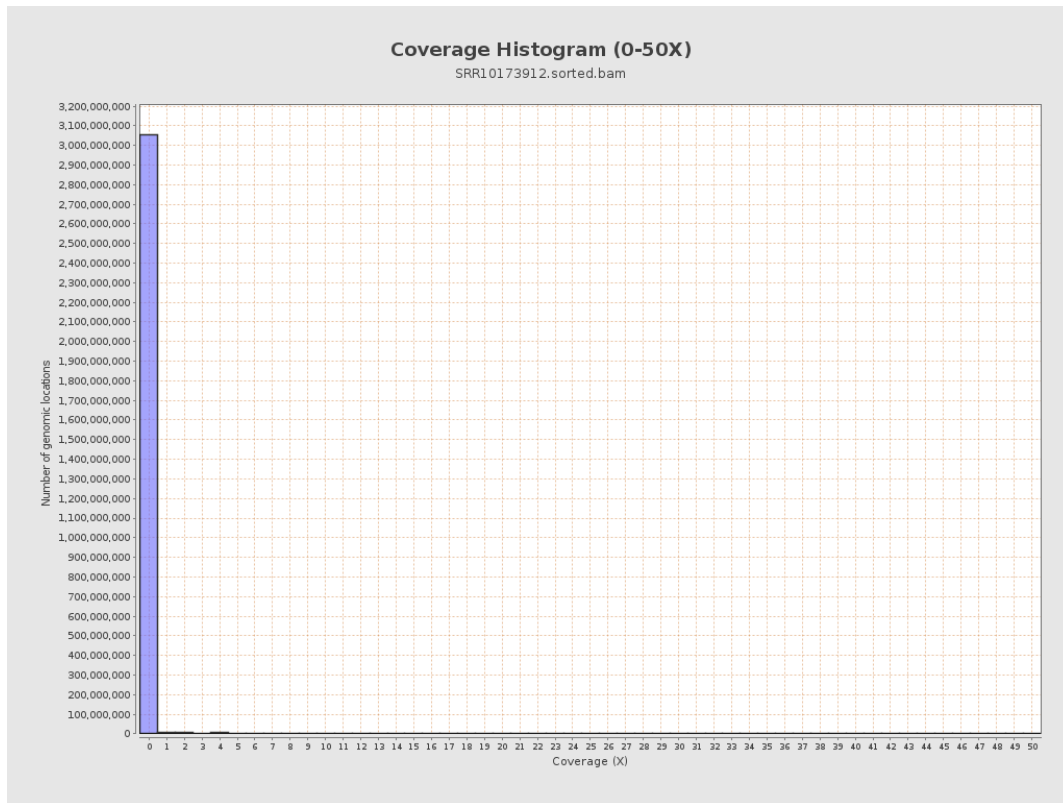
3. Results : Coverage across reference



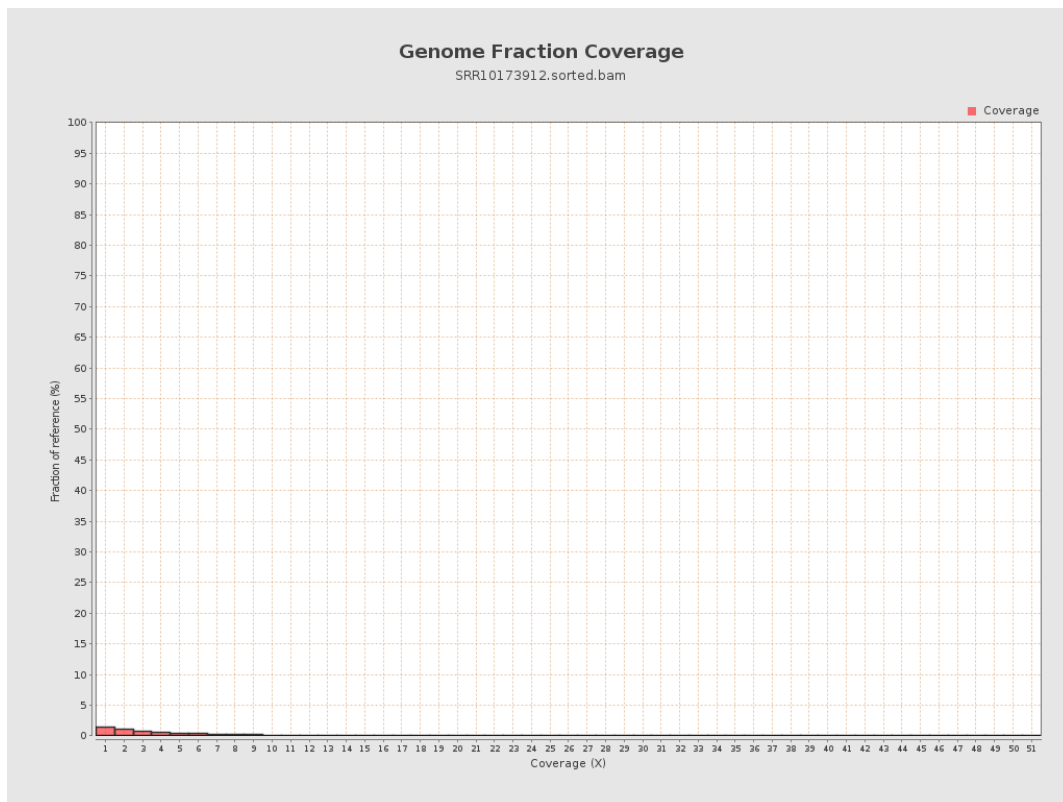
4. Results : Coverage Histogram



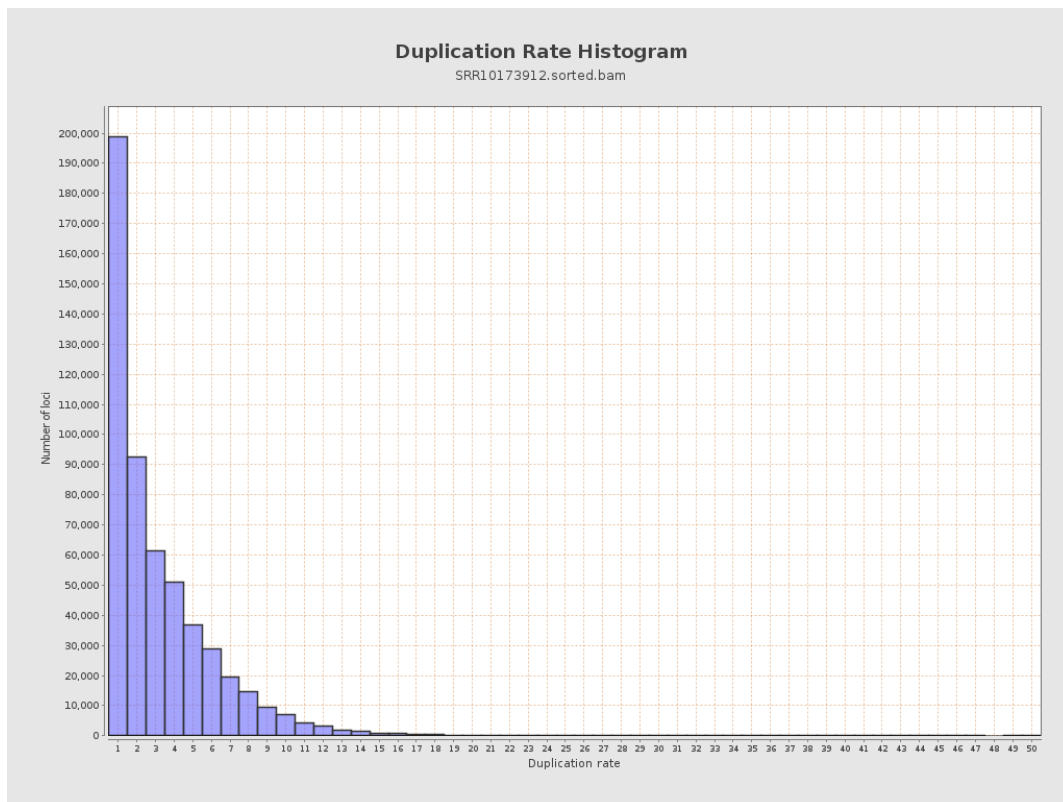
5. Results : Coverage Histogram (0-50X)



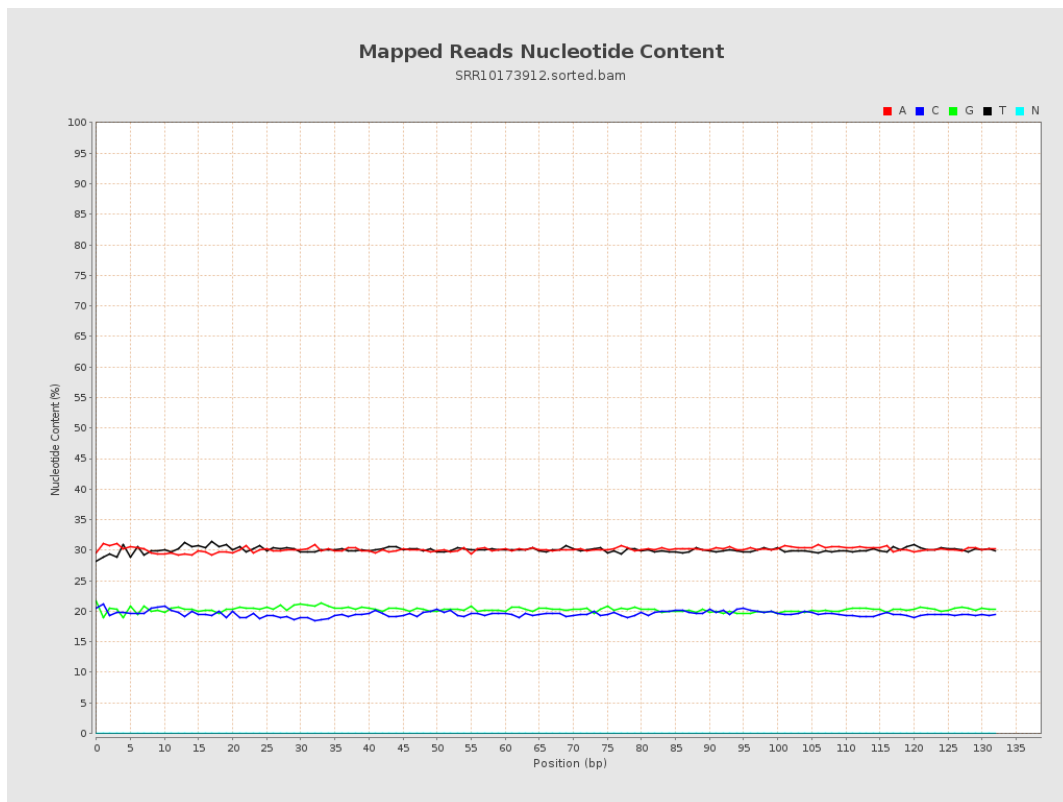
6. Results : Genome Fraction Coverage



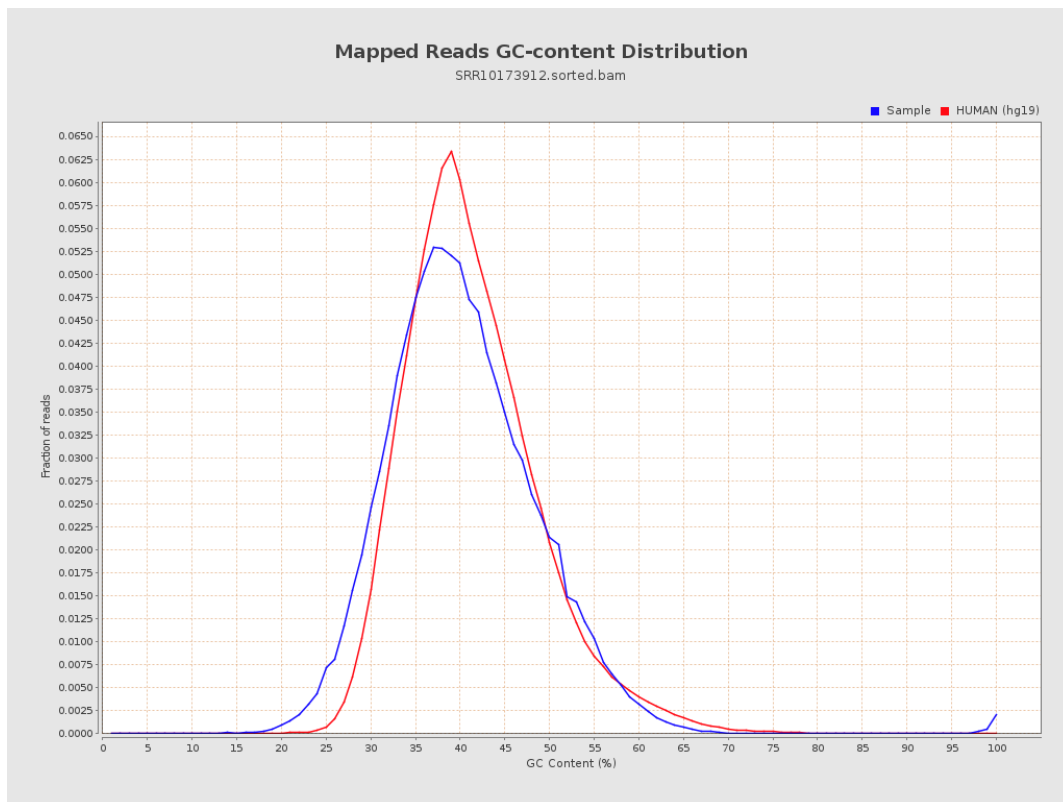
7. Results : Duplication Rate Histogram



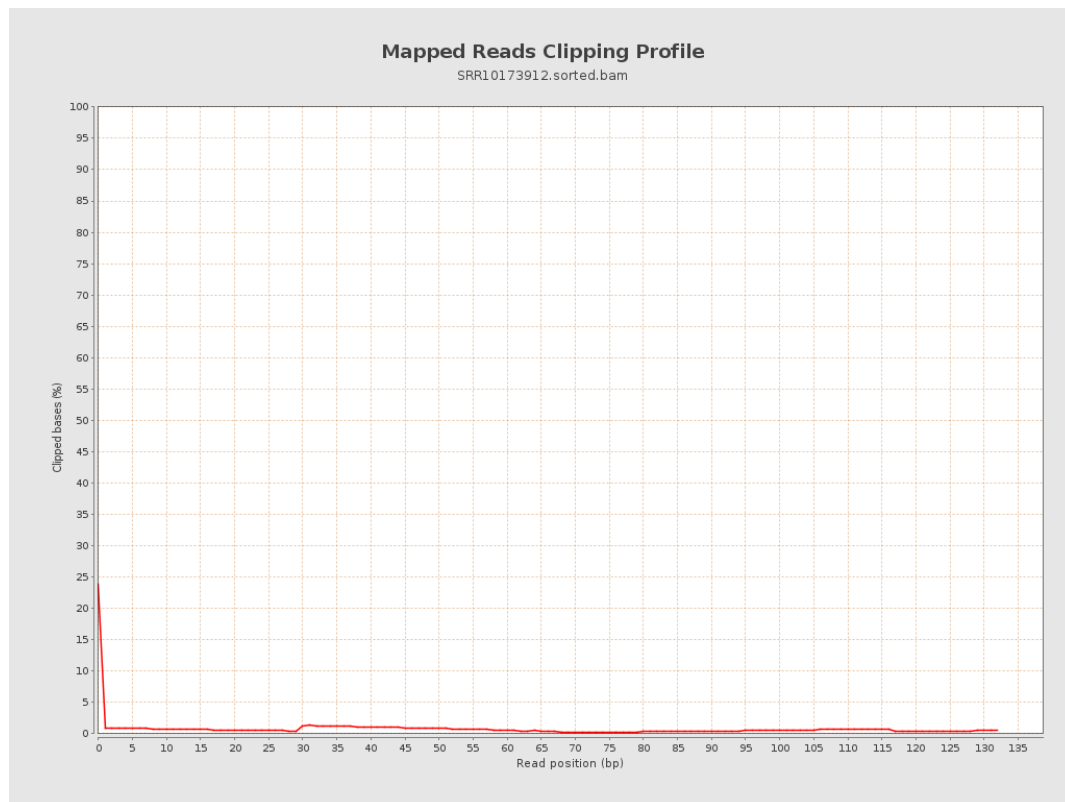
8. Results : Mapped Reads Nucleotide Content



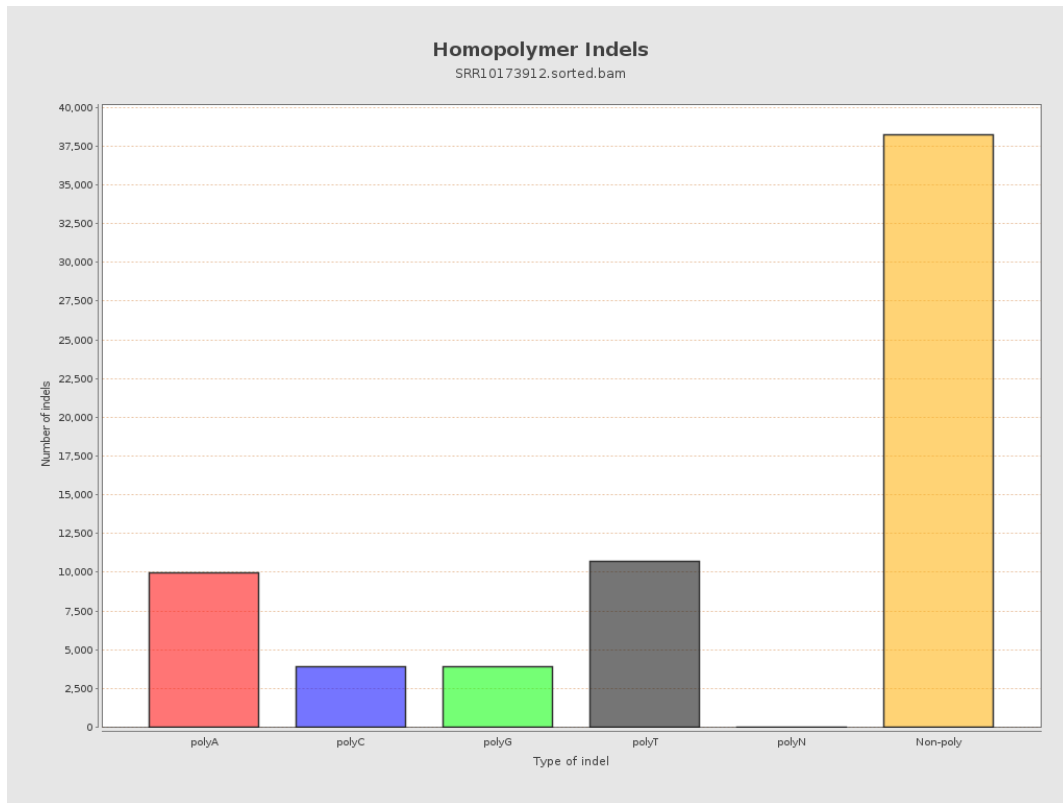
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



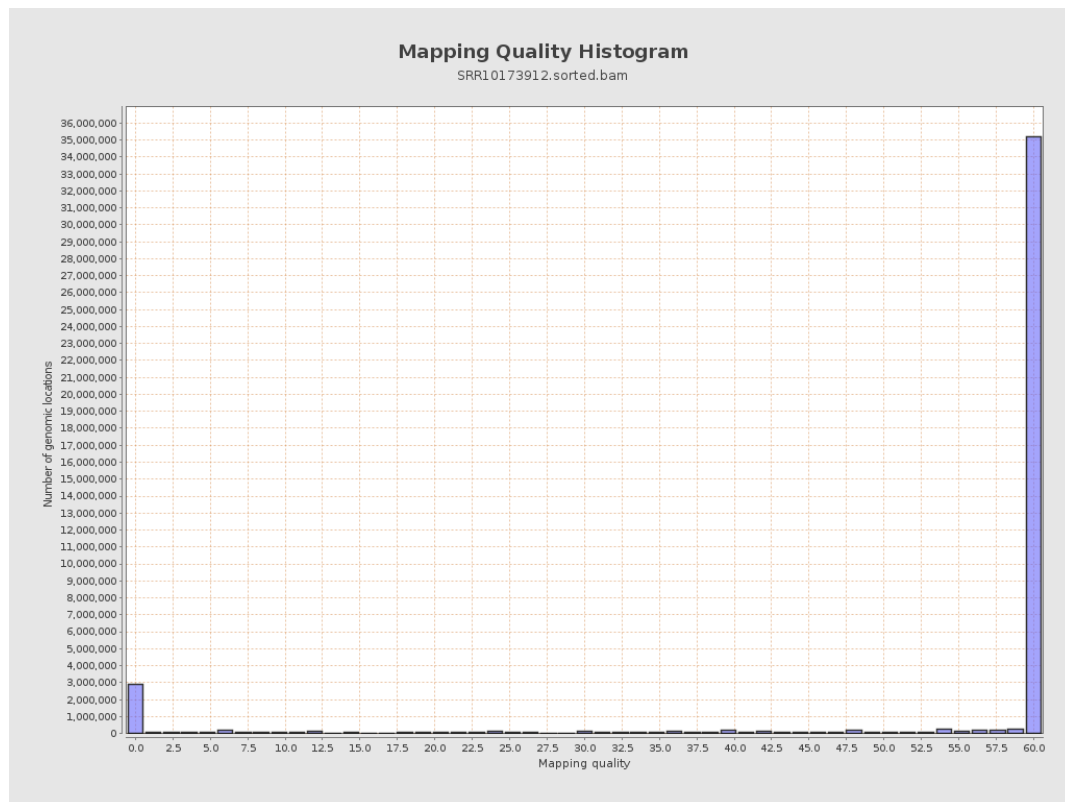
11. Results : Homopolymer Indels



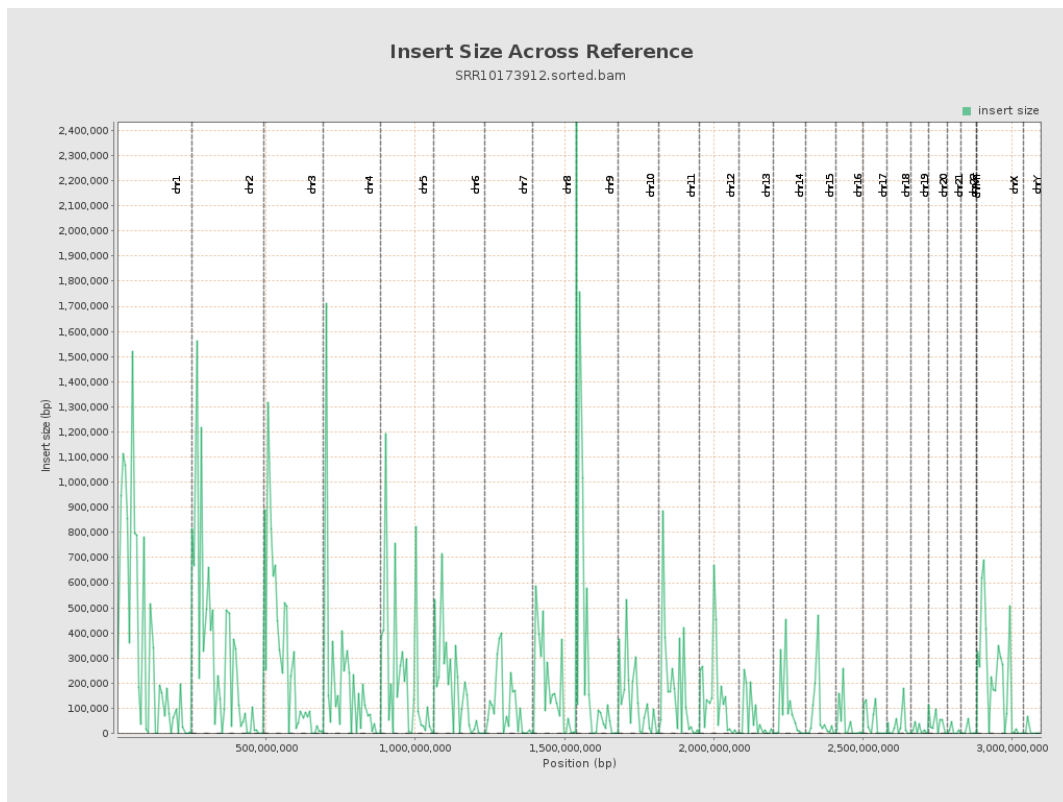
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

