

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:22:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173901.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_SRR10173901 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173901_1.fastq.gz SRR10173901_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:22:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173901.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,037,410
Mapped reads	1,986,457 / 97.5%
Unmapped reads	50,953 / 2.5%
Mapped paired reads	1,986,457 / 97.5%
Mapped reads, first in pair	995,475 / 48.86%
Mapped reads, second in pair	990,982 / 48.64%
Mapped reads, both in pair	1,953,124 / 95.86%
Mapped reads, singletons	33,333 / 1.64%
Secondary alignments	0
Supplementary alignments	196,229 / 9.63%
Read min/max/mean length	30 / 133 / 127.98
Duplicated reads (estimated)	1,493,563 / 73.31%
Duplication rate	62.99%
Clipped reads	810,964 / 39.8%

2.2. ACGT Content

Number/percentage of A's	70,822,676 / 30.24%
Number/percentage of C's	45,532,412 / 19.44%
Number/percentage of T's	70,694,975 / 30.19%
Number/percentage of G's	47,138,224 / 20.13%
Number/percentage of N's	2,920 / 0%

GC Percentage	39.57%
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2.3. Coverage

Mean	0.0757
Standard Deviation	1.2104

2.4. Mapping Quality

Mean Mapping Quality	53.15
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2.5. Insert size

Mean	999,204.9
Standard Deviation	9,339,771.85
P25/Median/P75	141 / 195 / 276

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	2,366,400
Insertions	25,439
Mapped reads with at least one insertion	1.24%
Deletions	53,763
Mapped reads with at least one deletion	2.64%
Homopolymer indels	42.62%

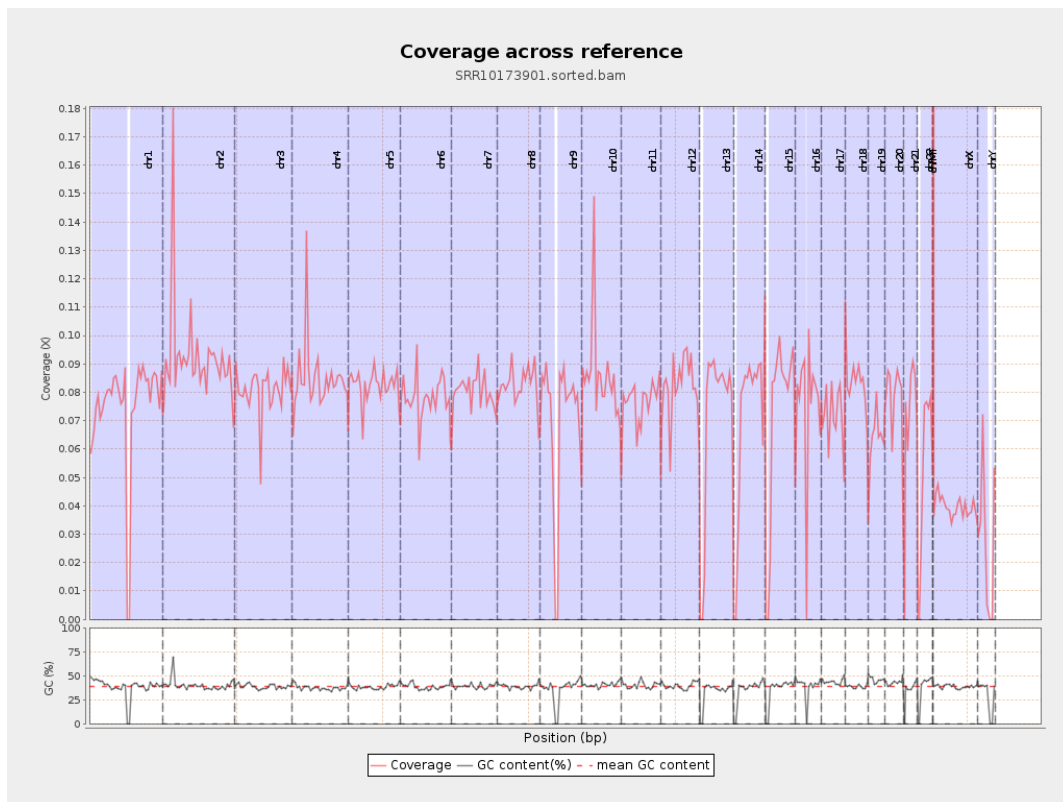
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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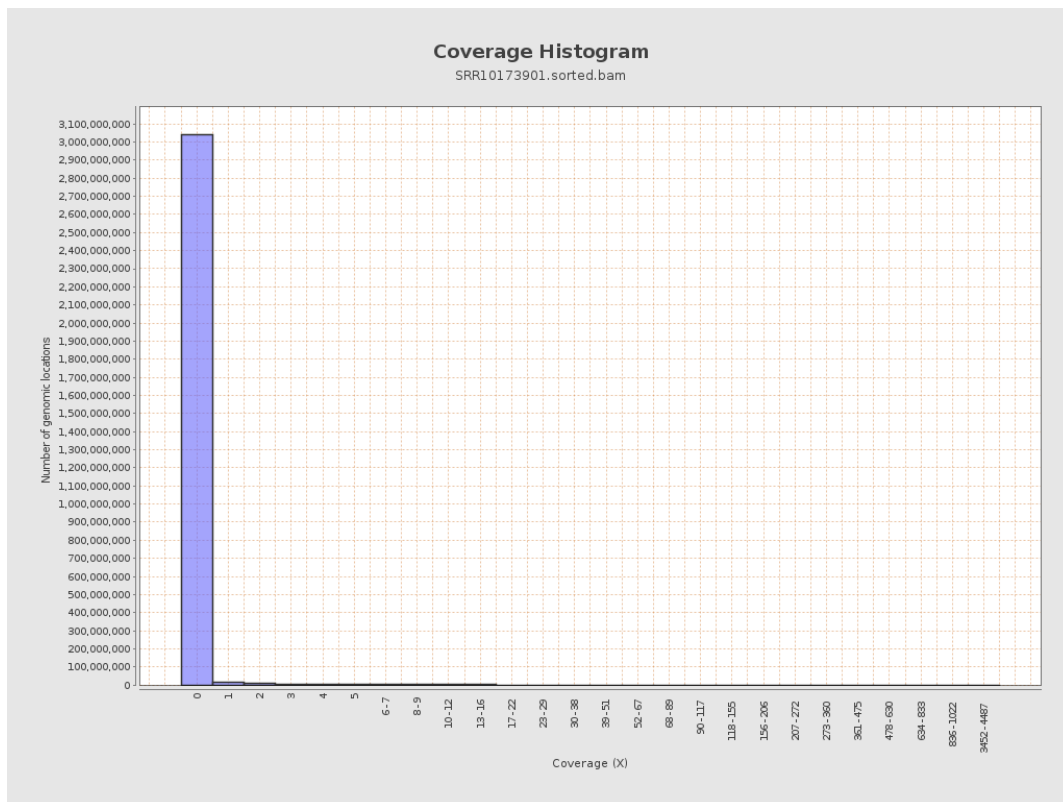
		bases	coverage	deviation
chr1	249250621	18627698	0.0747	0.9057
chr2	243199373	22365885	0.092	3.2143
chr3	198022430	15997708	0.0808	0.8033
chr4	191154276	16191954	0.0847	0.911
chr5	180915260	14891957	0.0823	0.8009
chr6	171115067	13405916	0.0783	0.826
chr7	159138663	12743499	0.0801	0.8944
chr8	146364022	12086420	0.0826	1.0587
chr9	141213431	9942582	0.0704	0.8522
chr10	135534747	11635780	0.0859	1.0864
chr11	135006516	10332499	0.0765	0.771
chr12	133851895	11012097	0.0823	0.7957
chr13	115169878	8136672	0.0706	0.7542
chr14	107349540	7534048	0.0702	0.7374
chr15	102531392	7226497	0.0705	0.7357
chr16	90354753	6685772	0.074	0.8114
chr17	81195210	5834994	0.0719	0.7604
chr18	78077248	6552450	0.0839	1.038
chr19	59128983	3823250	0.0647	0.7592
chr20	63025520	4972897	0.0789	0.7948
chr21	48129895	3427293	0.0712	0.8366
chr22	51304566	2683194	0.0523	0.6378
chrMT	16571	364214	21.979	18.6756
chrX	155270560	6133589	0.0395	0.5545

chrY	59373566	1712029	0.0288	0.5777
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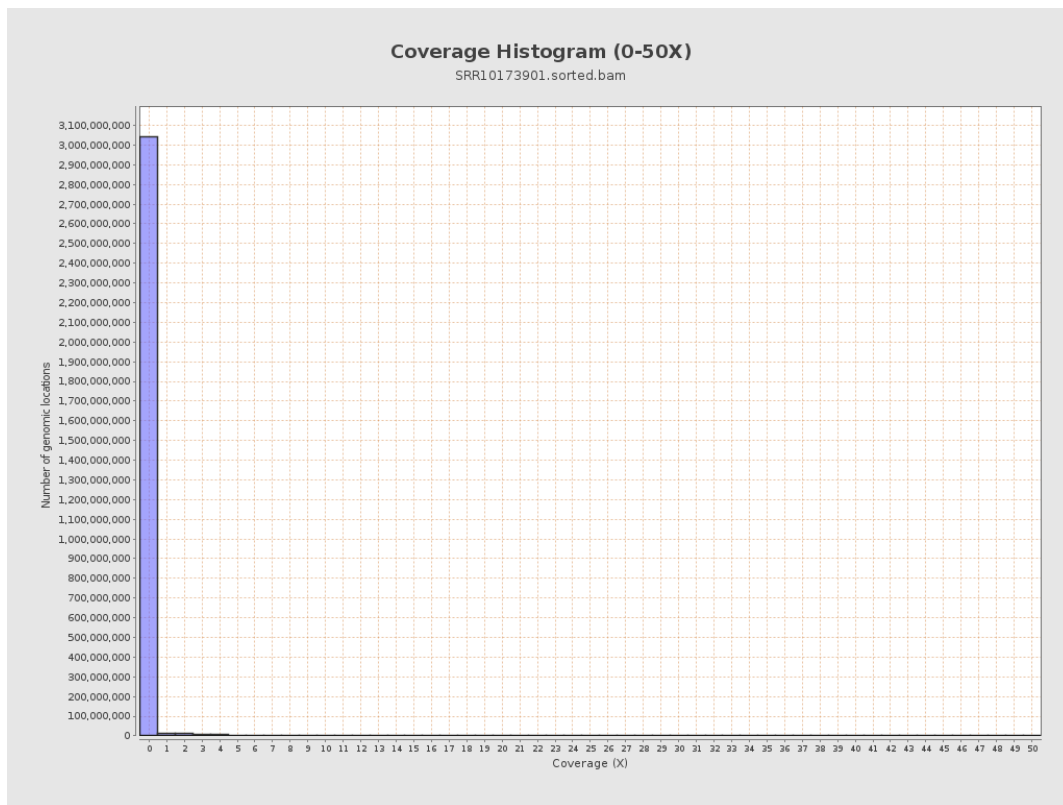
3. Results : Coverage across reference



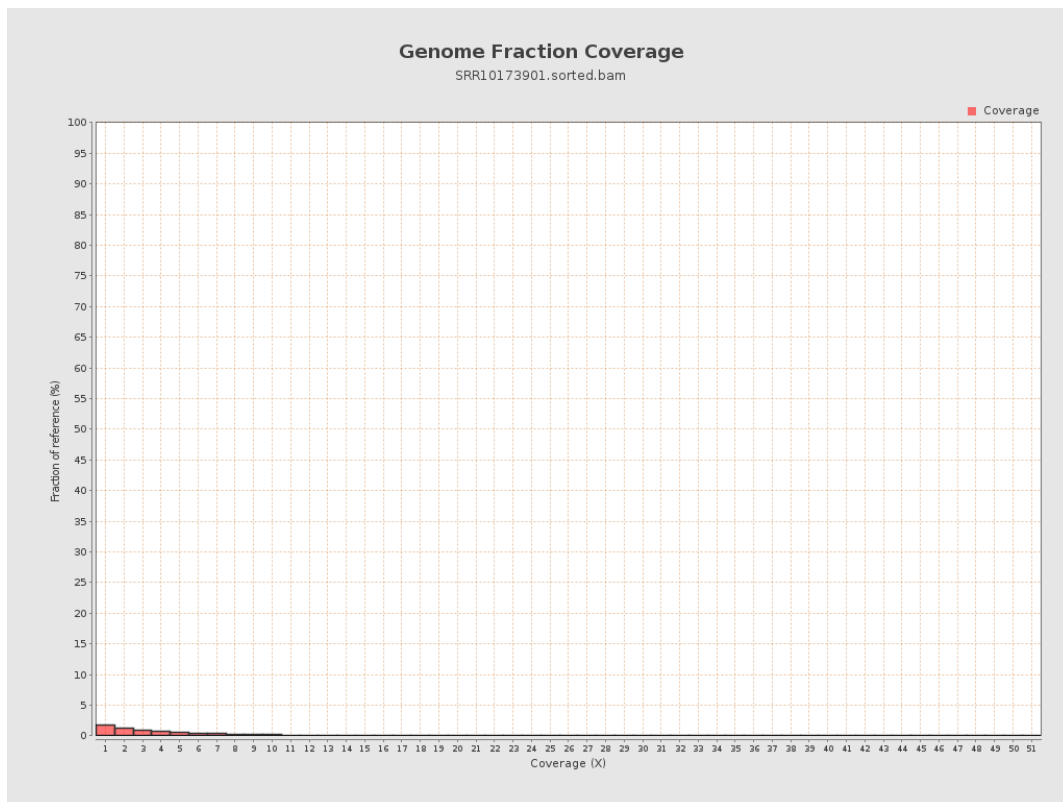
4. Results : Coverage Histogram



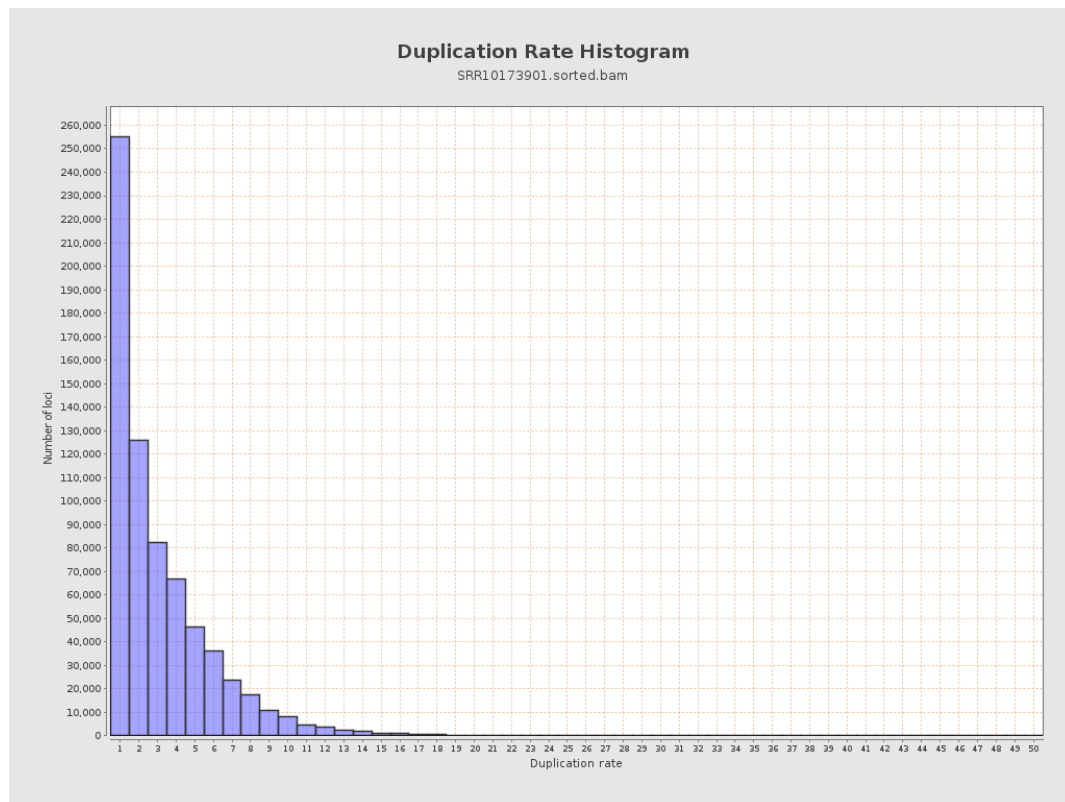
5. Results : Coverage Histogram (0-50X)



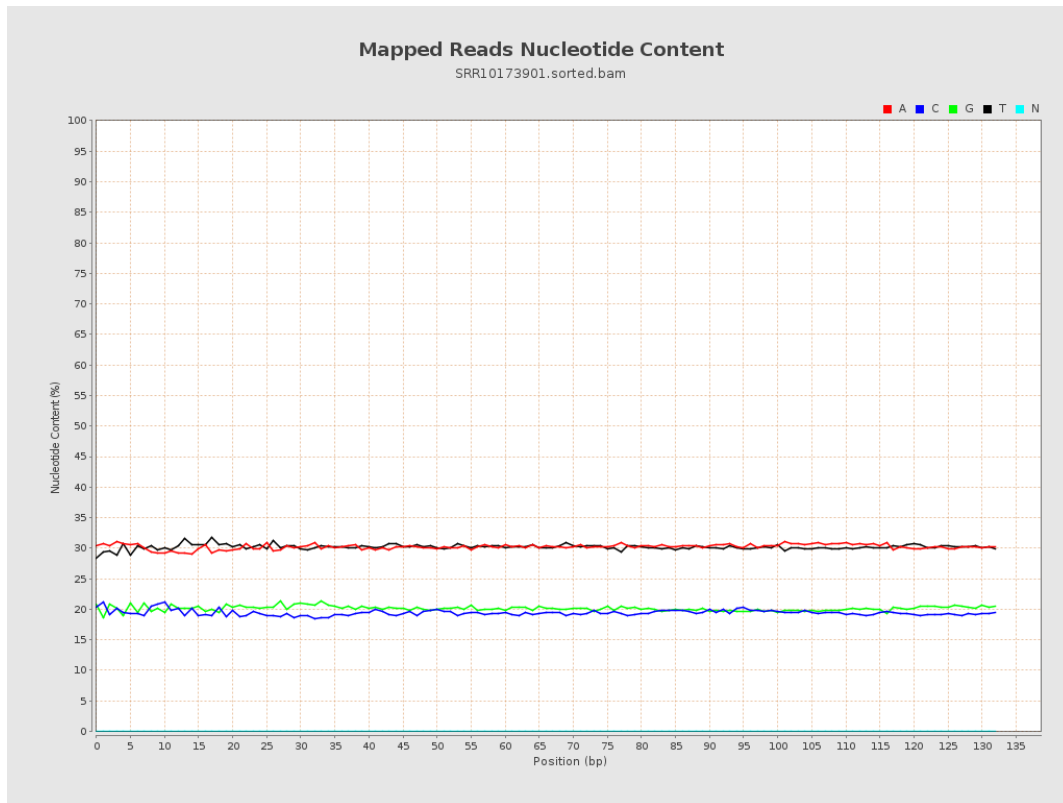
6. Results : Genome Fraction Coverage



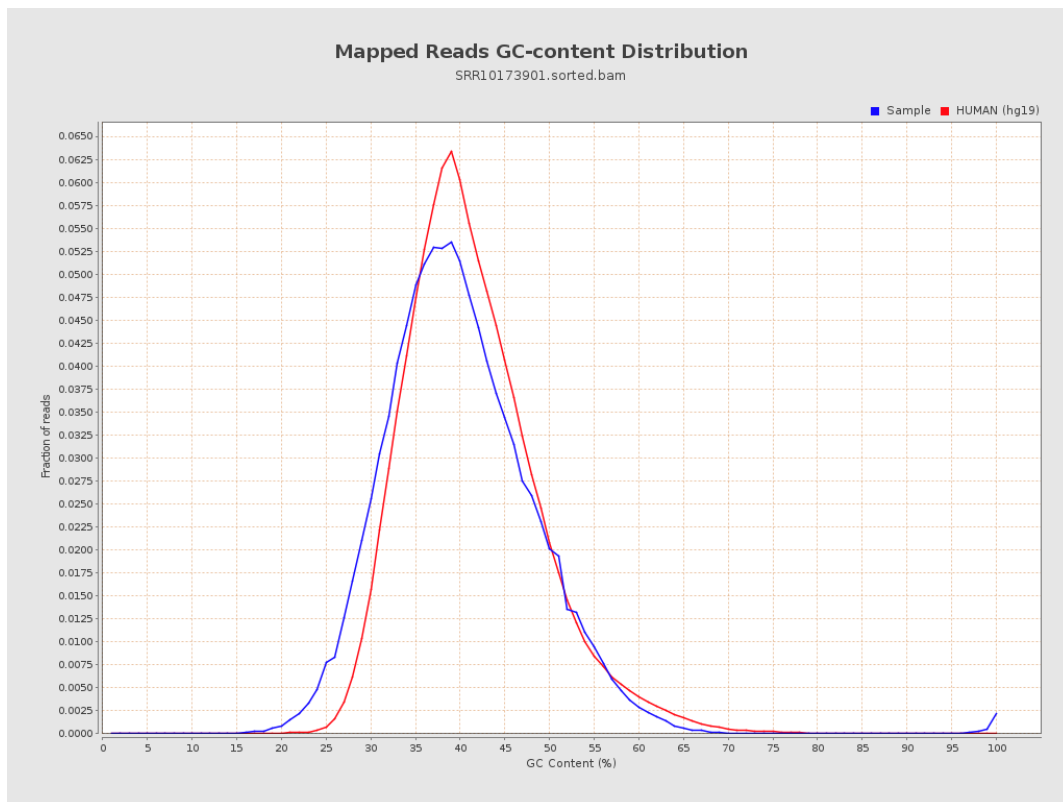
7. Results : Duplication Rate Histogram



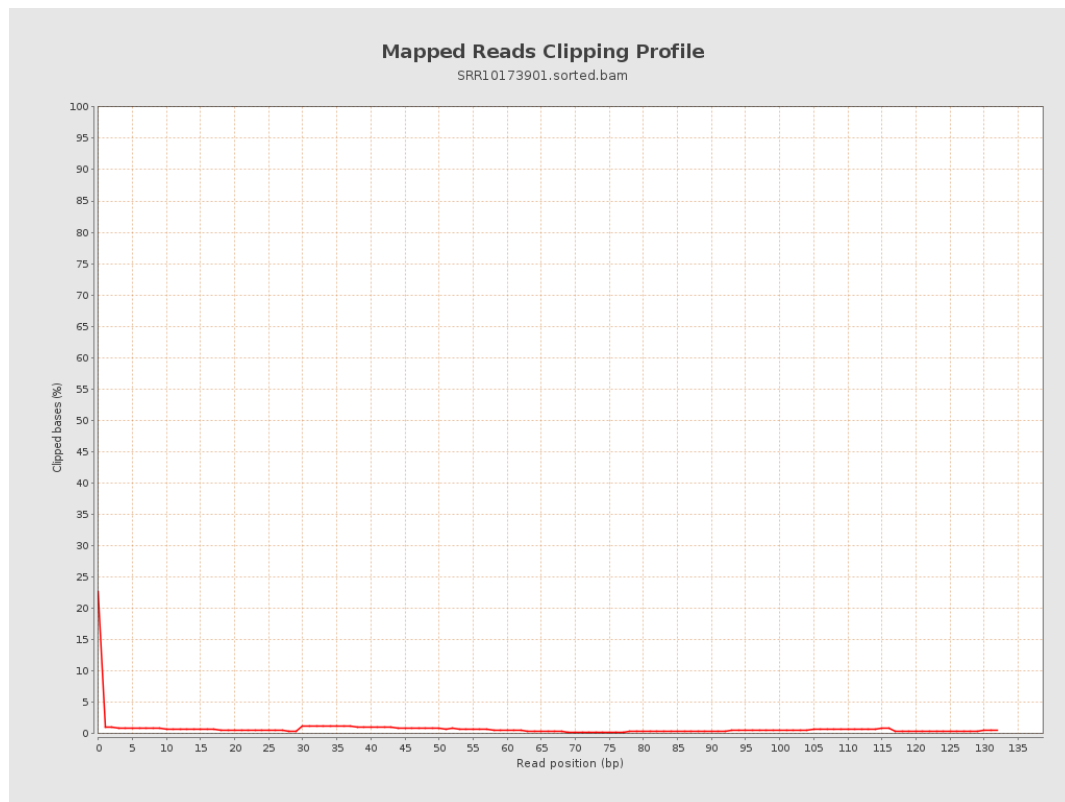
8. Results : Mapped Reads Nucleotide Content



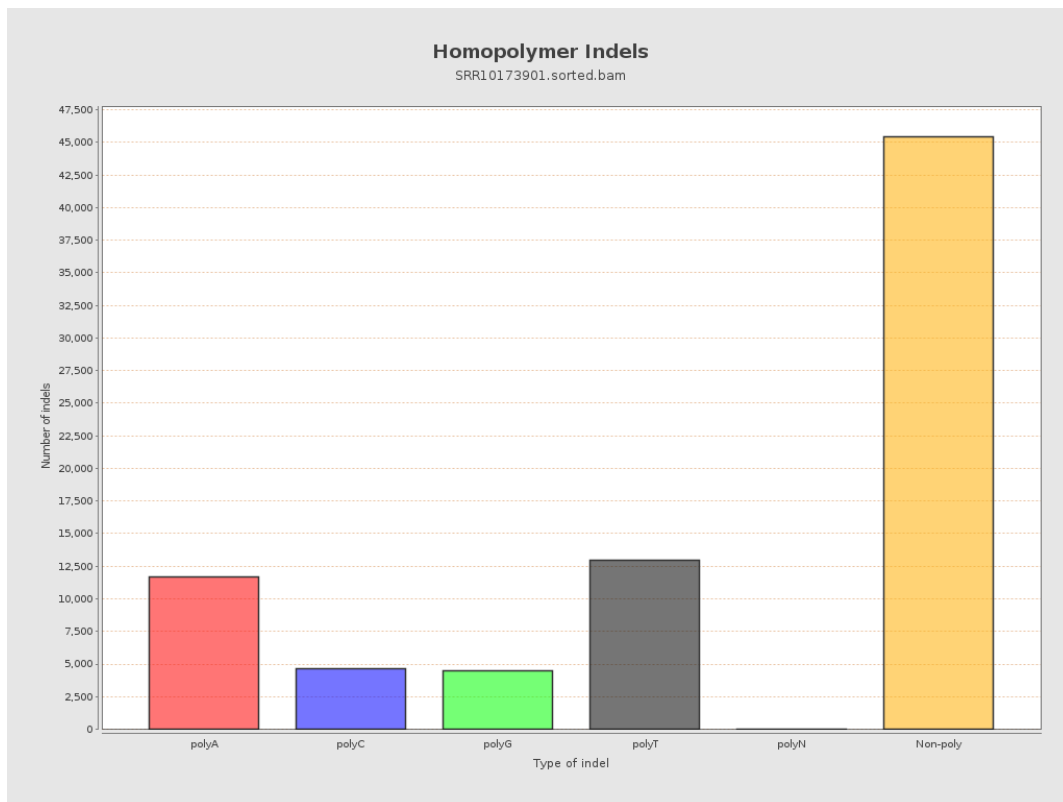
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



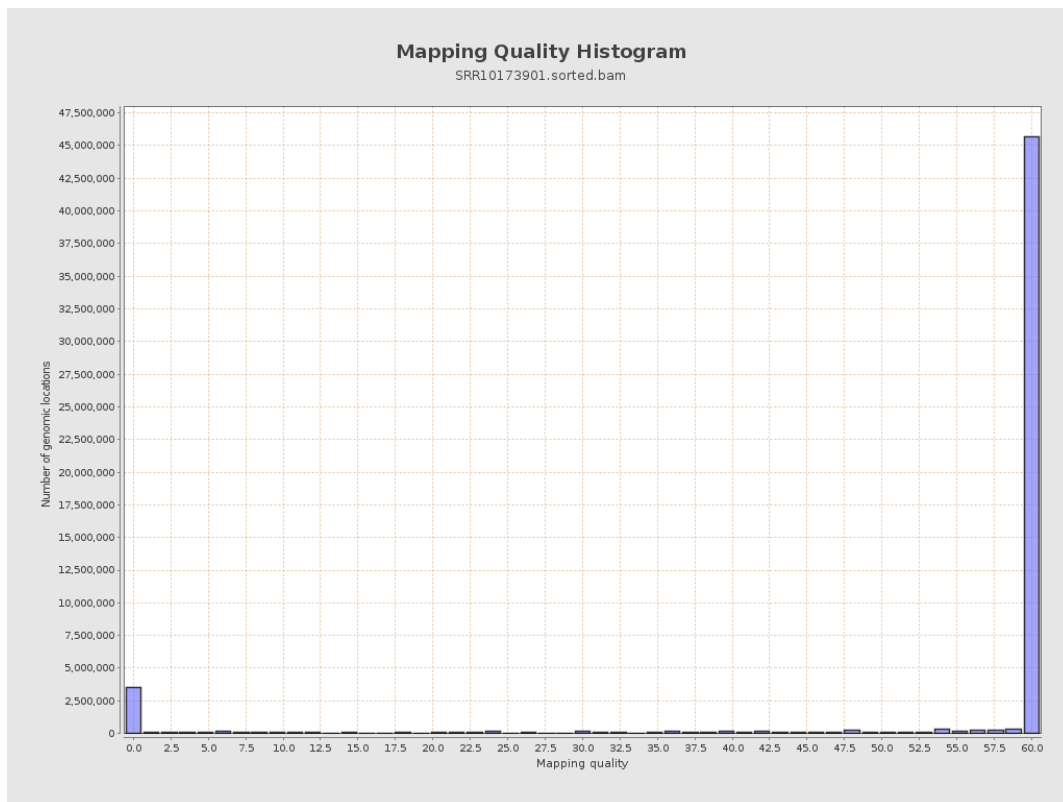
11. Results : Homopolymer Indels



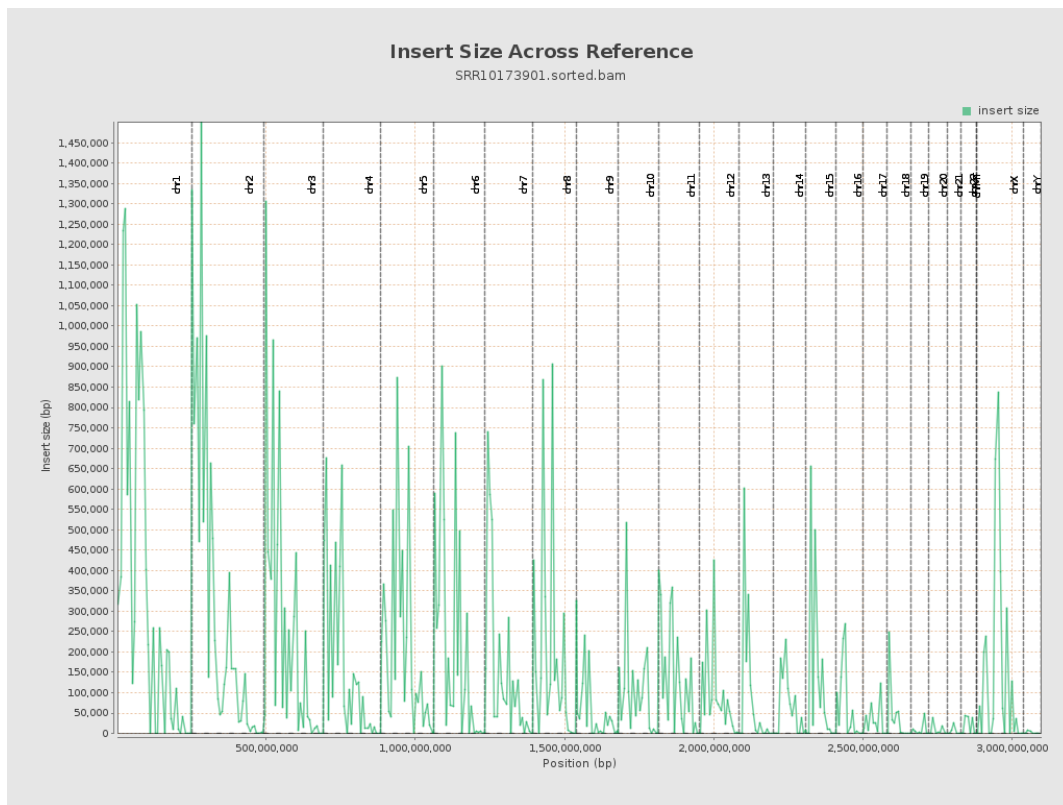
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

