

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:26:13

1. Input data & parameters

1.1. QualiMap command line

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qualimap bamqc -bam SRR10173907.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_SRR10173907 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173907_1.fastq.gz SRR10173907_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:26:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173907.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,740,742
Mapped reads	1,698,564 / 97.58%
Unmapped reads	42,178 / 2.42%
Mapped paired reads	1,698,564 / 97.58%
Mapped reads, first in pair	850,419 / 48.85%
Mapped reads, second in pair	848,145 / 48.72%
Mapped reads, both in pair	1,672,248 / 96.07%
Mapped reads, singletons	26,316 / 1.51%
Secondary alignments	0
Supplementary alignments	157,918 / 9.07%
Read min/max/mean length	30 / 133 / 128.04
Duplicated reads (estimated)	1,310,432 / 75.28%
Duplication rate	65%
Clipped reads	625,184 / 35.91%

2.2. ACGT Content

Number/percentage of A's	60,741,577 / 30.05%
Number/percentage of C's	39,711,856 / 19.65%
Number/percentage of T's	60,529,877 / 29.95%
Number/percentage of G's	41,130,907 / 20.35%
Number/percentage of N's	2,338 / 0%

GC Percentage	40%
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2.3. Coverage

Mean	0.0653
Standard Deviation	1.0738

2.4. Mapping Quality

Mean Mapping Quality	53.15
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2.5. Insert size

Mean	1,096,044.09
Standard Deviation	9,739,021.04
P25/Median/P75	150 / 207 / 293

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	2,083,333
Insertions	22,777
Mapped reads with at least one insertion	1.29%
Deletions	46,142
Mapped reads with at least one deletion	2.64%
Homopolymer indels	42.32%

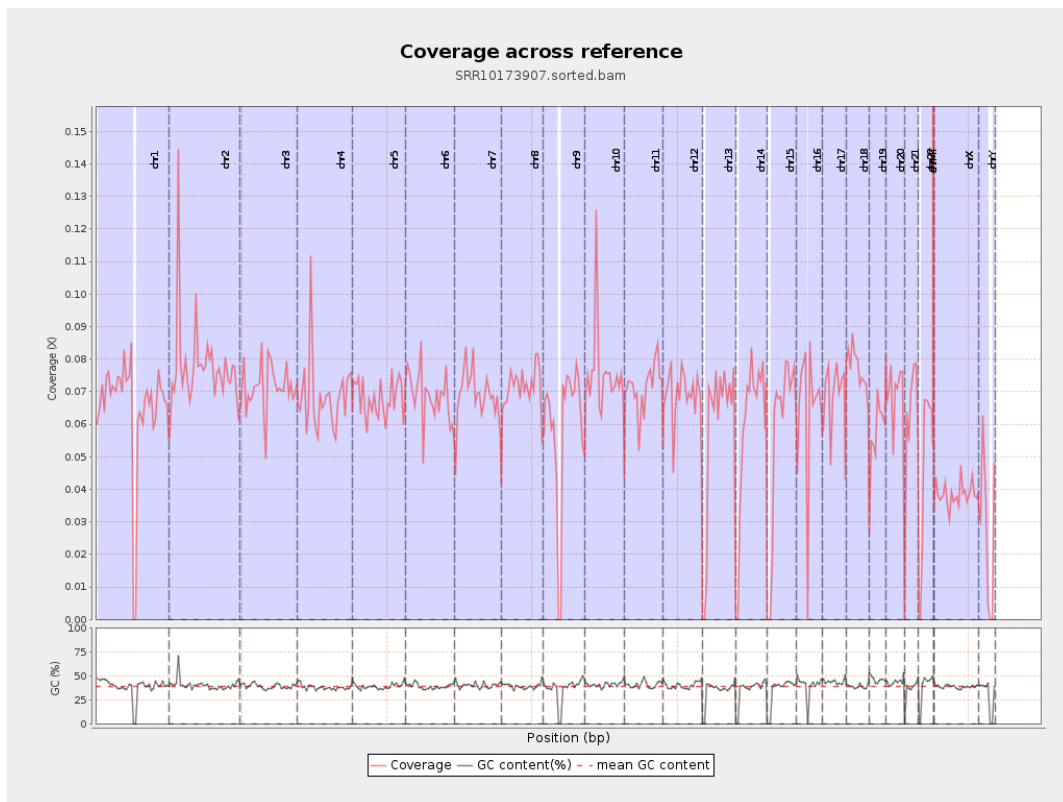
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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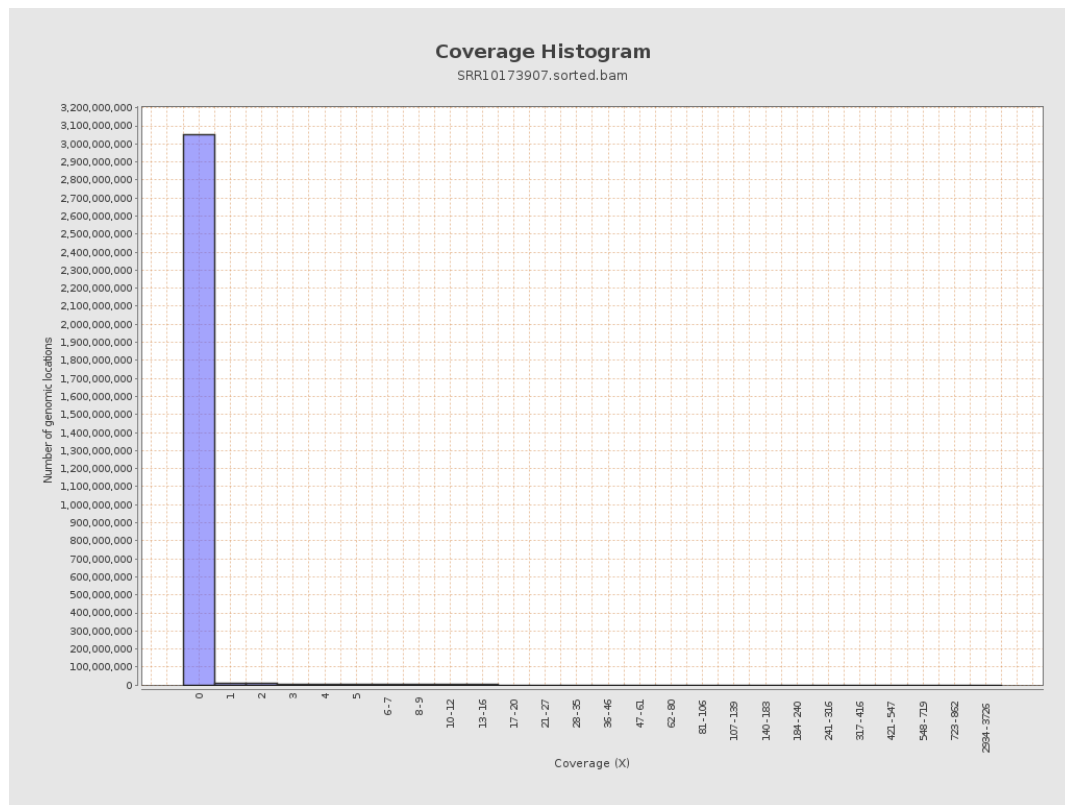
		bases	coverage	deviation
chr1	249250621	16260518	0.0652	0.8707
chr2	243199373	18902401	0.0777	2.7143
chr3	198022430	14060488	0.071	0.7611
chr4	191154276	13008438	0.0681	0.8452
chr5	180915260	12242807	0.0677	0.7427
chr6	171115067	11725366	0.0685	0.7908
chr7	159138663	11029967	0.0693	0.8411
chr8	146364022	10474065	0.0716	0.9467
chr9	141213431	8345865	0.0591	0.7908
chr10	135534747	10220263	0.0754	0.9823
chr11	135006516	9570827	0.0709	0.7595
chr12	133851895	9173195	0.0685	0.7445
chr13	115169878	6699279	0.0582	0.6942
chr14	107349540	6317872	0.0589	0.691
chr15	102531392	5844870	0.057	0.6679
chr16	90354753	5875314	0.065	0.7562
chr17	81195210	5555580	0.0684	0.753
chr18	78077248	6026278	0.0772	0.9826
chr19	59128983	3476540	0.0588	0.7462
chr20	63025520	4338806	0.0688	0.7597
chr21	48129895	2935576	0.061	0.7436
chr22	51304566	2329793	0.0454	0.6038
chrMT	16571	272454	16.4416	17.491
chrX	155270560	5968447	0.0384	0.5573

chrY	59373566	1576372	0.0266	0.5481
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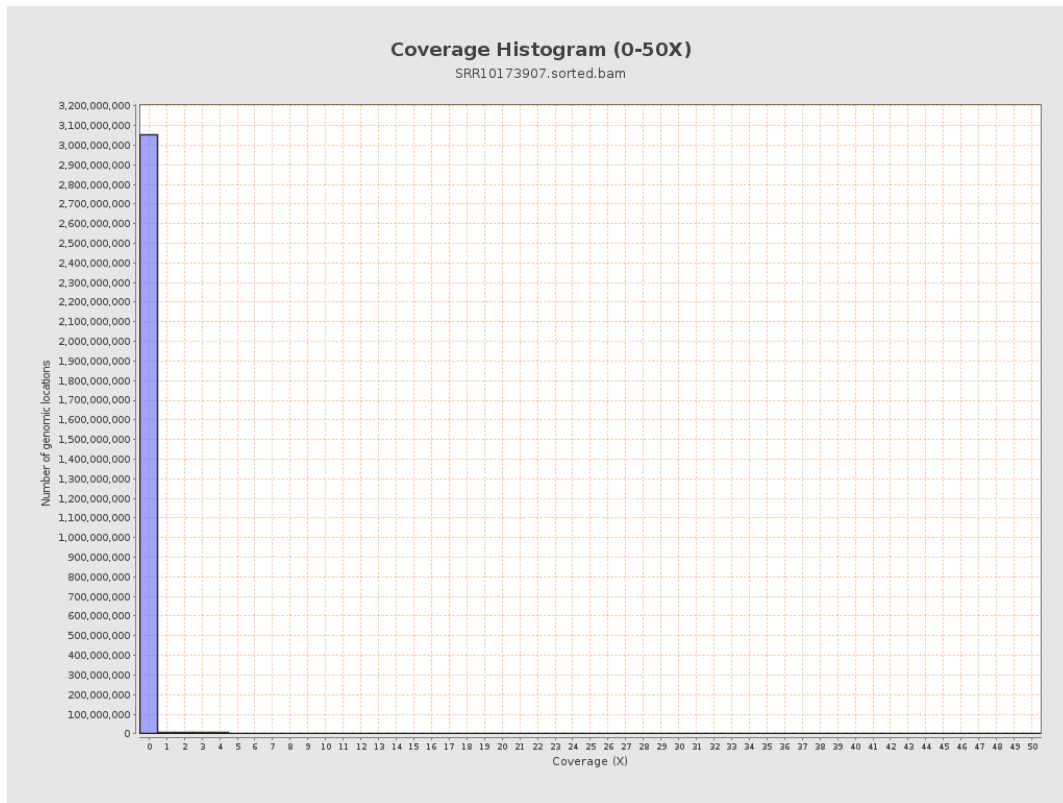
3. Results : Coverage across reference



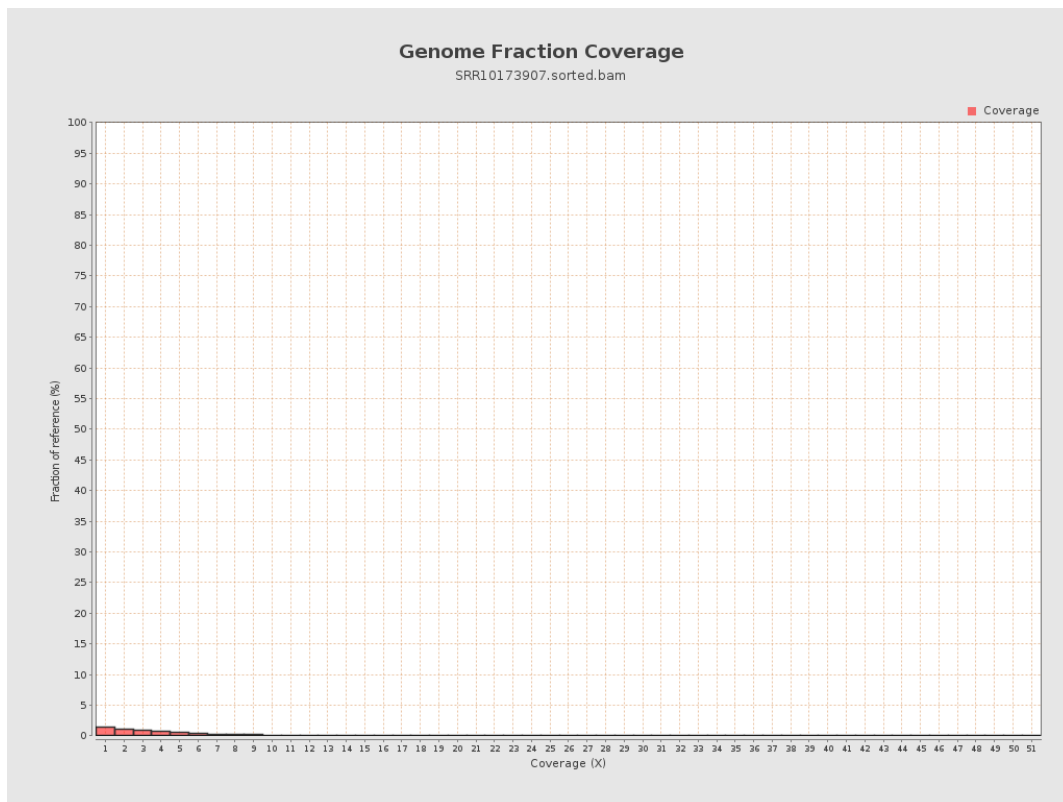
4. Results : Coverage Histogram



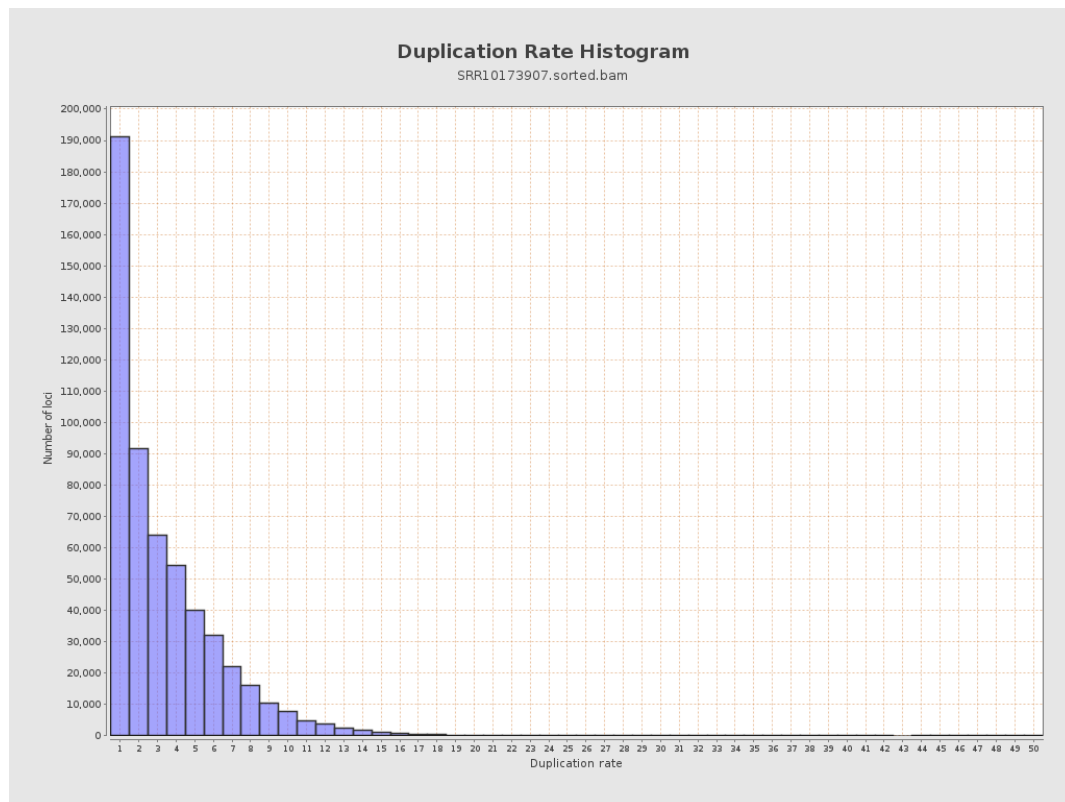
5. Results : Coverage Histogram (0-50X)



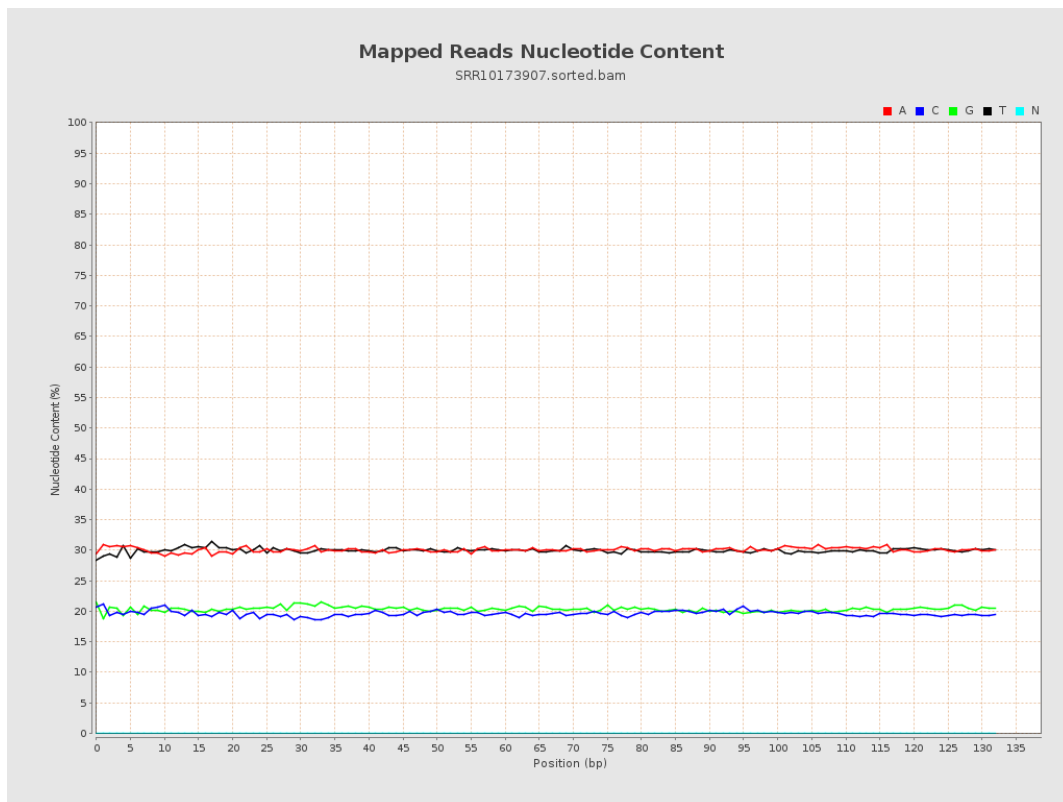
6. Results : Genome Fraction Coverage



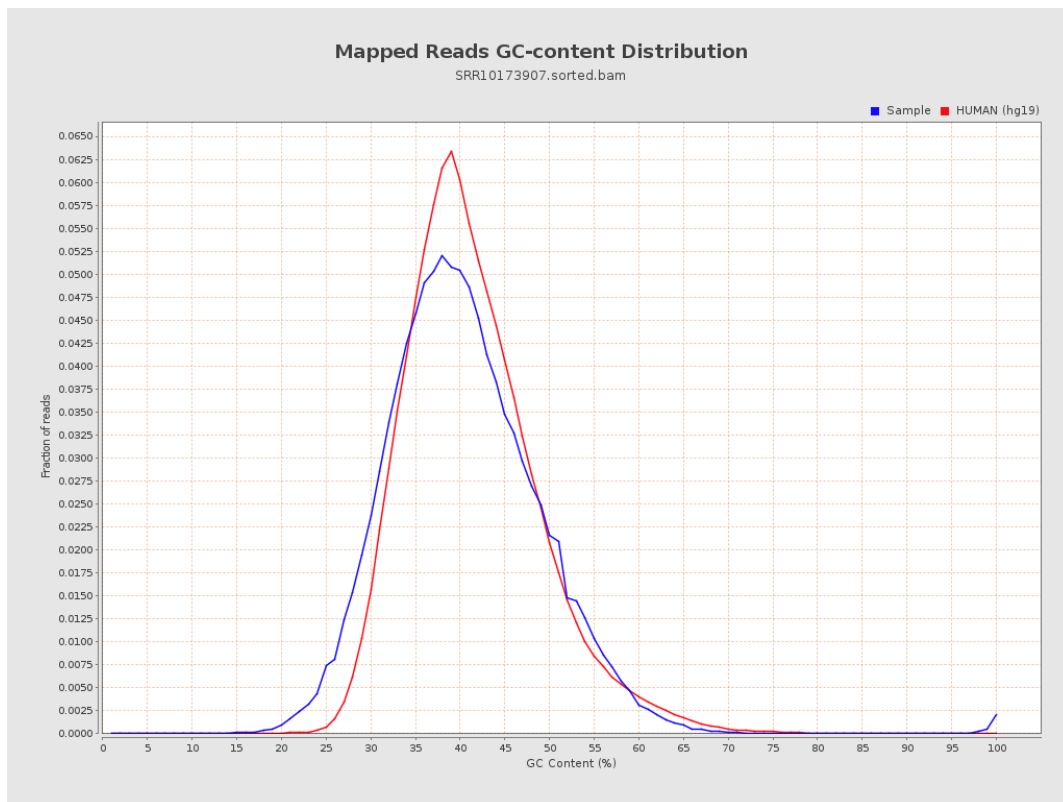
7. Results : Duplication Rate Histogram



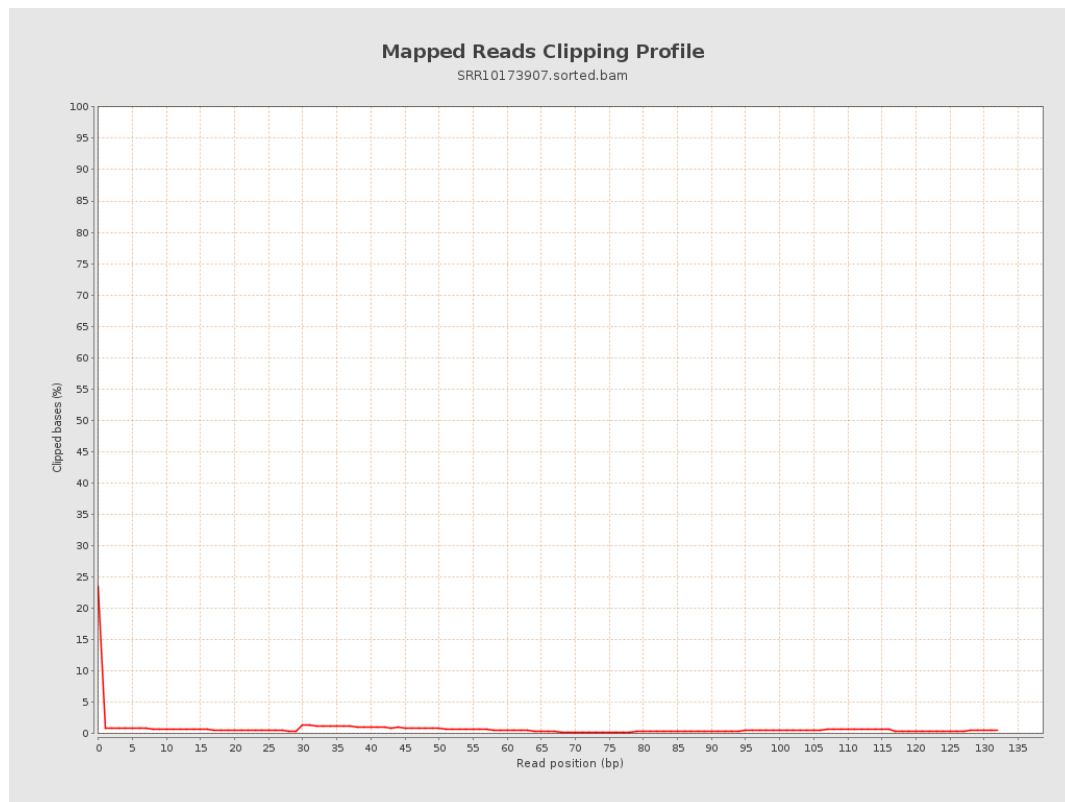
8. Results : Mapped Reads Nucleotide Content



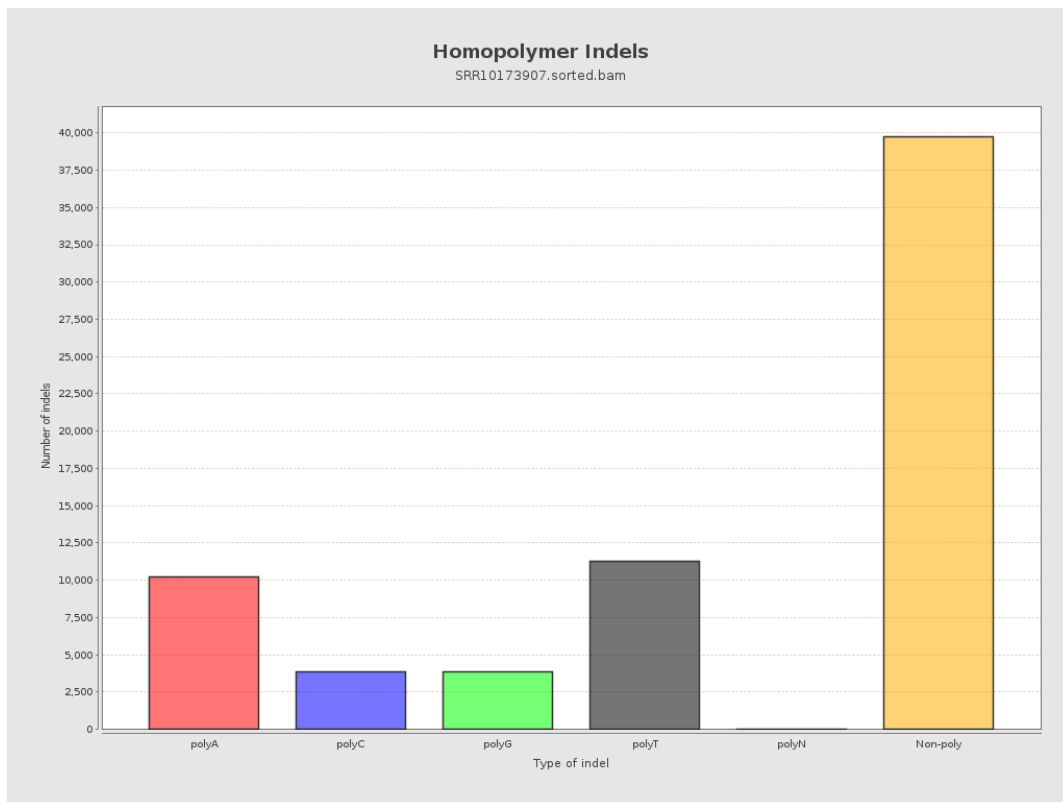
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



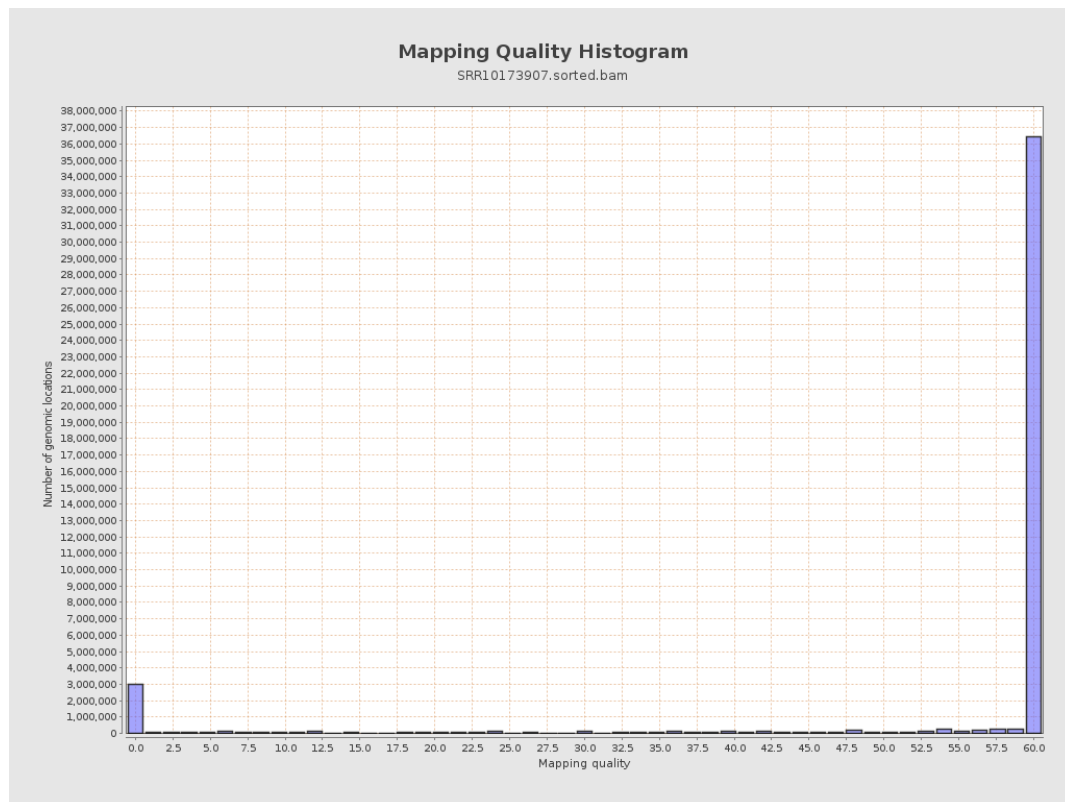
11. Results : Homopolymer Indels



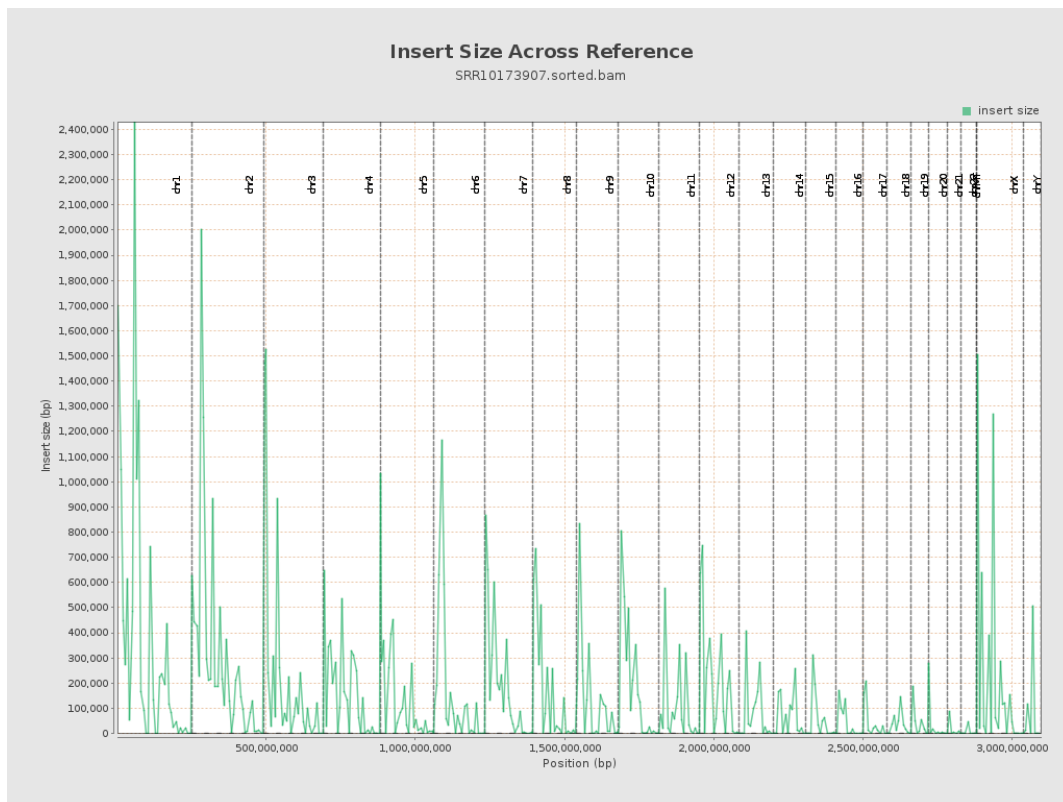
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

