

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 05:05:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174073.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_SRR10174073 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174073_1.fastq.gz SRR10174073_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 05:05:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174073.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,638,424
Mapped reads	7,472,338 / 97.83%
Unmapped reads	166,086 / 2.17%
Mapped paired reads	7,472,338 / 97.83%
Mapped reads, first in pair	3,735,860 / 48.91%
Mapped reads, second in pair	3,736,478 / 48.92%
Mapped reads, both in pair	7,363,956 / 96.41%
Mapped reads, singletons	108,382 / 1.42%
Secondary alignments	0
Supplementary alignments	1,039,750 / 13.61%
Read min/max/mean length	30 / 133 / 125.86
Duplicated reads (estimated)	6,060,930 / 79.35%
Duplication rate	65.13%
Clipped reads	4,091,436 / 53.56%

2.2. ACGT Content

Number/percentage of A's	252,353,015 / 29.9%
Number/percentage of C's	167,129,993 / 19.8%
Number/percentage of T's	250,535,309 / 29.68%
Number/percentage of G's	174,002,405 / 20.62%
Number/percentage of N's	6,655 / 0%

GC Percentage	40.42%
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2.3. Coverage

Mean	0.2728
Standard Deviation	5.1316

2.4. Mapping Quality

Mean Mapping Quality	52.43
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2.5. Insert size

Mean	1,347,894.43
Standard Deviation	10,984,157.74
P25/Median/P75	105 / 156 / 243

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	7,076,810
Insertions	92,579
Mapped reads with at least one insertion	1.19%
Deletions	244,787
Mapped reads with at least one deletion	3.19%
Homopolymer indels	40.75%

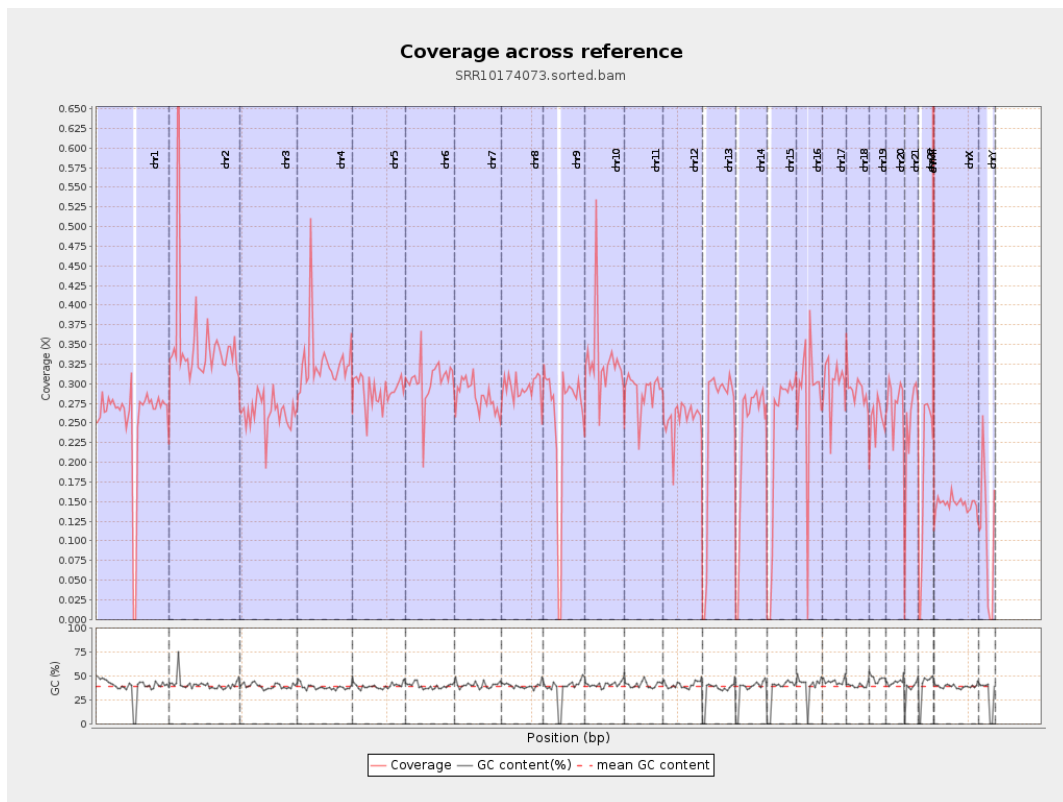
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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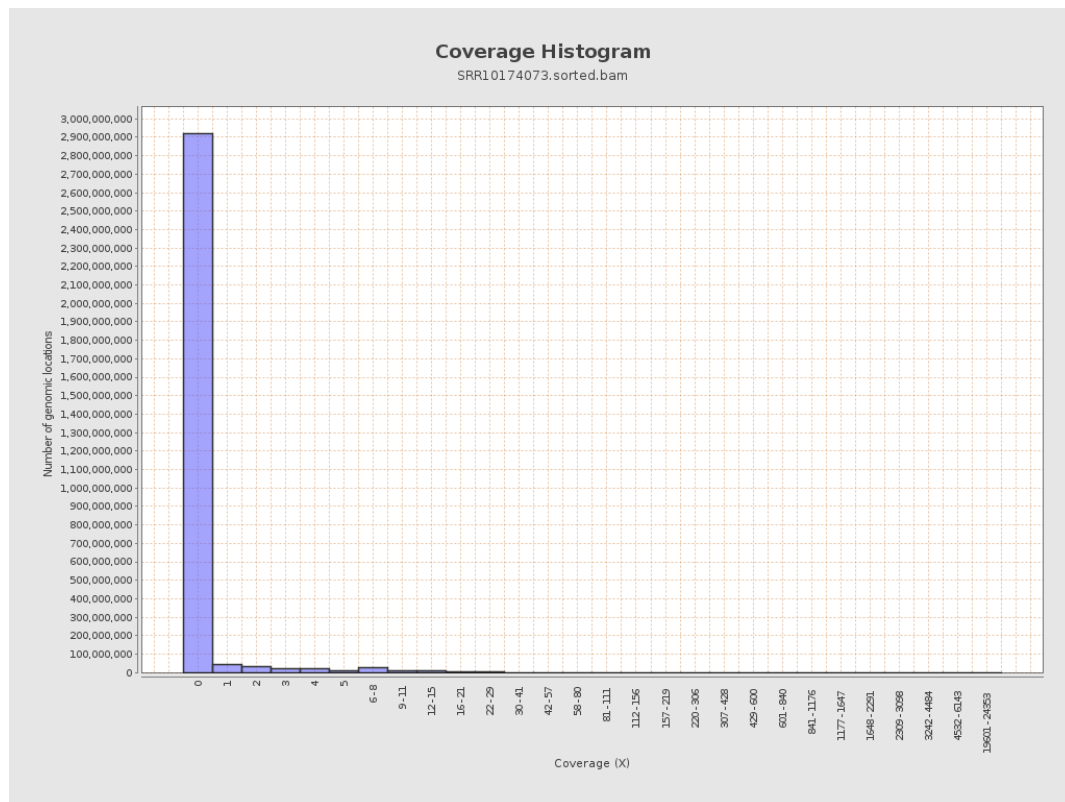
		bases	coverage	deviation
chr1	249250621	63564963	0.255	2.2355
chr2	243199373	85794511	0.3528	16.9875
chr3	198022430	52173488	0.2635	1.5435
chr4	191154276	62489059	0.3269	2.4456
chr5	180915260	52493136	0.2902	1.6379
chr6	171115067	52092622	0.3044	1.9162
chr7	159138663	45249876	0.2843	2.2005
chr8	146364022	43189820	0.2951	2.5162
chr9	141213431	36164494	0.2561	2.2203
chr10	135534747	44625872	0.3293	2.7532
chr11	135006516	39211568	0.2904	1.7142
chr12	133851895	34143930	0.2551	1.5854
chr13	115169878	28496419	0.2474	1.5233
chr14	107349540	24873715	0.2317	1.4723
chr15	102531392	23878020	0.2329	1.4797
chr16	90354753	25648618	0.2839	2.0899
chr17	81195210	24285027	0.2991	1.7867
chr18	78077248	22852344	0.2927	2.9706
chr19	59128983	15104093	0.2554	1.8853
chr20	63025520	17450153	0.2769	1.6787
chr21	48129895	11701505	0.2431	1.9001
chr22	51304566	9477974	0.1847	1.5526
chrMT	16571	860230	51.9118	42.1654
chrX	155270560	22776535	0.1467	1.1689

chrY	59373566	6014803	0.1013	1.6654
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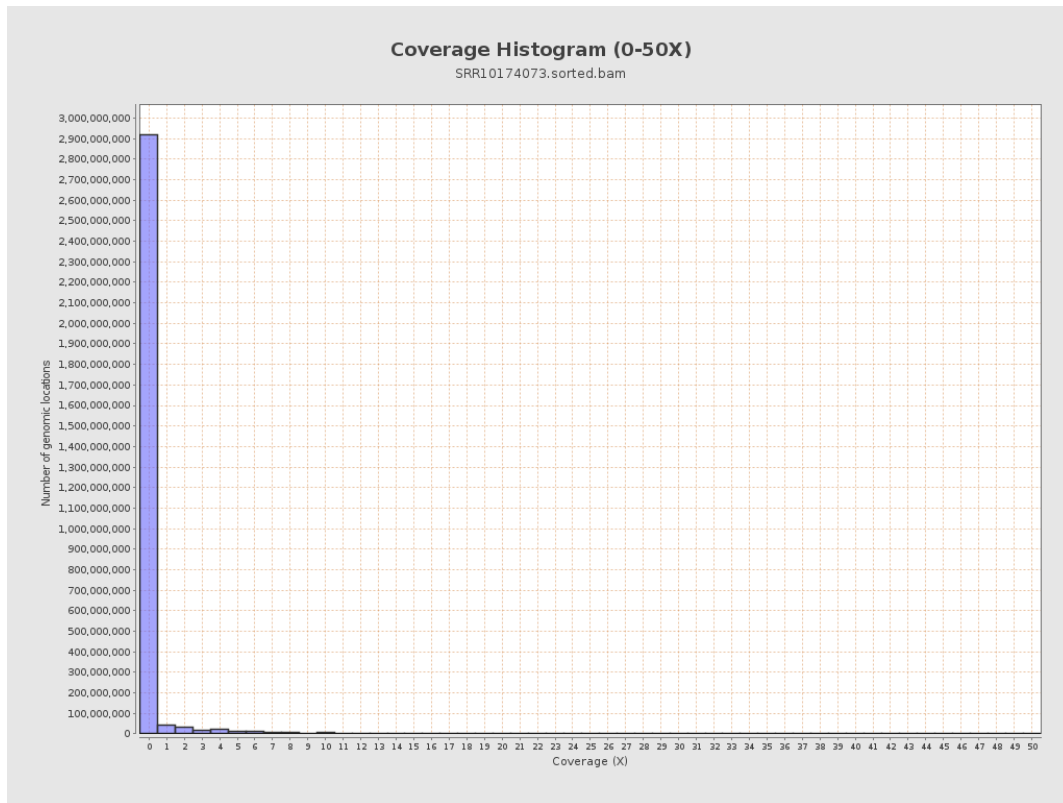
3. Results : Coverage across reference



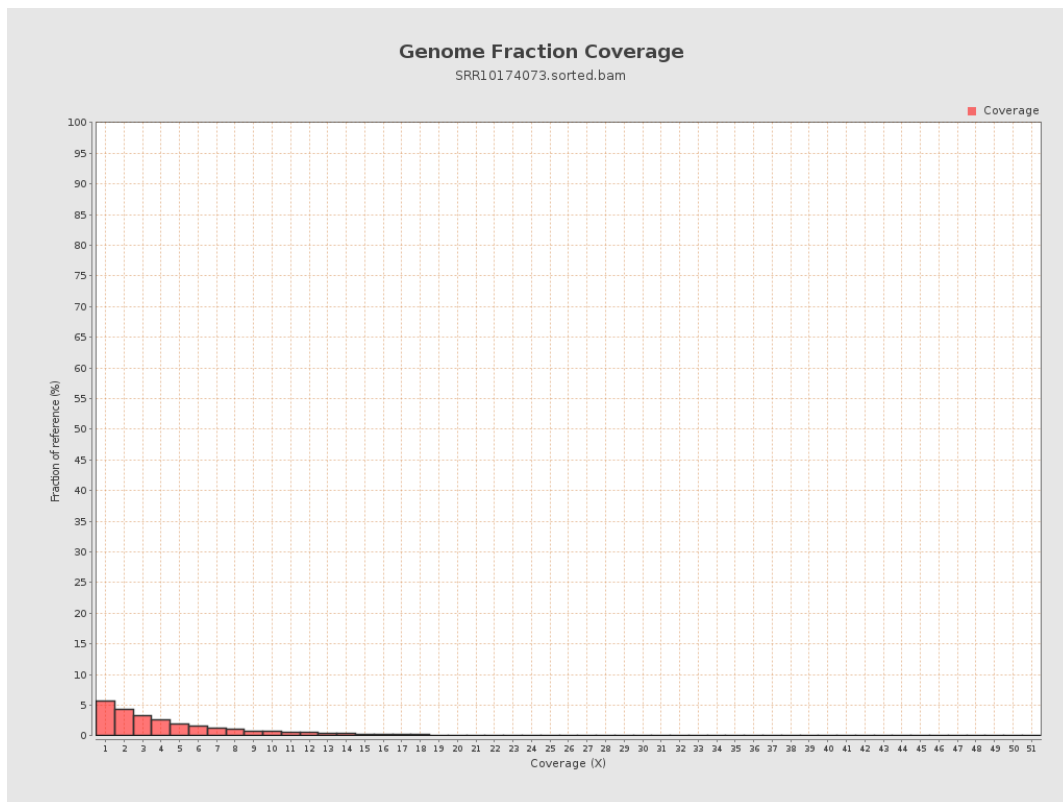
4. Results : Coverage Histogram



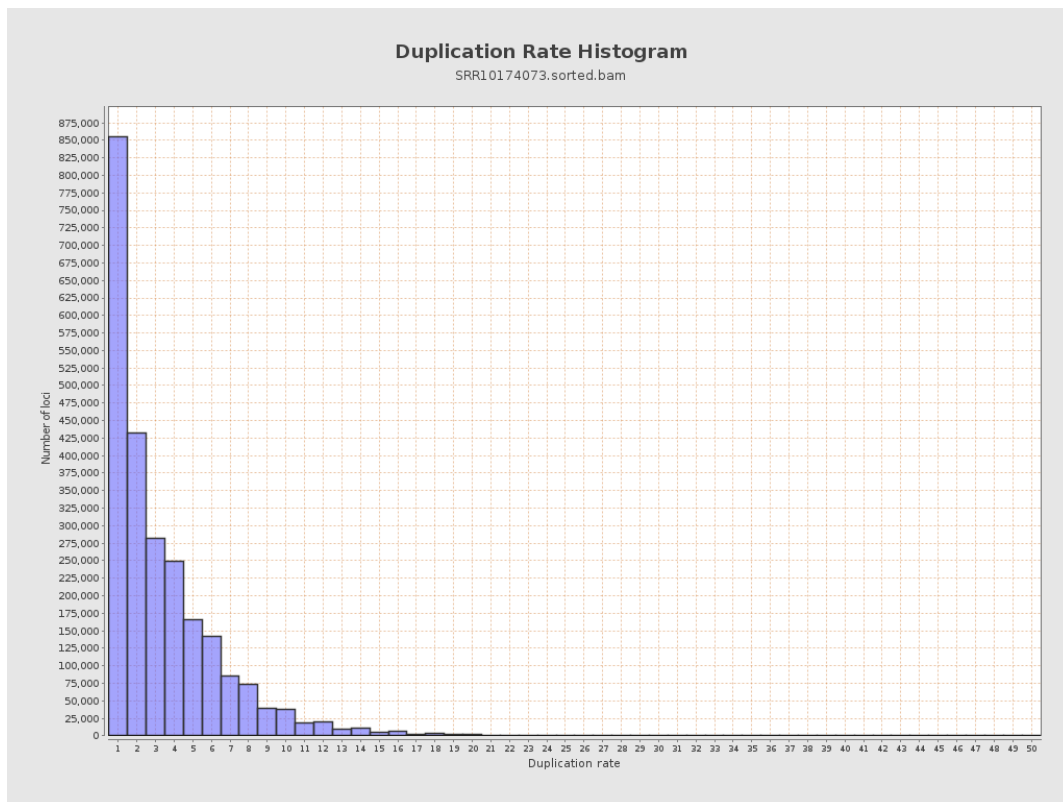
5. Results : Coverage Histogram (0-50X)



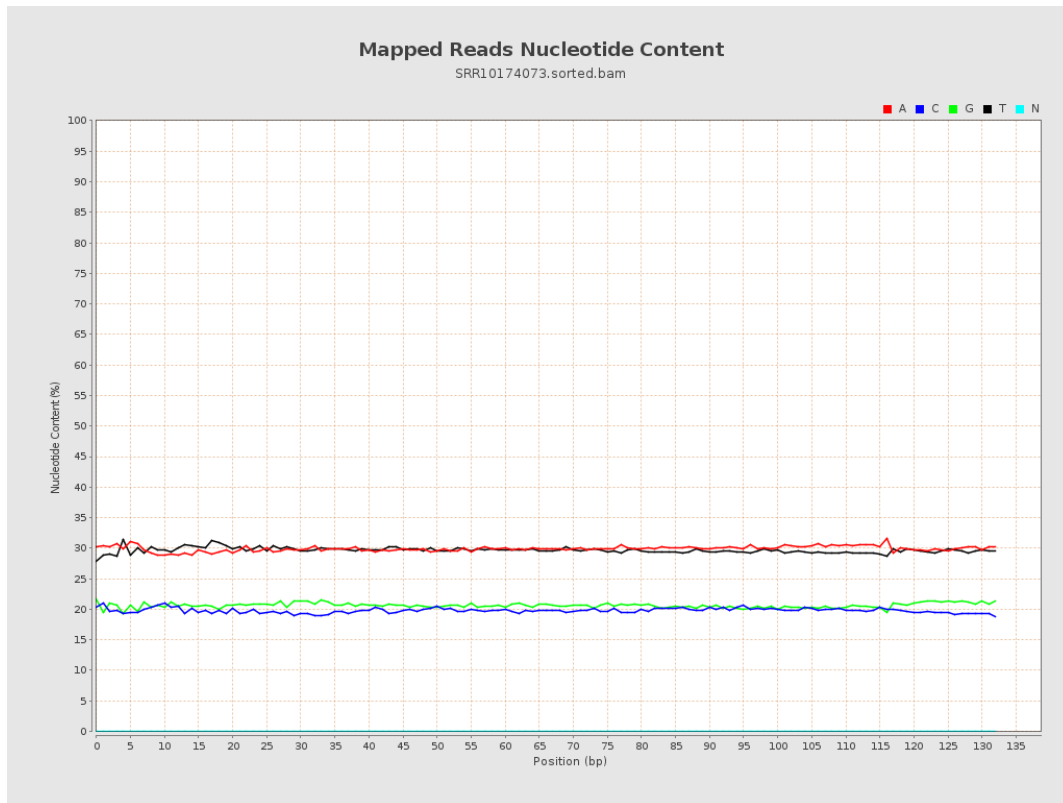
6. Results : Genome Fraction Coverage



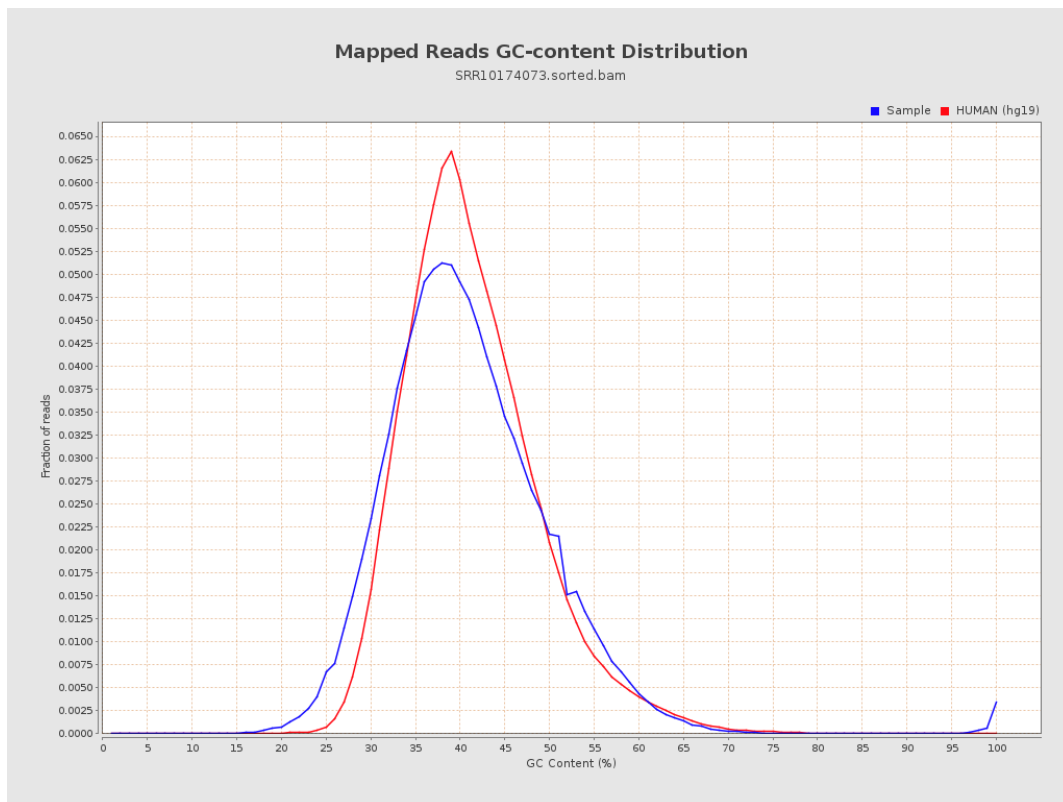
7. Results : Duplication Rate Histogram



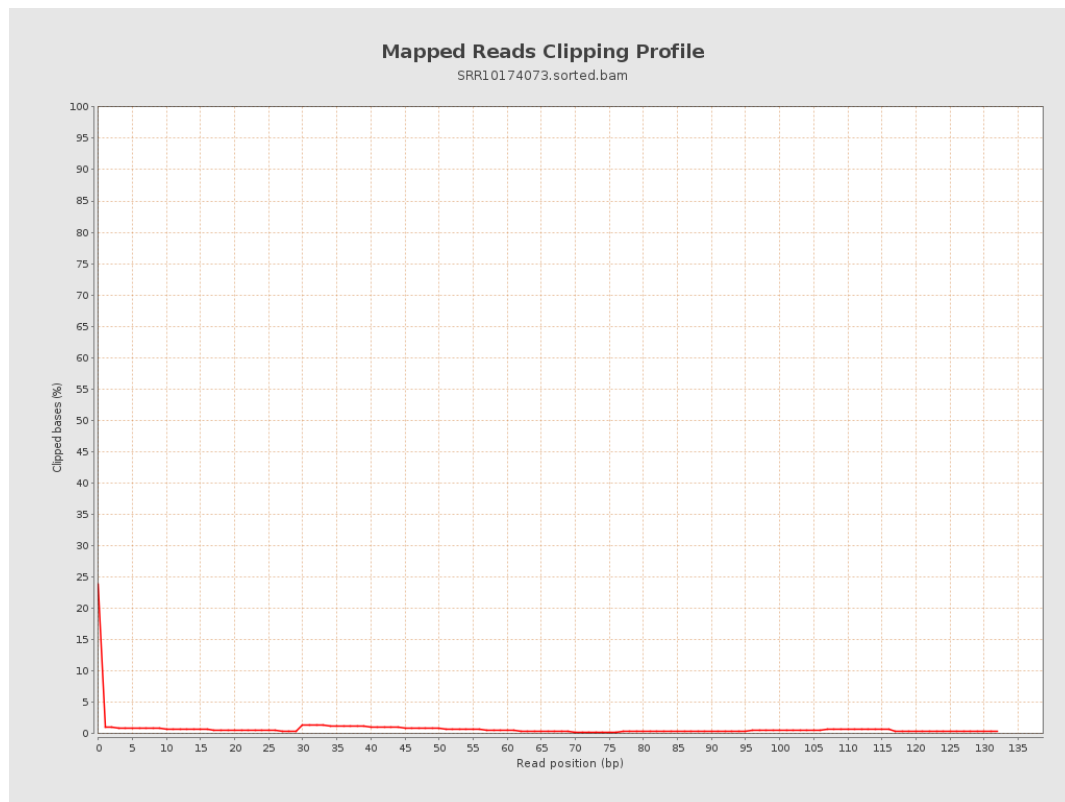
8. Results : Mapped Reads Nucleotide Content



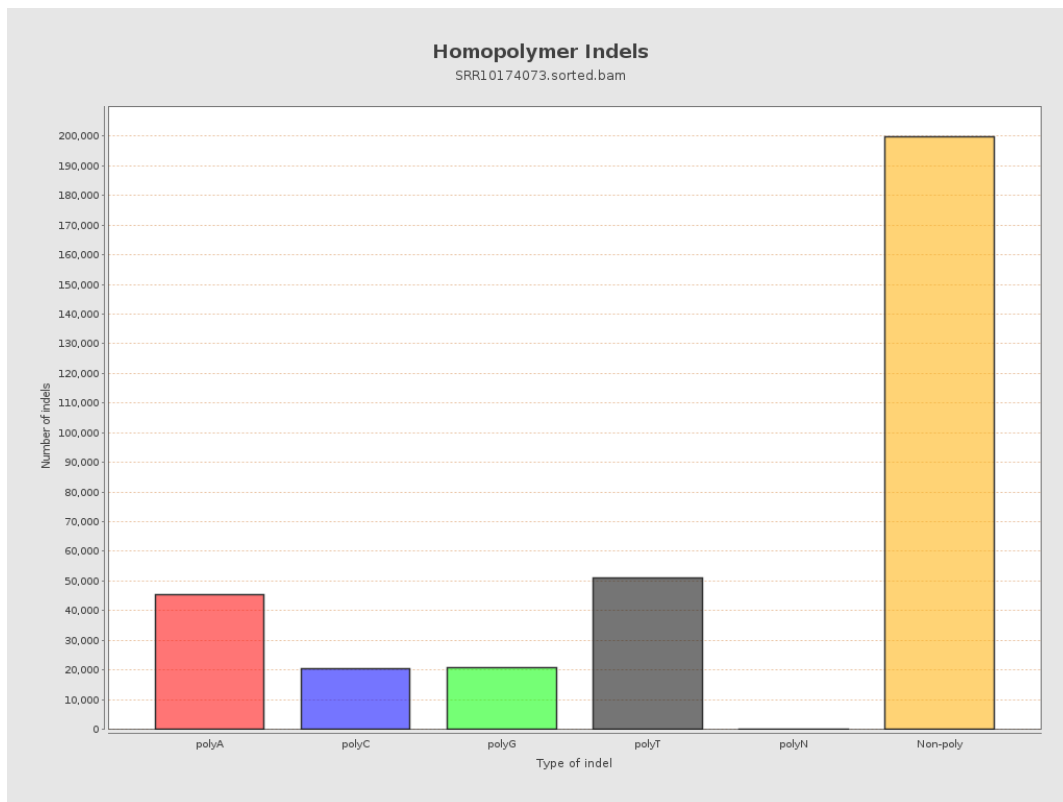
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



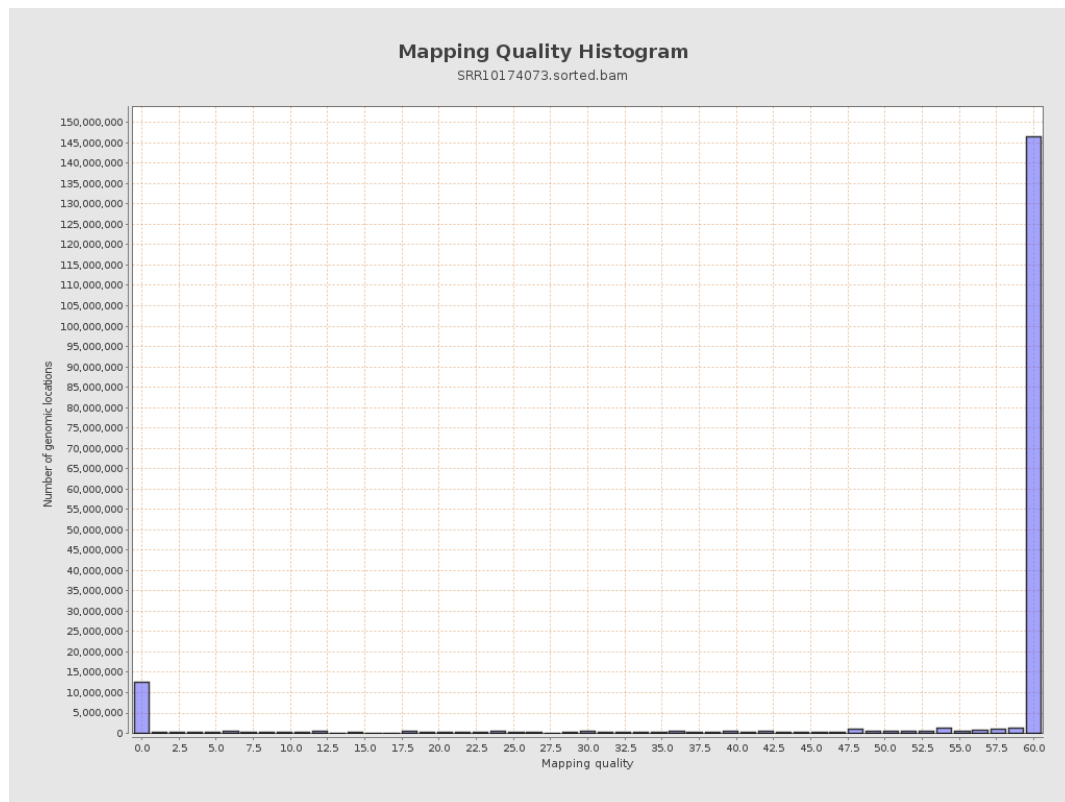
11. Results : Homopolymer Indels



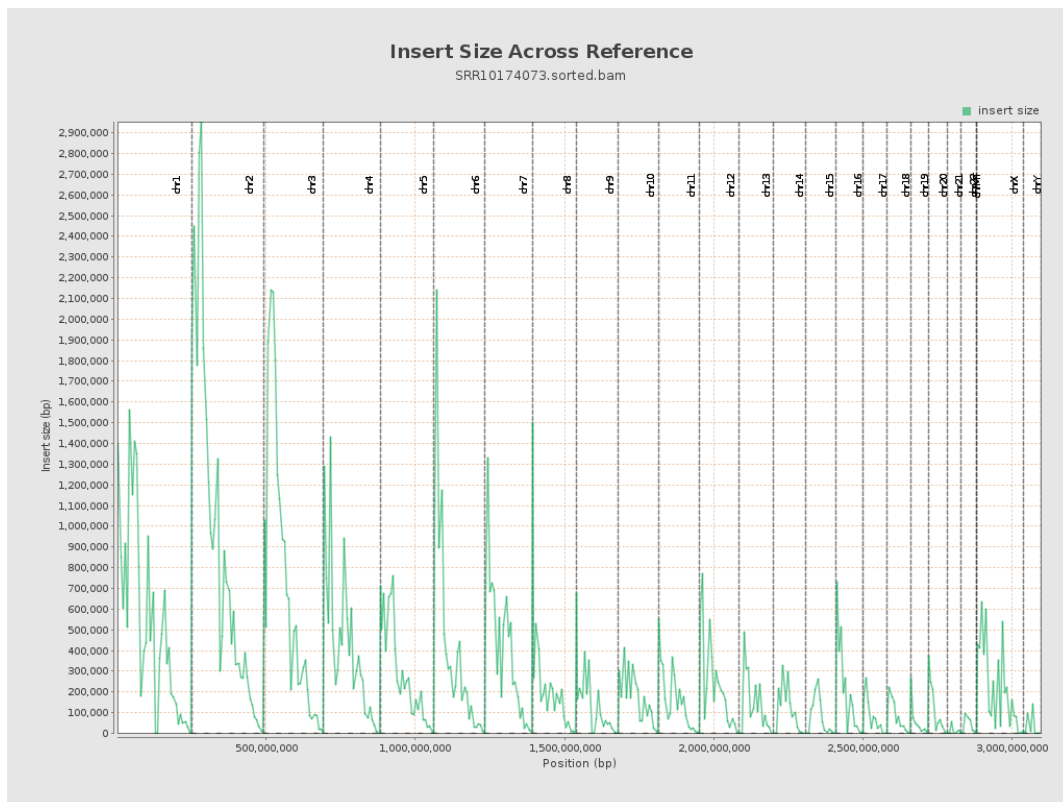
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

