

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 01:56:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174053.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_SRR10174053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174053_1.fastq.gz SRR10174053_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 01:56:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,693,574
Mapped reads	10,416,792 / 97.41%
Unmapped reads	276,782 / 2.59%
Mapped paired reads	10,416,792 / 97.41%
Mapped reads, first in pair	5,220,849 / 48.82%
Mapped reads, second in pair	5,195,943 / 48.59%
Mapped reads, both in pair	10,226,600 / 95.63%
Mapped reads, singletons	190,192 / 1.78%
Secondary alignments	0
Supplementary alignments	1,017,901 / 9.52%
Read min/max/mean length	30 / 133 / 128.19
Duplicated reads (estimated)	8,280,105 / 77.43%
Duplication rate	65.83%
Clipped reads	4,553,344 / 42.58%

2.2. ACGT Content

Number/percentage of A's	368,724,146 / 30.16%
Number/percentage of C's	238,294,693 / 19.49%
Number/percentage of T's	368,404,462 / 30.13%
Number/percentage of G's	247,093,148 / 20.21%
Number/percentage of N's	14,228 / 0%

GC Percentage	39.7%
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2.3. Coverage

Mean	0.3951
Standard Deviation	5.6306

2.4. Mapping Quality

Mean Mapping Quality	52.73
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2.5. Insert size

Mean	952,929.26
Standard Deviation	8,771,725.64
P25/Median/P75	146 / 202 / 288

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	12,323,214
Insertions	126,188
Mapped reads with at least one insertion	1.17%
Deletions	280,392
Mapped reads with at least one deletion	2.62%
Homopolymer indels	42.86%

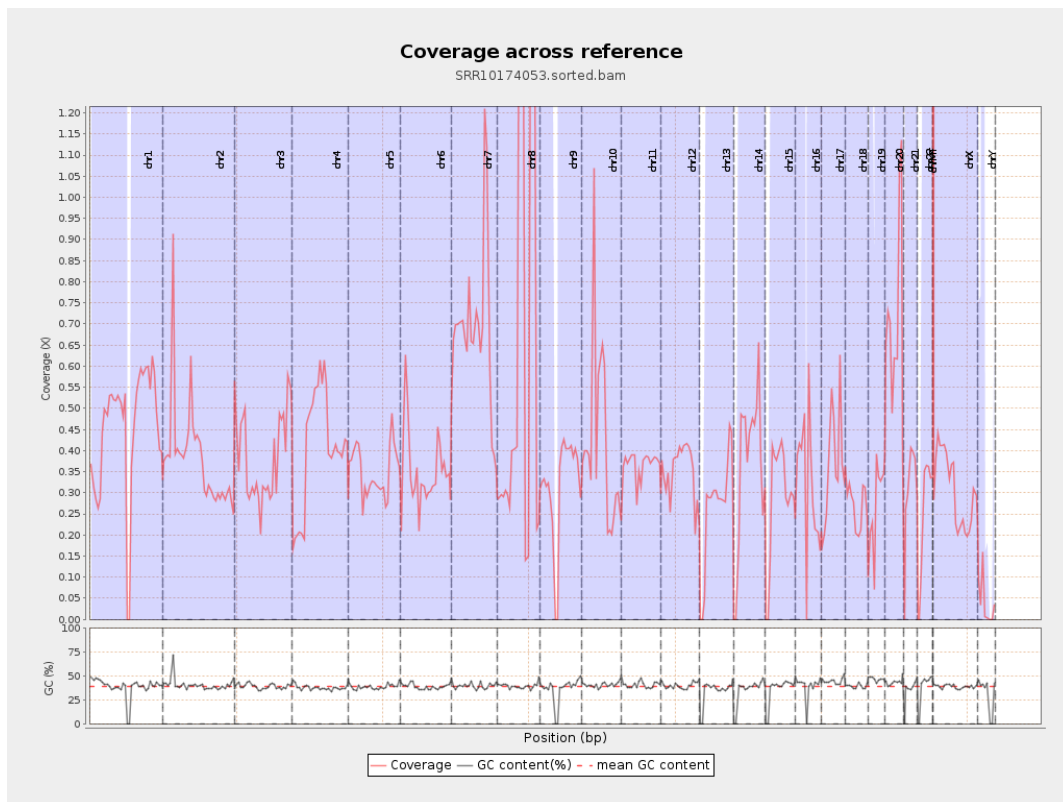
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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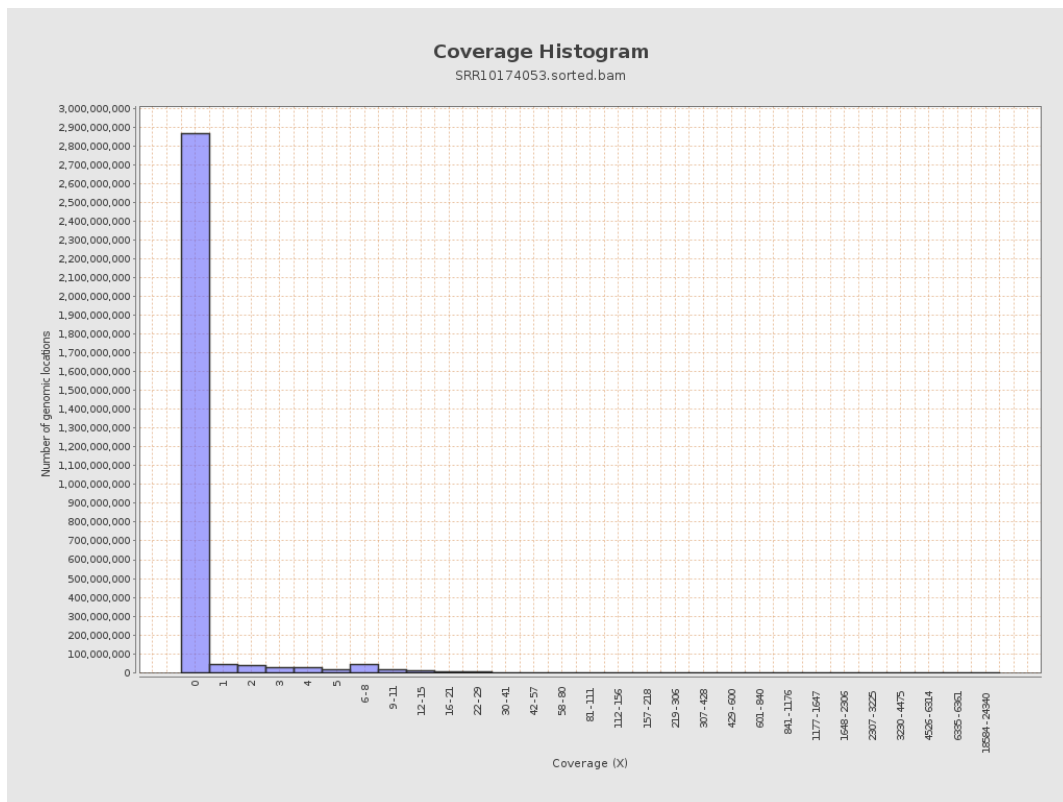
		bases	coverage	deviation
chr1	249250621	112463177	0.4512	3.101
chr2	243199373	92469794	0.3802	16.9912
chr3	198022430	76220385	0.3849	1.8734
chr4	191154276	78167043	0.4089	2.7023
chr5	180915260	63224121	0.3495	1.7621
chr6	171115067	60532860	0.3538	1.9298
chr7	159138663	108474947	0.6816	6.2822
chr8	146364022	111833133	0.7641	3.6472
chr9	141213431	44655395	0.3162	2.48
chr10	135534747	56669524	0.4181	7.3889
chr11	135006516	49200635	0.3644	1.9033
chr12	133851895	47224811	0.3528	1.7886
chr13	115169878	31064202	0.2697	1.5683
chr14	107349540	40298246	0.3754	1.8705
chr15	102531392	29379100	0.2865	1.5841
chr16	90354753	28740254	0.3181	2.8751
chr17	81195210	29828071	0.3674	2.1387
chr18	78077248	21330793	0.2732	3.3198
chr19	59128983	15873294	0.2685	2.058
chr20	63025520	46422136	0.7366	2.6687
chr21	48129895	14915420	0.3099	1.9196
chr22	51304566	12575922	0.2451	1.4124
chrMT	16571	1787468	107.8672	83.0932
chrX	155270560	47537822	0.3062	1.6913

chrY	59373566	2332596	0.0393	1.5962
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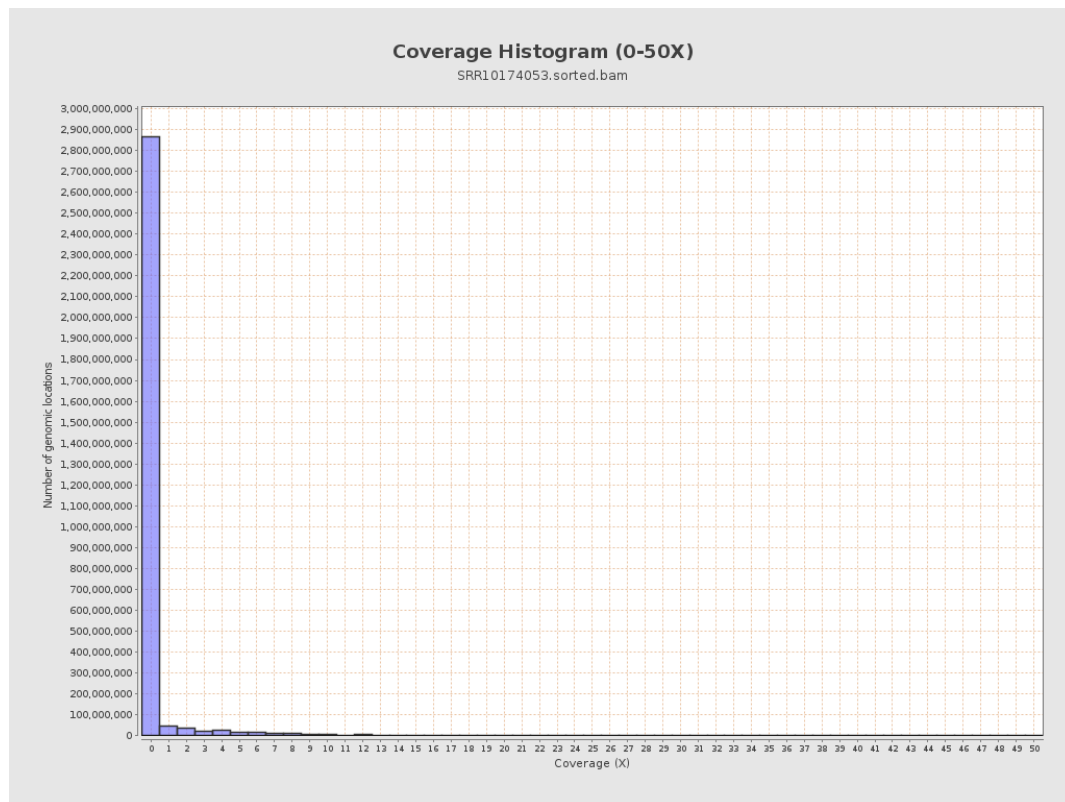
3. Results : Coverage across reference



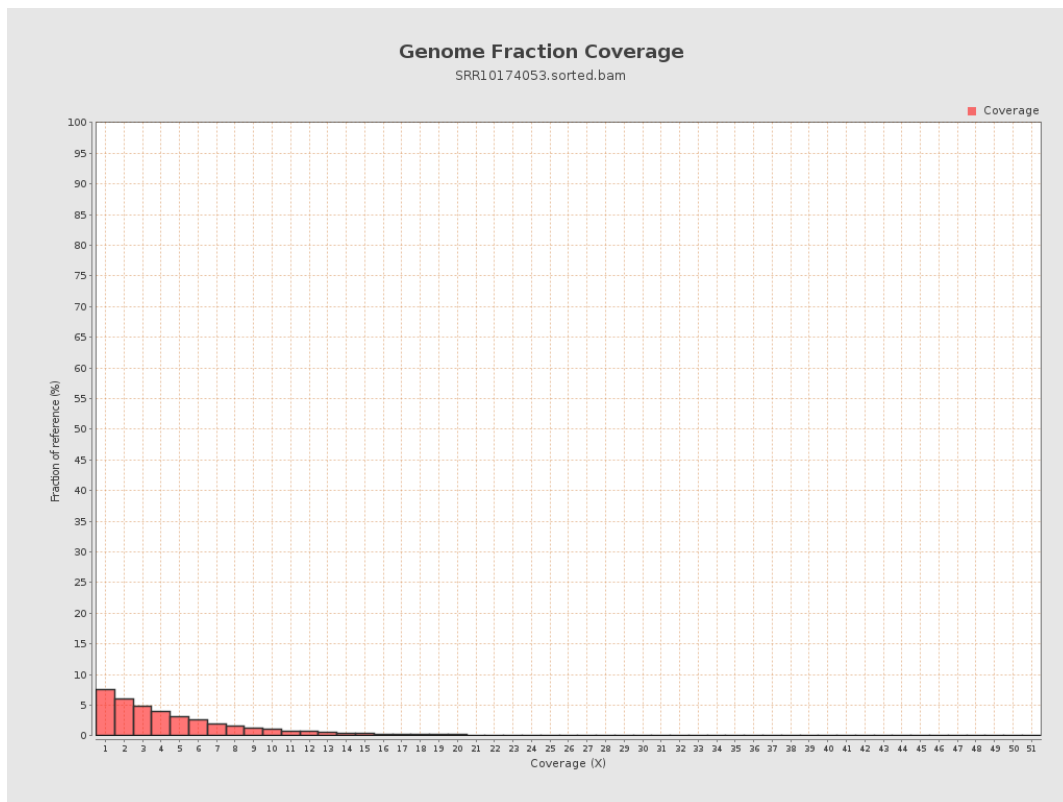
4. Results : Coverage Histogram



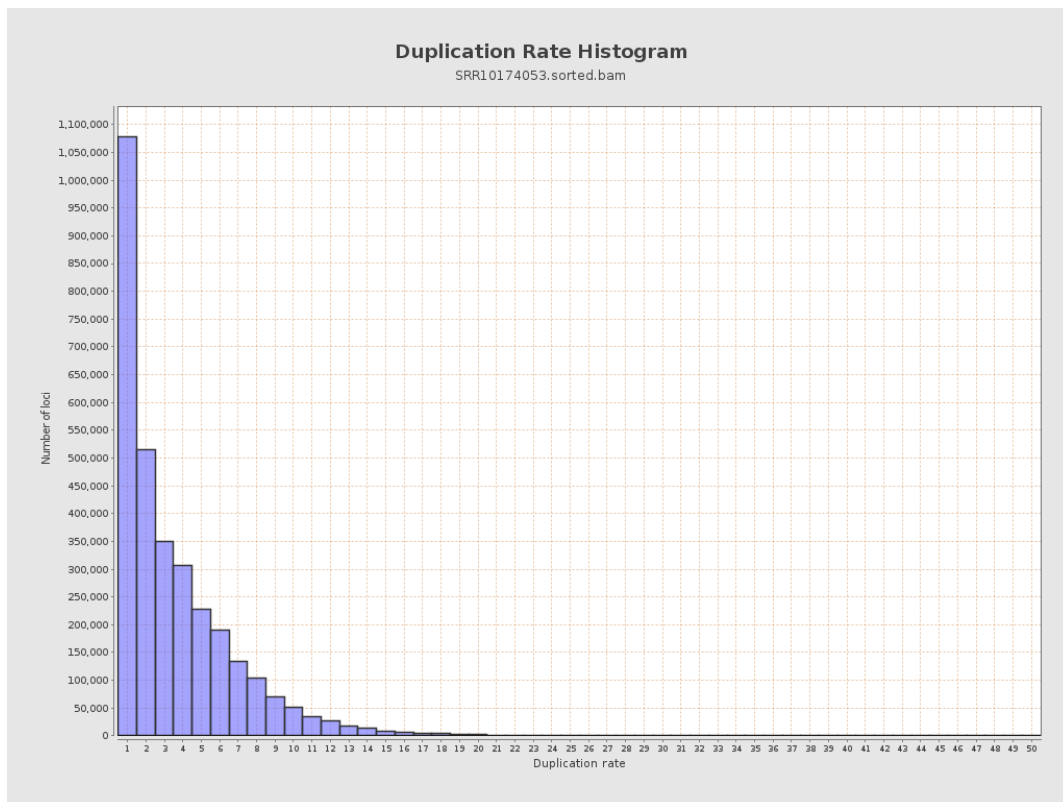
5. Results : Coverage Histogram (0-50X)



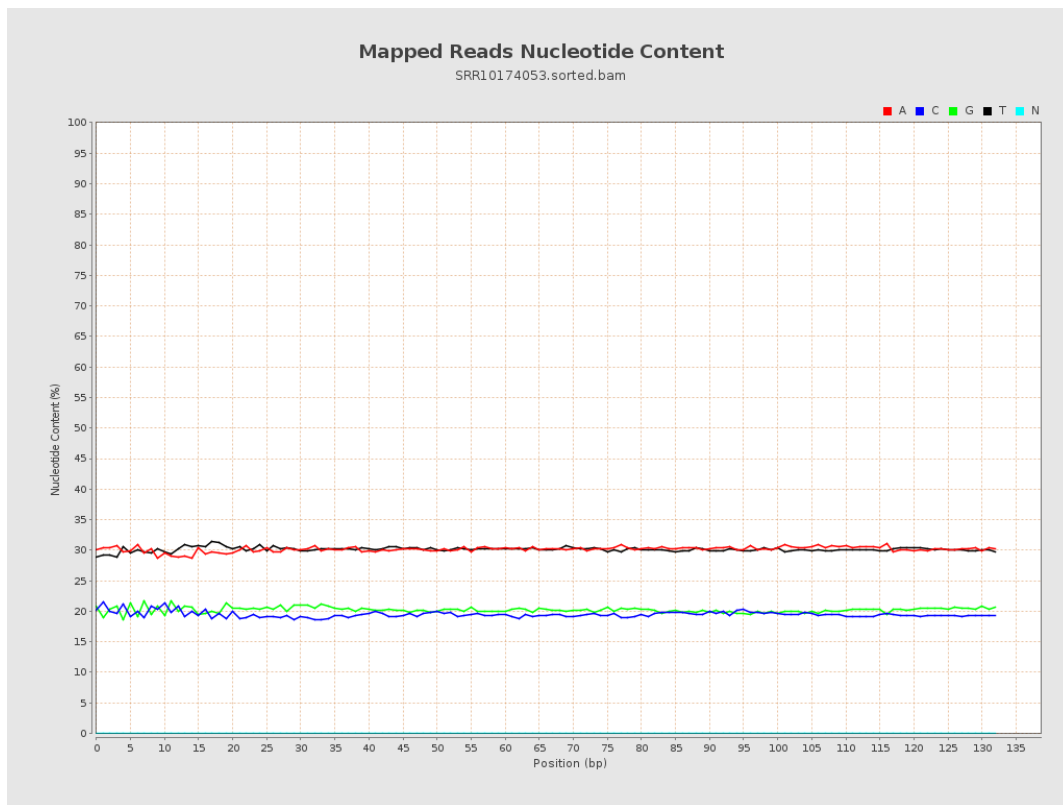
6. Results : Genome Fraction Coverage



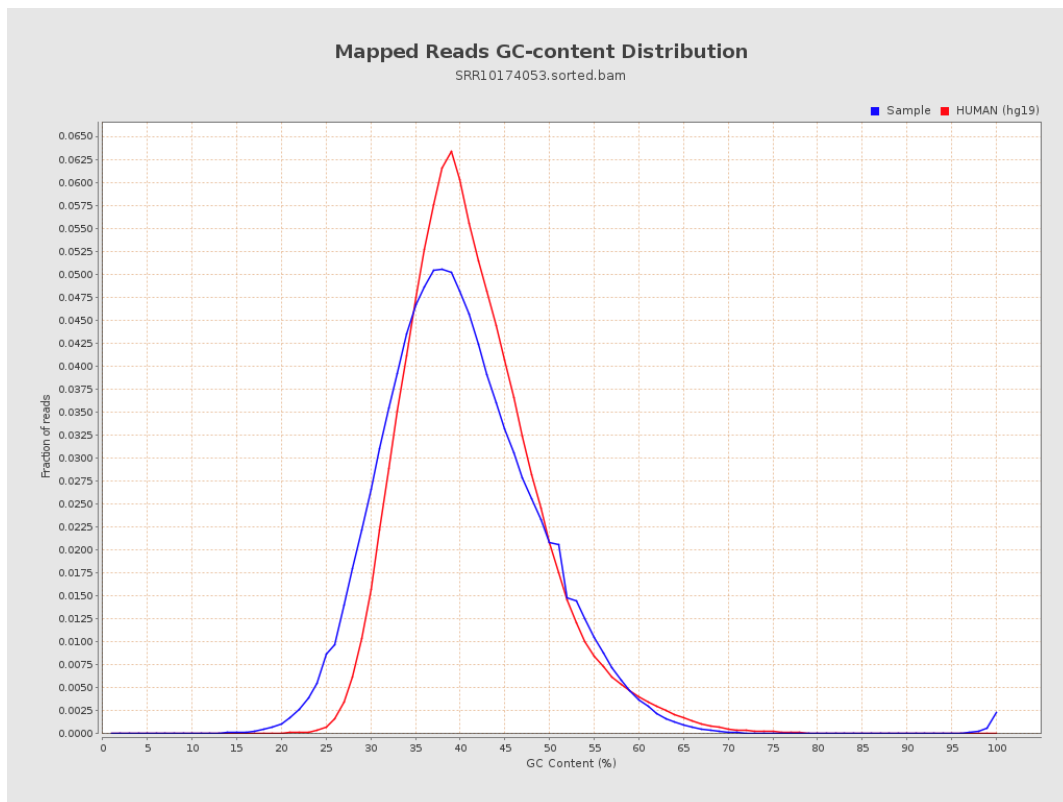
7. Results : Duplication Rate Histogram



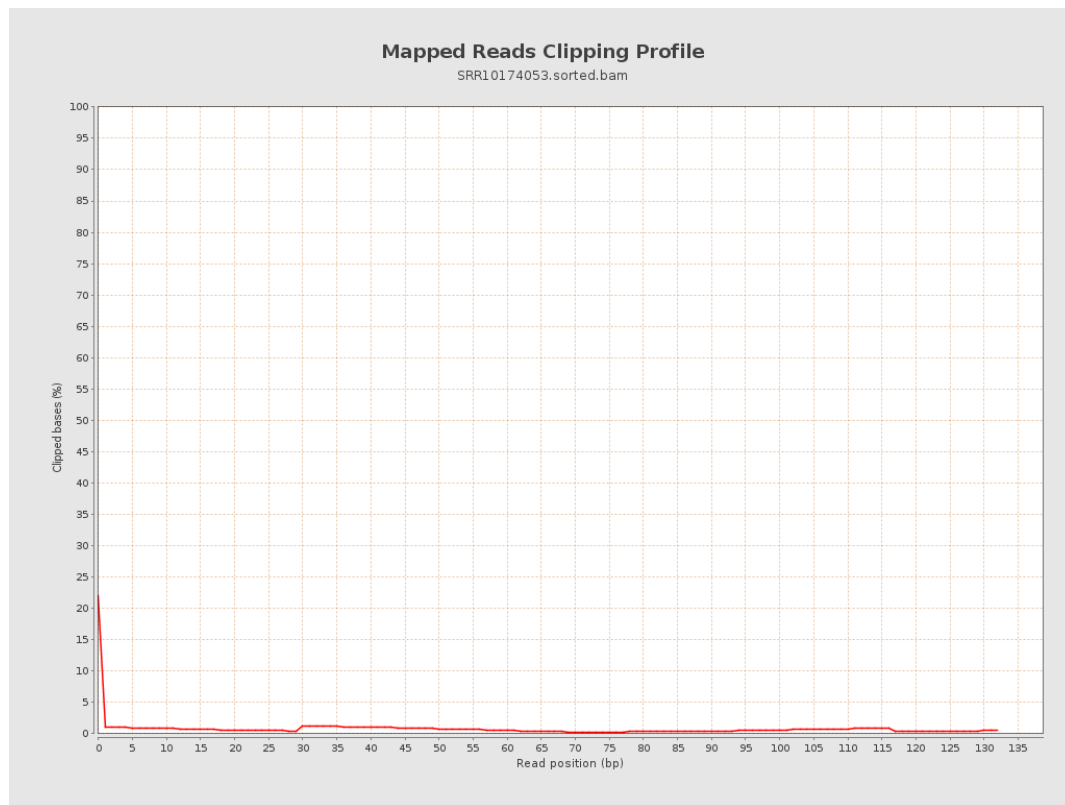
8. Results : Mapped Reads Nucleotide Content



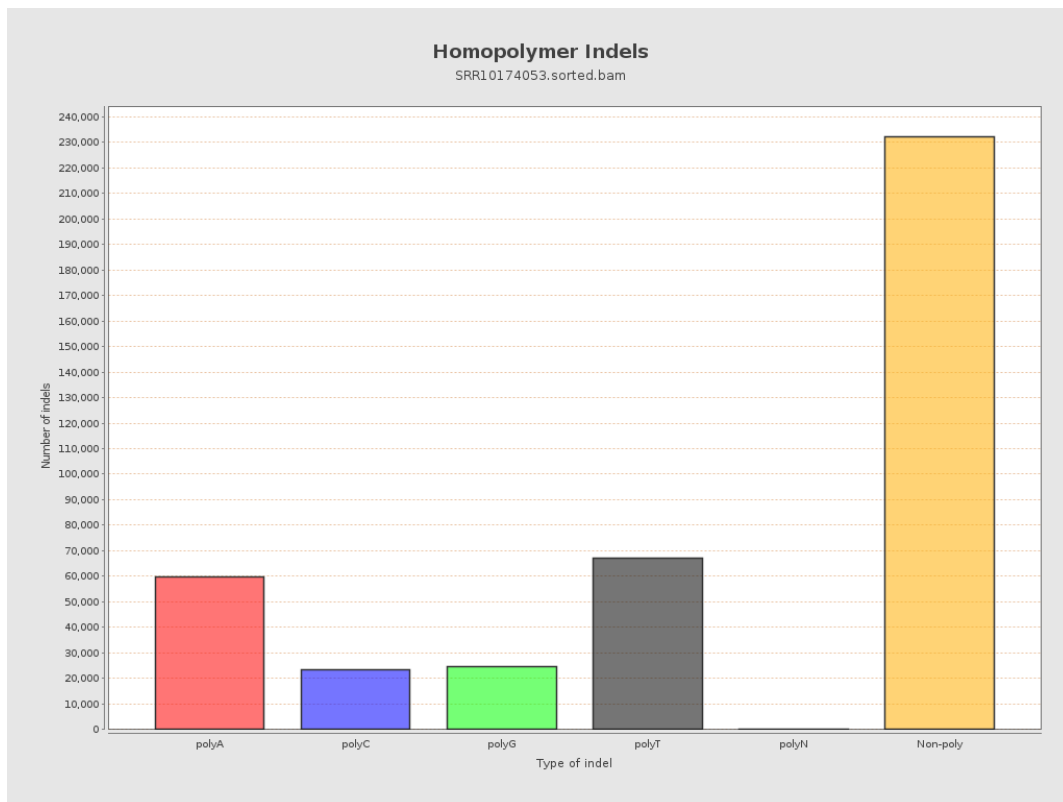
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



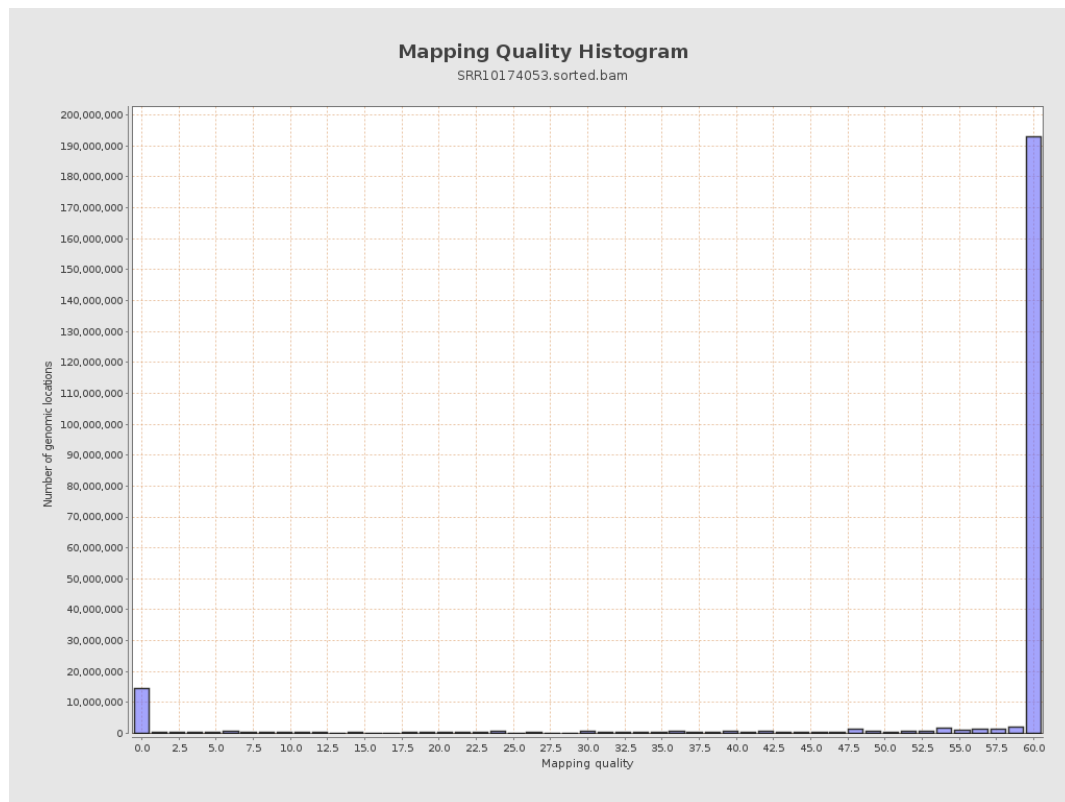
11. Results : Homopolymer Indels



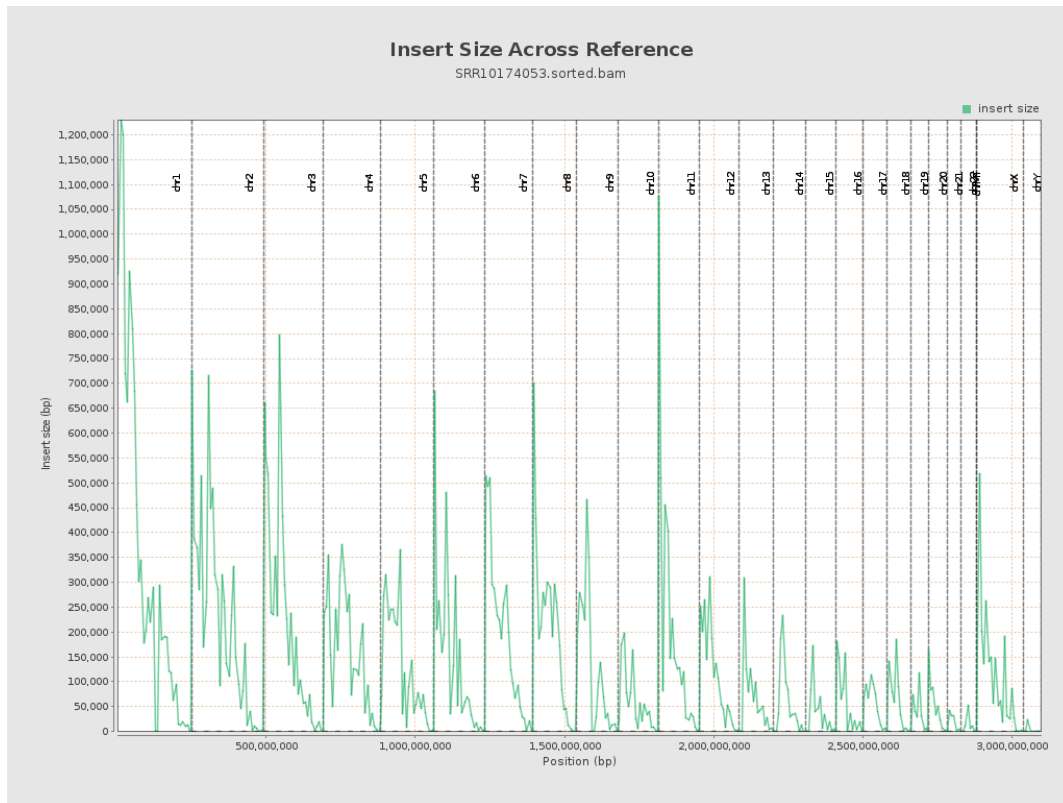
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

