

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 06:48:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354864.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_SRR22354864 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354864_1.fastq.gz SRR22354864_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 06:47:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354864.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	245,911,020
Mapped reads	240,636,165 / 97.85%
Unmapped reads	5,274,855 / 2.15%
Mapped paired reads	240,636,165 / 97.85%
Mapped reads, first in pair	120,457,903 / 48.98%
Mapped reads, second in pair	120,178,262 / 48.87%
Mapped reads, both in pair	240,127,586 / 97.65%
Mapped reads, singletons	508,579 / 0.21%
Secondary alignments	0
Supplementary alignments	7,812,750 / 3.18%
Read min/max/mean length	30 / 150 / 151.17
Duplicated reads (estimated)	200,101,403 / 81.37%
Duplication rate	82.57%
Clipped reads	138,873,603 / 56.47%

2.2. ACGT Content

Number/percentage of A's	8,205,212,455 / 27.87%
Number/percentage of C's	6,324,356,929 / 21.48%
Number/percentage of T's	8,274,159,721 / 28.1%
Number/percentage of G's	6,637,972,785 / 22.55%
Number/percentage of N's	634,439 / 0%

GC Percentage	44.03%
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2.3. Coverage

Mean	9.5153
Standard Deviation	385.1501

2.4. Mapping Quality

Mean Mapping Quality	53.71
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2.5. Insert size

Mean	302,238.36
Standard Deviation	6,429,869.94
P25/Median/P75	97 / 143 / 206

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	177,470,779
Insertions	4,882,143
Mapped reads with at least one insertion	1.9%
Deletions	5,219,139
Mapped reads with at least one deletion	2.08%
Homopolymer indels	42.99%

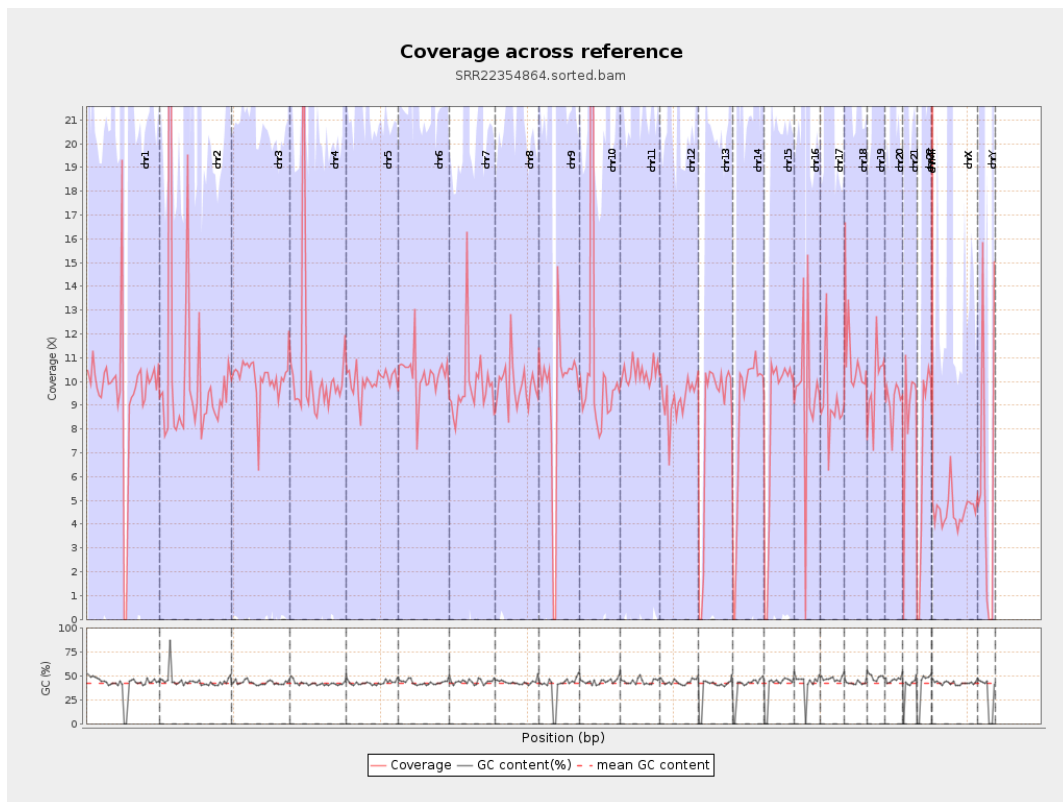
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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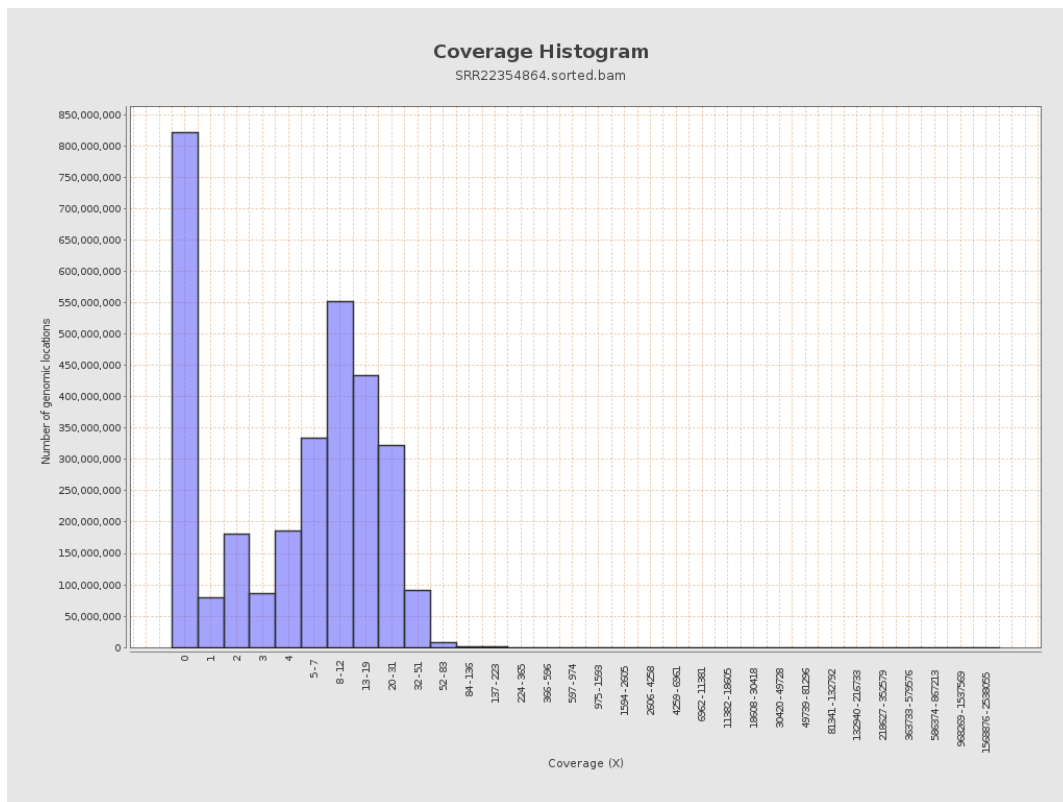
		bases	coverage	deviation
chr1	249250621	2392650846	9.5994	247.3679
chr2	243199373	2560465106	10.5283	1,301.9511
chr3	198022430	2003520322	10.1176	21.685
chr4	191154276	1980578764	10.3612	122.2216
chr5	180915260	1807411520	9.9904	12.0581
chr6	171115067	1766537280	10.3237	36.9479
chr7	159138663	1561669454	9.8133	170.5389
chr8	146364022	1446724548	9.8844	32.4404
chr9	141213431	1321999989	9.3617	119.4903
chr10	135534747	1562190479	11.5261	316.2544
chr11	135006516	1400163735	10.3711	49.6026
chr12	133851895	1237127046	9.2425	11.779
chr13	115169878	963086103	8.3623	10.2778
chr14	107349540	932018577	8.6821	53.4716
chr15	102531392	861787989	8.4051	10.1734
chr16	90354753	863303527	9.5546	60.7286
chr17	81195210	731131280	9.0046	56.3009
chr18	78077248	847770885	10.8581	126.0254
chr19	59128983	587468472	9.9354	119.8534
chr20	63025520	577707707	9.1663	41.1101
chr21	48129895	418748944	8.7004	70.1338
chr22	51304566	357547454	6.9691	30.2002
chrMT	16571	207956900	12,549.4478	2,547.5665
chrX	155270560	712906411	4.5914	21.8796

chrY	59373566	353837144	5.9595	165.0007
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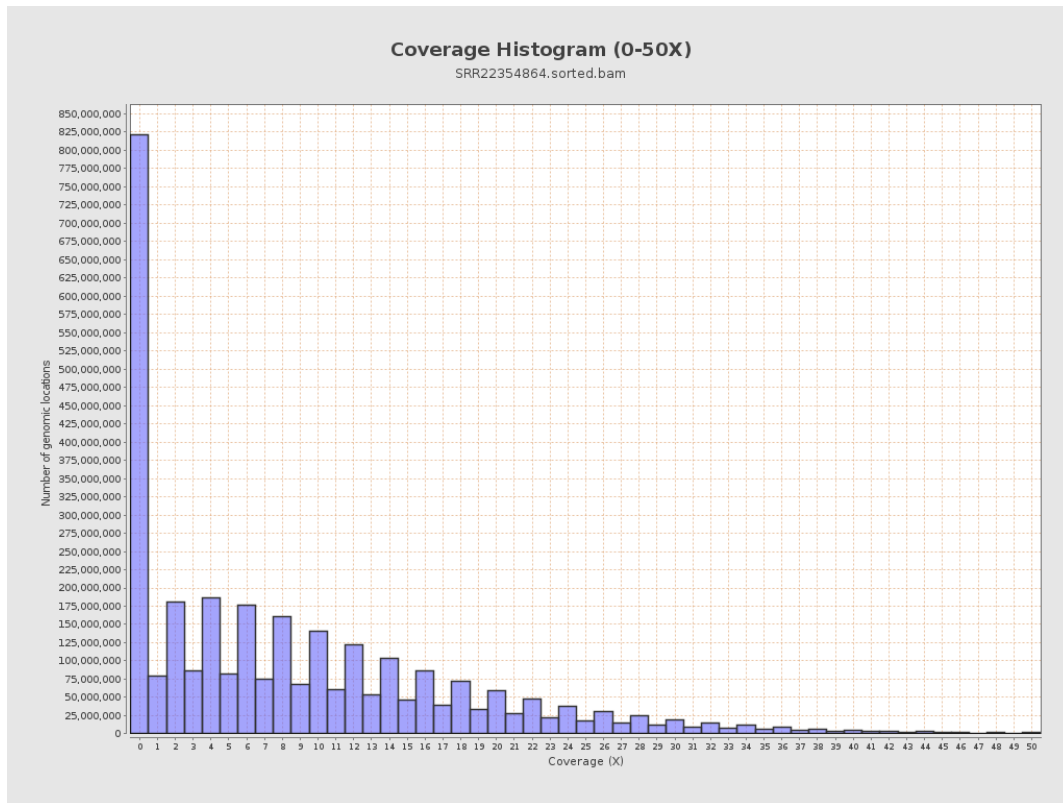
3. Results : Coverage across reference



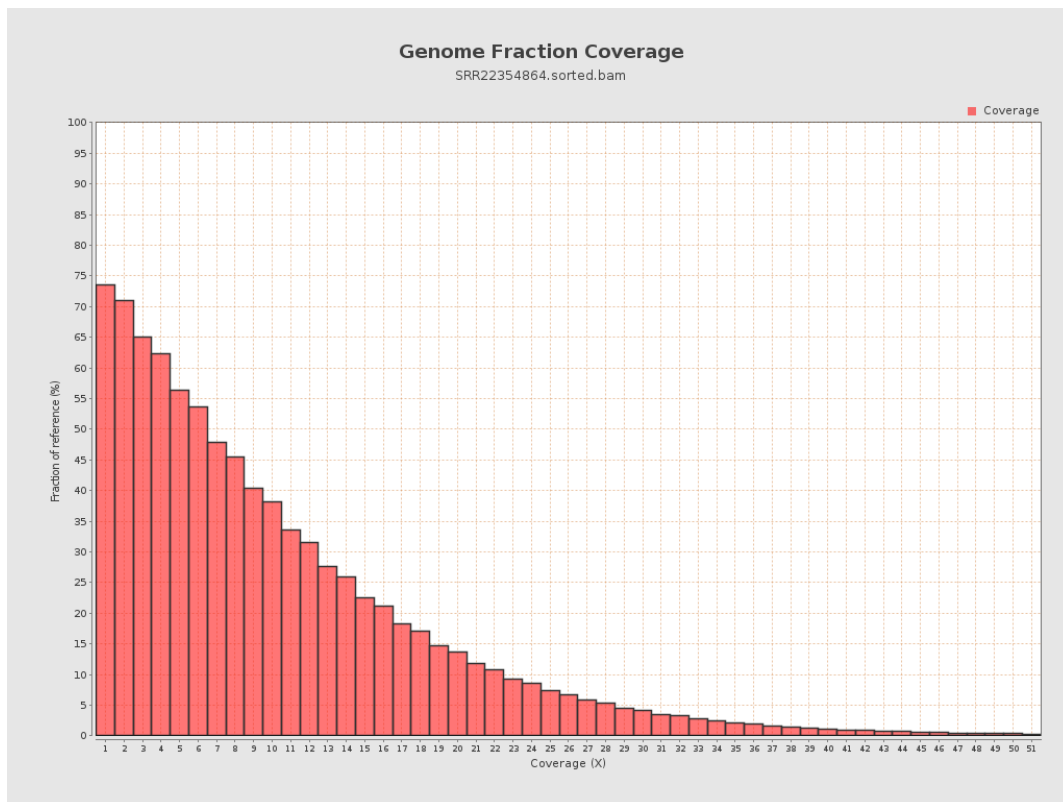
4. Results : Coverage Histogram



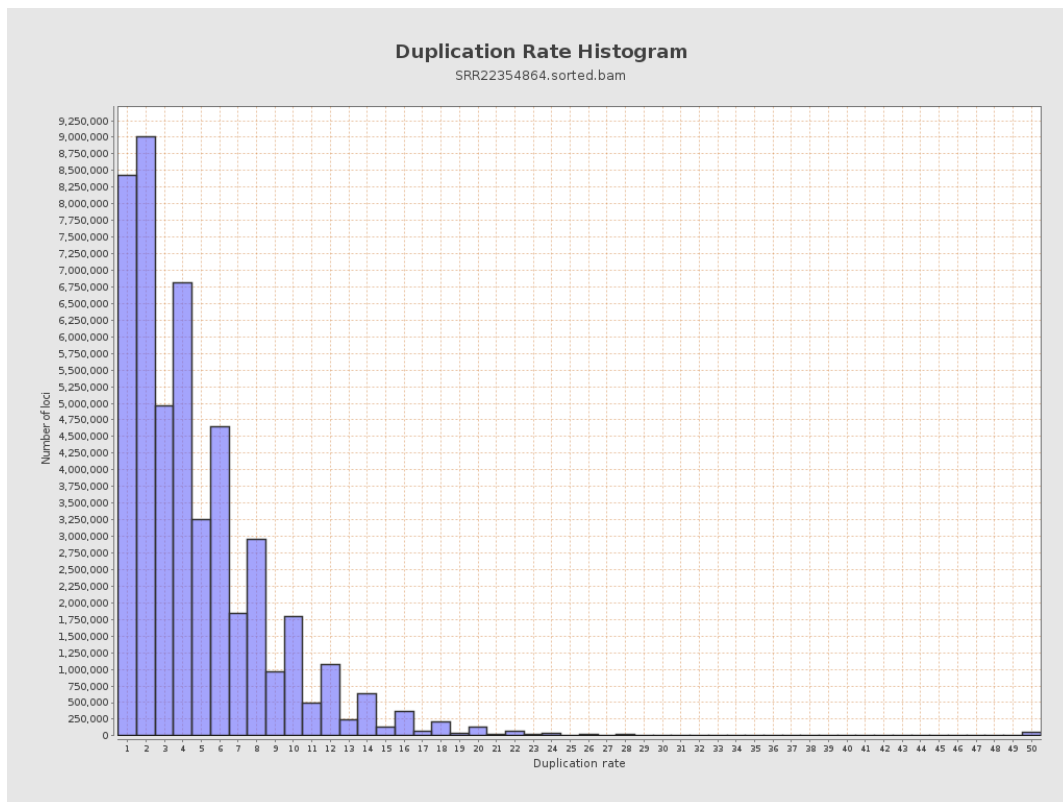
5. Results : Coverage Histogram (0-50X)



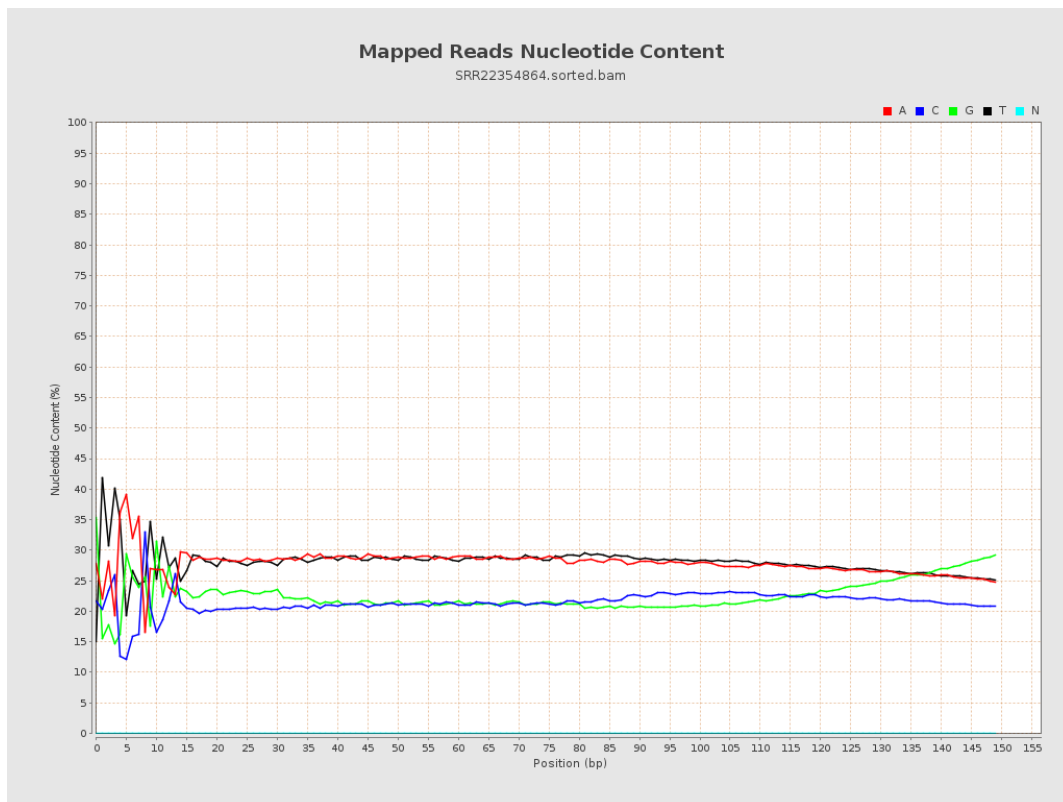
6. Results : Genome Fraction Coverage



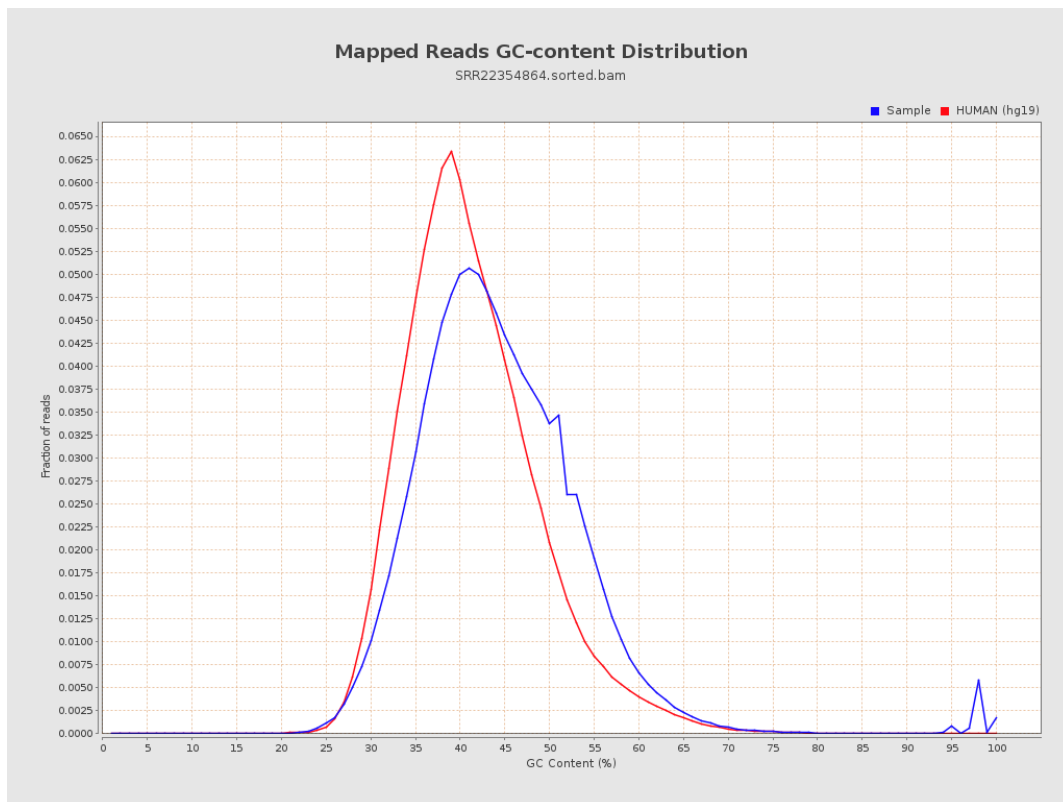
7. Results : Duplication Rate Histogram



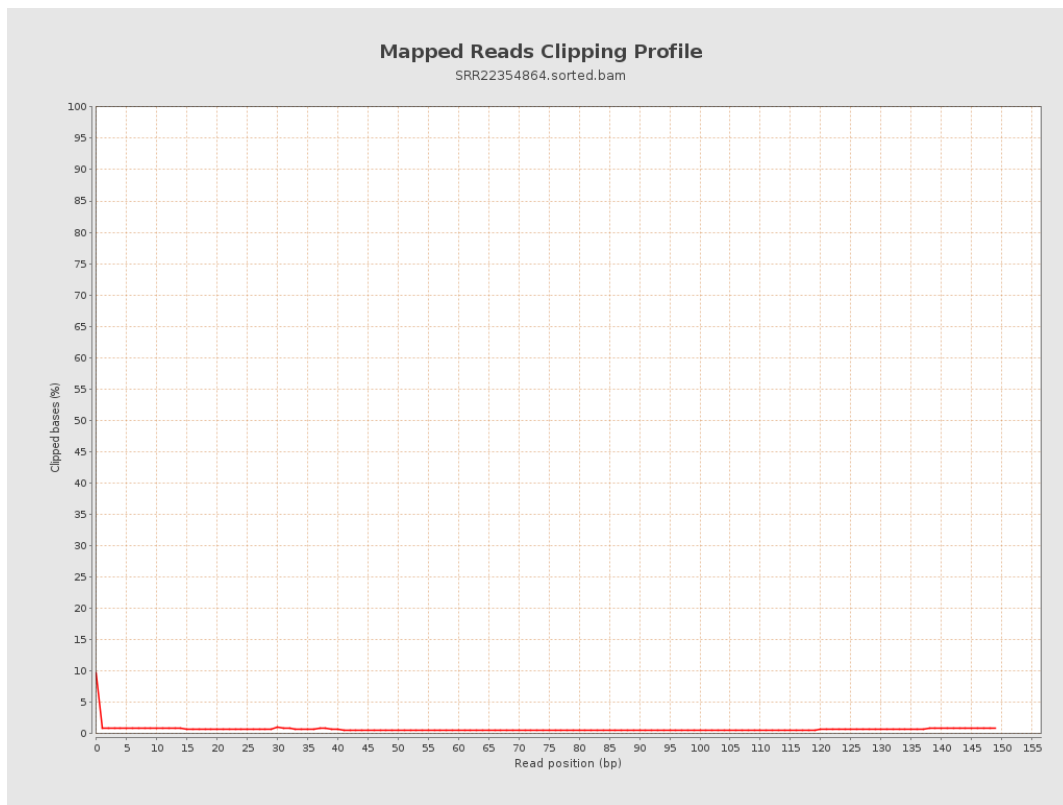
8. Results : Mapped Reads Nucleotide Content



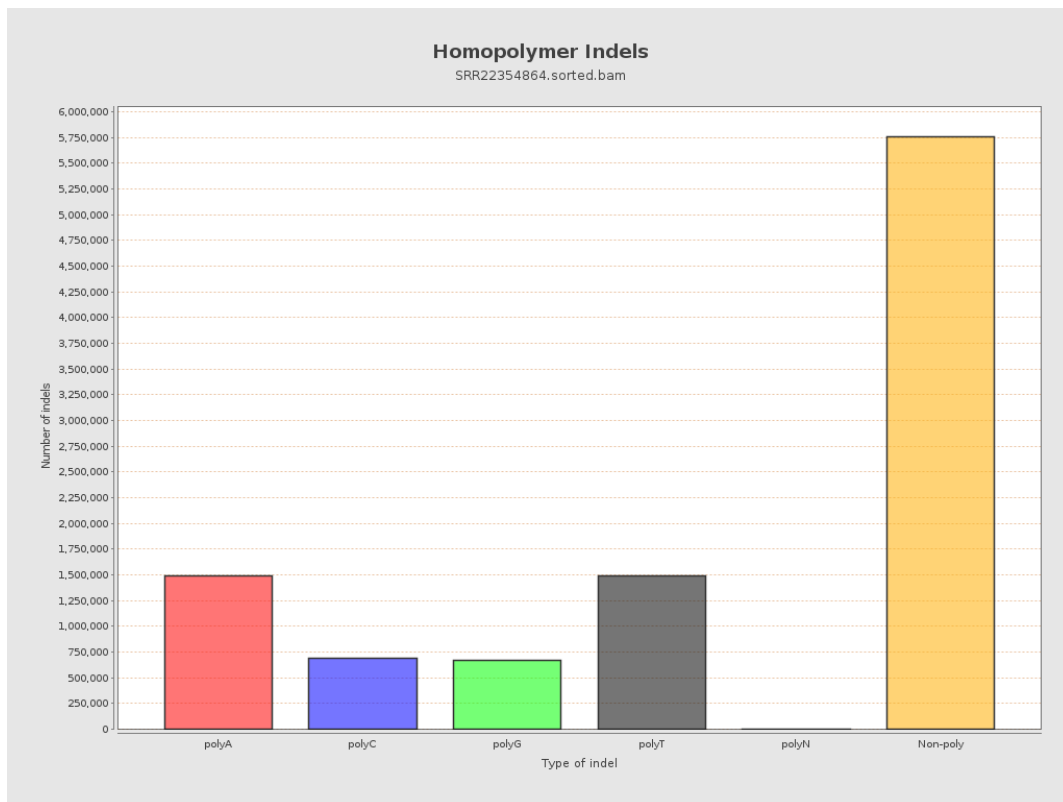
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



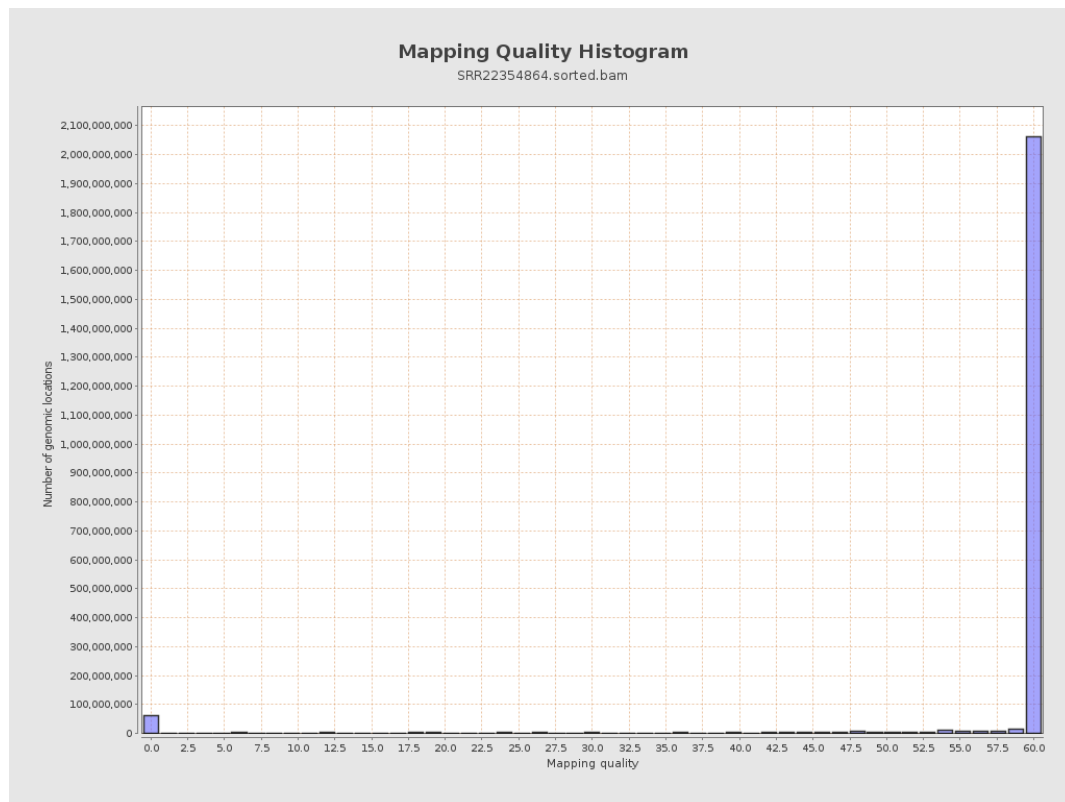
11. Results : Homopolymer Indels



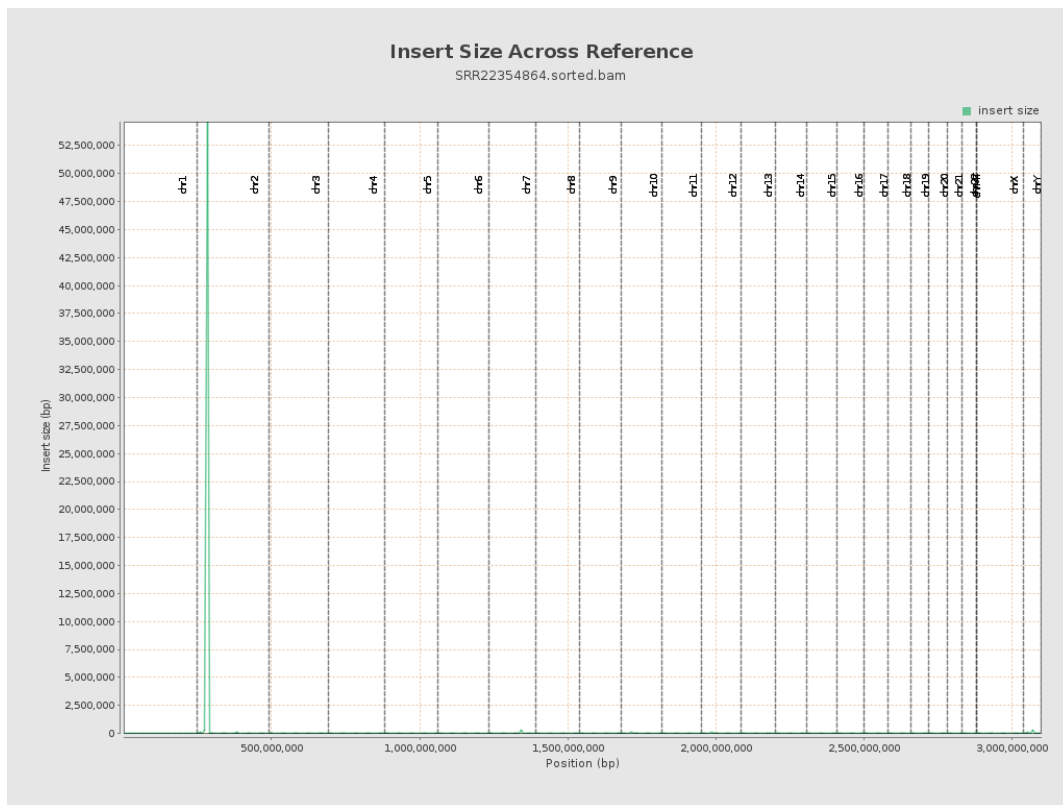
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

