

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 05:13:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354876.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_SRR22354876 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354876_1.fastq.gz SRR22354876_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 05:13:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354876.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	173,454,974
Mapped reads	172,386,263 / 99.38%
Unmapped reads	1,068,711 / 0.62%
Mapped paired reads	172,386,263 / 99.38%
Mapped reads, first in pair	86,340,276 / 49.78%
Mapped reads, second in pair	86,045,987 / 49.61%
Mapped reads, both in pair	171,841,674 / 99.07%
Mapped reads, singletons	544,589 / 0.31%
Secondary alignments	0
Supplementary alignments	875,411 / 0.5%
Read min/max/mean length	30 / 150 / 150.25
Duplicated reads (estimated)	47,903,647 / 27.62%
Duplication rate	24.52%
Clipped reads	11,354,843 / 6.55%

2.2. ACGT Content

Number/percentage of A's	7,341,178,133 / 28.79%
Number/percentage of C's	5,406,374,608 / 21.2%
Number/percentage of T's	7,284,397,530 / 28.57%
Number/percentage of G's	5,465,040,751 / 21.43%
Number/percentage of N's	474,596 / 0%

GC Percentage	42.64%
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2.3. Coverage

Mean	8.2397
Standard Deviation	97.1584

2.4. Mapping Quality

Mean Mapping Quality	54.5
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2.5. Insert size

Mean	35,288.3
Standard Deviation	1,870,117.67
P25/Median/P75	254 / 295 / 340

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	217,758,526
Insertions	3,561,149
Mapped reads with at least one insertion	1.94%
Deletions	3,657,264
Mapped reads with at least one deletion	2.03%
Homopolymer indels	44.81%

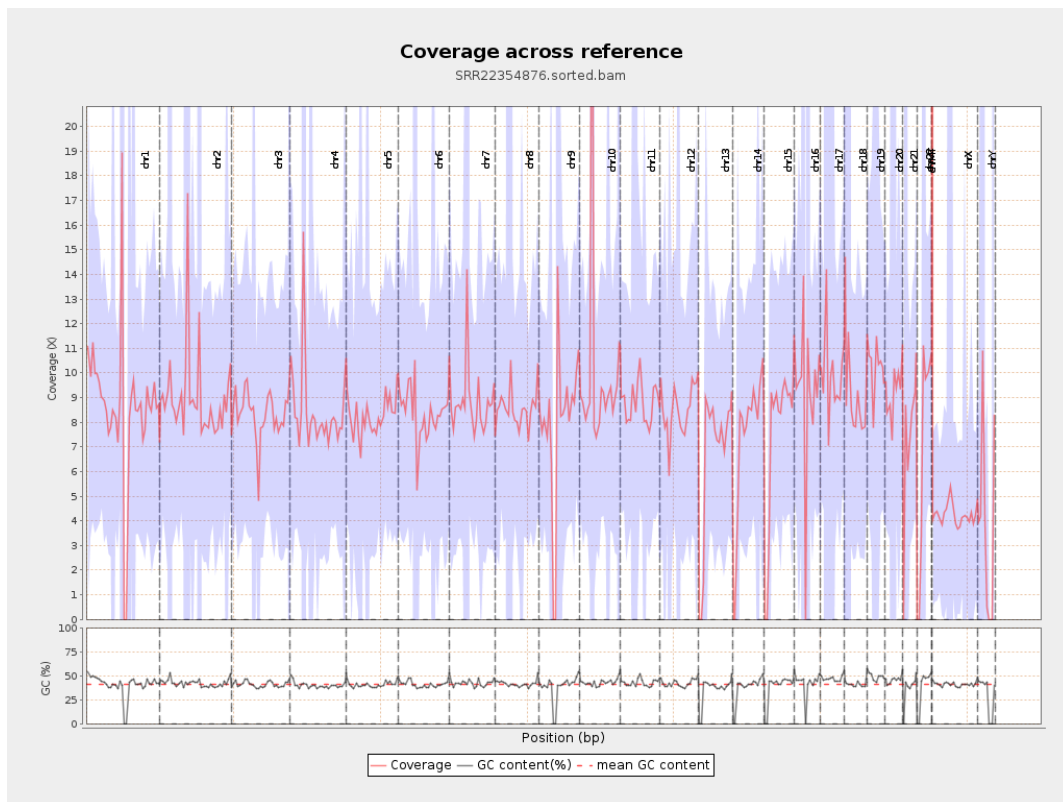
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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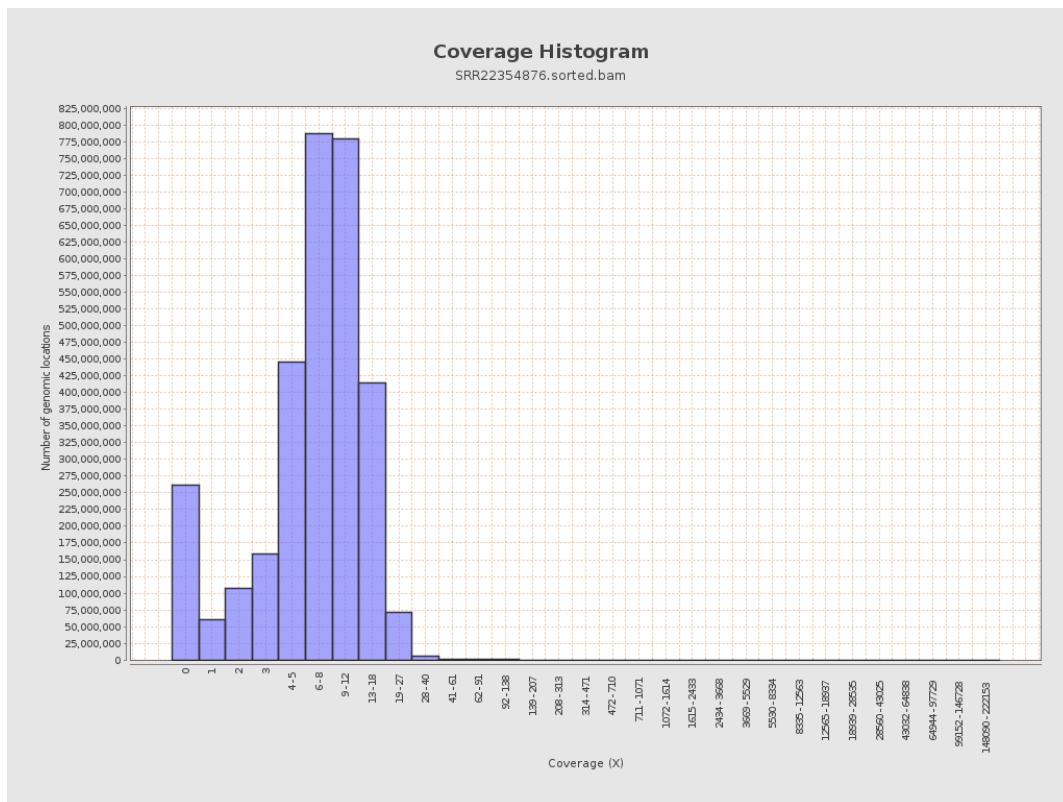
		bases	coverage	deviation
chr1	249250621	2151801642	8.6331	229.8068
chr2	243199373	2188575585	8.9991	80.9501
chr3	198022430	1648735048	8.326	6.4906
chr4	191154276	1604594457	8.3942	69.9185
chr5	180915260	1497002715	8.2746	7.7418
chr6	171115067	1429619967	8.3547	31.2877
chr7	159138663	1409769531	8.8587	115.9893
chr8	146364022	1257975212	8.5948	46.3264
chr9	141213431	1123363036	7.9551	141.0009
chr10	135534747	1366555662	10.0827	195.8758
chr11	135006516	1196121530	8.8597	44.8944
chr12	133851895	1136249229	8.4889	8.3123
chr13	115169878	771350225	6.6975	5.8387
chr14	107349540	781753599	7.2823	7.6675
chr15	102531392	749508864	7.31	6.1499
chr16	90354753	842896088	9.3287	36.1396
chr17	81195210	804088099	9.9031	56.1736
chr18	78077248	697780715	8.9371	106.7933
chr19	59128983	607318809	10.2711	103.0451
chr20	63025520	579290625	9.1914	25.6116
chr21	48129895	360080013	7.4814	35.7822
chr22	51304566	368784836	7.1881	19.9751
chrMT	16571	39179213	2,364.324	255.5266
chrX	155270560	657326046	4.2334	15.9116

chrY	59373566	237902044	4.0069	85.3473
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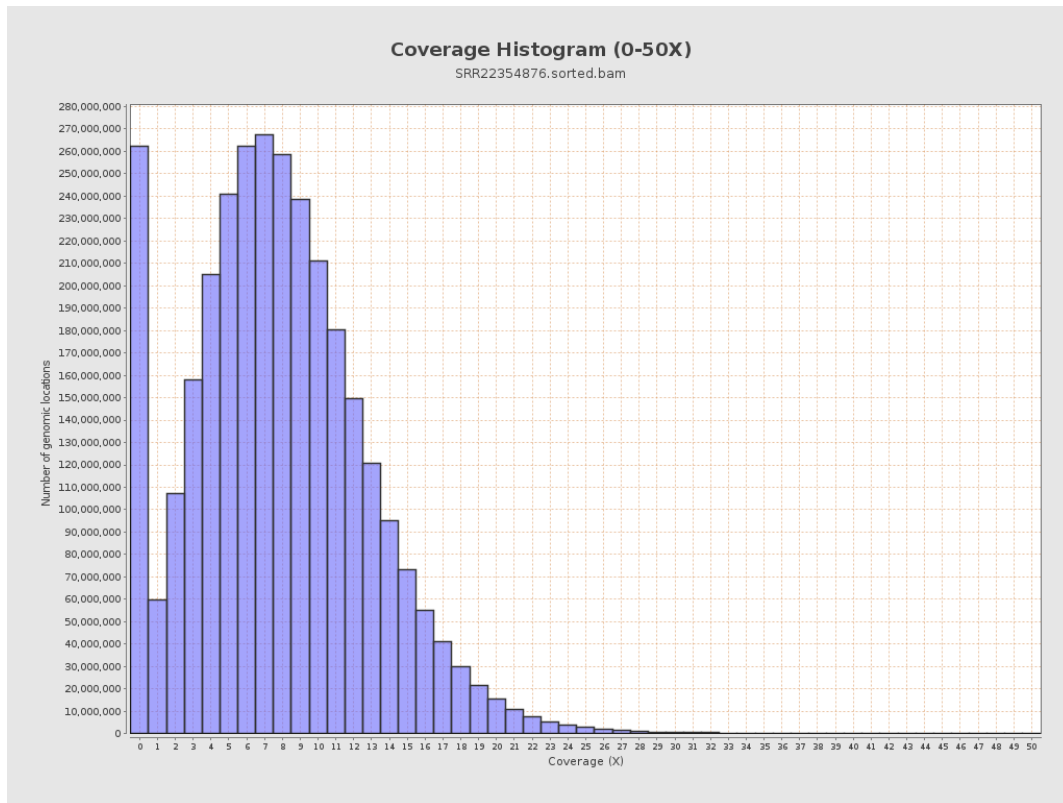
3. Results : Coverage across reference



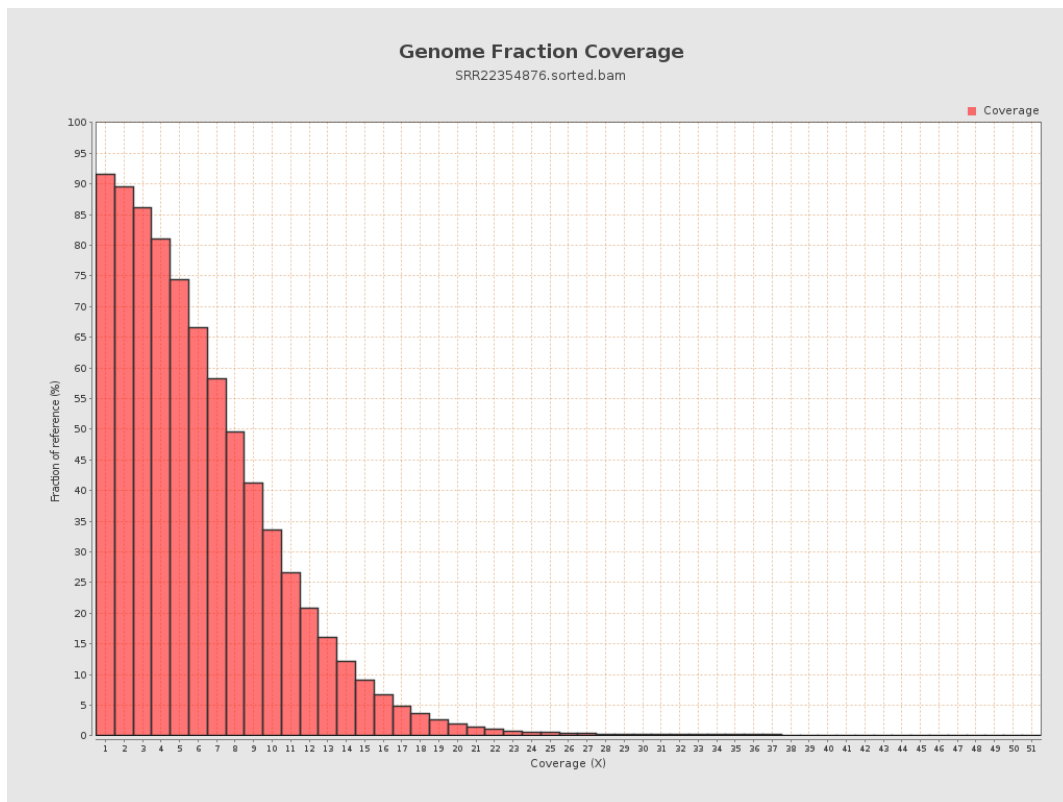
4. Results : Coverage Histogram



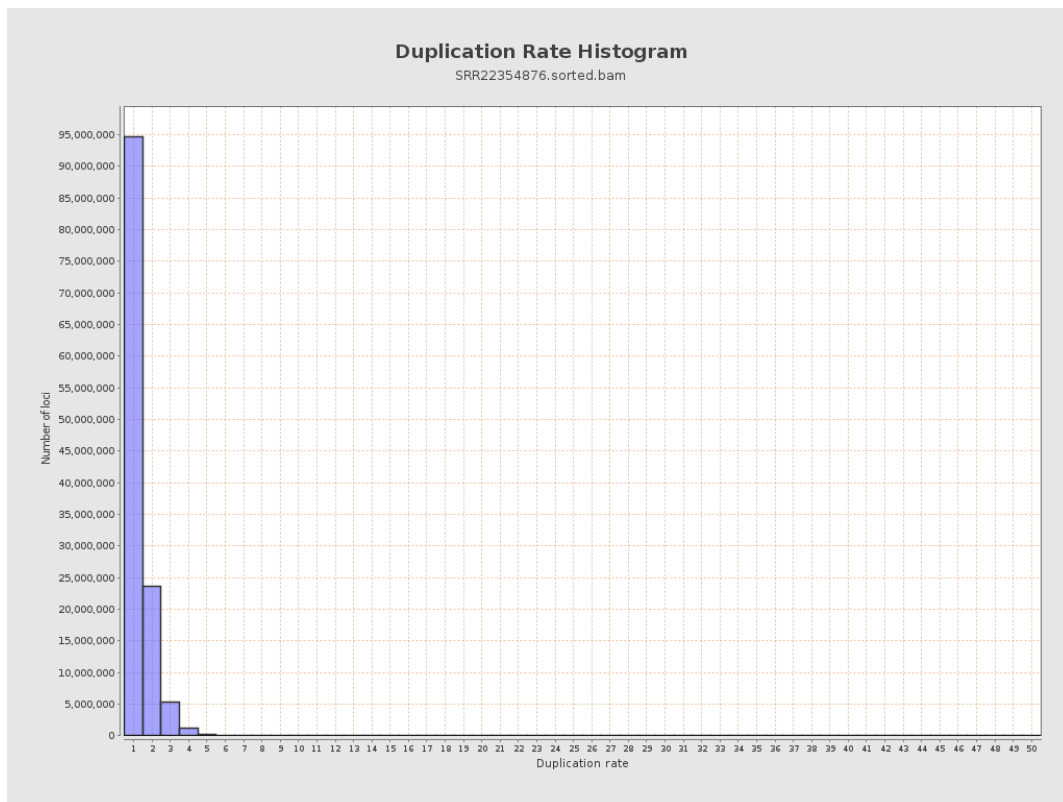
5. Results : Coverage Histogram (0-50X)



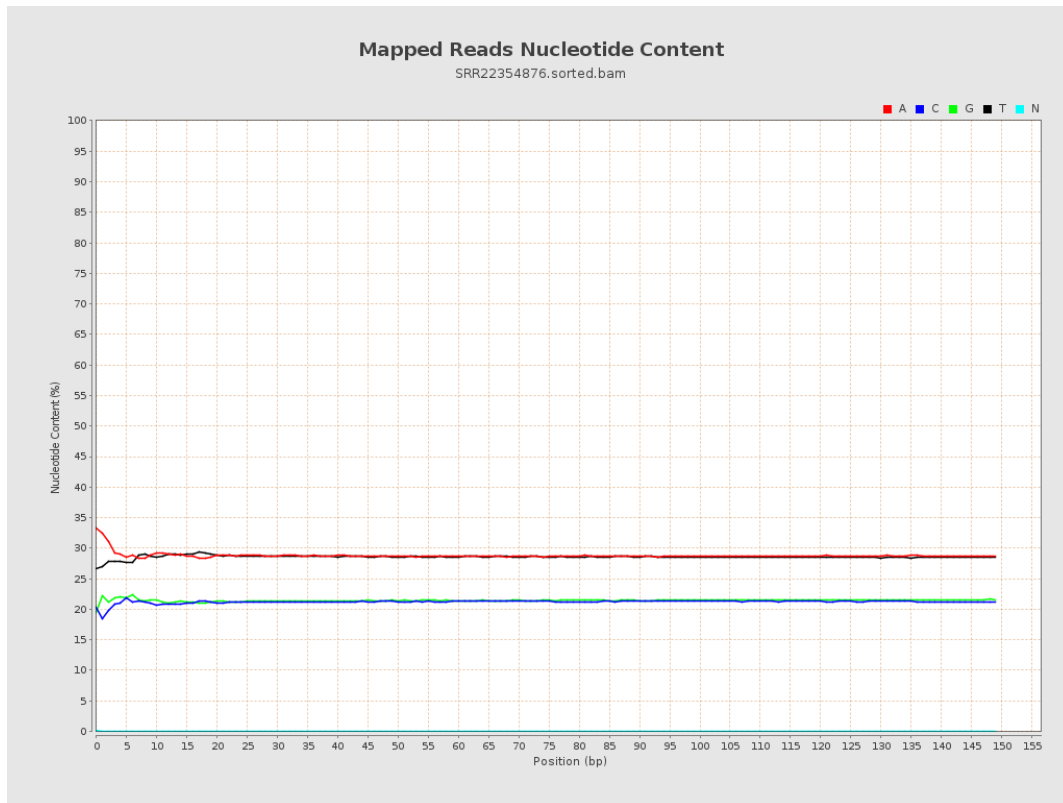
6. Results : Genome Fraction Coverage



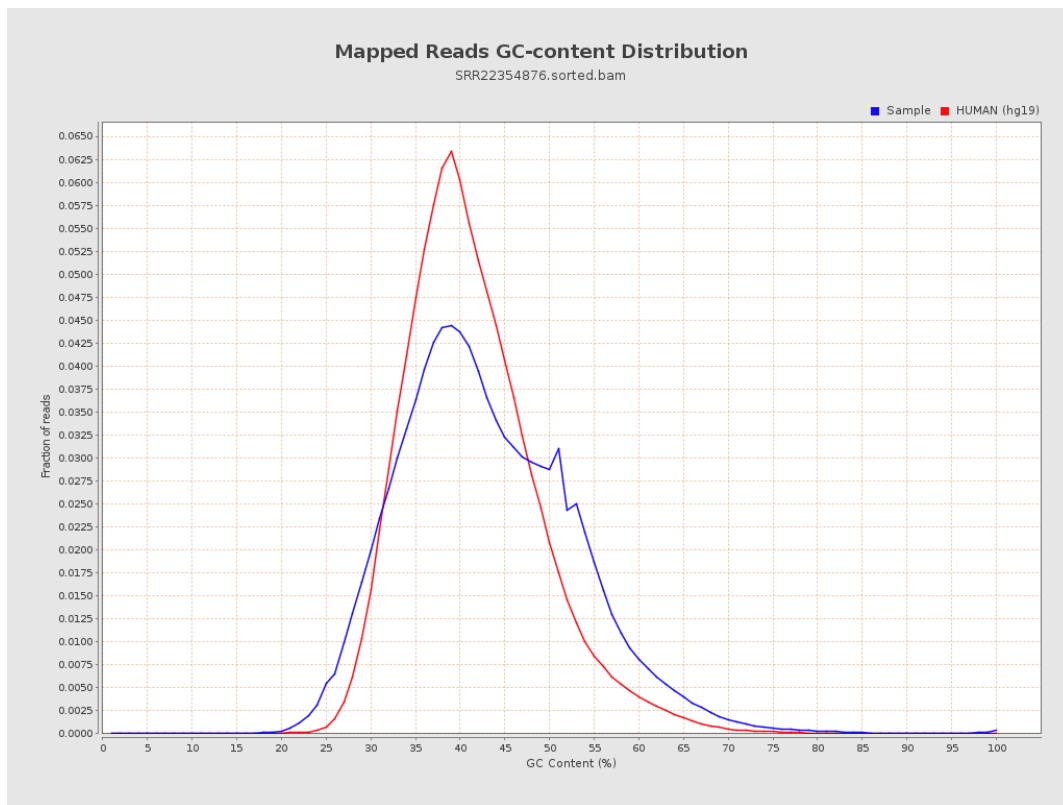
7. Results : Duplication Rate Histogram



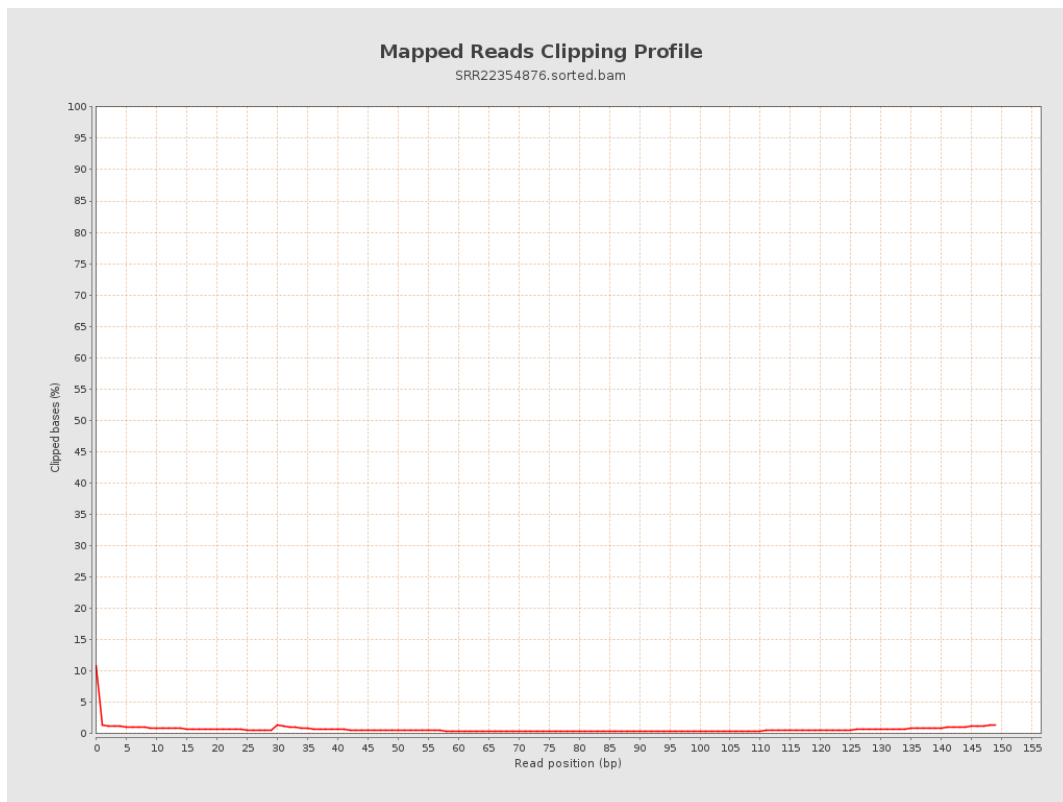
8. Results : Mapped Reads Nucleotide Content



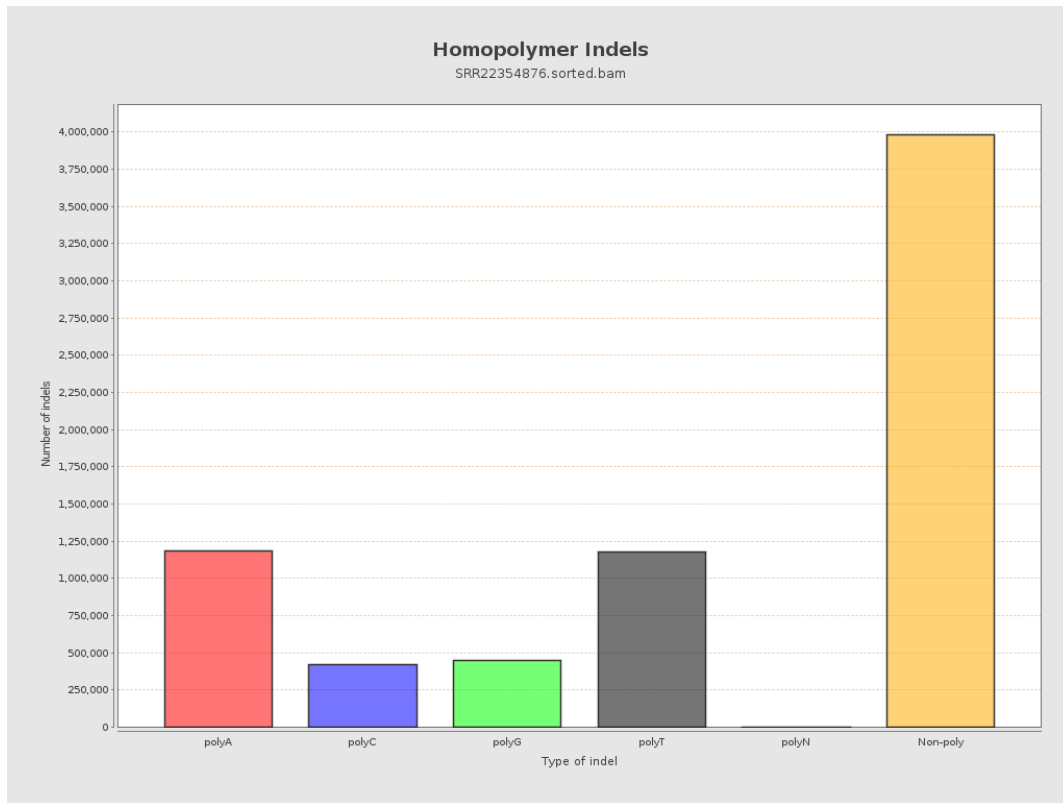
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



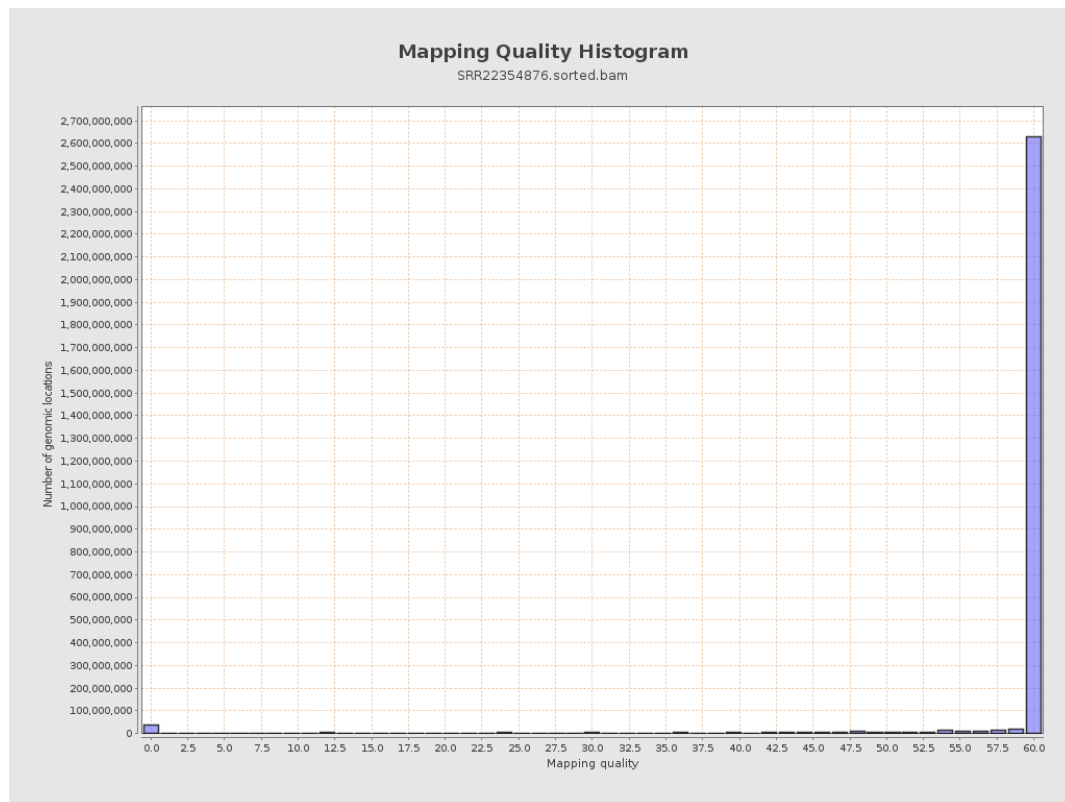
11. Results : Homopolymer Indels



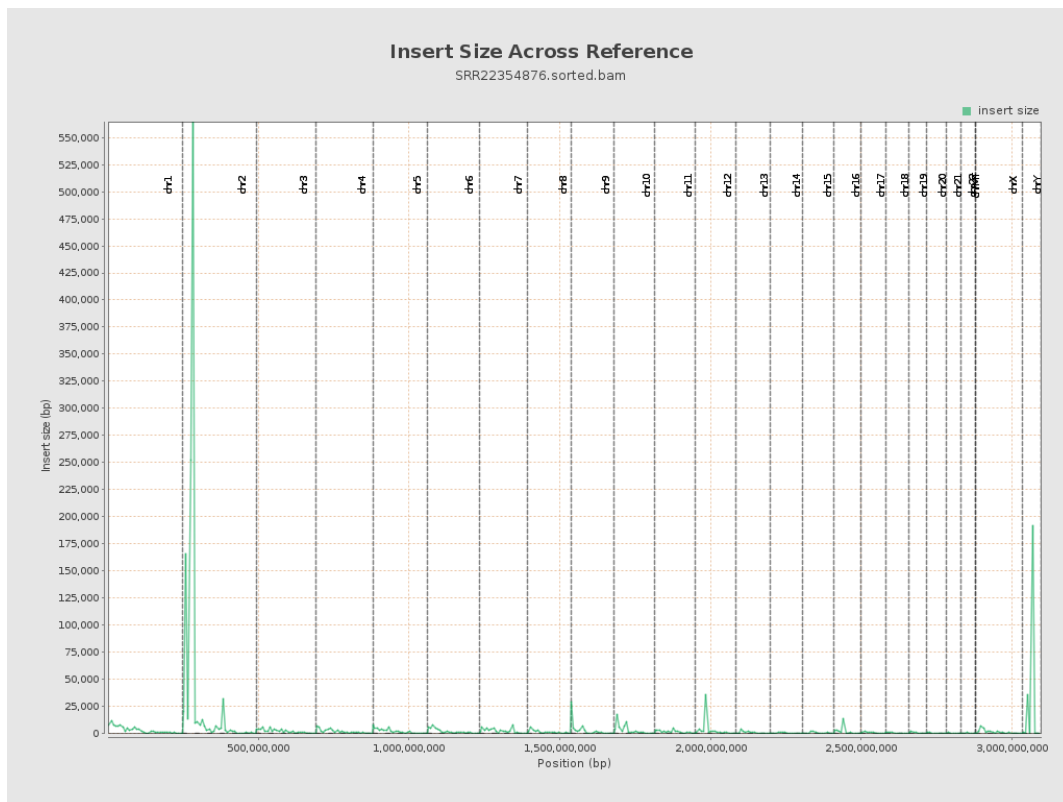
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

