

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 17:09:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354870.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_SRR22354870 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354870_1.fastq.gz SRR22354870_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 17:09:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354870.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,767,118
Mapped reads	25,511,874 / 99.01%
Unmapped reads	255,244 / 0.99%
Mapped paired reads	25,511,874 / 99.01%
Mapped reads, first in pair	12,767,278 / 49.55%
Mapped reads, second in pair	12,744,596 / 49.46%
Mapped reads, both in pair	25,470,008 / 98.85%
Mapped reads, singletons	41,866 / 0.16%
Secondary alignments	0
Supplementary alignments	1,186,085 / 4.6%
Read min/max/mean length	30 / 150 / 151.68
Duplicated reads (estimated)	16,426,992 / 63.75%
Duplication rate	64.51%
Clipped reads	13,338,416 / 51.77%

2.2. ACGT Content

Number/percentage of A's	890,000,093 / 27.87%
Number/percentage of C's	674,212,133 / 21.12%
Number/percentage of T's	900,877,179 / 28.21%
Number/percentage of G's	727,889,977 / 22.8%
Number/percentage of N's	29,232 / 0%

GC Percentage	43.91%
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2.3. Coverage

Mean	1.0319
Standard Deviation	62.0755

2.4. Mapping Quality

Mean Mapping Quality	53.63
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2.5. Insert size

Mean	440,047.54
Standard Deviation	7,677,871.48
P25/Median/P75	103 / 160 / 241

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	17,395,986
Insertions	531,941
Mapped reads with at least one insertion	1.95%
Deletions	550,564
Mapped reads with at least one deletion	2.06%
Homopolymer indels	44.2%

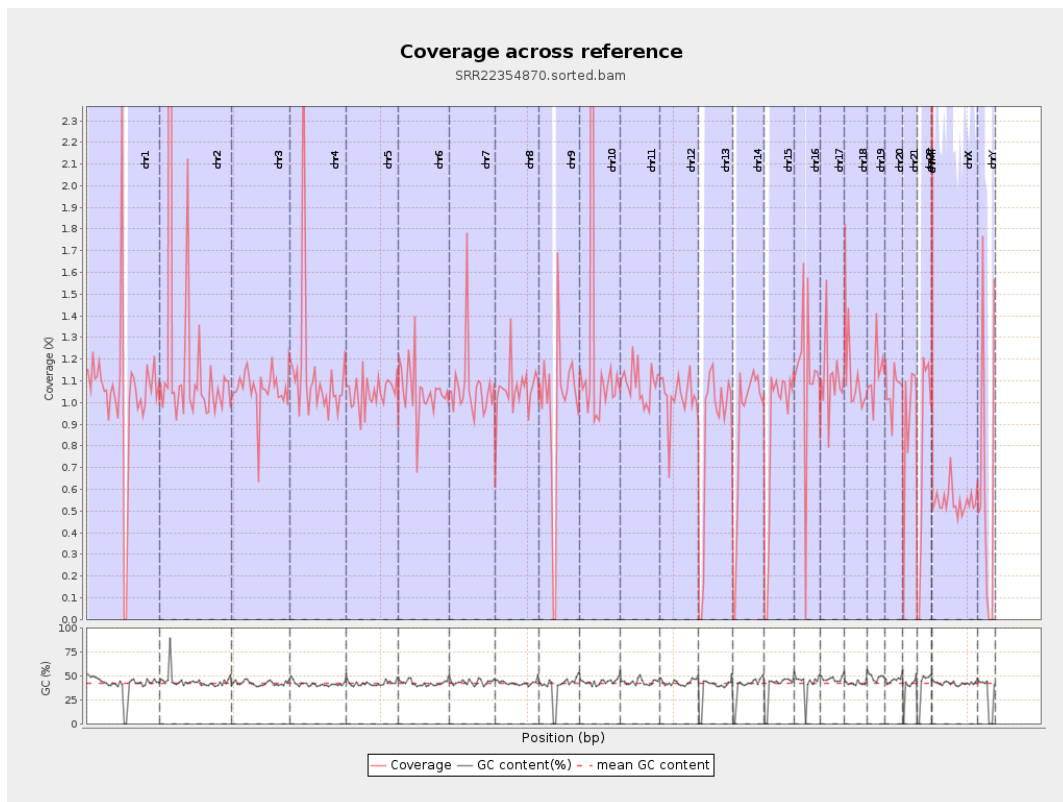
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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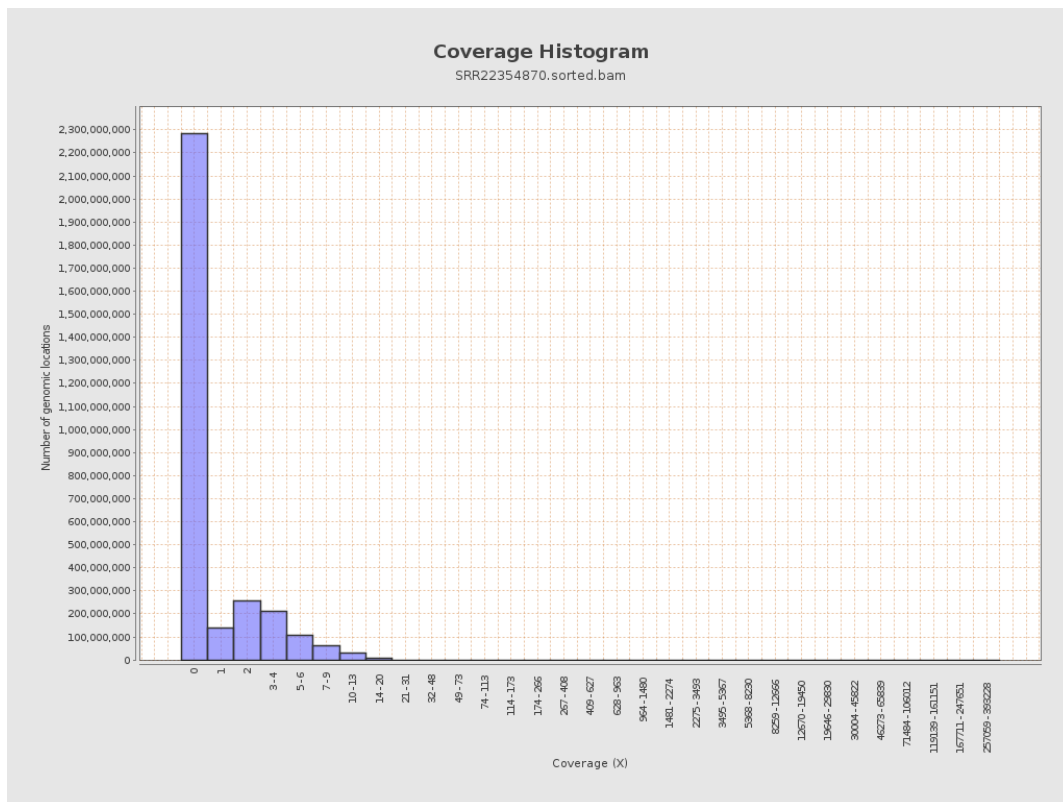
		bases	coverage	deviation
chr1	249250621	261256621	1.0482	30.5409
chr2	243199373	307931666	1.2662	215.8147
chr3	198022430	210010173	1.0605	2.8477
chr4	191154276	216788977	1.1341	13.0486
chr5	180915260	189232165	1.046	2.3746
chr6	171115067	180494323	1.0548	5.225
chr7	159138663	170443126	1.071	17.9403
chr8	146364022	156940605	1.0723	5.8329
chr9	141213431	136525409	0.9668	15.5784
chr10	135534747	174154262	1.2849	35.0159
chr11	135006516	146358577	1.0841	5.7805
chr12	133851895	137268955	1.0255	2.3099
chr13	115169878	99156495	0.861	2.0715
chr14	107349540	96329406	0.8973	7.5339
chr15	102531392	88606406	0.8642	2.0819
chr16	90354753	101316046	1.1213	6.1946
chr17	81195210	90120791	1.1099	6.8824
chr18	78077248	86983155	1.1141	13.712
chr19	59128983	67032534	1.1337	15.3579
chr20	63025520	67080939	1.0643	4.8398
chr21	48129895	44529584	0.9252	7.3449
chr22	51304566	40369146	0.7869	3.2338
chrMT	16571	3854690	232.6166	49.0194
chrX	155270560	84369192	0.5434	2.5102

chrY	59373566	37399008	0.6299	17.3219
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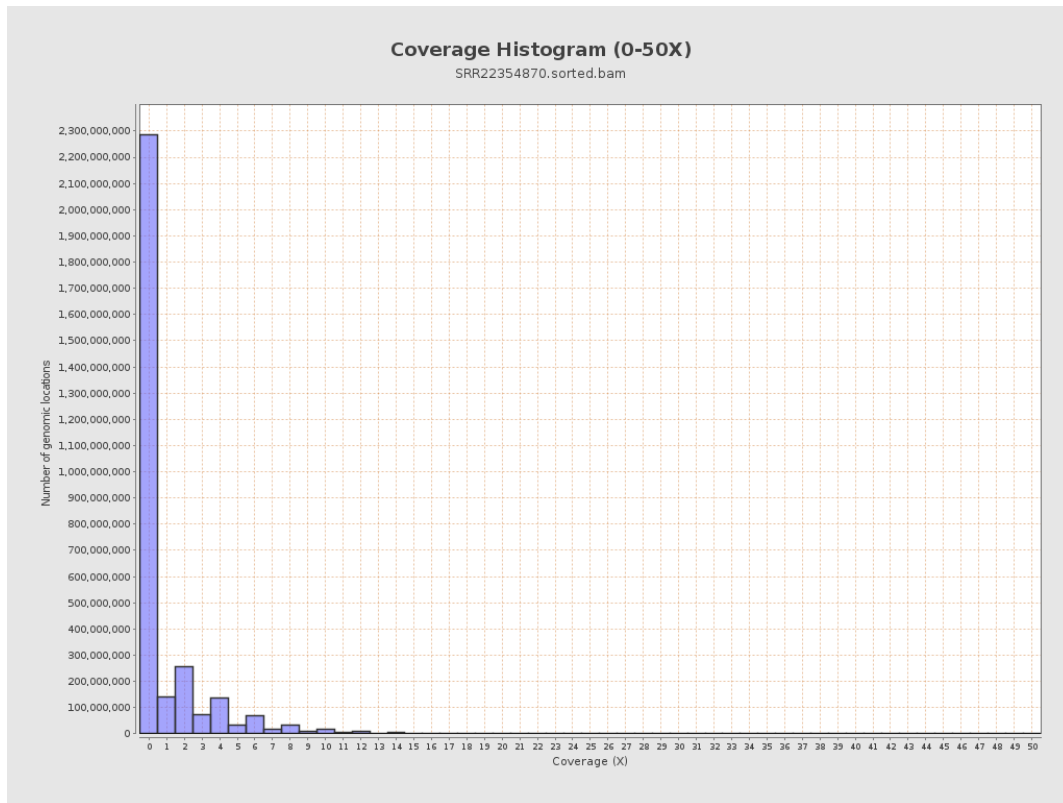
3. Results : Coverage across reference



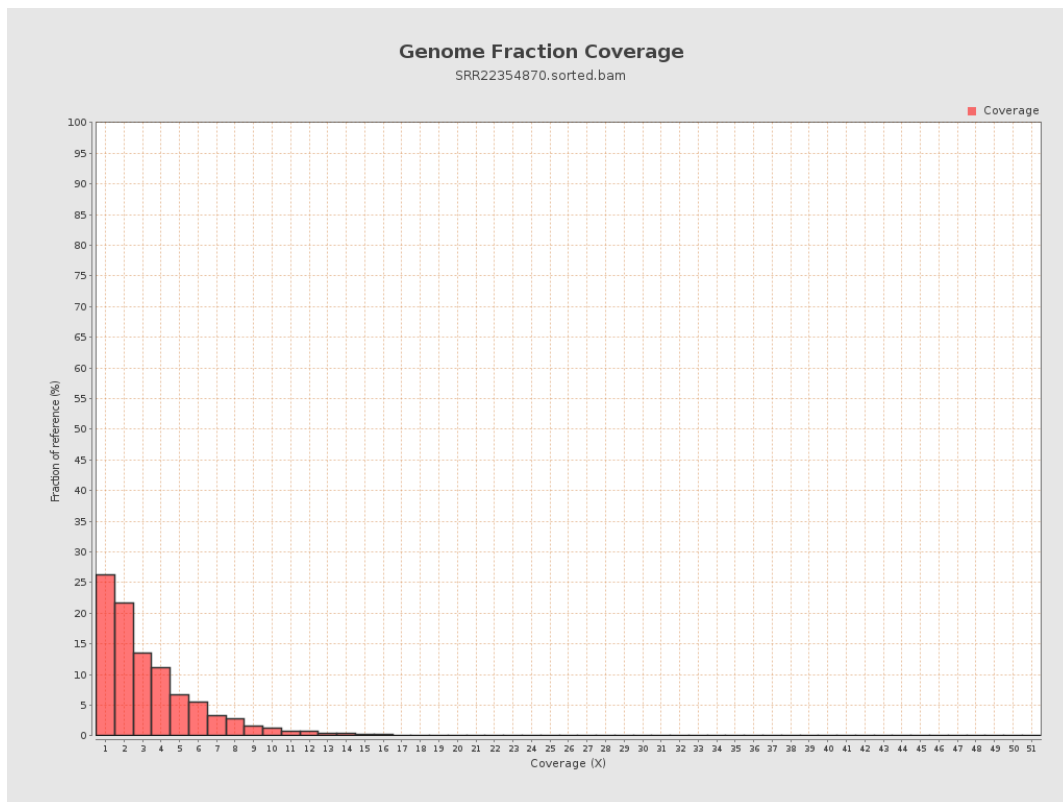
4. Results : Coverage Histogram



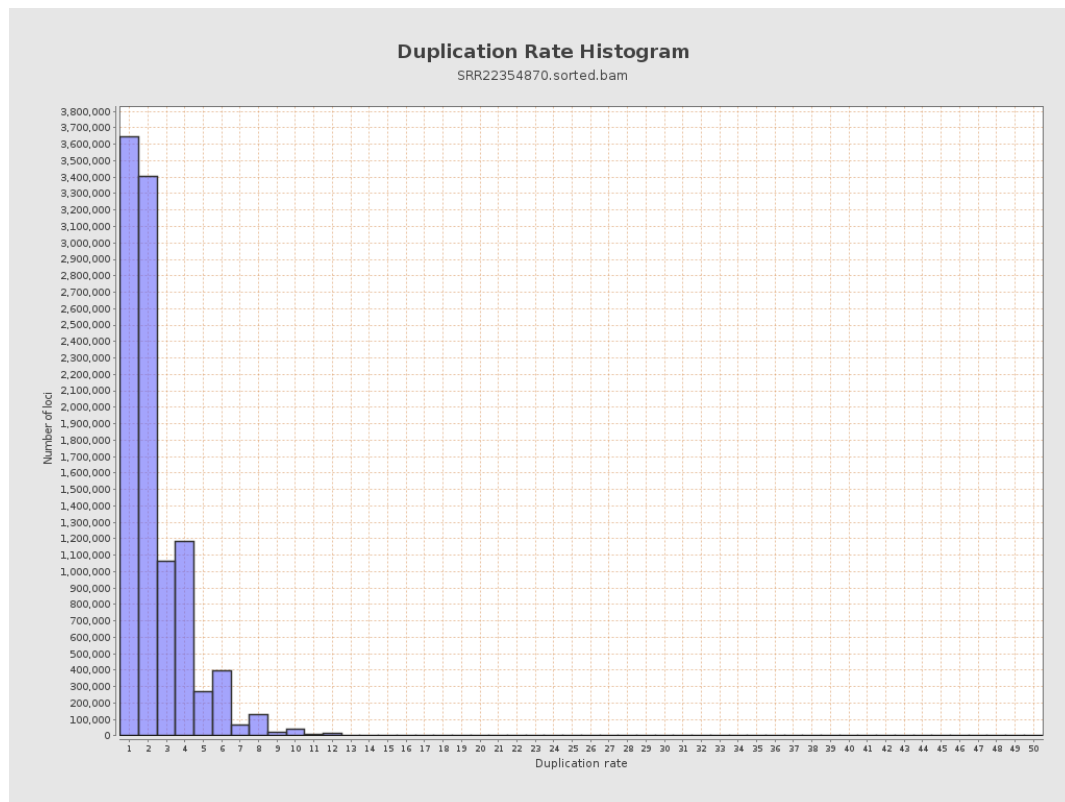
5. Results : Coverage Histogram (0-50X)



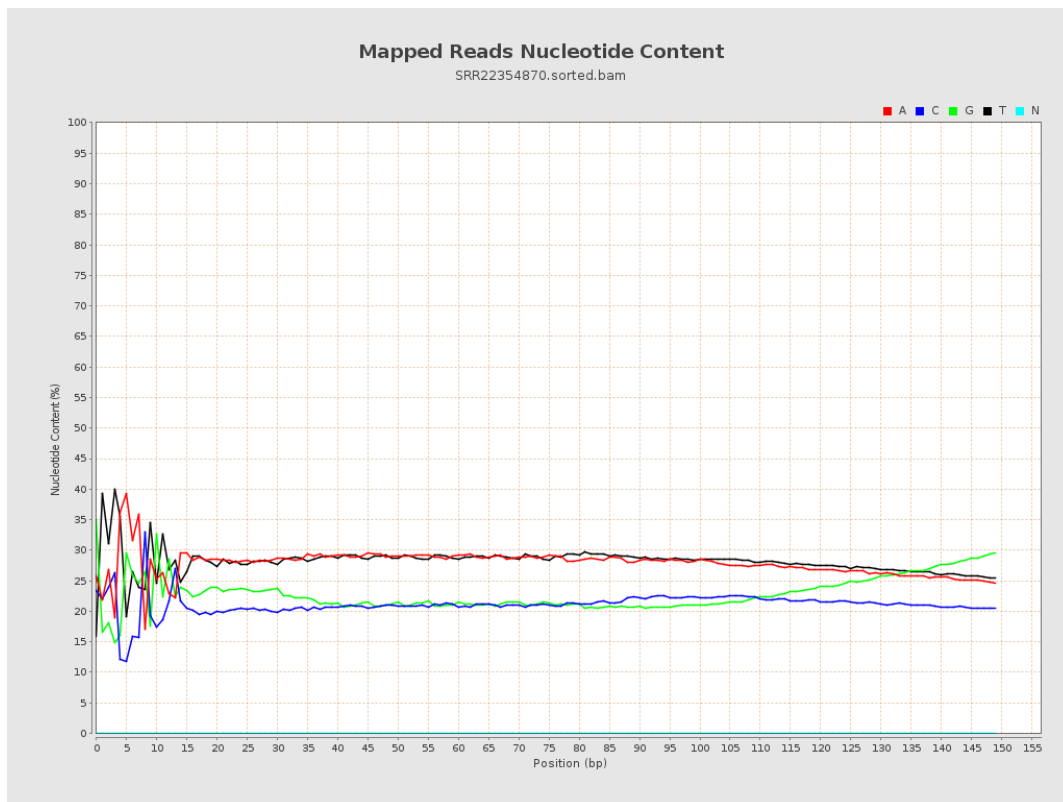
6. Results : Genome Fraction Coverage



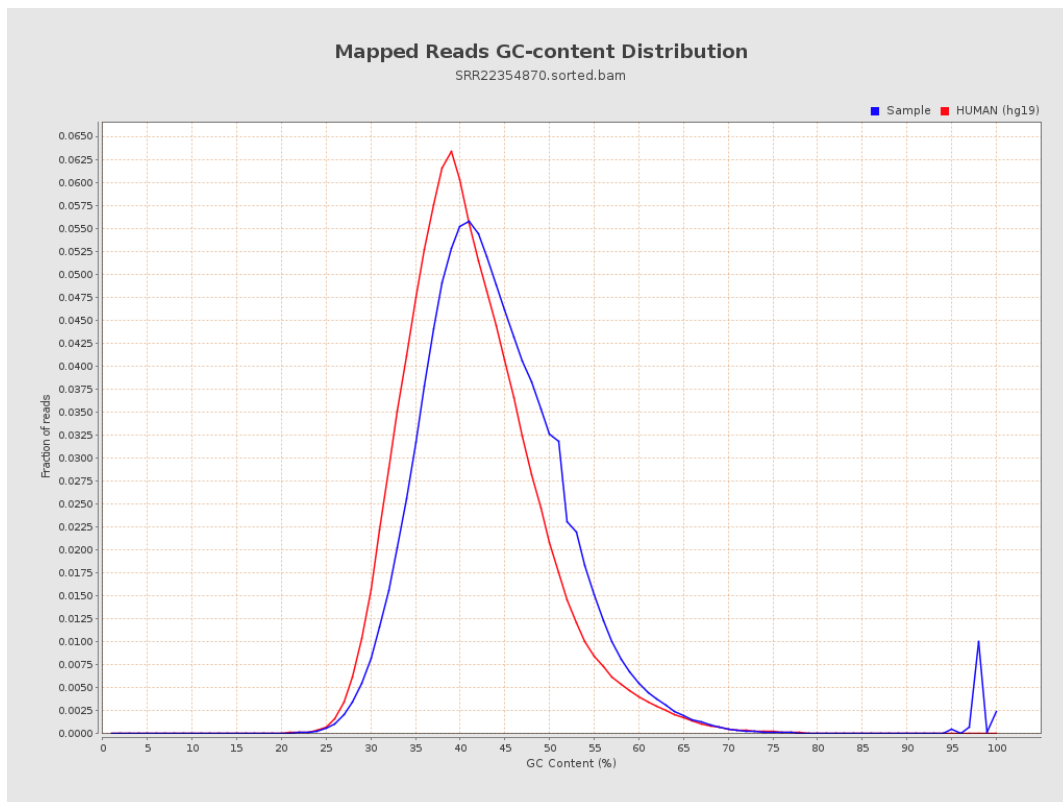
7. Results : Duplication Rate Histogram



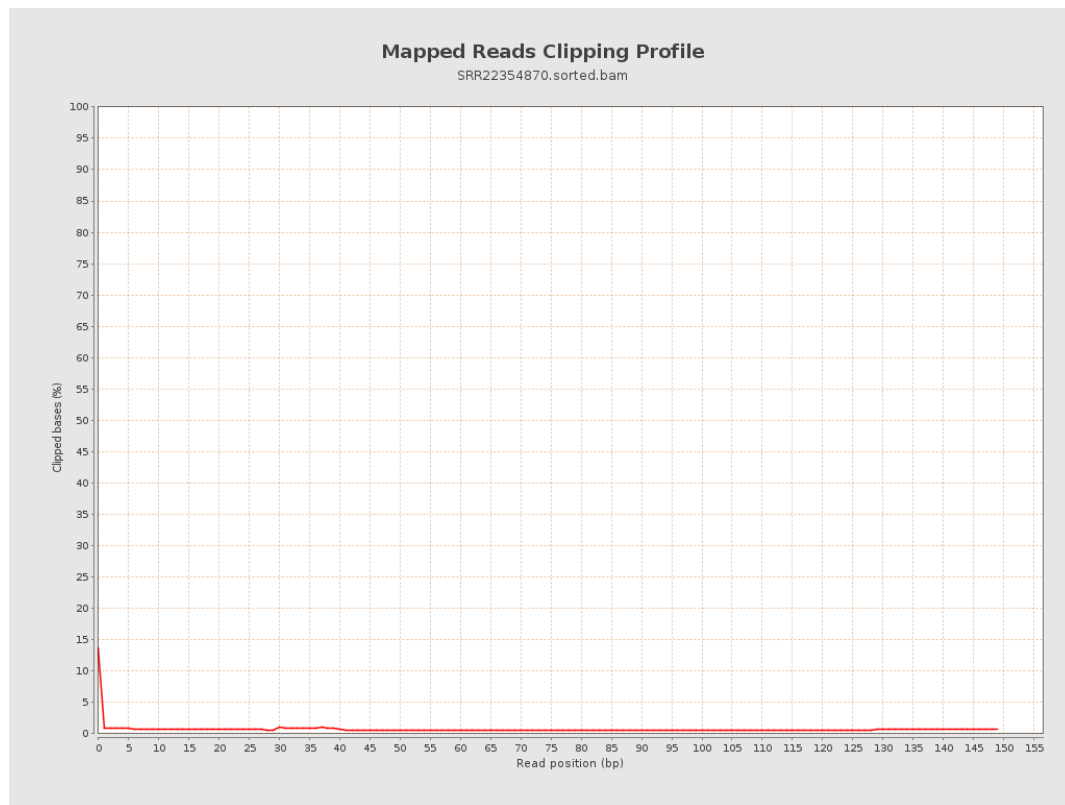
8. Results : Mapped Reads Nucleotide Content



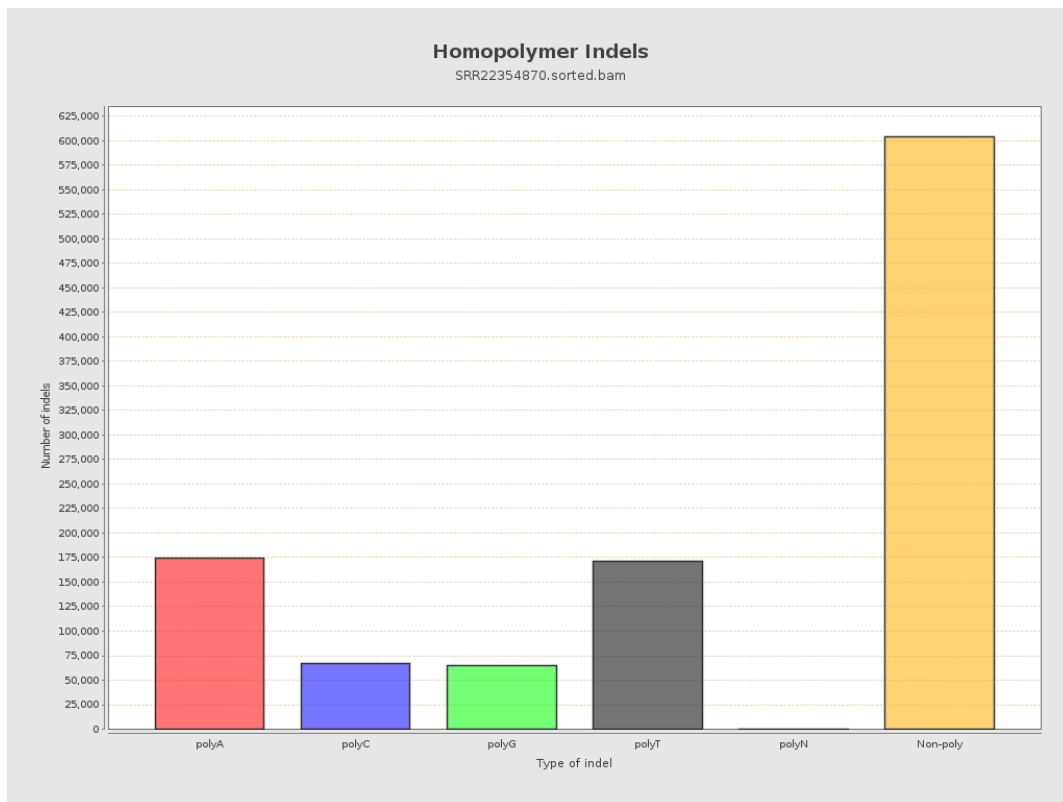
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



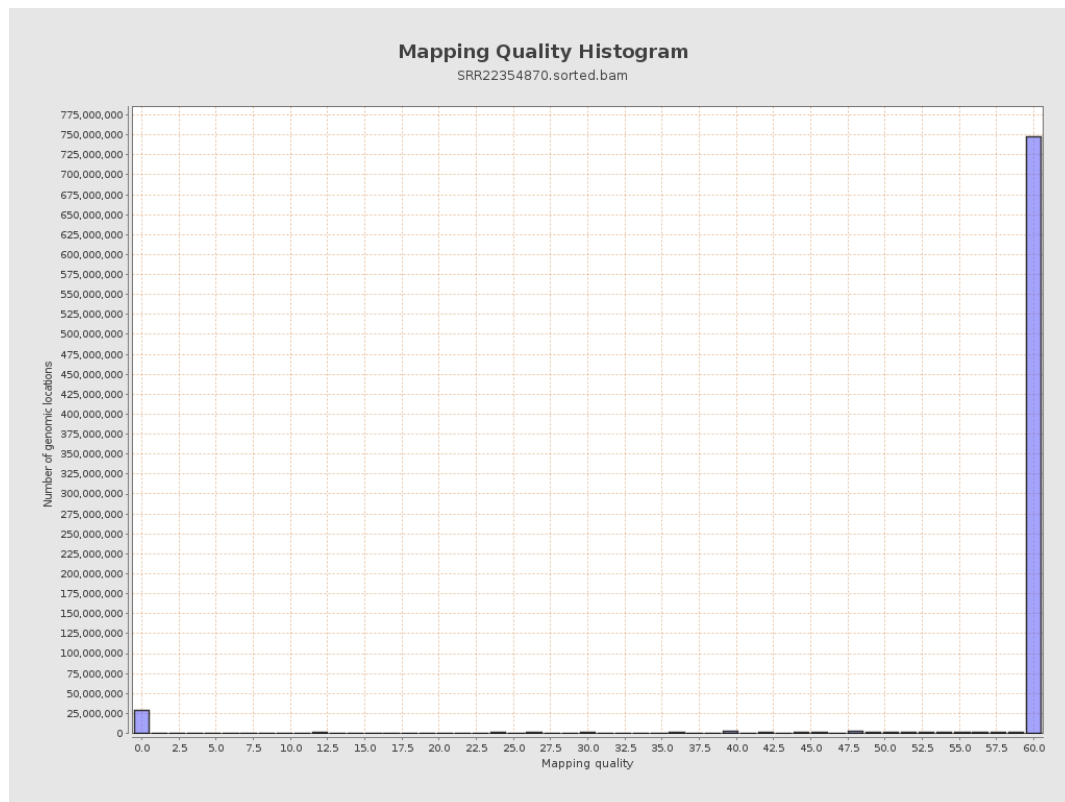
11. Results : Homopolymer Indels



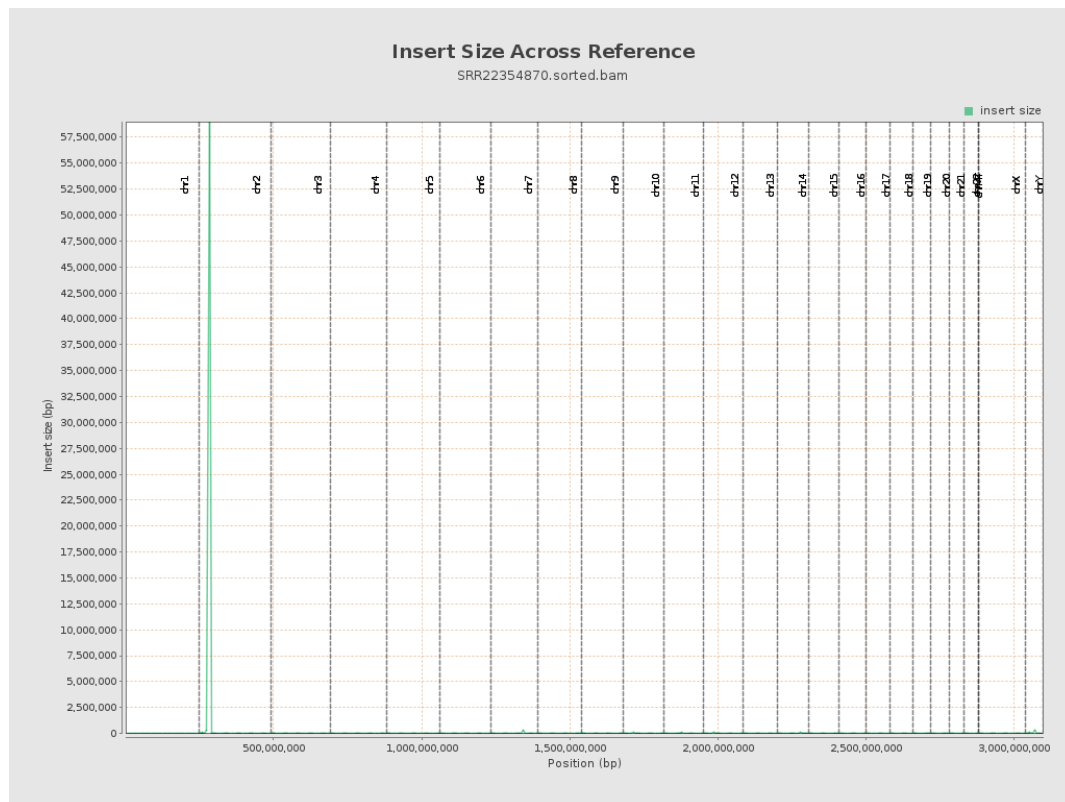
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

