

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:08:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354860.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_SRR22354860 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354860_1.fastq.gz SRR22354860_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:08:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354860.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,614,402
Mapped reads	20,269,240 / 98.33%
Unmapped reads	345,162 / 1.67%
Mapped paired reads	20,269,240 / 98.33%
Mapped reads, first in pair	10,163,037 / 49.3%
Mapped reads, second in pair	10,106,203 / 49.02%
Mapped reads, both in pair	20,190,438 / 97.94%
Mapped reads, singletons	78,802 / 0.38%
Secondary alignments	0
Supplementary alignments	647,570 / 3.14%
Read min/max/mean length	30 / 150 / 151.2
Duplicated reads (estimated)	14,550,877 / 70.59%
Duplication rate	64.93%
Clipped reads	8,959,028 / 43.46%

2.2. ACGT Content

Number/percentage of A's	731,768,113 / 27.83%
Number/percentage of C's	563,793,441 / 21.44%
Number/percentage of T's	741,462,144 / 28.2%
Number/percentage of G's	592,679,676 / 22.54%
Number/percentage of N's	20,188 / 0%

GC Percentage	43.98%
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2.3. Coverage

Mean	0.8499
Standard Deviation	30.9931

2.4. Mapping Quality

Mean Mapping Quality	53.6
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2.5. Insert size

Mean	306,832.66
Standard Deviation	6,372,744.74
P25/Median/P75	116 / 181 / 286

2.6. Mismatches and indels

General error rate	0.74%
Mismatches	18,114,710
Insertions	401,169
Mapped reads with at least one insertion	1.82%
Deletions	410,311
Mapped reads with at least one deletion	1.91%
Homopolymer indels	39.7%

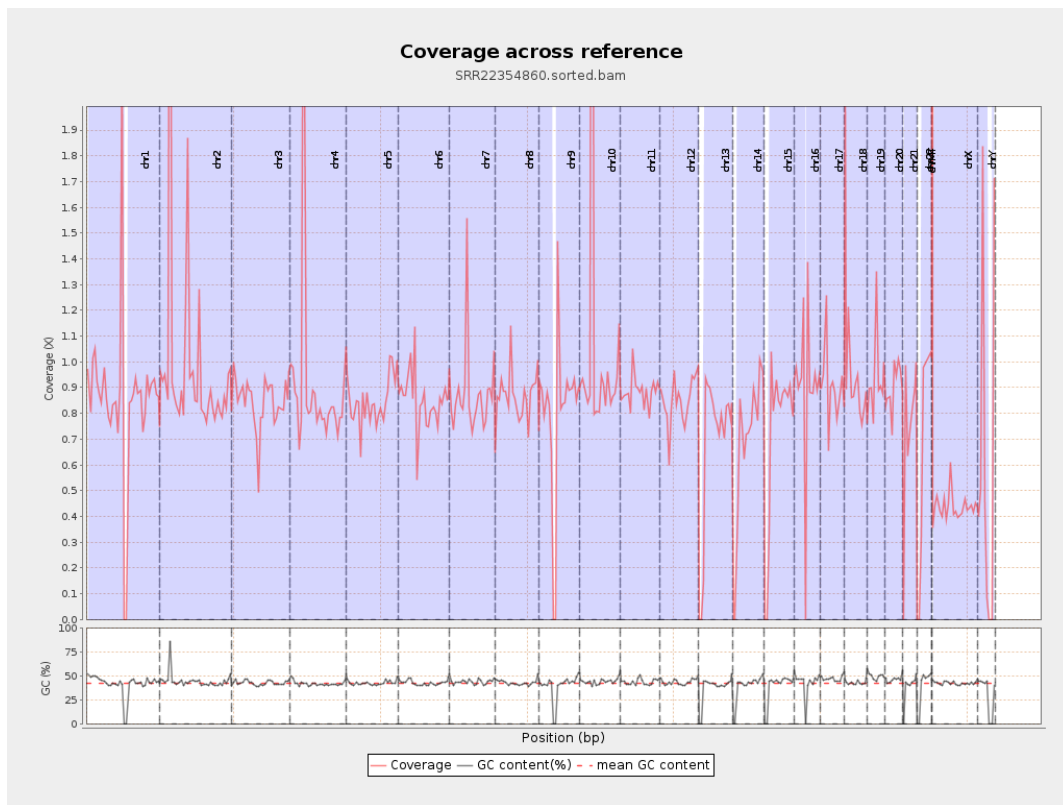
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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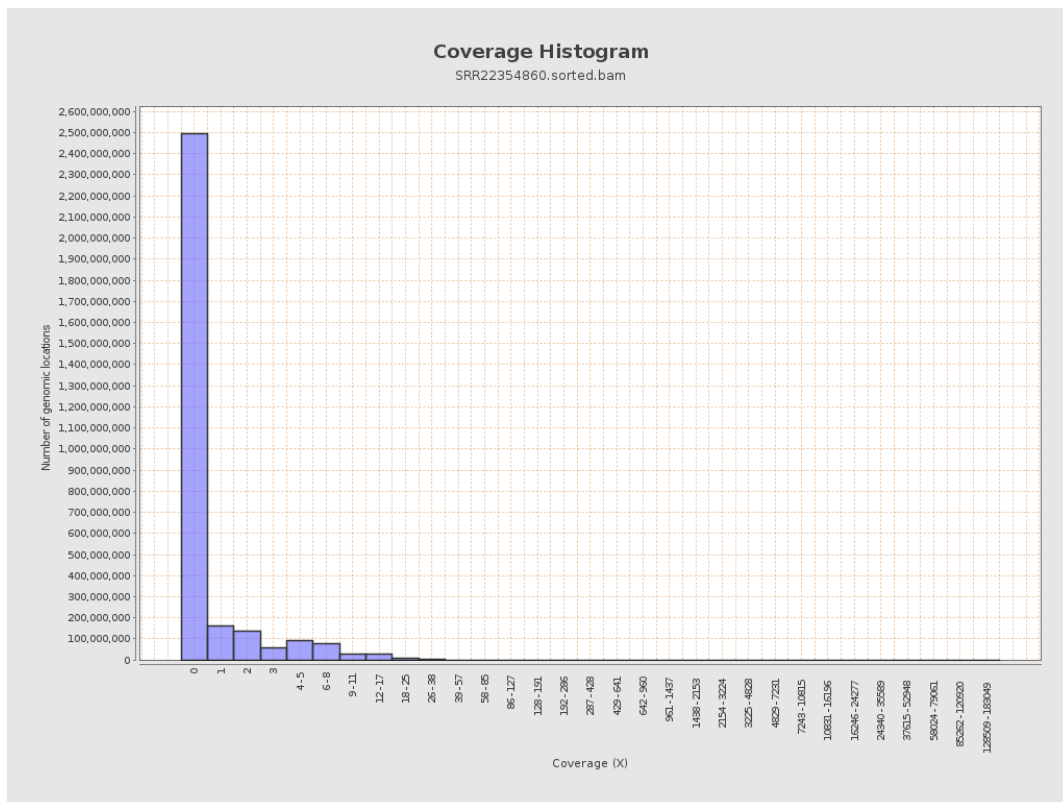
		bases	coverage	deviation
chr1	249250621	214831031	0.8619	30.3634
chr2	243199373	243127145	0.9997	98.4136
chr3	198022430	167202869	0.8444	2.8188
chr4	191154276	172402947	0.9019	15.1047
chr5	180915260	153805460	0.8502	2.5504
chr6	171115067	145797932	0.852	4.298
chr7	159138663	139587898	0.8771	15.4202
chr8	146364022	128303339	0.8766	6.2957
chr9	141213431	112338061	0.7955	13.9556
chr10	135534747	151752471	1.1197	33.02
chr11	135006516	119369641	0.8842	5.4901
chr12	133851895	113456478	0.8476	2.5501
chr13	115169878	78690763	0.6833	2.2241
chr14	107349540	73131706	0.6812	4.4391
chr15	102531392	73154847	0.7135	2.2841
chr16	90354753	82293971	0.9108	5.9276
chr17	81195210	73306701	0.9028	5.6437
chr18	78077248	74599393	0.9555	15.6091
chr19	59128983	55200192	0.9336	18.2407
chr20	63025520	56840242	0.9019	5.4274
chr21	48129895	36336341	0.755	8.2276
chr22	51304566	35693642	0.6957	2.8937
chrMT	16571	24581166	1,483.3846	412.2097
chrX	155270560	67583193	0.4353	2.3363

chrY	59373566	37582555	0.633	19.1014
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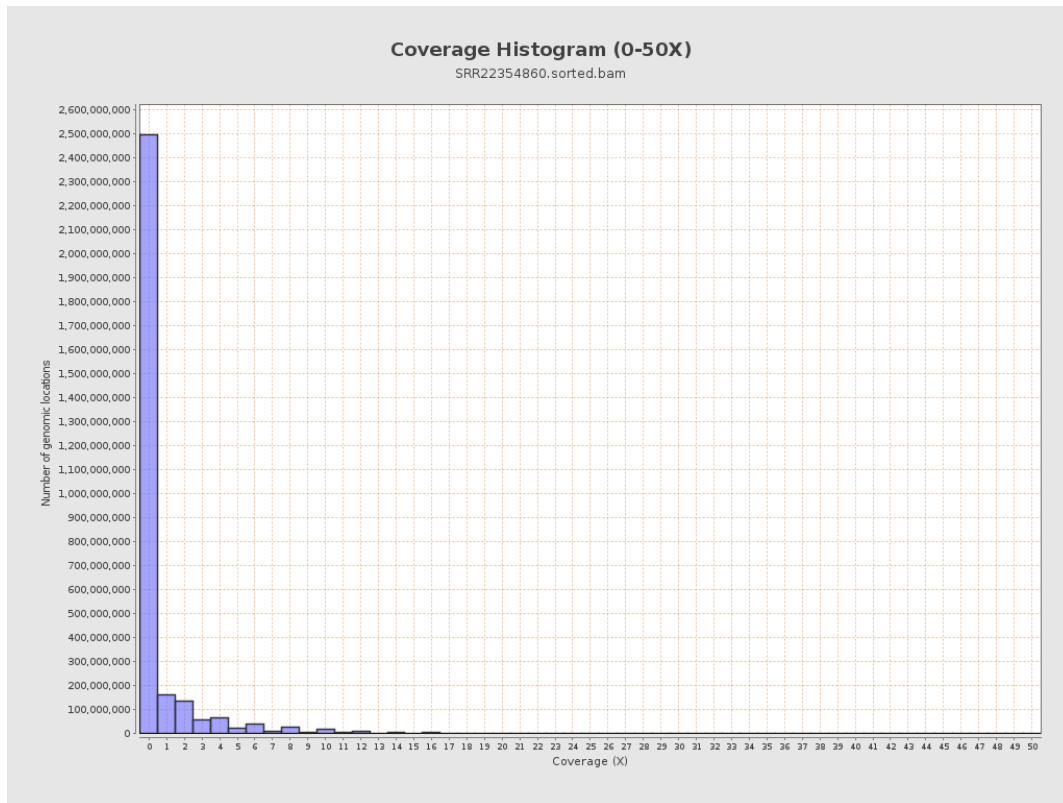
3. Results : Coverage across reference



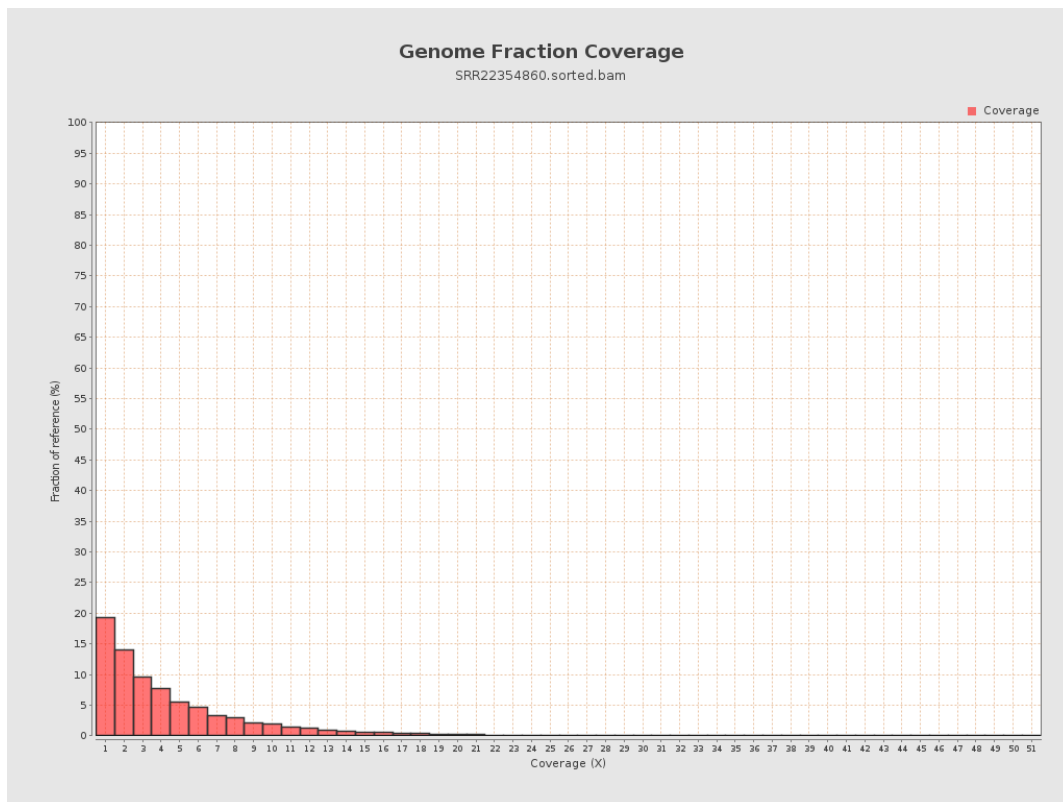
4. Results : Coverage Histogram



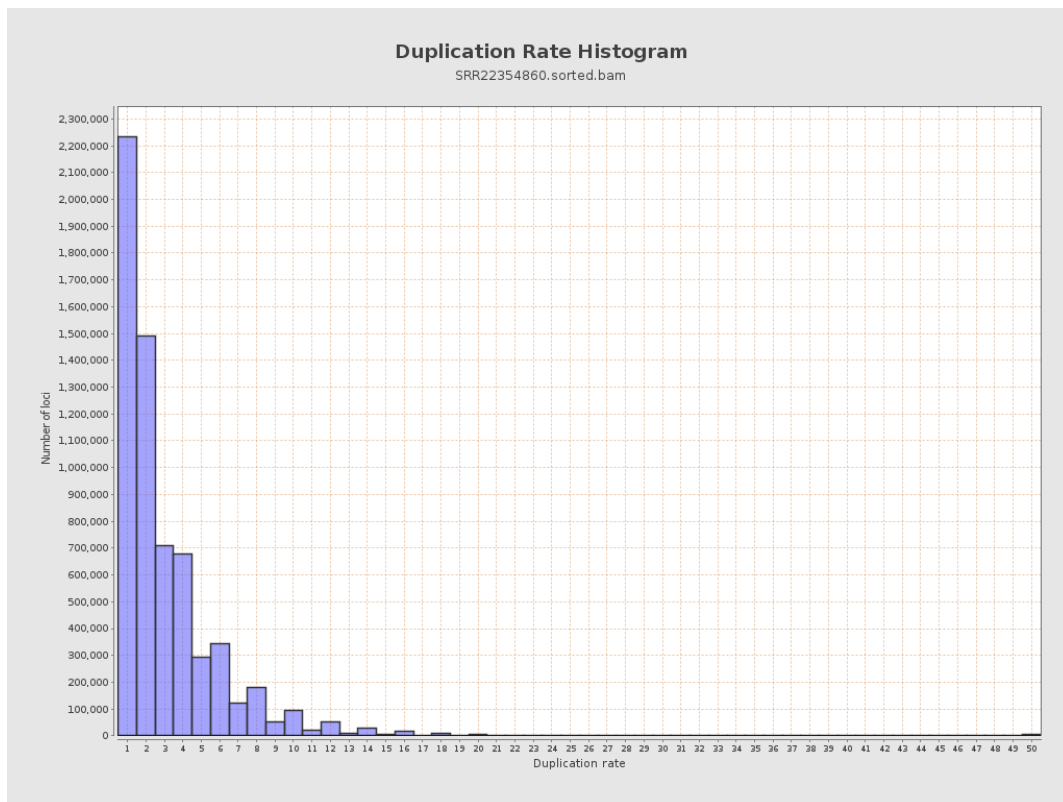
5. Results : Coverage Histogram (0-50X)



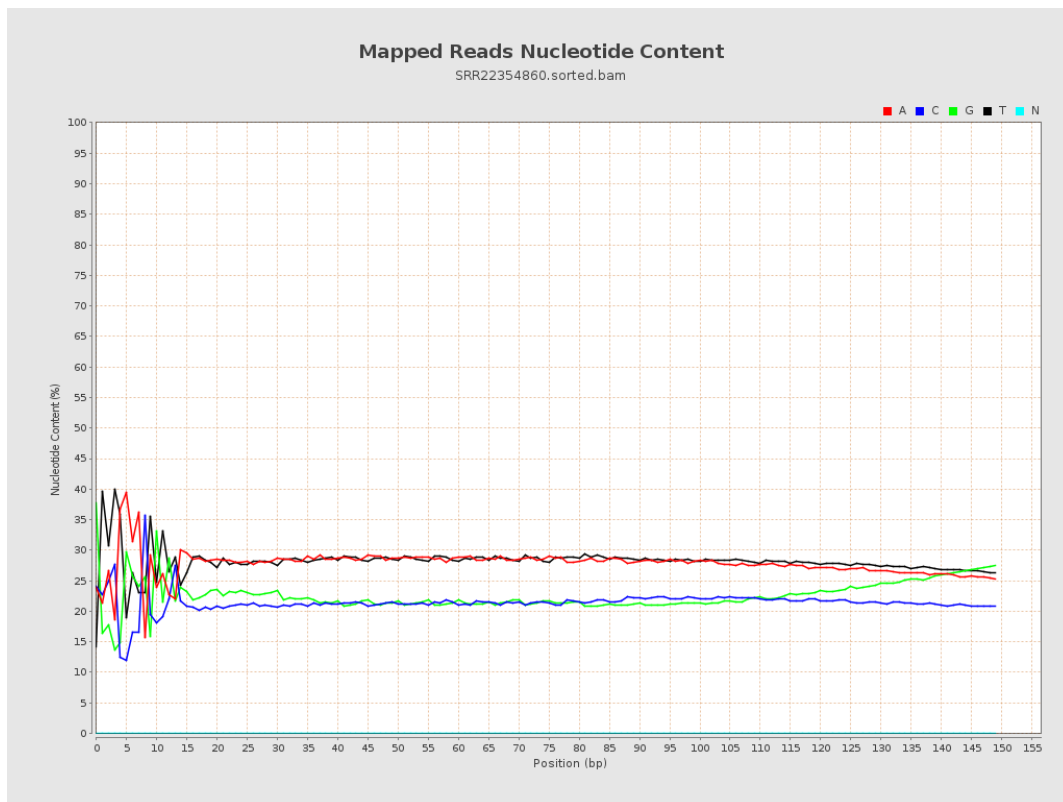
6. Results : Genome Fraction Coverage



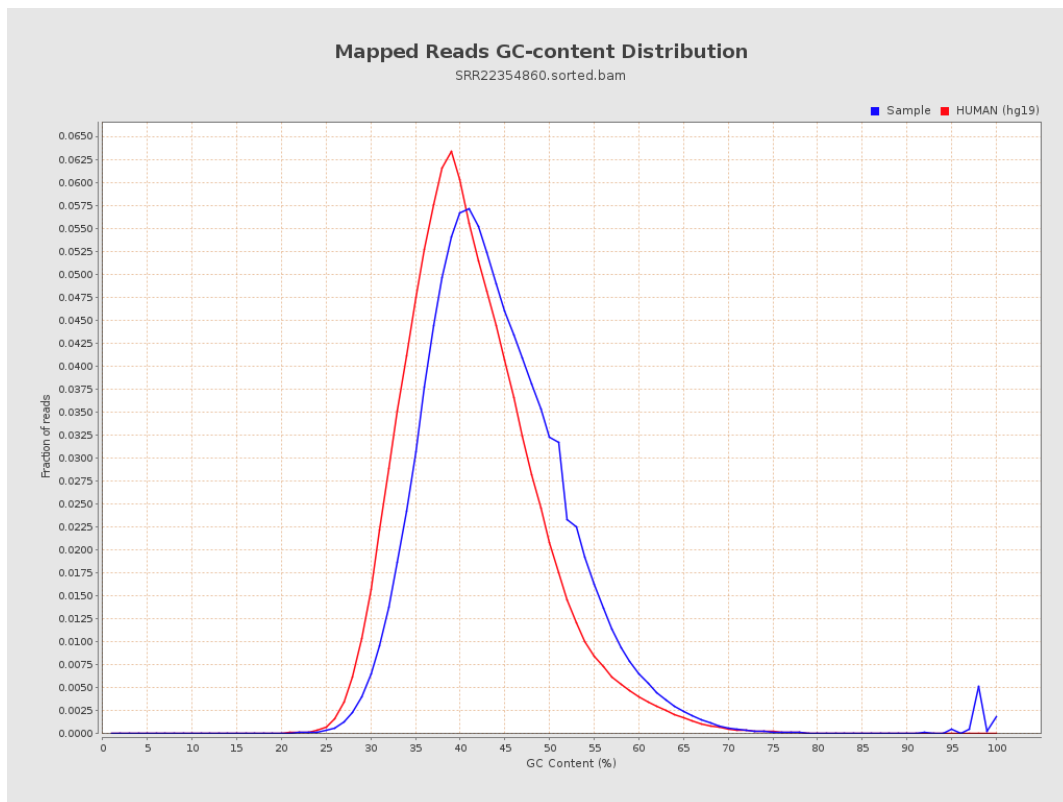
7. Results : Duplication Rate Histogram



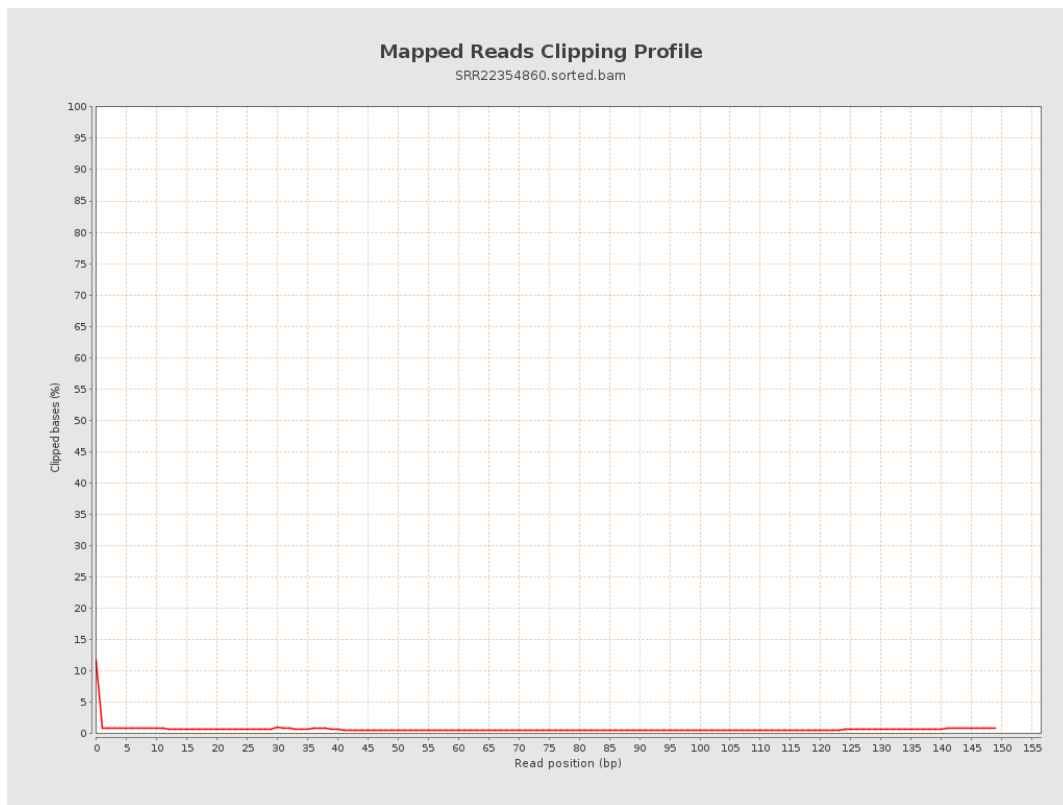
8. Results : Mapped Reads Nucleotide Content



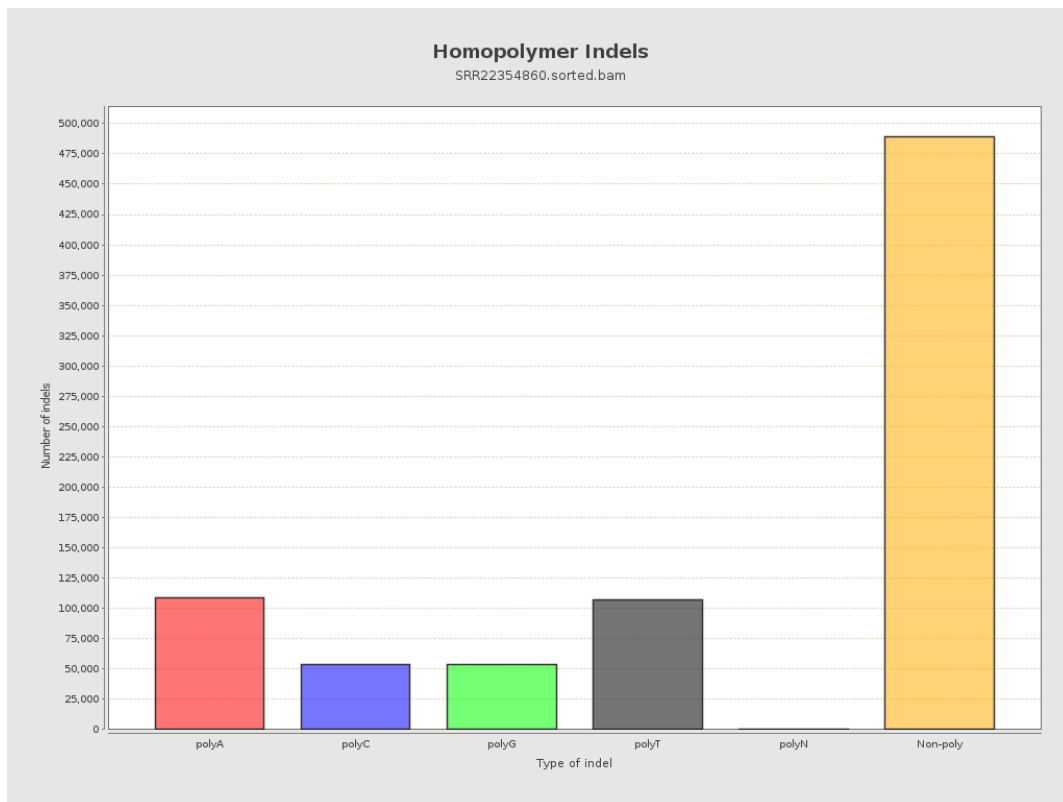
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



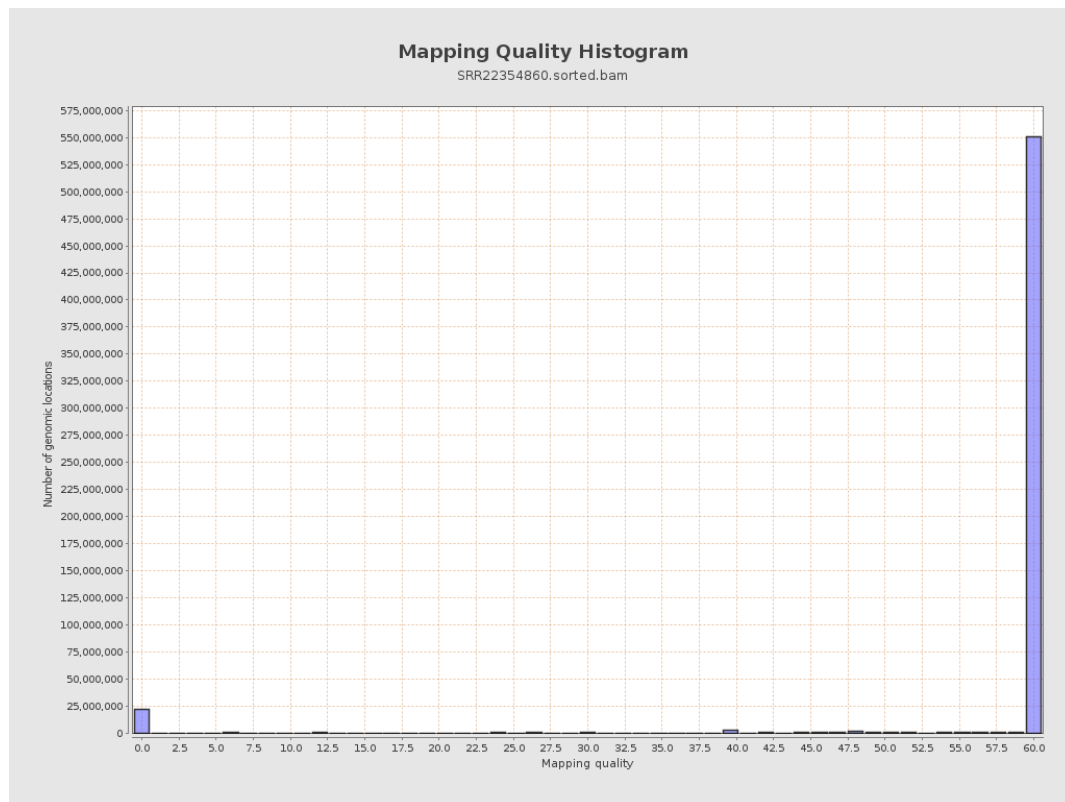
11. Results : Homopolymer Indels



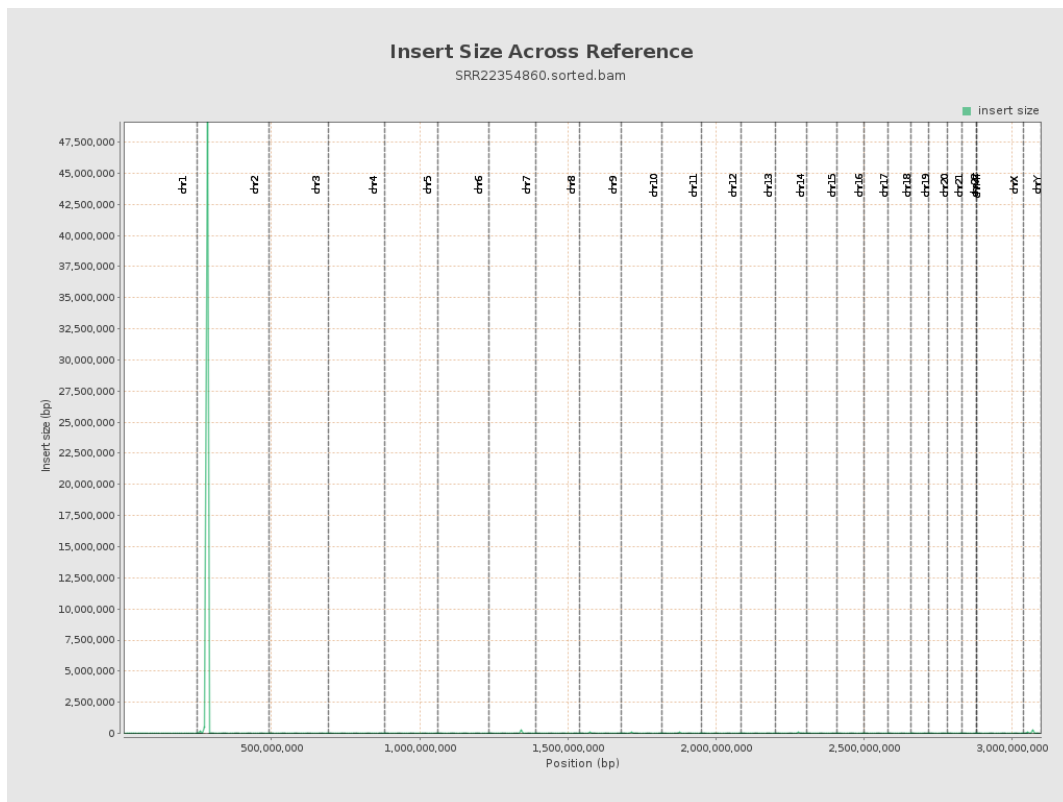
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

