

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:12:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354848.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_SRR22354848 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354848_1.fastq.gz SRR22354848_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:12:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354848.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,307,742
Mapped reads	19,129,860 / 99.08%
Unmapped reads	177,882 / 0.92%
Mapped paired reads	19,129,860 / 99.08%
Mapped reads, first in pair	9,572,570 / 49.58%
Mapped reads, second in pair	9,557,290 / 49.5%
Mapped reads, both in pair	19,102,284 / 98.94%
Mapped reads, singletons	27,576 / 0.14%
Secondary alignments	0
Supplementary alignments	582,385 / 3.02%
Read min/max/mean length	30 / 150 / 151.1
Duplicated reads (estimated)	15,576,652 / 80.68%
Duplication rate	78.75%
Clipped reads	11,554,728 / 59.85%

2.2. ACGT Content

Number/percentage of A's	676,044,916 / 28.9%
Number/percentage of C's	478,020,177 / 20.43%
Number/percentage of T's	687,541,049 / 29.39%
Number/percentage of G's	497,829,242 / 21.28%
Number/percentage of N's	5,777 / 0%

GC Percentage	41.71%
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2.3. Coverage

Mean	0.756
Standard Deviation	27.8506

2.4. Mapping Quality

Mean Mapping Quality	53.86
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2.5. Insert size

Mean	295,867.99
Standard Deviation	6,318,495.31
P25/Median/P75	98 / 138 / 191

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	13,929,359
Insertions	340,579
Mapped reads with at least one insertion	1.68%
Deletions	372,180
Mapped reads with at least one deletion	1.87%
Homopolymer indels	44.23%

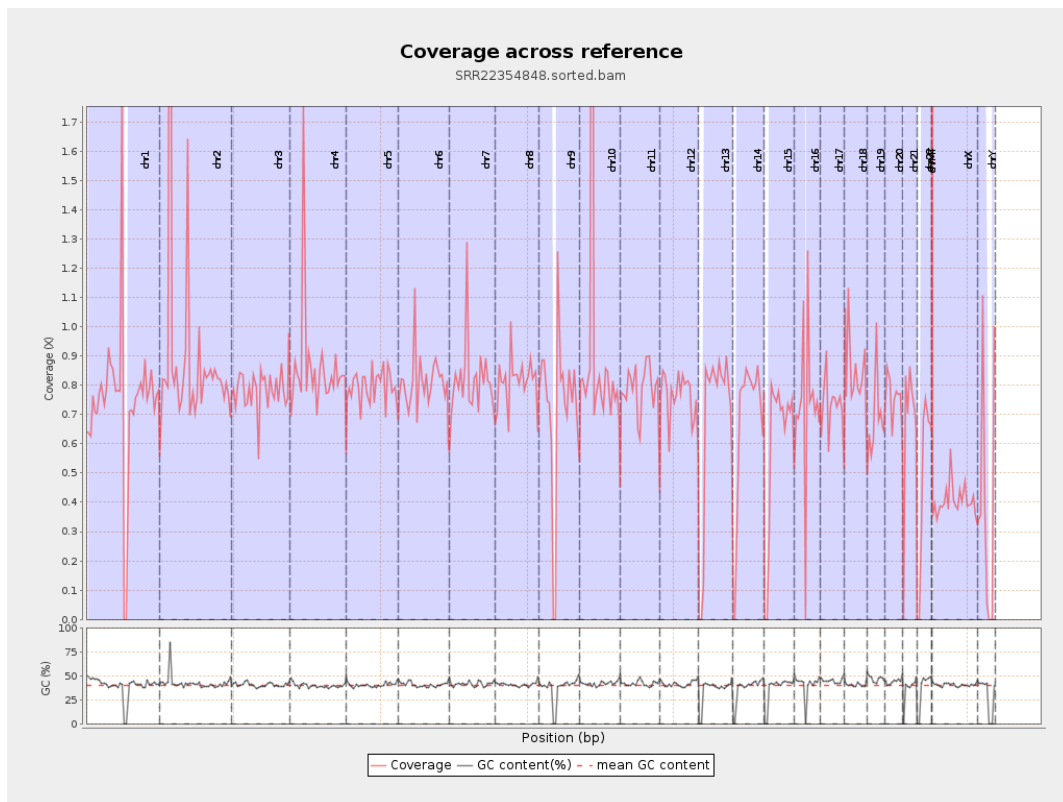
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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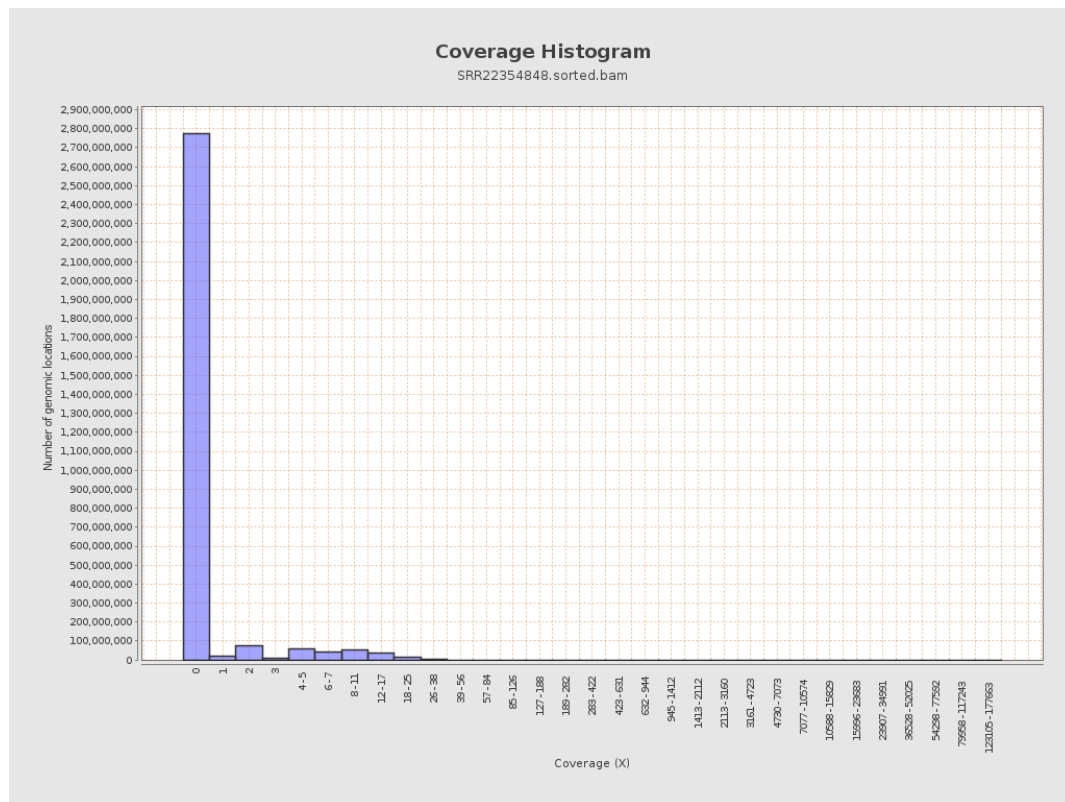
		bases	coverage	deviation
chr1	249250621	187599211	0.7527	23.3387
chr2	243199373	220714474	0.9075	92.3307
chr3	198022430	154526700	0.7803	3.3591
chr4	191154276	164225878	0.8591	7.2926
chr5	180915260	143576642	0.7936	3.1318
chr6	171115067	139230494	0.8137	4.5439
chr7	159138663	129545454	0.814	13.8503
chr8	146364022	119526794	0.8166	4.6052
chr9	141213431	100210377	0.7096	11.4984
chr10	135534747	127637039	0.9417	23.5318
chr11	135006516	105796427	0.7836	5.1394
chr12	133851895	102182160	0.7634	3.0756
chr13	115169878	79003236	0.686	2.8821
chr14	107349540	71843425	0.6692	5.3115
chr15	102531392	61295778	0.5978	2.6266
chr16	90354753	65762078	0.7278	5.3002
chr17	81195210	58583658	0.7215	4.9591
chr18	78077248	65940923	0.8446	10.4277
chr19	59128983	40415539	0.6835	13.0056
chr20	63025520	47775683	0.758	3.7407
chr21	48129895	33283269	0.6915	5.0141
chr22	51304566	25049996	0.4883	2.7343
chrMT	16571	9618483	580.4407	131.1725
chrX	155270560	62833707	0.4047	2.6173

chrY	59373566	24232404	0.4081	9.2791
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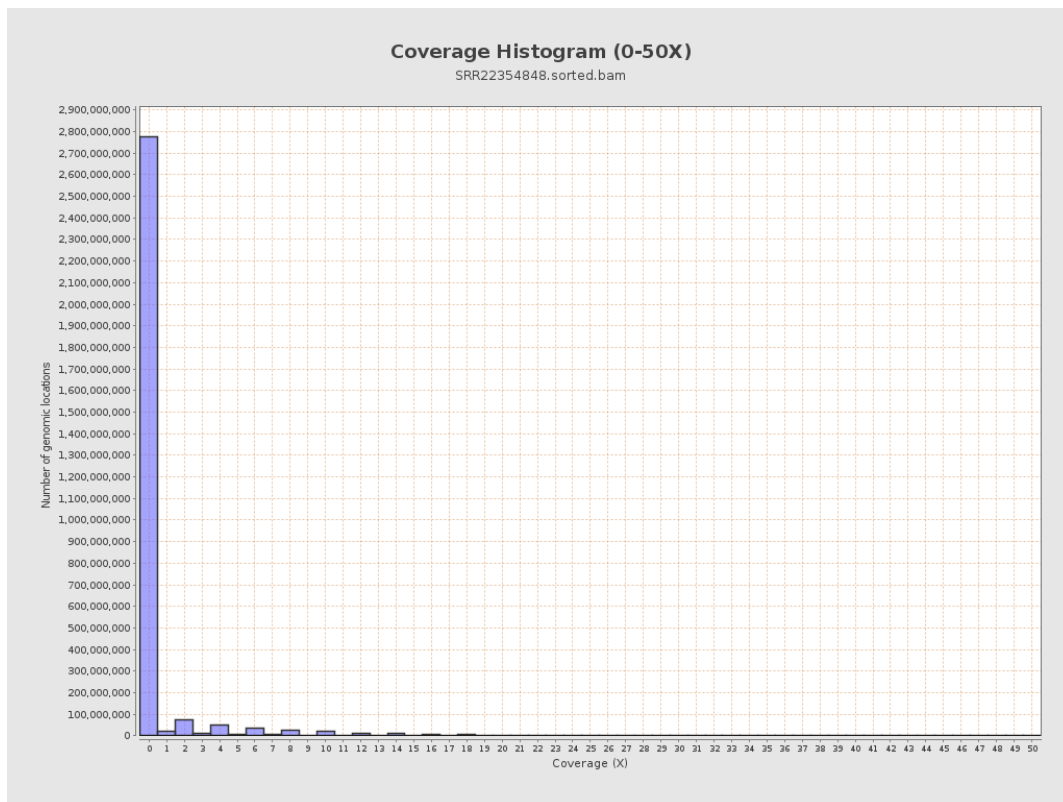
3. Results : Coverage across reference



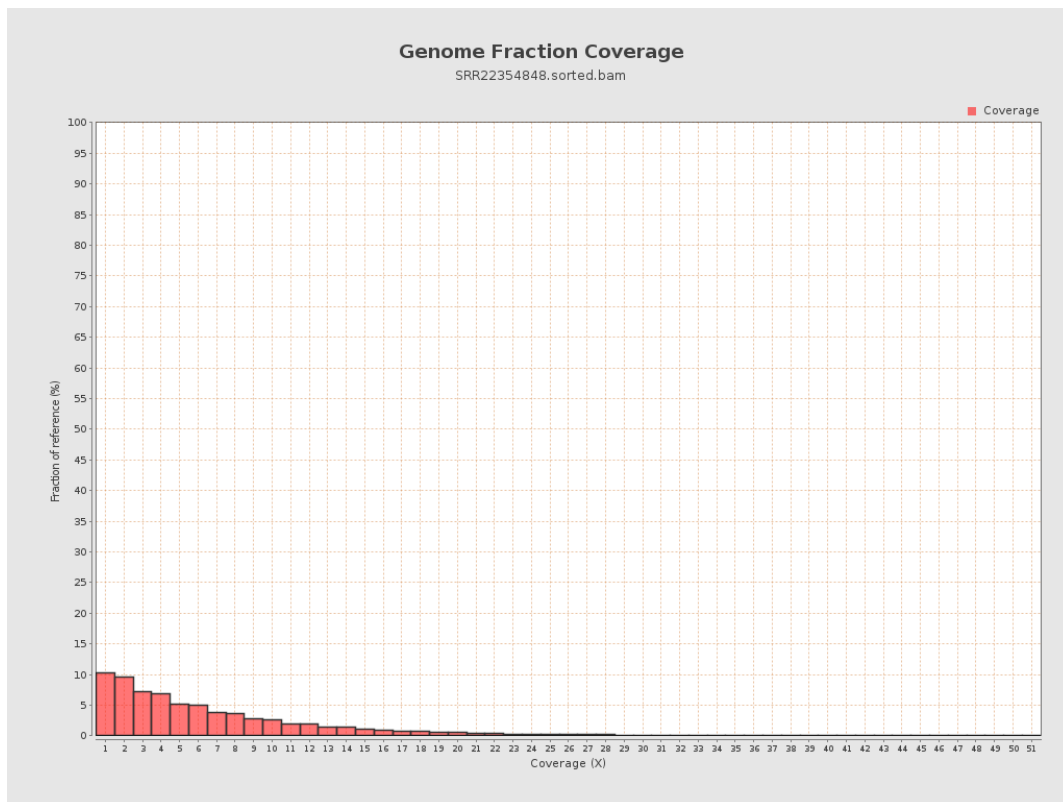
4. Results : Coverage Histogram



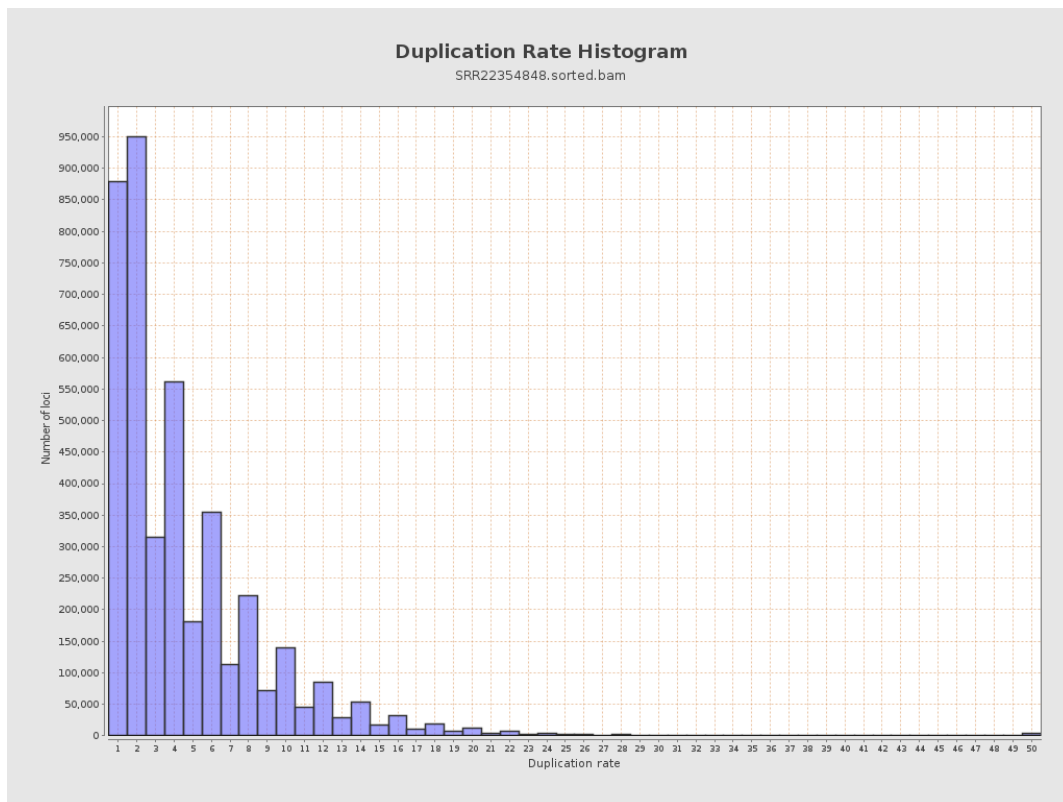
5. Results : Coverage Histogram (0-50X)



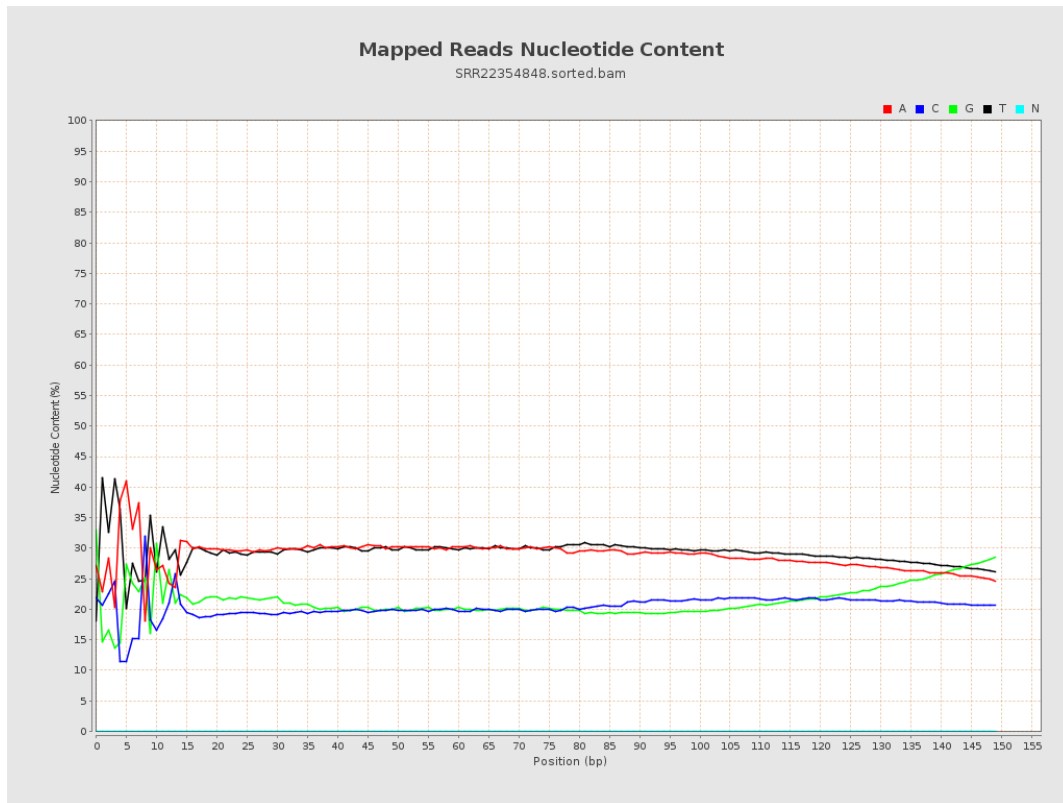
6. Results : Genome Fraction Coverage



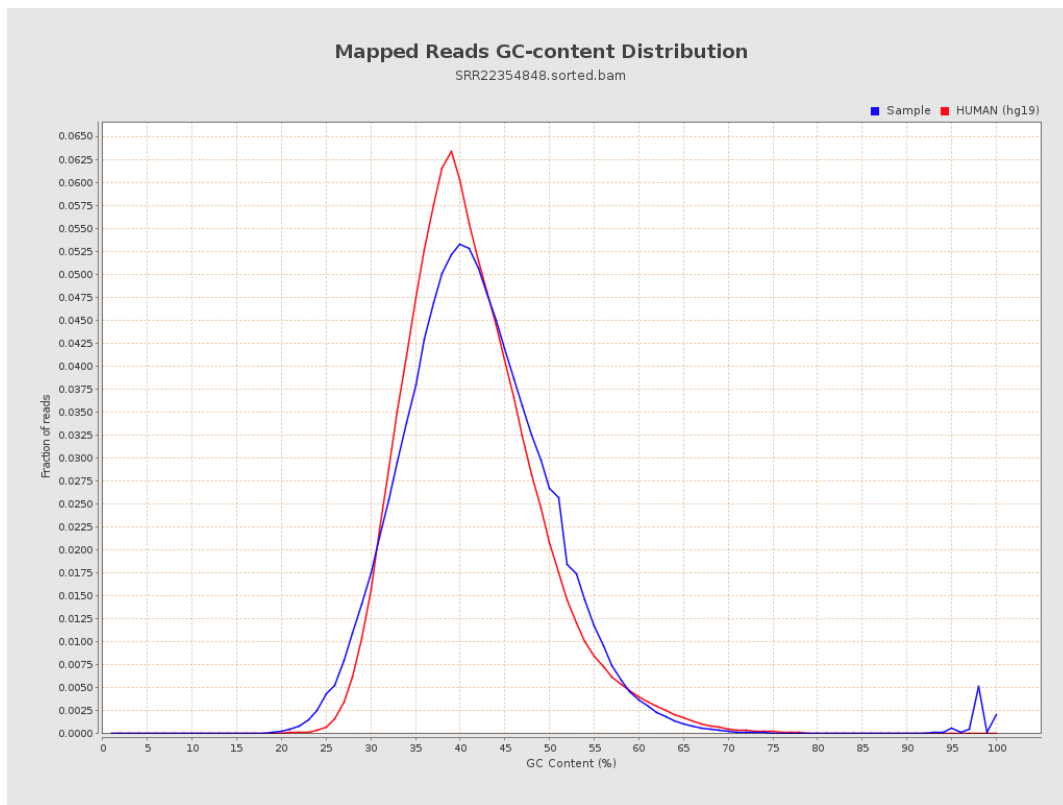
7. Results : Duplication Rate Histogram



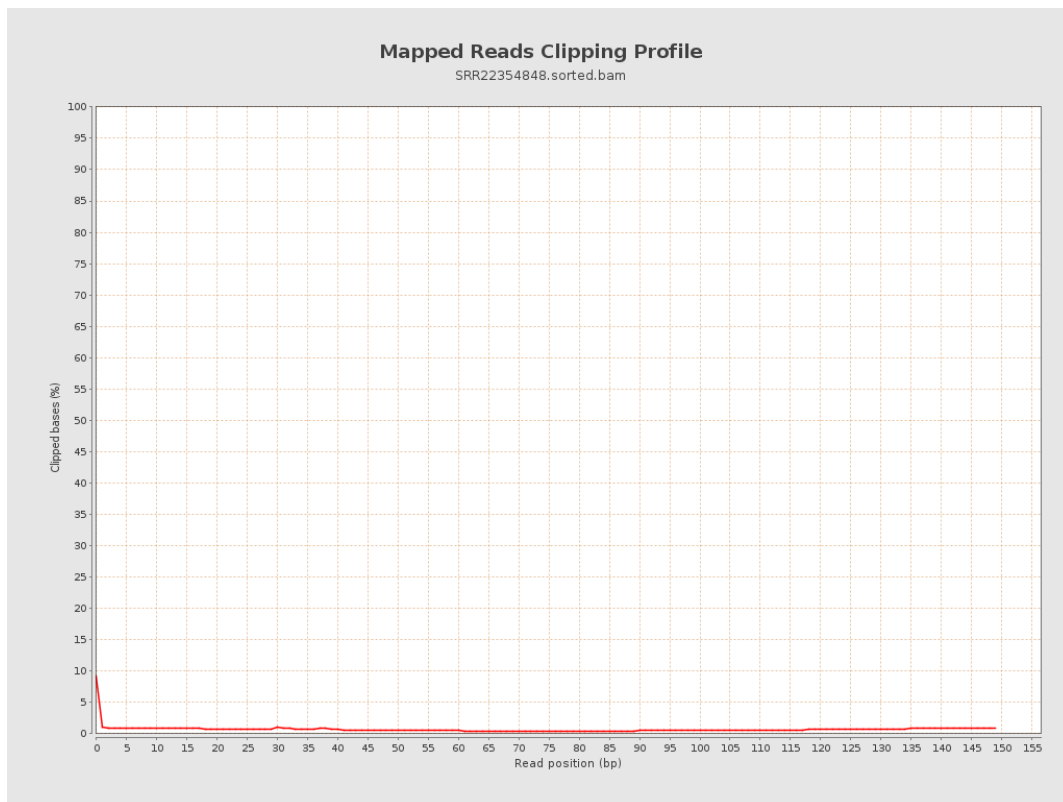
8. Results : Mapped Reads Nucleotide Content



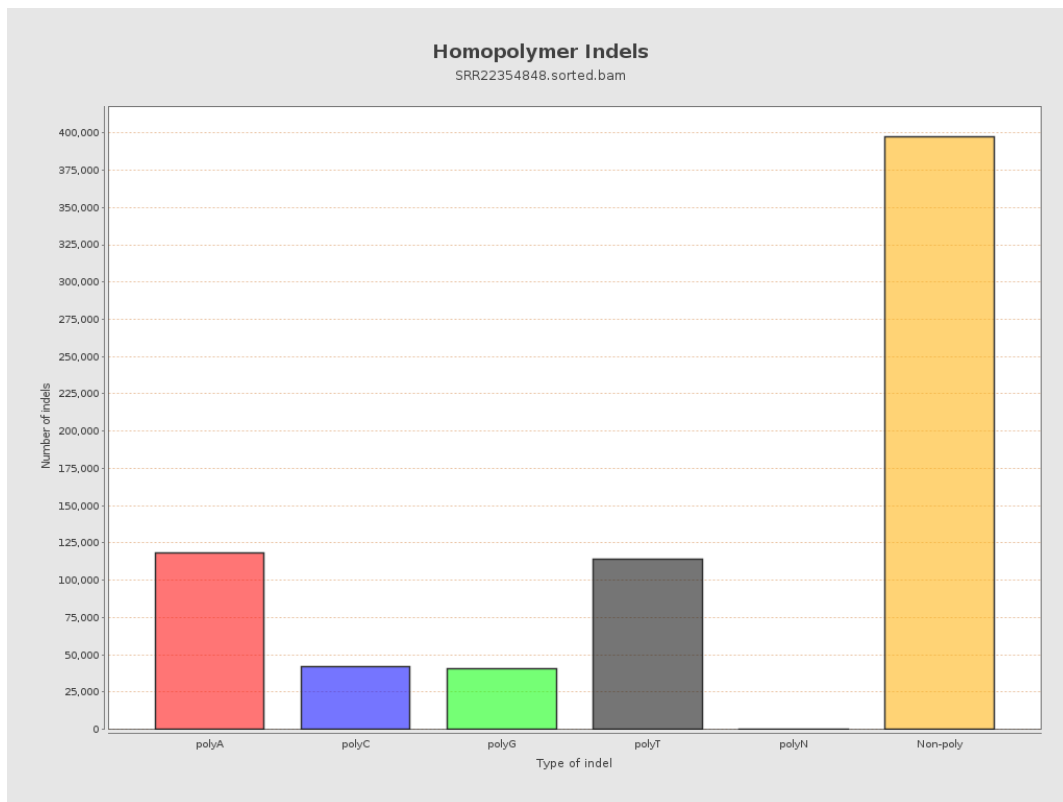
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



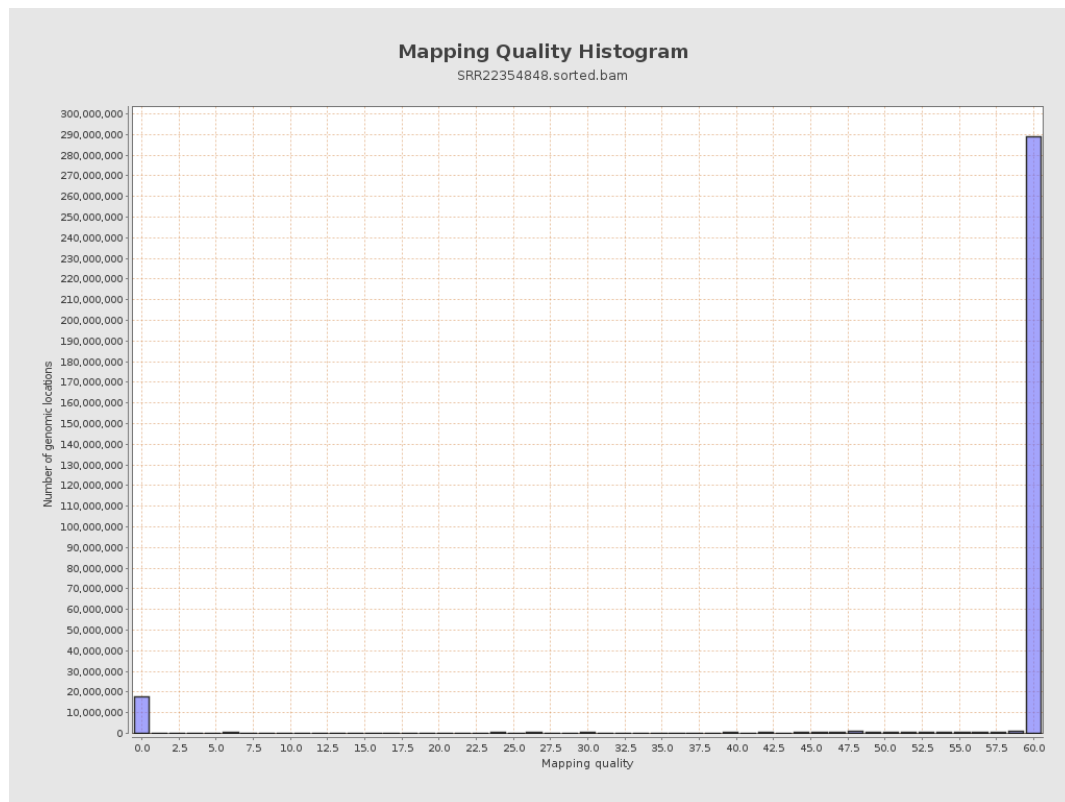
11. Results : Homopolymer Indels



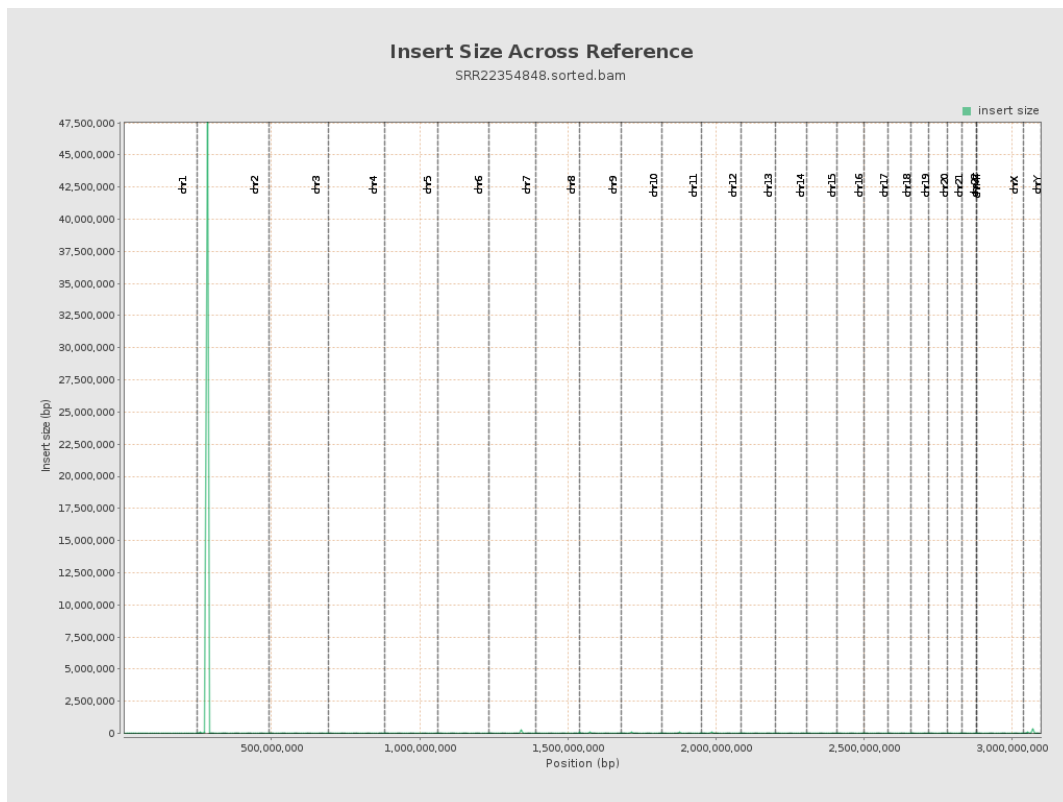
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

