

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/07 00:27:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124838.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_SRR3124838 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124838_1.fastq.gz SRR3124838_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 07 00:27:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124838.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	143,354,098
Mapped reads	139,722,382 / 97.47%
Unmapped reads	3,631,716 / 2.53%
Mapped paired reads	139,722,382 / 97.47%
Mapped reads, first in pair	70,519,017 / 49.19%
Mapped reads, second in pair	69,203,365 / 48.27%
Mapped reads, both in pair	137,959,944 / 96.24%
Mapped reads, singletons	1,762,438 / 1.23%
Secondary alignments	0
Supplementary alignments	1,155,513 / 0.81%
Read min/max/mean length	30 / 150 / 150.39
Duplicated reads (estimated)	49,859,364 / 34.78%
Duplication rate	27.63%
Clipped reads	53,219,257 / 37.12%

2.2. ACGT Content

Number/percentage of A's	5,499,523,594 / 28.48%
Number/percentage of C's	3,901,281,685 / 20.2%
Number/percentage of T's	5,582,167,952 / 28.91%
Number/percentage of G's	4,326,540,036 / 22.41%
Number/percentage of N's	46,534 / 0%

GC Percentage	42.61%
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2.3. Coverage

Mean	6.2414
Standard Deviation	51.5667

2.4. Mapping Quality

Mean Mapping Quality	54.03
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2.5. Insert size

Mean	40,454.04
Standard Deviation	1,925,218.91
P25/Median/P75	207 / 262 / 328

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	223,392,505
Insertions	2,872,418
Mapped reads with at least one insertion	1.94%
Deletions	6,349,542
Mapped reads with at least one deletion	4.38%
Homopolymer indels	46.79%

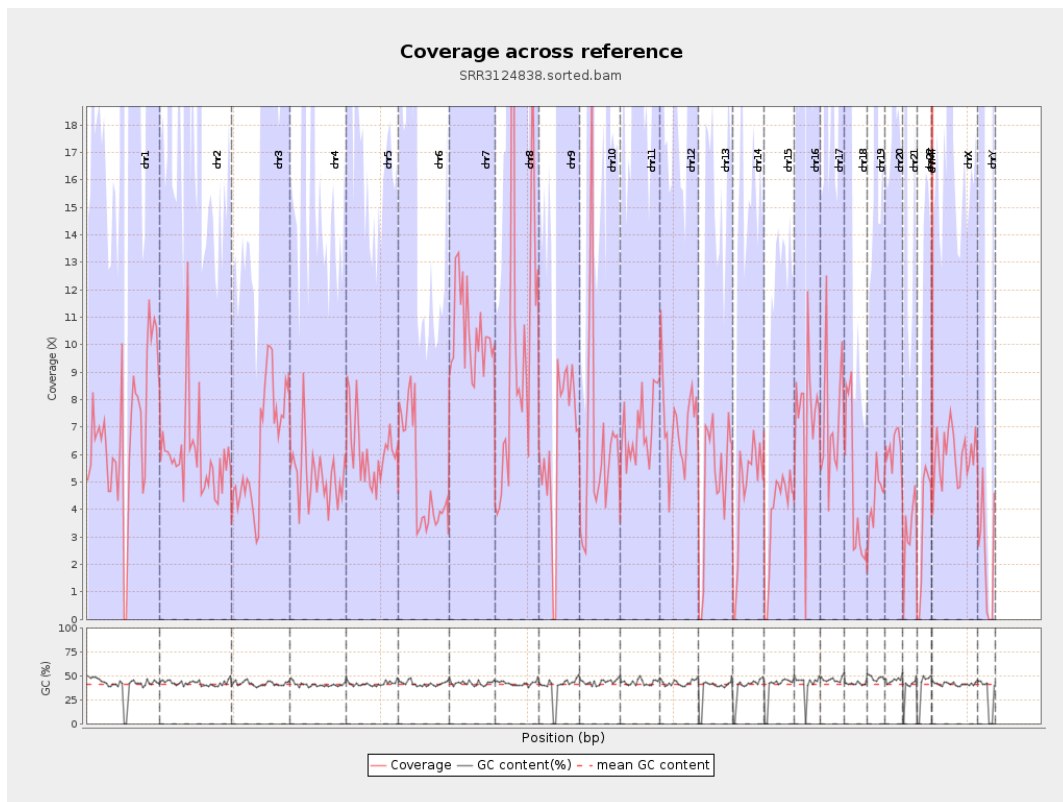
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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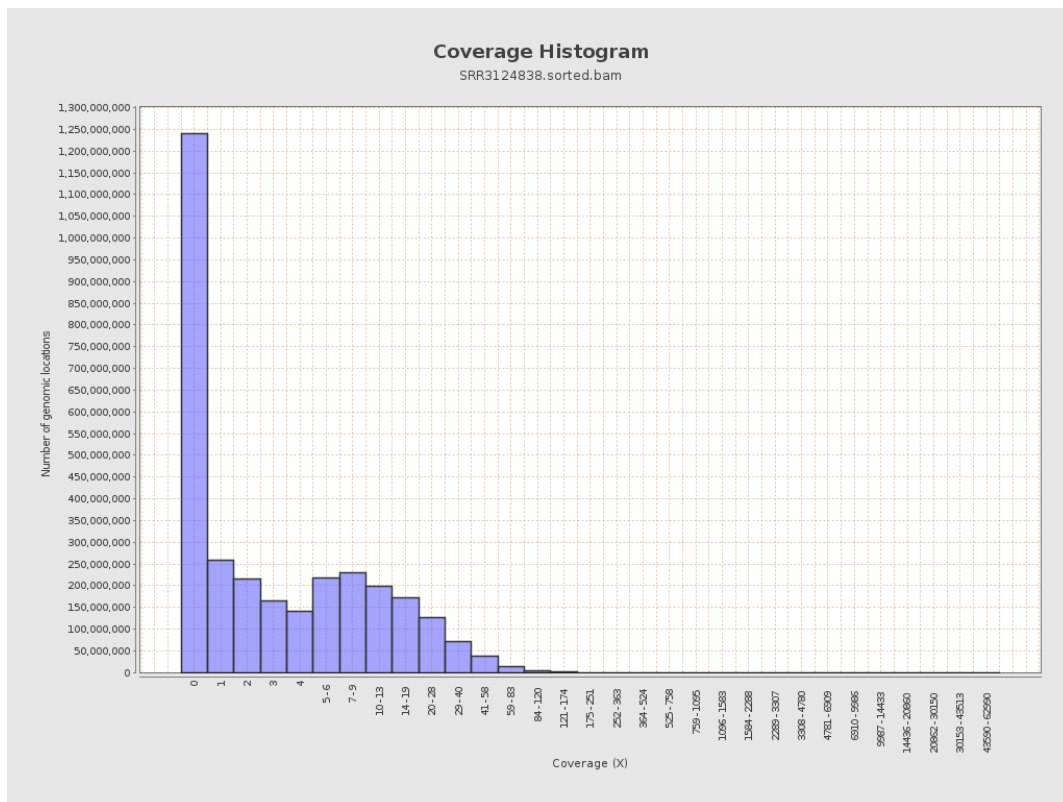
		bases	coverage	deviation
chr1	249250621	1706918365	6.8482	63.6492
chr2	243199373	1457304902	5.9922	52.8249
chr3	198022430	1251602751	6.3205	10.7157
chr4	191154276	997136429	5.2164	37.3722
chr5	180915260	1108287419	6.126	10.7008
chr6	171115067	879064446	5.1373	26.2964
chr7	159138663	1658706392	10.423	86.3426
chr8	146364022	1489377066	10.1758	29.7982
chr9	141213431	896186285	6.3463	90.4104
chr10	135534747	877314097	6.473	115.5155
chr11	135006516	925681145	6.8566	33.4713
chr12	133851895	951651179	7.1097	11.7946
chr13	115169878	575136979	4.9938	9.2431
chr14	107349540	500611615	4.6634	9.7818
chr15	102531392	389065693	3.7946	7.5805
chr16	90354753	664710086	7.3567	49.7399
chr17	81195210	576972837	7.106	100.204
chr18	78077248	358253569	4.5885	61.7409
chr19	59128983	259788172	4.3936	34.6462
chr20	63025520	393544379	6.2442	14.8609
chr21	48129895	158861502	3.3007	18.0658
chr22	51304566	179081460	3.4906	8.3915
chrMT	16571	5867732	354.0964	172.6535
chrX	155270560	921622295	5.9356	19.0331

chrY	59373566	138831873	2.3383	46.9935
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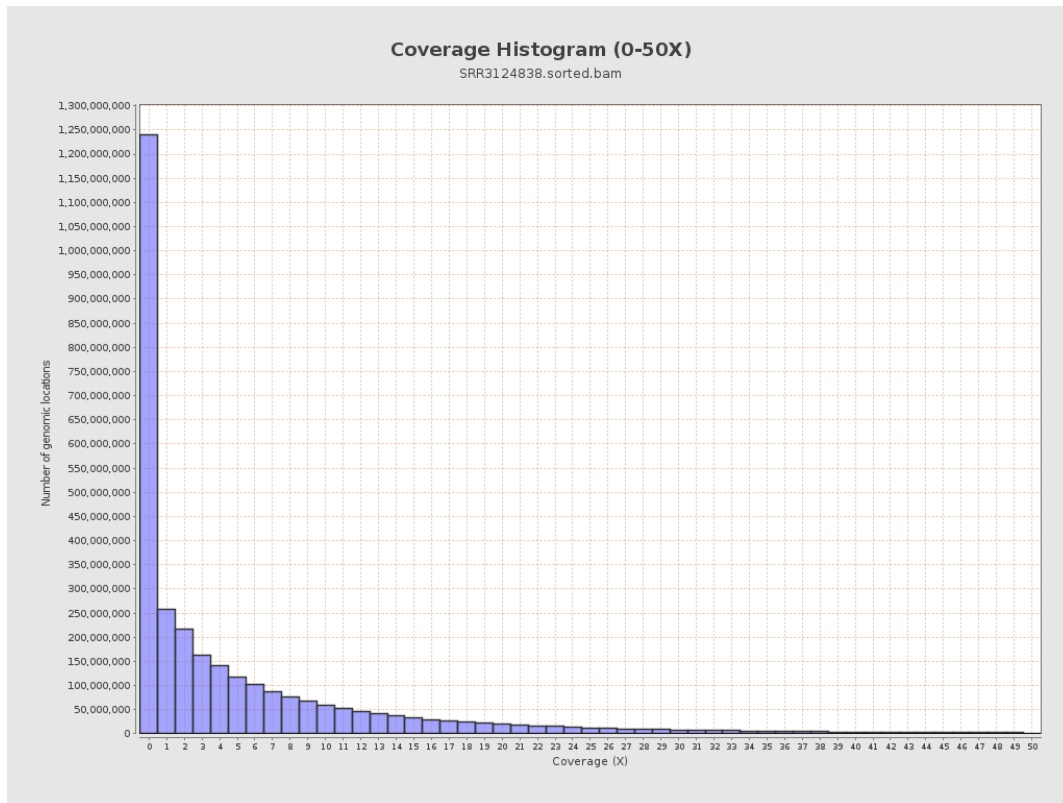
3. Results : Coverage across reference



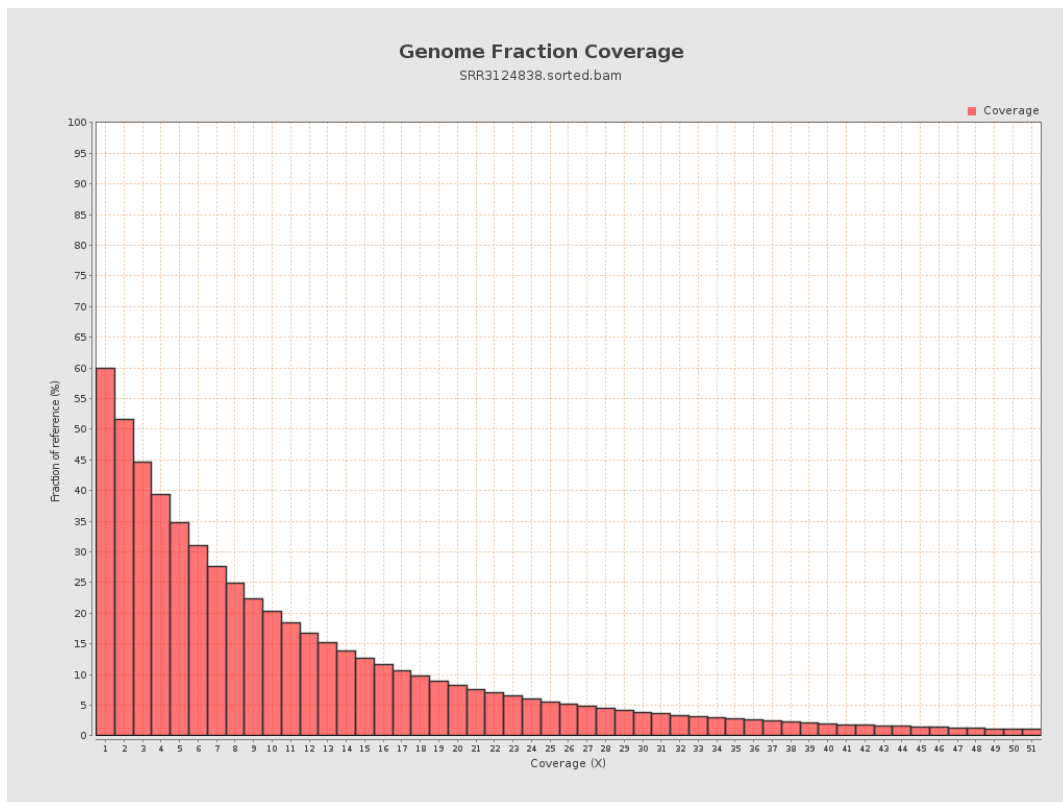
4. Results : Coverage Histogram



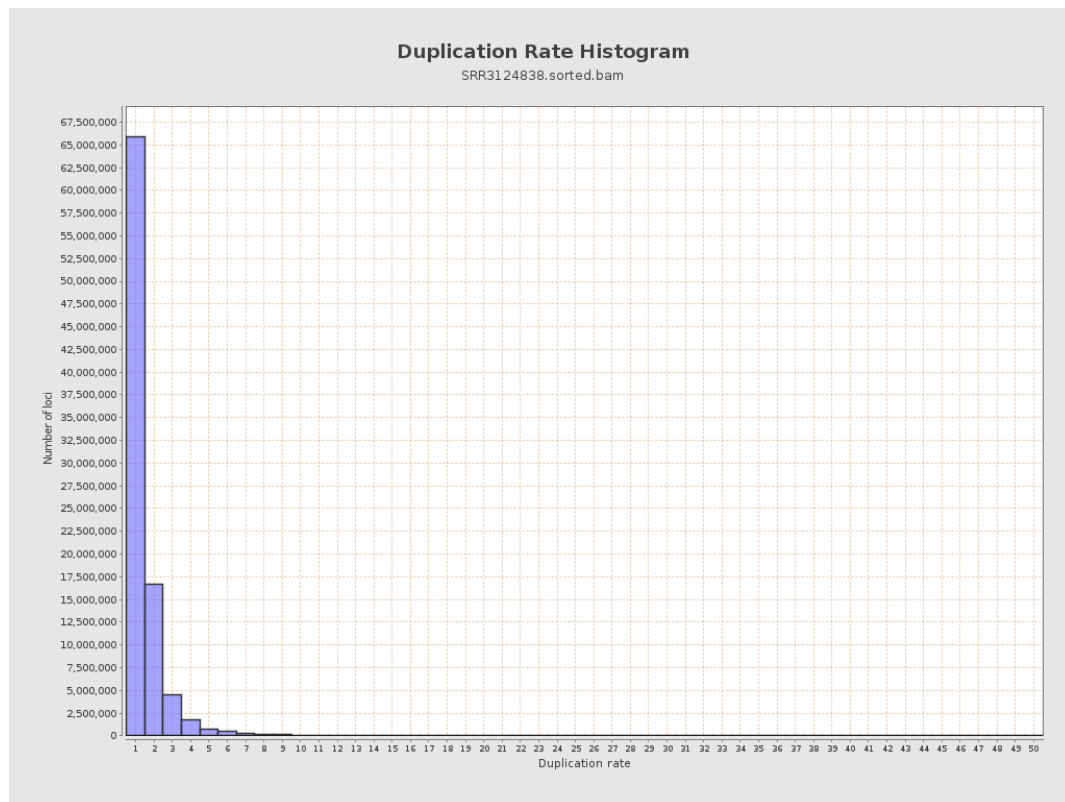
5. Results : Coverage Histogram (0-50X)



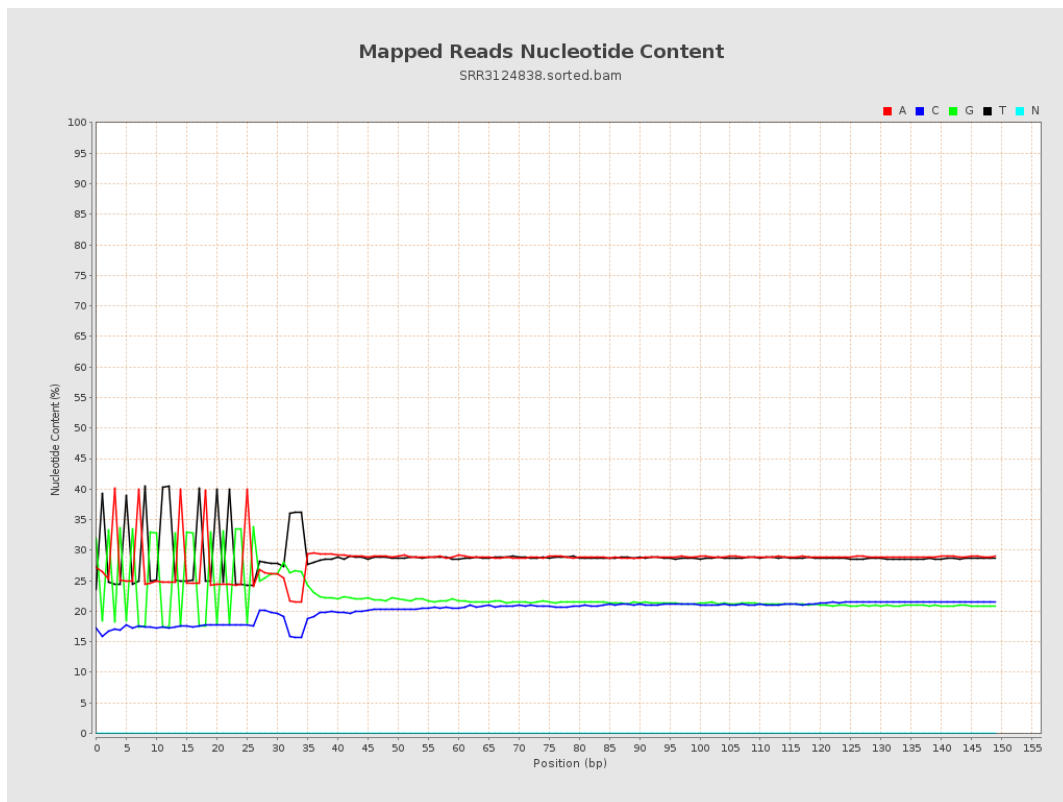
6. Results : Genome Fraction Coverage



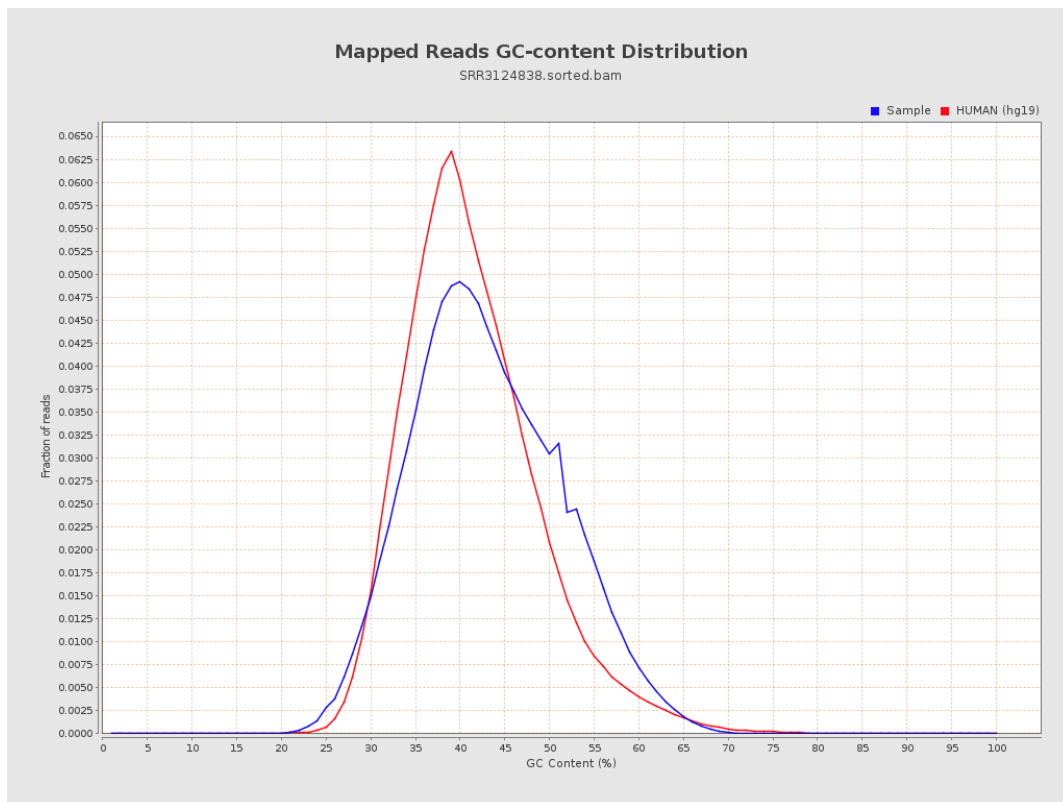
7. Results : Duplication Rate Histogram



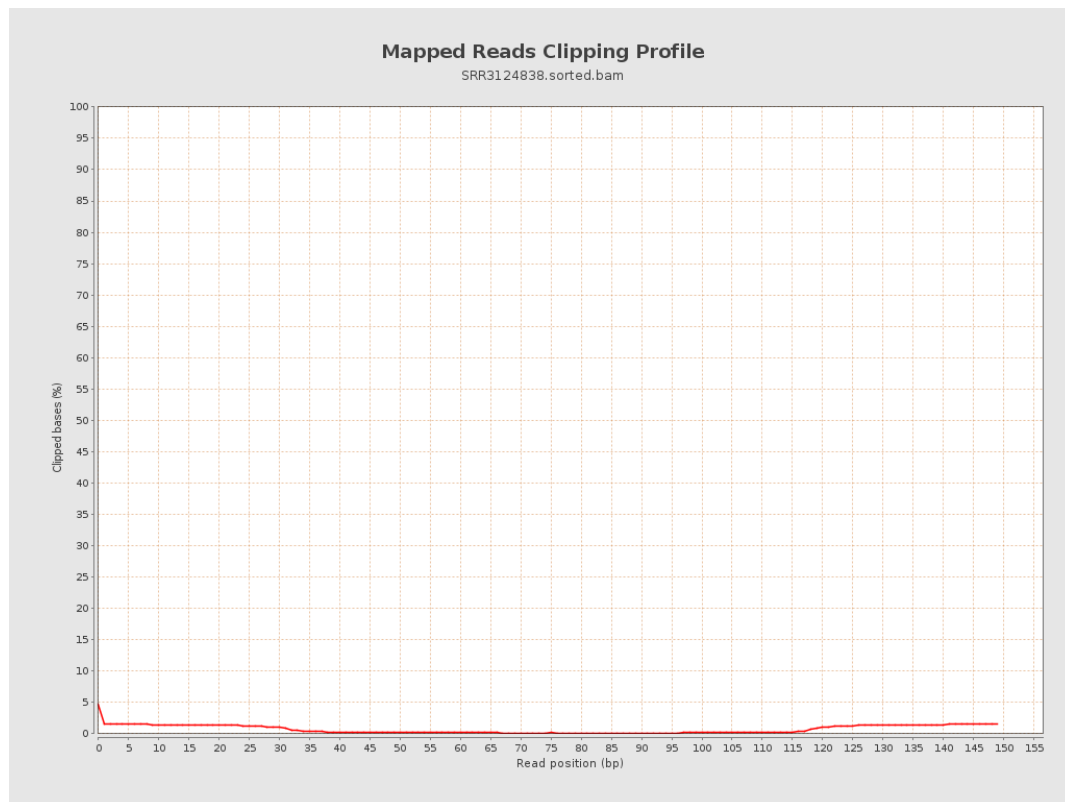
8. Results : Mapped Reads Nucleotide Content



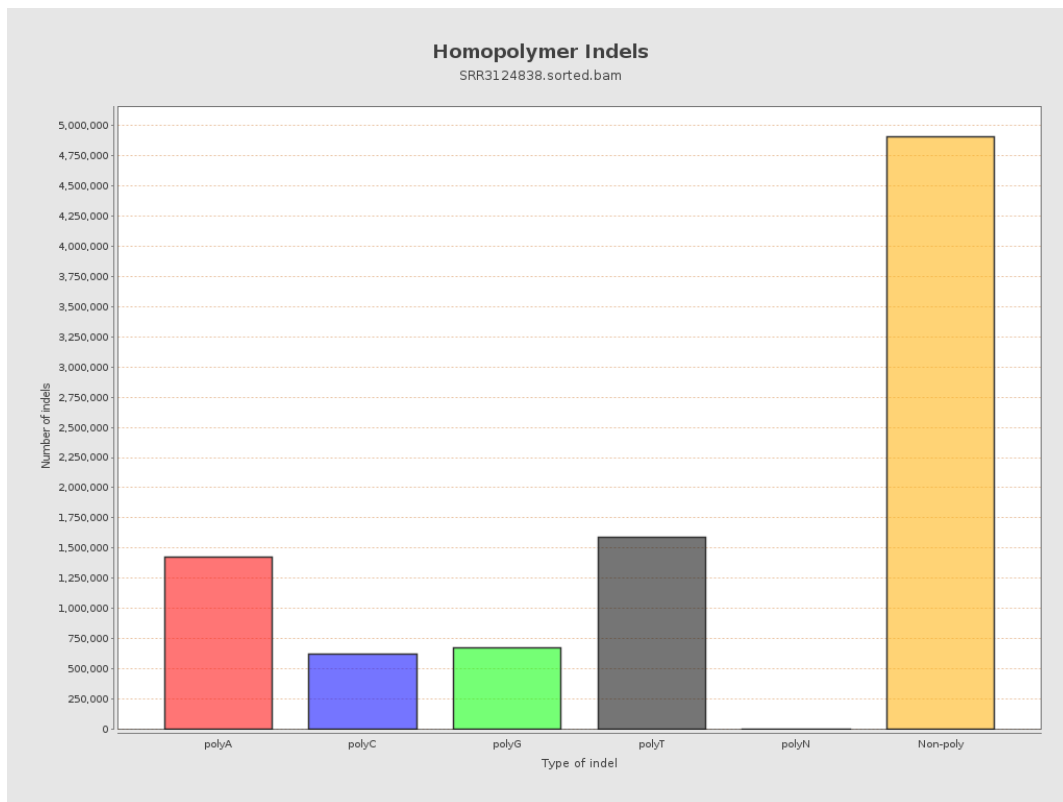
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



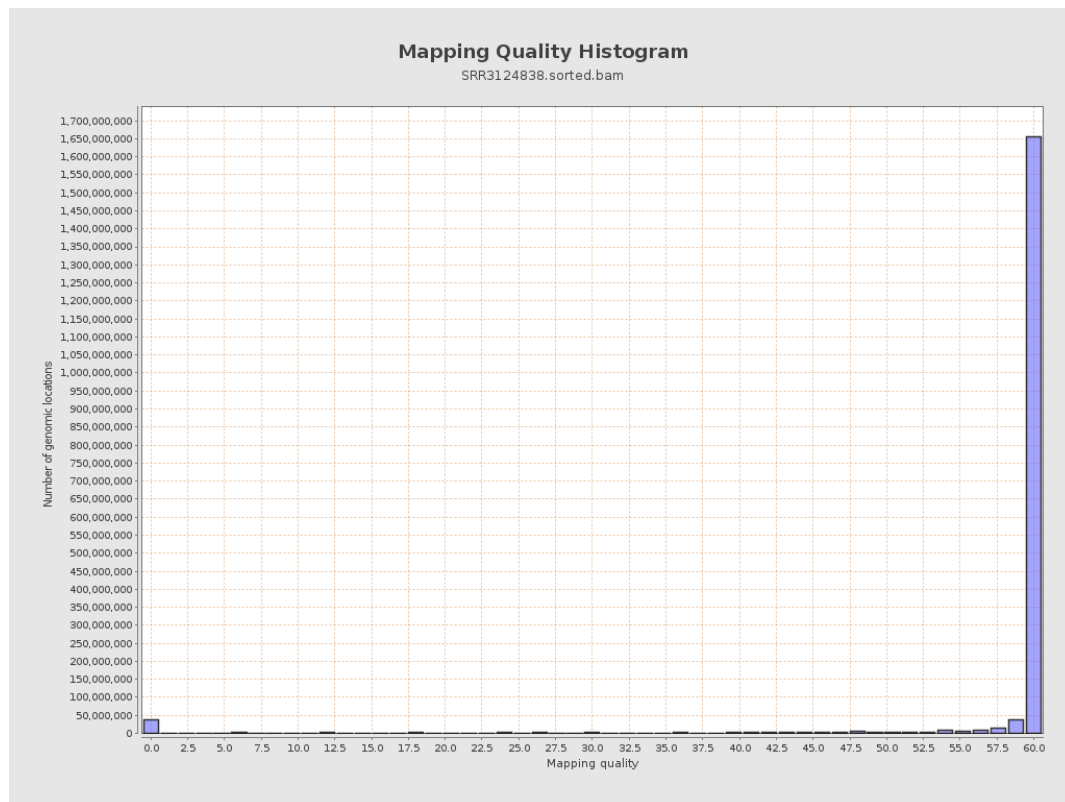
11. Results : Homopolymer Indels



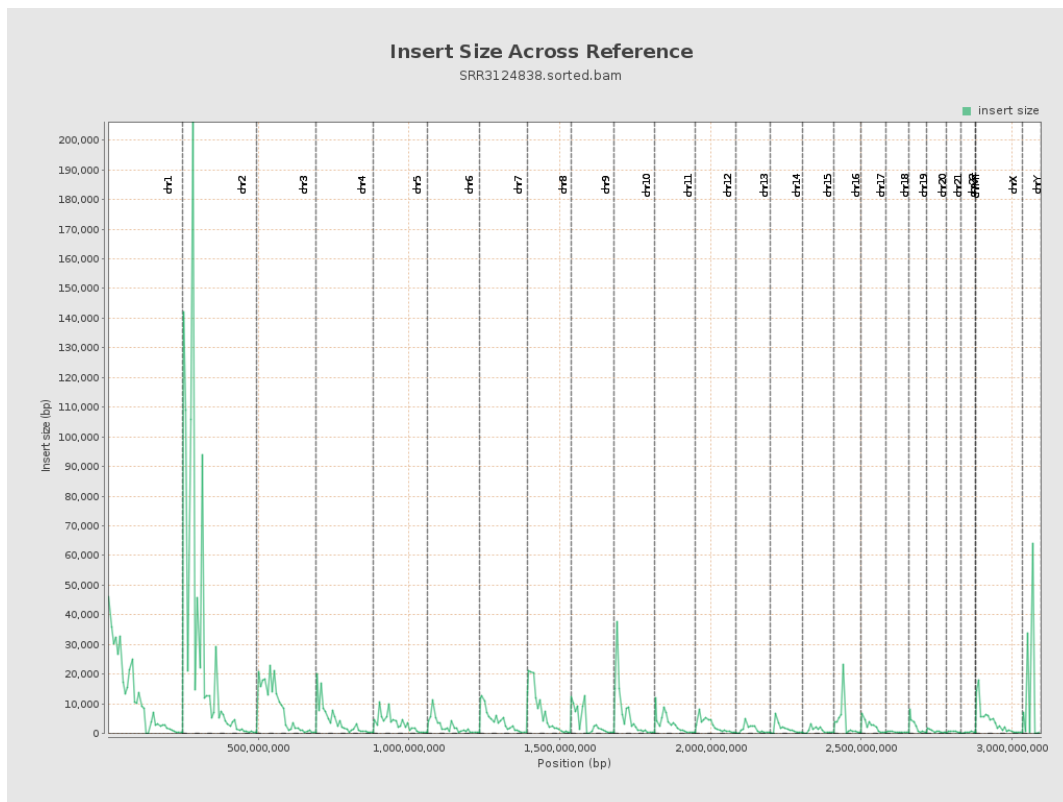
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

