

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 09:42:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21672009.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_SRR21672009 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21672009_1.fastq.gz SRR21672009_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 09:42:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21672009.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	480,982,134
Mapped reads	476,173,000 / 99%
Unmapped reads	4,809,134 / 1%
Mapped paired reads	476,173,000 / 99%
Mapped reads, first in pair	238,150,512 / 49.51%
Mapped reads, second in pair	238,022,488 / 49.49%
Mapped reads, both in pair	475,381,158 / 98.84%
Mapped reads, singletons	791,842 / 0.16%
Secondary alignments	0
Supplementary alignments	2,059,318 / 0.43%
Read min/max/mean length	15 / 150 / 149.68
Duplicated reads (estimated)	106,866,634 / 22.22%
Duplication rate	18.79%
Clipped reads	21,090,256 / 4.38%

2.2. ACGT Content

Number/percentage of A's	20,944,827,201 / 29.65%
Number/percentage of C's	14,449,532,689 / 20.46%
Number/percentage of T's	20,744,989,801 / 29.37%
Number/percentage of G's	14,489,483,874 / 20.51%
Number/percentage of N's	243,294 / 0%

GC Percentage	40.97%
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2.3. Coverage

Mean	22.8245
Standard Deviation	223.9669

2.4. Mapping Quality

Mean Mapping Quality	54.52
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2.5. Insert size

Mean	31,723.44
Standard Deviation	1,667,969.03
P25/Median/P75	296 / 343 / 388

2.6. Mismatches and indels

General error rate	0.73%
Mismatches	485,914,790
Insertions	9,977,326
Mapped reads with at least one insertion	1.99%
Deletions	10,418,733
Mapped reads with at least one deletion	2.1%
Homopolymer indels	45.72%

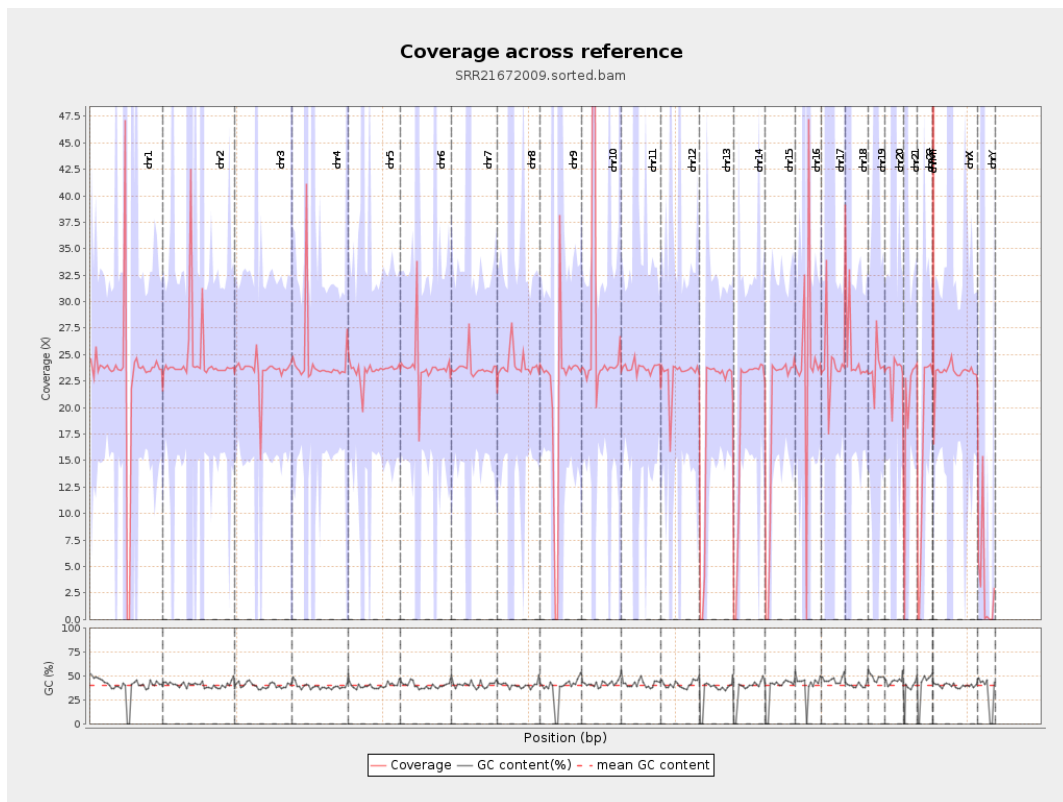
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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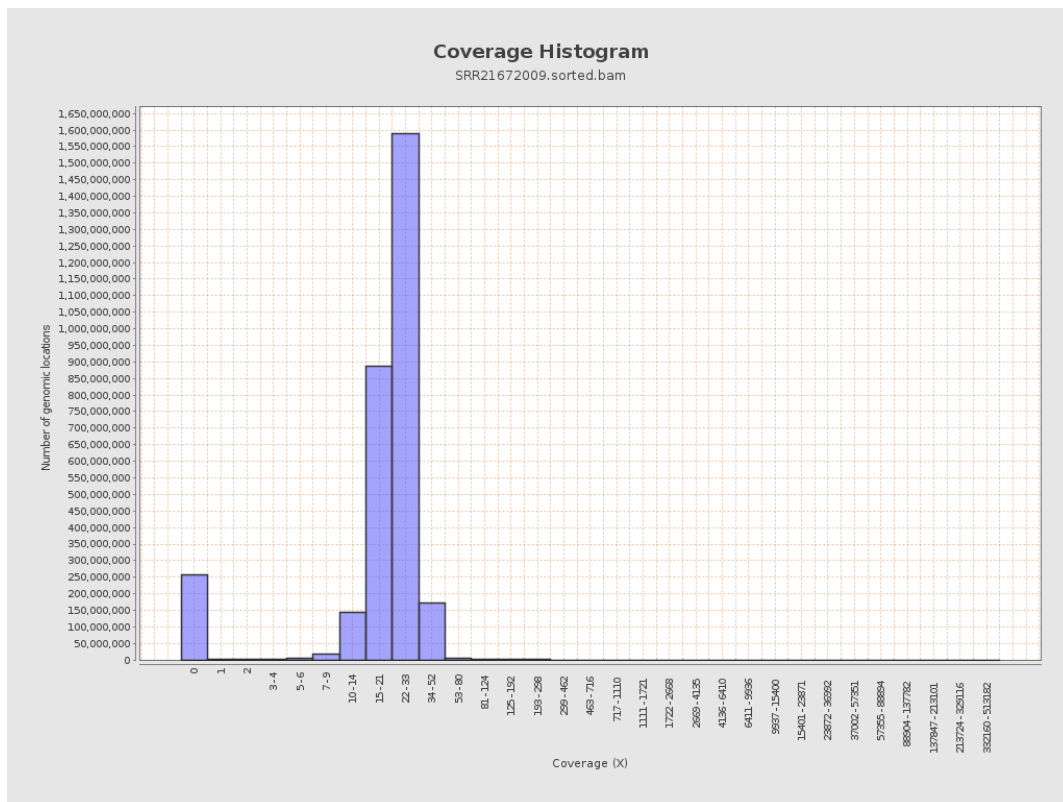
		bases	coverage	deviation
chr1	249250621	5734306243	23.0062	531.6166
chr2	243199373	5982419591	24.5988	120.8867
chr3	198022430	4642104196	23.4423	15.709
chr4	191154276	4659529467	24.3758	172.635
chr5	180915260	4246304040	23.4712	18.1202
chr6	171115067	4074434393	23.8111	119.5034
chr7	159138663	3782942559	23.7714	137.3836
chr8	146364022	3519656036	24.0473	224.1877
chr9	141213431	3049402069	21.5943	299
chr10	135534747	3633784919	26.8107	480.2558
chr11	135006516	3207370854	23.7572	103.4504
chr12	133851895	3100153764	23.1611	17.1133
chr13	115169878	2251732477	19.5514	12.3622
chr14	107349540	2117618549	19.7264	15.2177
chr15	102531392	1974195299	19.2545	12.5713
chr16	90354753	2209967075	24.4588	181.9519
chr17	81195210	1967738870	24.2347	135.1207
chr18	78077248	1966530377	25.187	296.774
chr19	59128983	1406437193	23.7859	227.828
chr20	63025520	1468573192	23.3012	63.1283
chr21	48129895	980670831	20.3755	81.4667
chr22	51304566	851166237	16.5905	15.8769
chrMT	16571	25912302	1,563.7138	176.079
chrX	155270560	3608431175	23.2396	49.7688

chrY	59373566	196346461	3.307	173.6027
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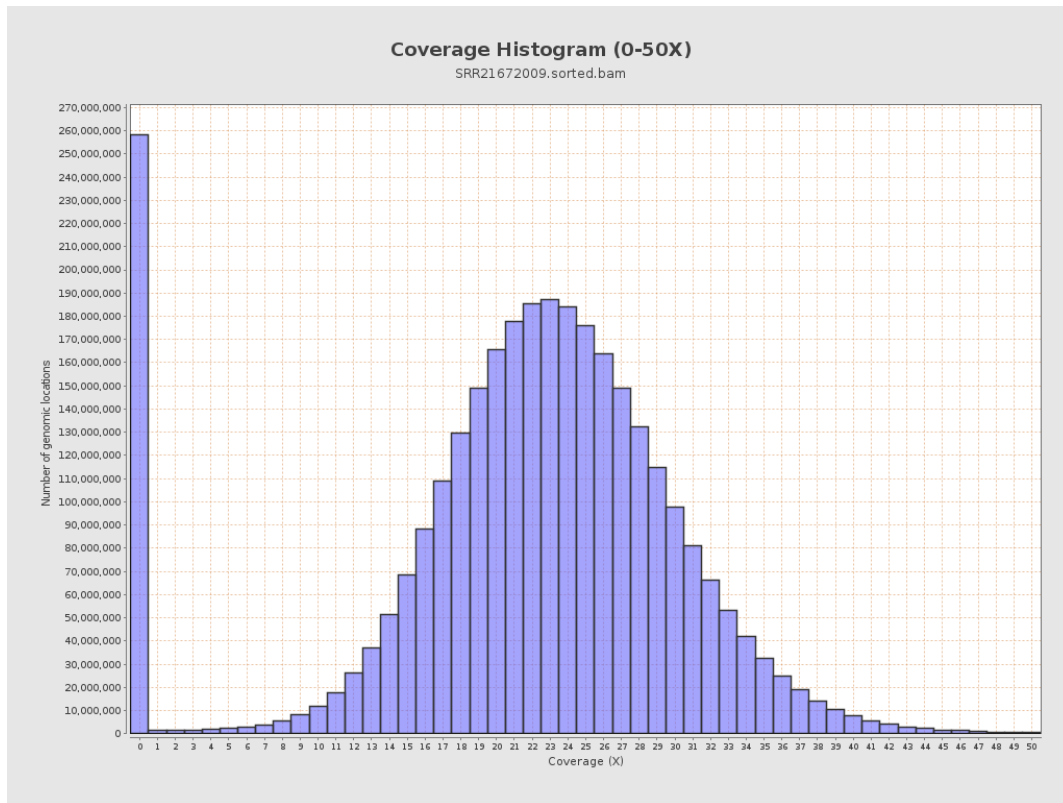
3. Results : Coverage across reference



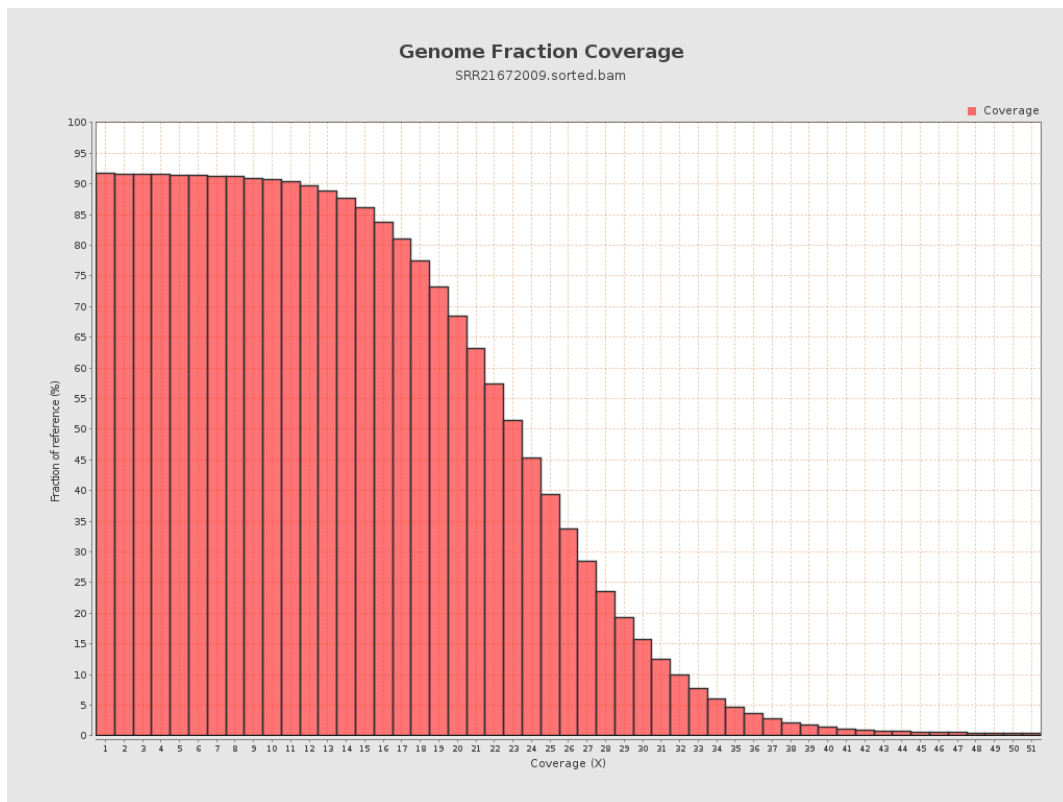
4. Results : Coverage Histogram



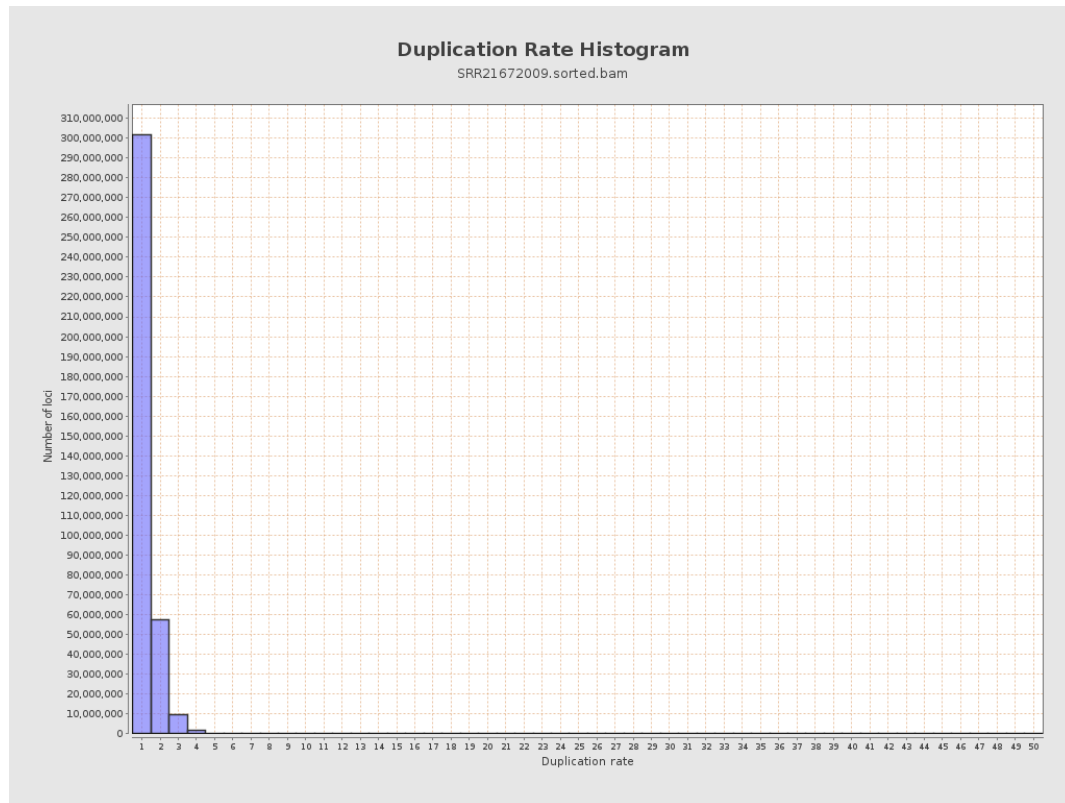
5. Results : Coverage Histogram (0-50X)



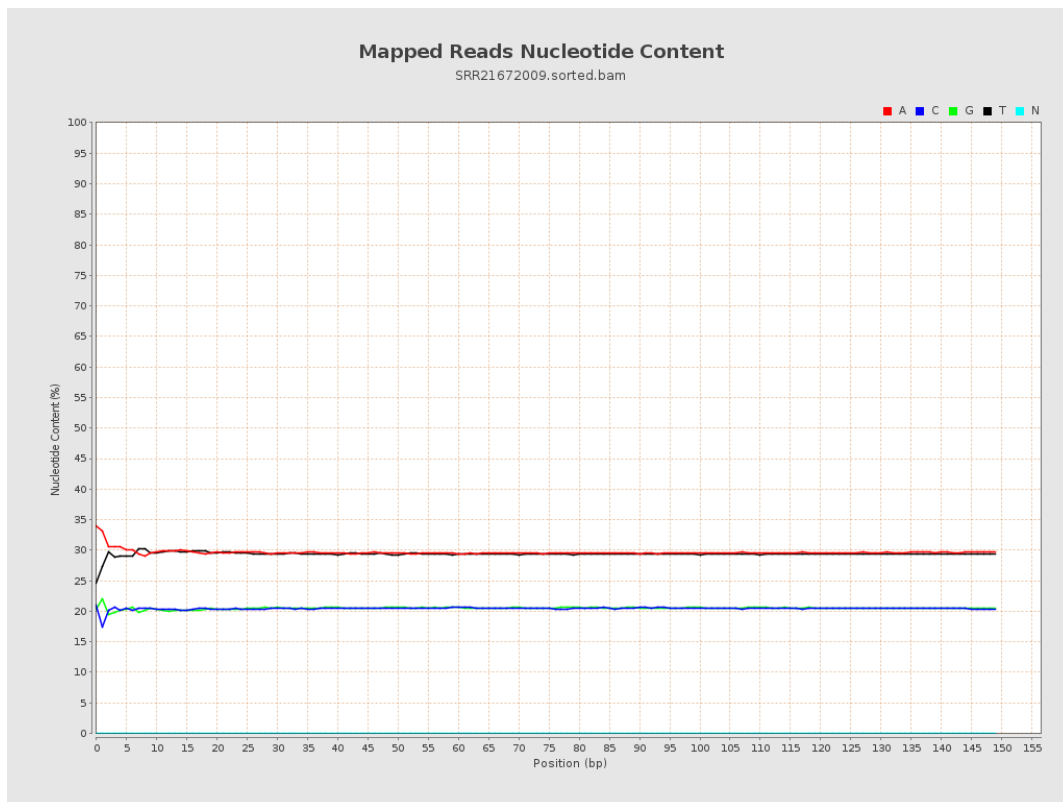
6. Results : Genome Fraction Coverage



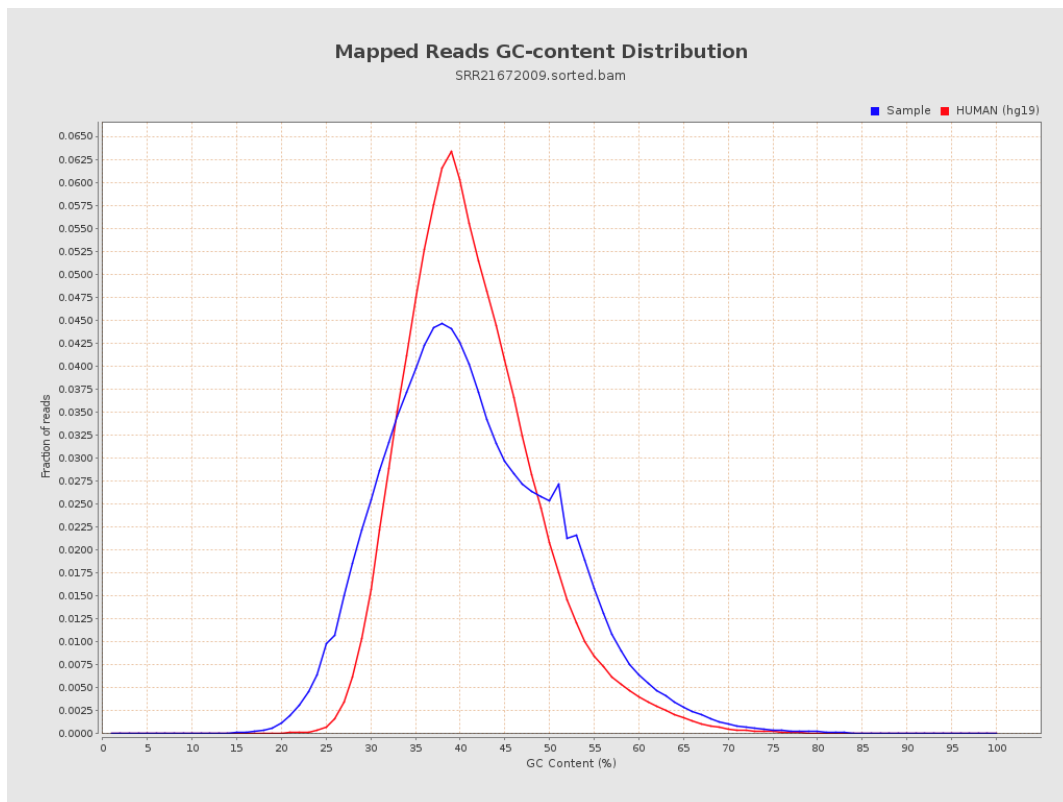
7. Results : Duplication Rate Histogram



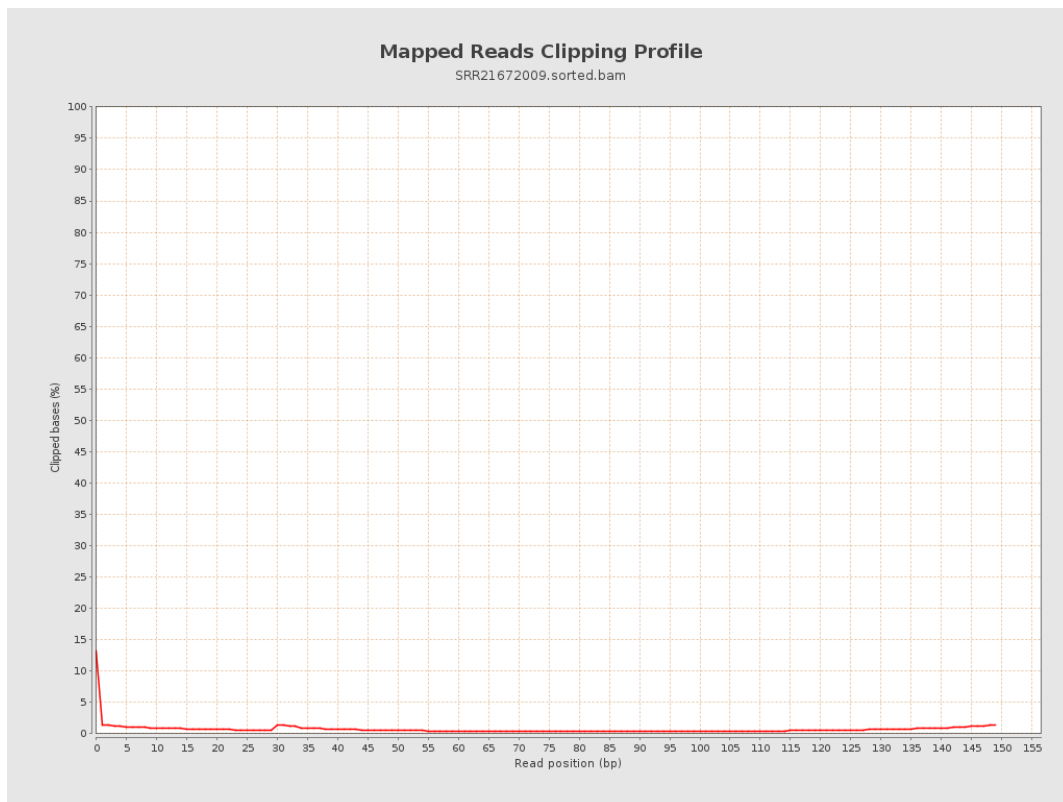
8. Results : Mapped Reads Nucleotide Content



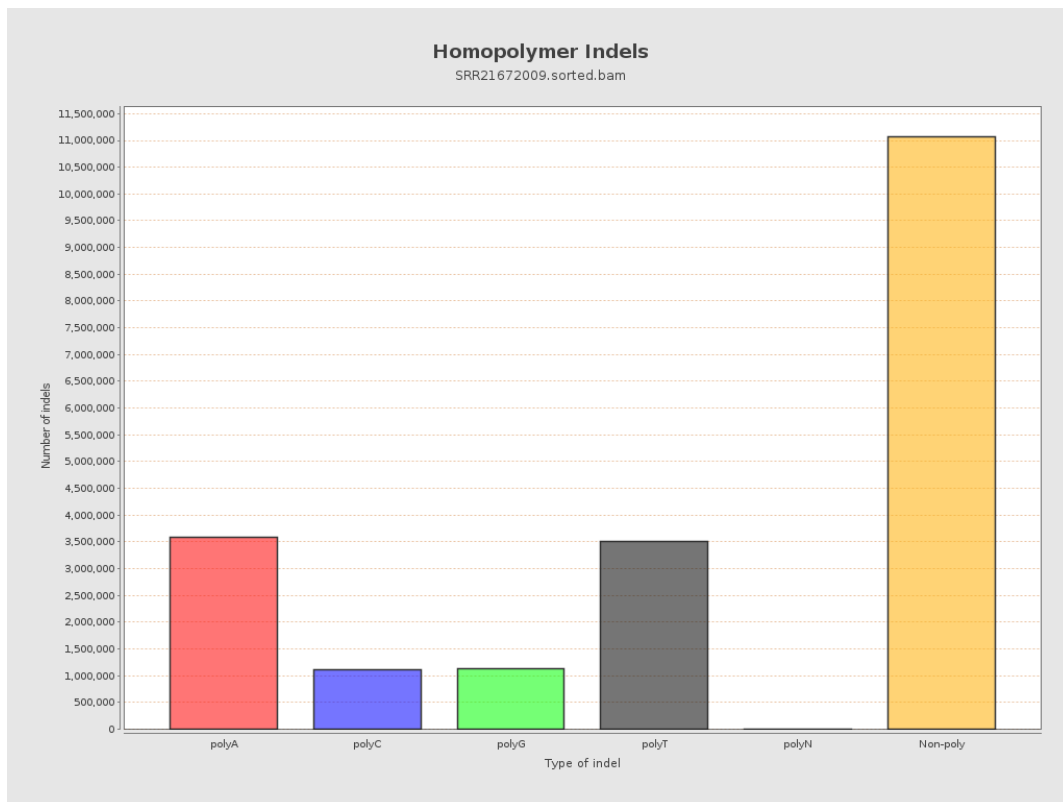
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



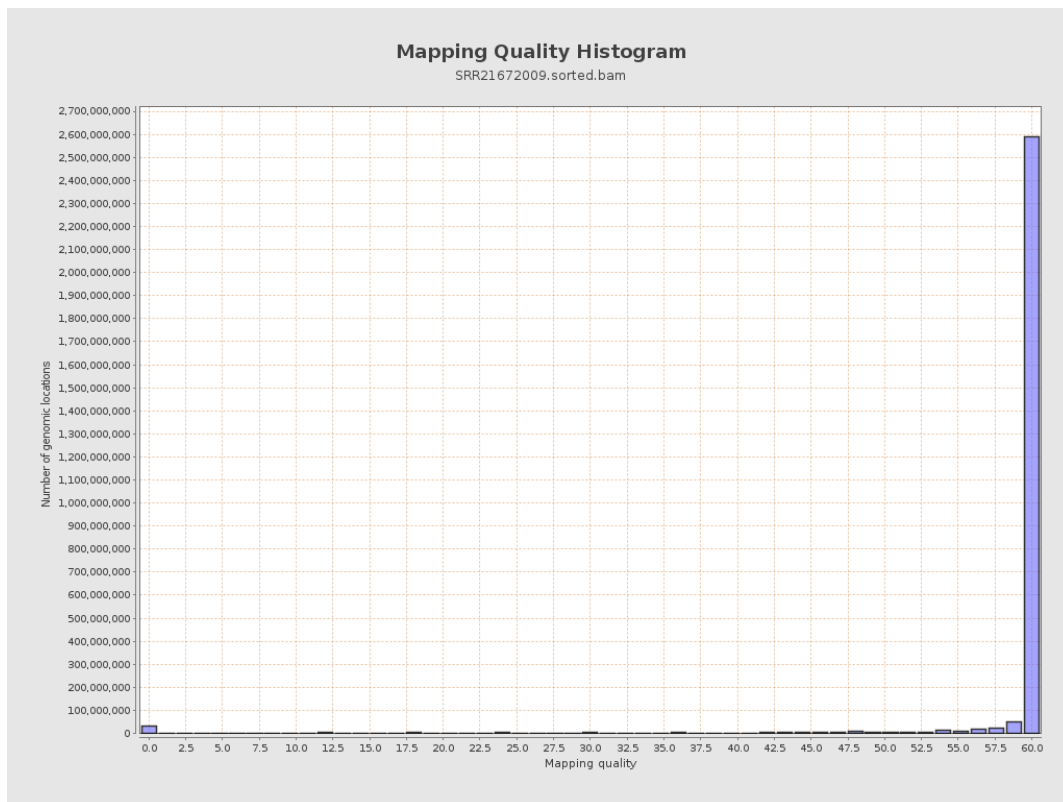
11. Results : Homopolymer Indels



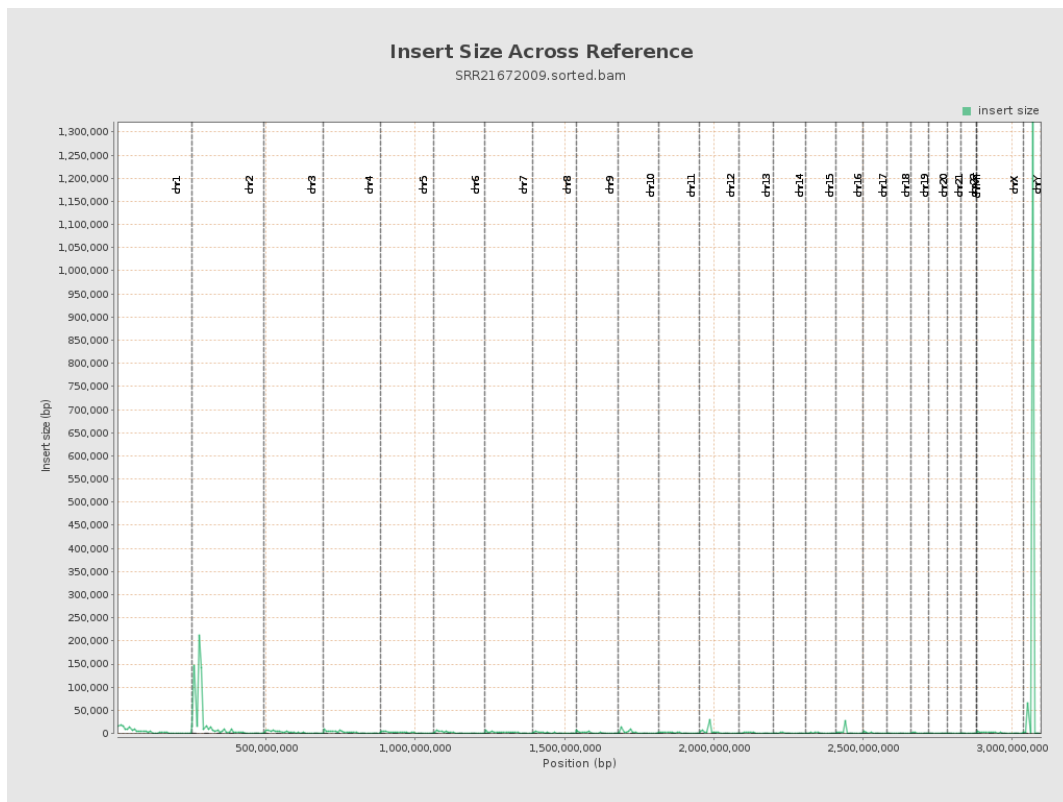
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

