

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 05:17:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124919.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_SRR3124919 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124919_1.fastq.gz SRR3124919_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 05:17:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124919.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,274,710
Mapped reads	5,144,696 / 97.54%
Unmapped reads	130,014 / 2.46%
Mapped paired reads	5,144,696 / 97.54%
Mapped reads, first in pair	2,602,434 / 49.34%
Mapped reads, second in pair	2,542,262 / 48.2%
Mapped reads, both in pair	5,068,256 / 96.09%
Mapped reads, singletons	76,440 / 1.45%
Secondary alignments	0
Supplementary alignments	5,156 / 0.1%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	281,448 / 5.34%
Duplication rate	3.88%
Clipped reads	2,373,183 / 44.99%

2.2. ACGT Content

Number/percentage of A's	87,344,862 / 27.36%
Number/percentage of C's	57,193,330 / 17.92%
Number/percentage of T's	95,300,859 / 29.85%
Number/percentage of G's	79,384,787 / 24.87%
Number/percentage of N's	2,592 / 0%

GC Percentage	42.78%
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2.3. Coverage

Mean	0.1032
Standard Deviation	0.7707

2.4. Mapping Quality

Mean Mapping Quality	52.04
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2.5. Insert size

Mean	25,953.58
Standard Deviation	1,542,906.93
P25/Median/P75	147 / 197 / 270

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	2,099,388
Insertions	33,070
Mapped reads with at least one insertion	0.64%
Deletions	91,158
Mapped reads with at least one deletion	1.75%
Homopolymer indels	48.46%

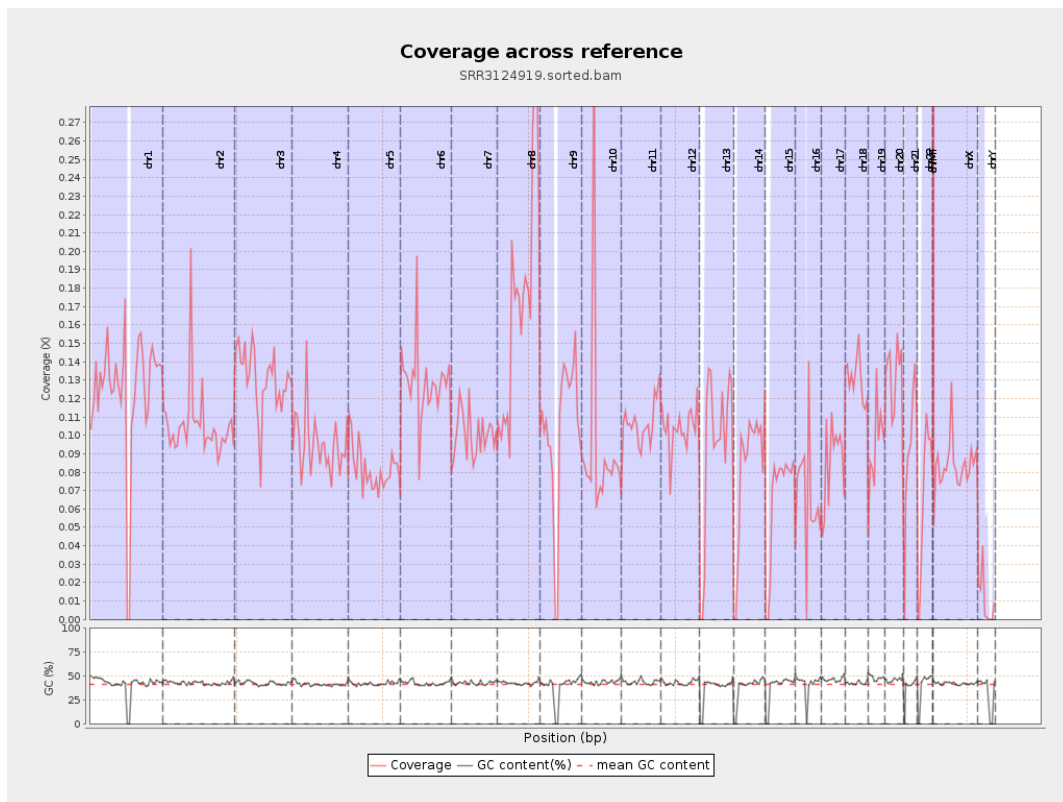
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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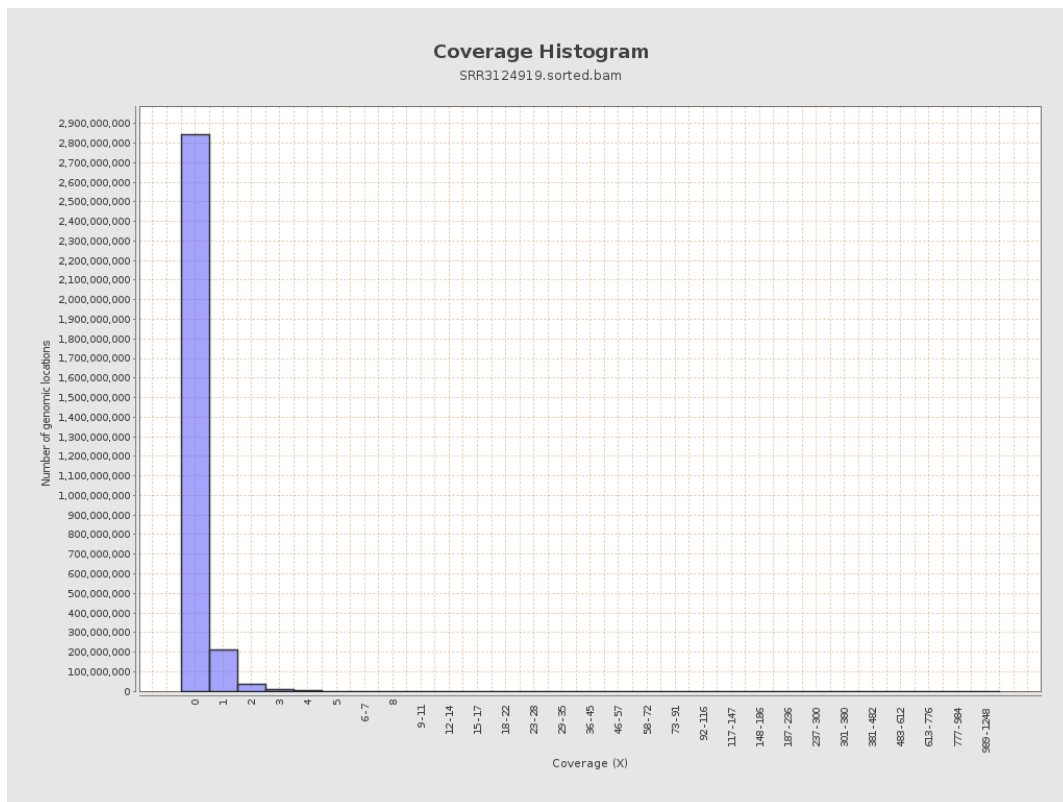
		bases	coverage	deviation
chr1	249250621	31026471	0.1245	0.852
chr2	243199373	25670636	0.1056	0.7898
chr3	198022430	25808102	0.1303	0.4368
chr4	191154276	18274359	0.0956	0.4684
chr5	180915260	14806480	0.0818	0.3364
chr6	171115067	22055187	0.1289	0.9315
chr7	159138663	15958016	0.1003	0.9451
chr8	146364022	25454354	0.1739	0.6203
chr9	141213431	14575262	0.1032	0.7092
chr10	135534747	12479838	0.0921	1.9408
chr11	135006516	14358934	0.1064	0.7605
chr12	133851895	13929233	0.1041	0.3843
chr13	115169878	10911588	0.0947	0.3617
chr14	107349540	8790101	0.0819	0.3841
chr15	102531392	6623292	0.0646	0.308
chr16	90354753	5961345	0.066	0.7336
chr17	81195210	6954285	0.0856	0.9084
chr18	78077248	10186454	0.1305	1.1615
chr19	59128983	5633219	0.0953	0.7202
chr20	63025520	8338750	0.1323	0.4513
chr21	48129895	4461553	0.0927	0.4083
chr22	51304566	3475414	0.0677	0.3096
chrMT	16571	49673	2.9976	2.6042
chrX	155270560	12952552	0.0834	0.554

chrY	59373566	624839	0.0105	0.439
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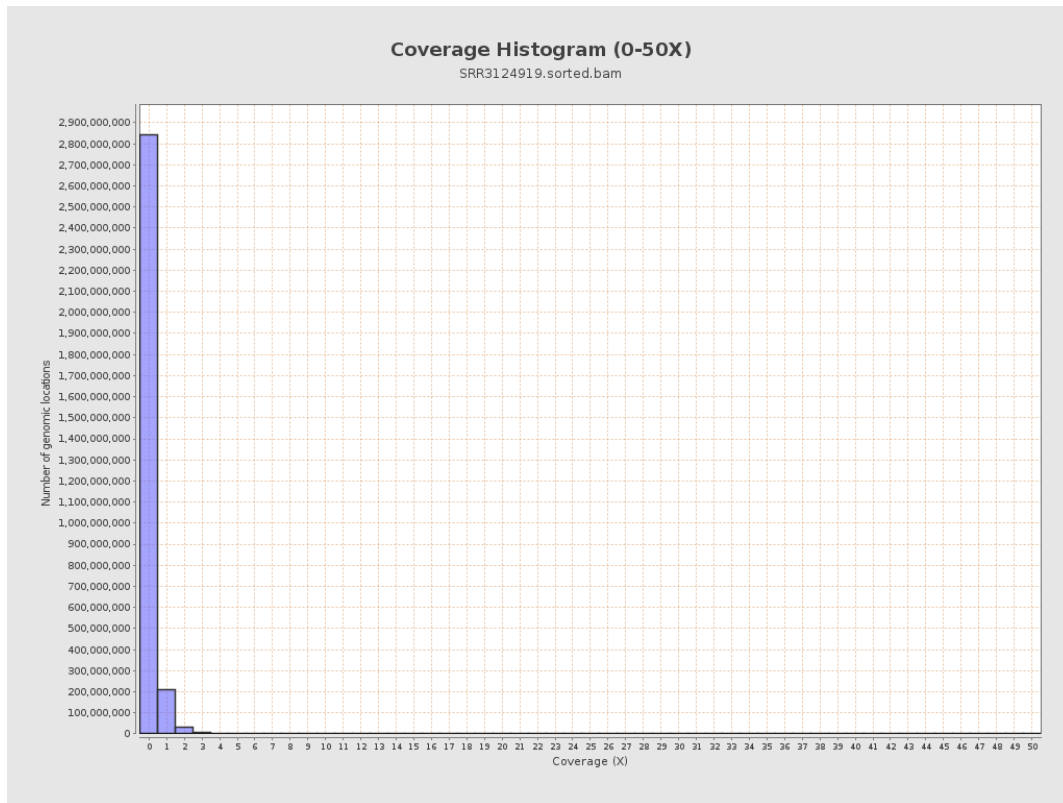
3. Results : Coverage across reference



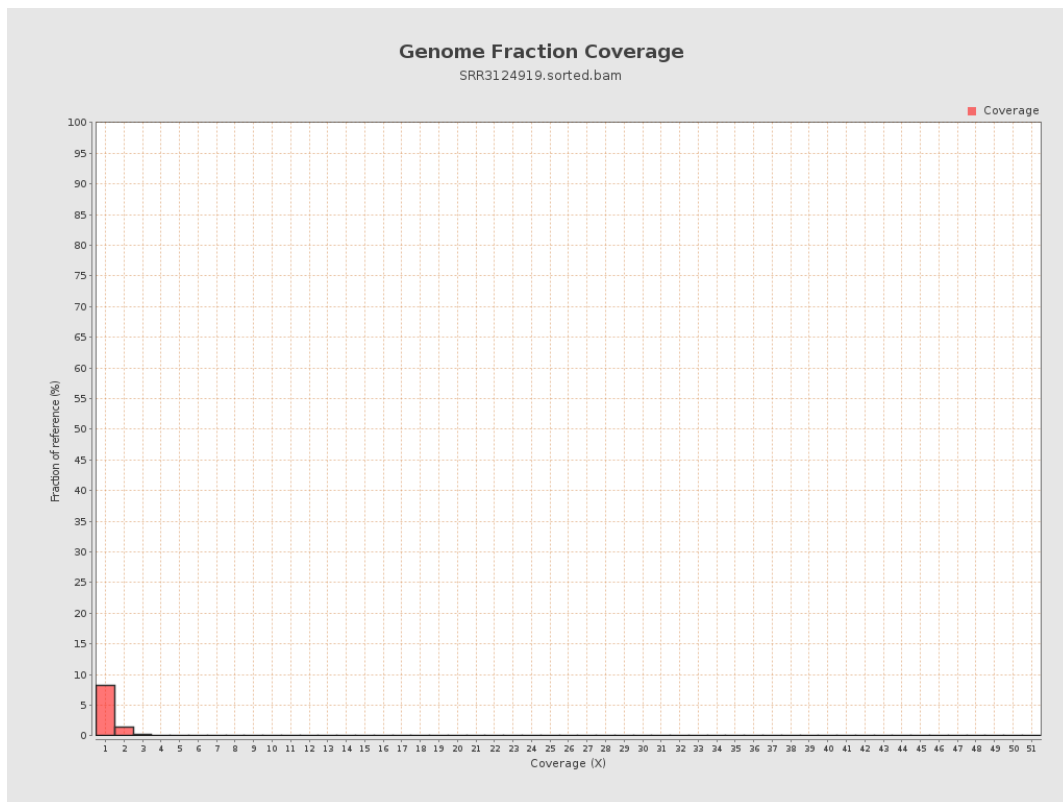
4. Results : Coverage Histogram



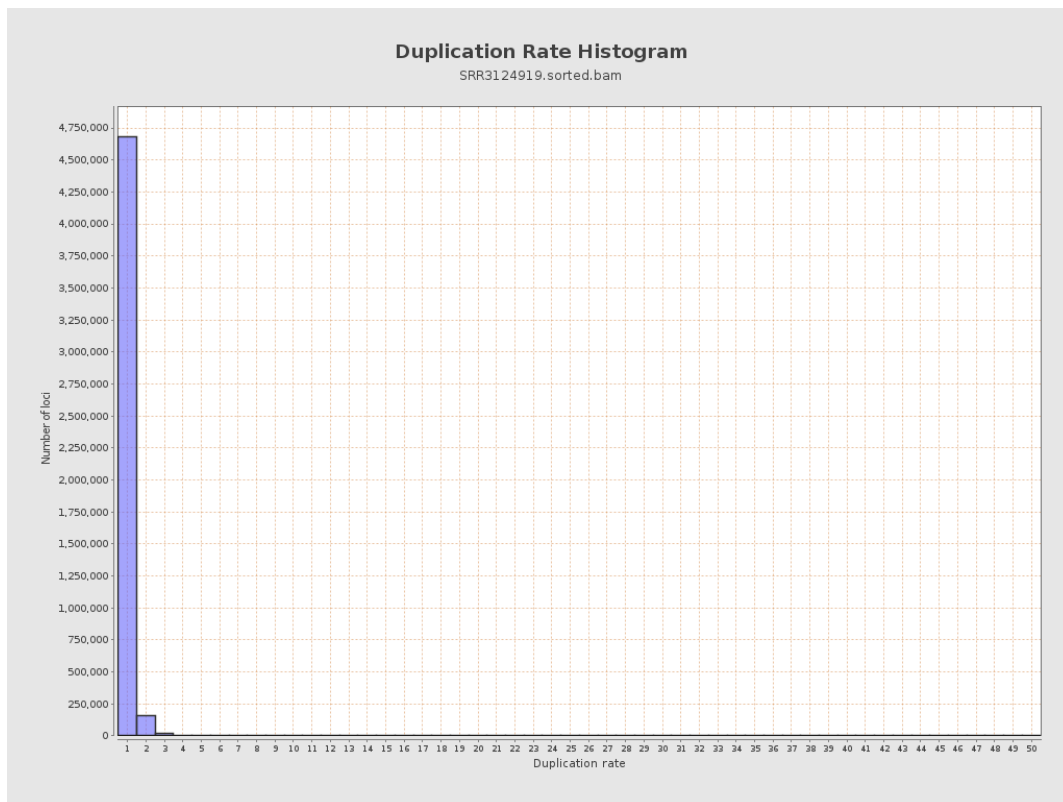
5. Results : Coverage Histogram (0-50X)



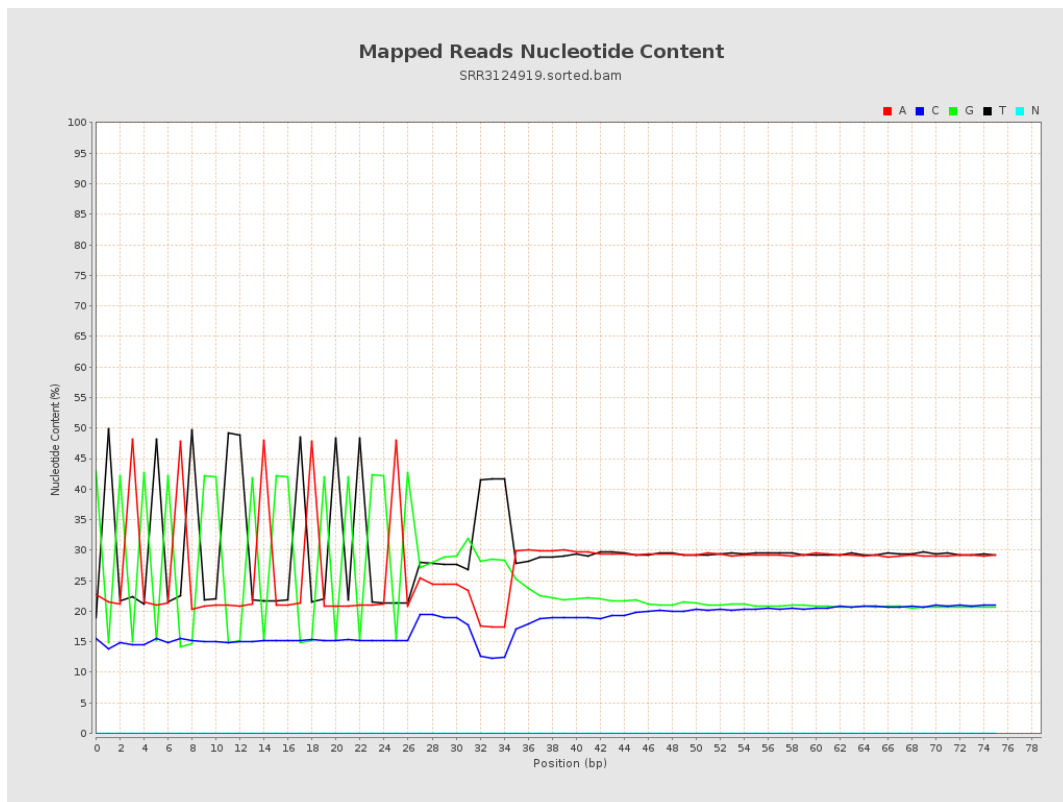
6. Results : Genome Fraction Coverage



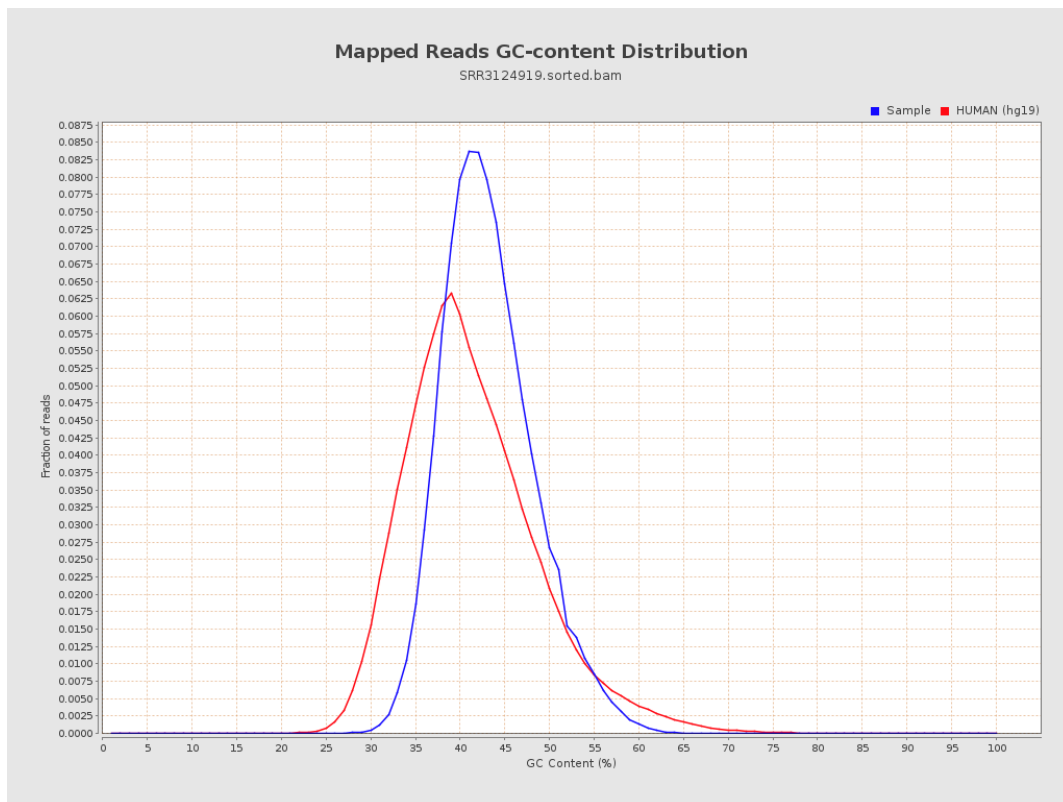
7. Results : Duplication Rate Histogram



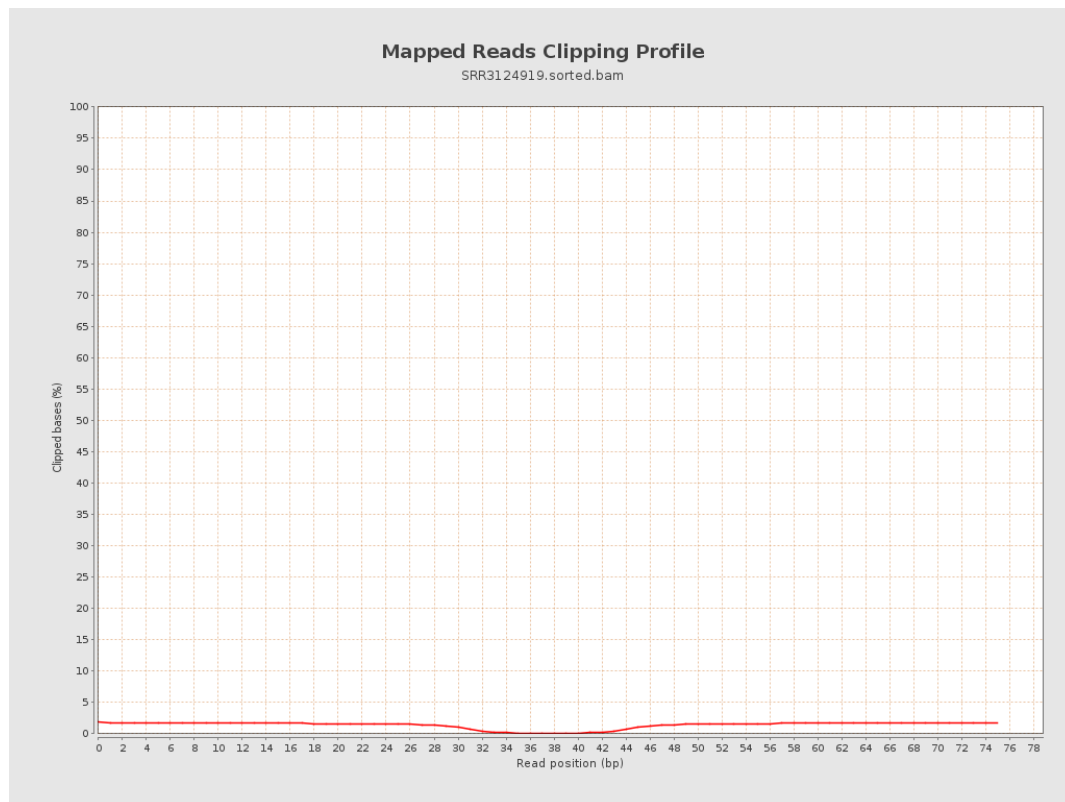
8. Results : Mapped Reads Nucleotide Content



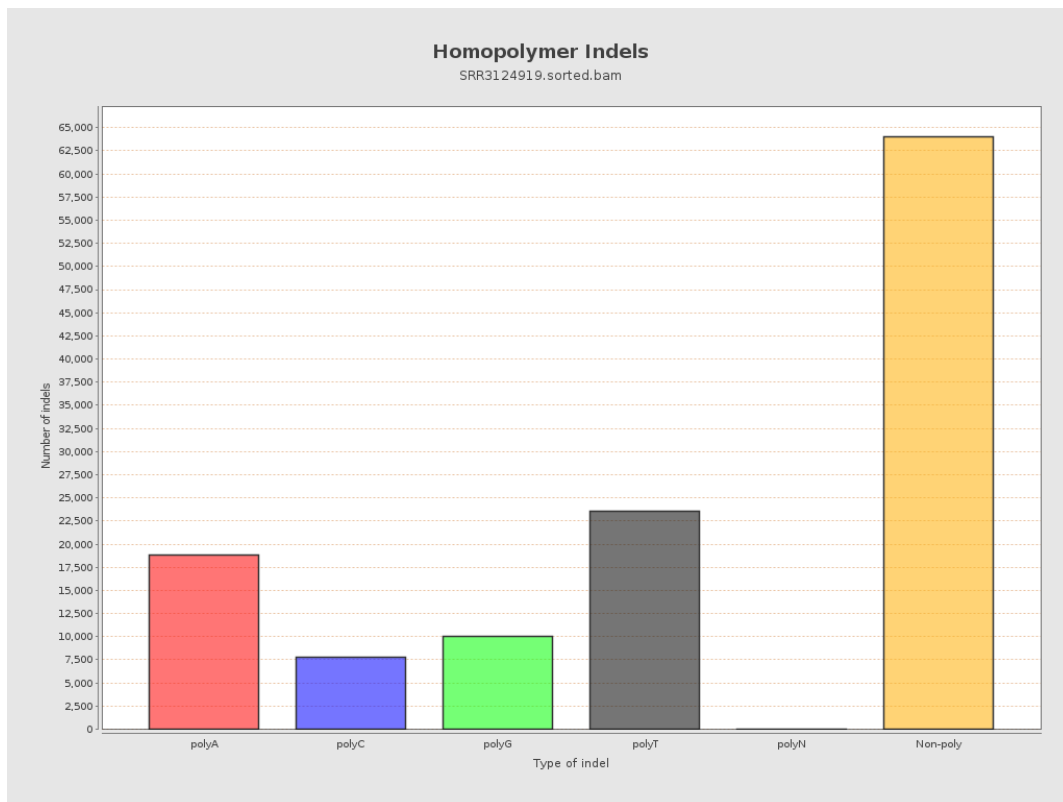
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



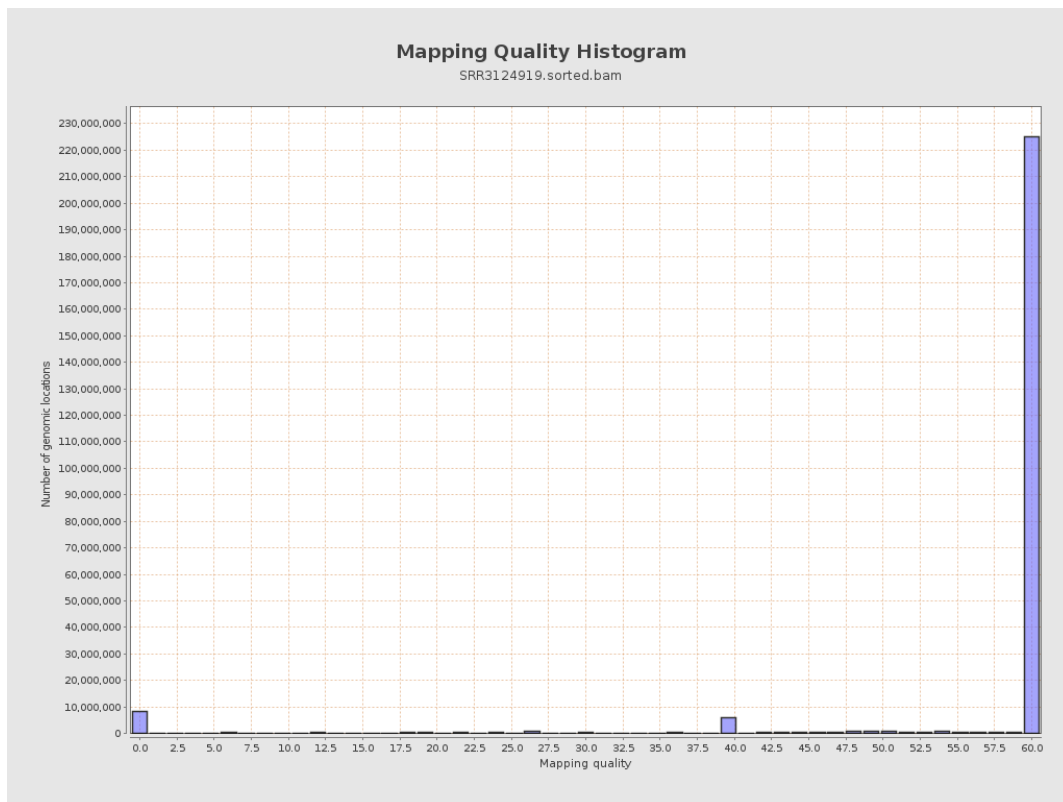
11. Results : Homopolymer Indels



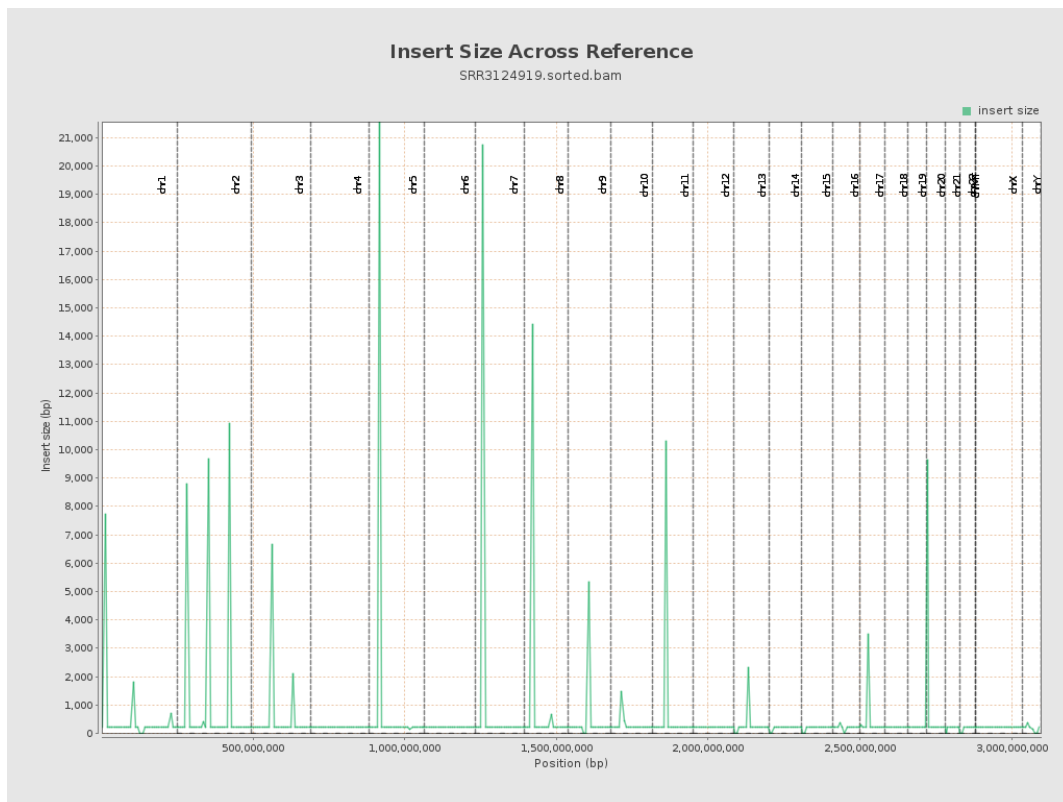
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

