

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 07:18:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124934.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_SRR3124934 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124934_1.fastq.gz SRR3124934_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 07:18:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124934.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,452,182
Mapped reads	4,407,330 / 98.99%
Unmapped reads	44,852 / 1.01%
Mapped paired reads	4,407,330 / 98.99%
Mapped reads, first in pair	2,205,895 / 49.55%
Mapped reads, second in pair	2,201,435 / 49.45%
Mapped reads, both in pair	4,388,966 / 98.58%
Mapped reads, singletons	18,364 / 0.41%
Secondary alignments	0
Supplementary alignments	32,267 / 0.72%
Read min/max/mean length	30 / 101 / 101.29
Duplicated reads (estimated)	237,392 / 5.33%
Duplication rate	3.64%
Clipped reads	1,936,670 / 43.5%

2.2. ACGT Content

Number/percentage of A's	111,884,365 / 28.53%
Number/percentage of C's	74,195,876 / 18.92%
Number/percentage of T's	116,817,278 / 29.79%
Number/percentage of G's	89,197,036 / 22.75%
Number/percentage of N's	5,823 / 0%

GC Percentage	41.67%
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2.3. Coverage

Mean	0.1267
Standard Deviation	1.0782

2.4. Mapping Quality

Mean Mapping Quality	52.97
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2.5. Insert size

Mean	75,206.9
Standard Deviation	2,600,292.85
P25/Median/P75	147 / 196 / 267

2.6. Mismatches and indels

General error rate	0.72%
Mismatches	2,712,519
Insertions	45,505
Mapped reads with at least one insertion	1.01%
Deletions	115,773
Mapped reads with at least one deletion	2.58%
Homopolymer indels	47.55%

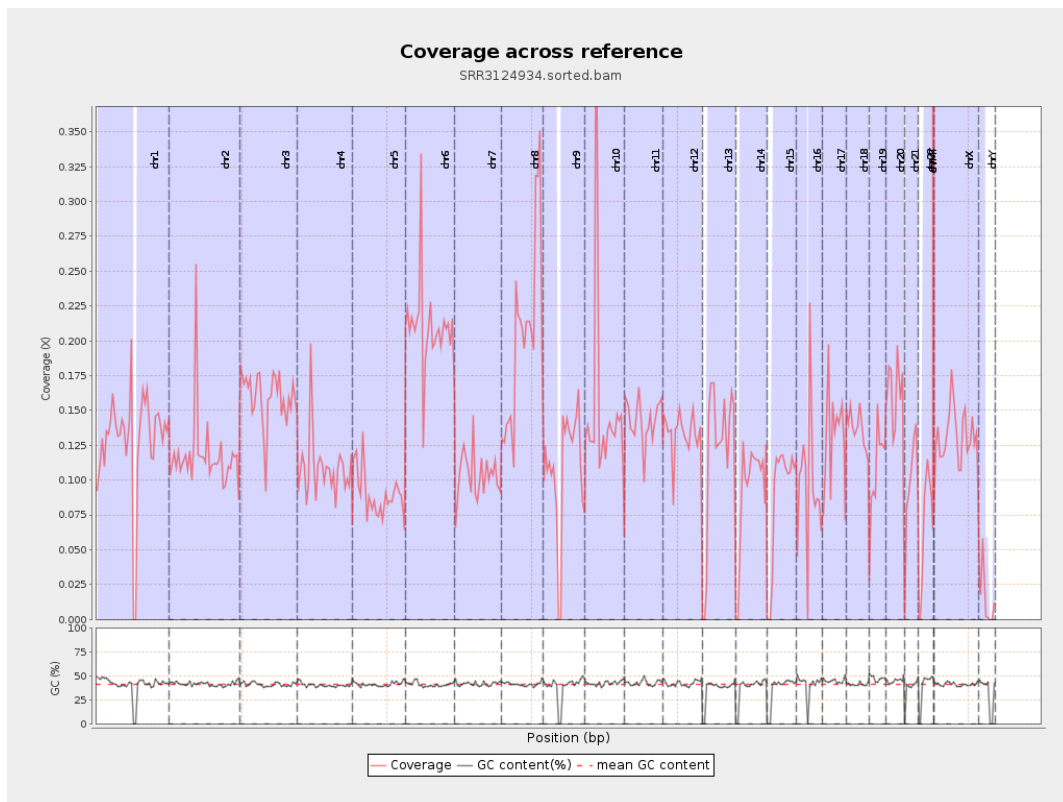
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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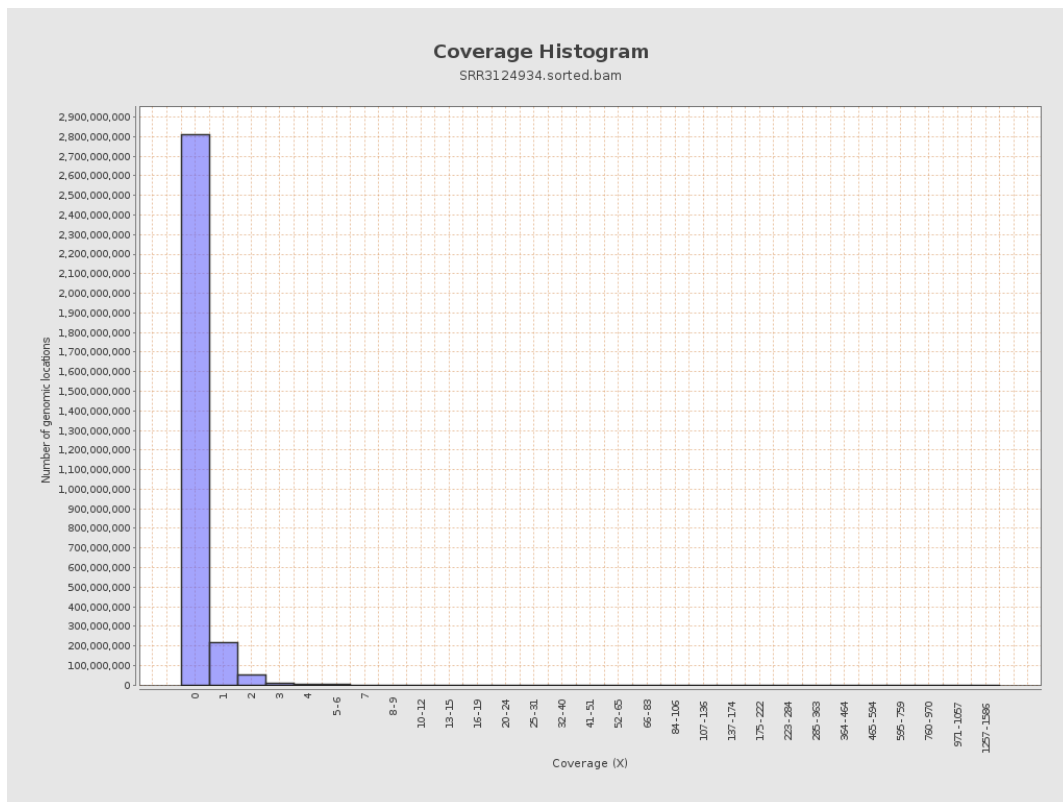
		bases	coverage	deviation
chr1	249250621	32069931	0.1287	1.1066
chr2	243199373	28610140	0.1176	1.0353
chr3	198022430	31560485	0.1594	0.5053
chr4	191154276	20592240	0.1077	0.7423
chr5	180915260	16236050	0.0897	0.3795
chr6	171115067	35877448	0.2097	1.5221
chr7	159138663	16558929	0.1041	1.1418
chr8	146364022	29912941	0.2044	0.7385
chr9	141213431	15401165	0.1091	1.2546
chr10	135534747	20273864	0.1496	2.73
chr11	135006516	19005553	0.1408	1.2194
chr12	133851895	17763477	0.1327	0.4638
chr13	115169878	13694323	0.1189	0.4268
chr14	107349540	9792157	0.0912	0.4092
chr15	102531392	9110598	0.0889	0.378
chr16	90354753	8640389	0.0956	1.0965
chr17	81195210	10507070	0.1294	1.5812
chr18	78077248	10716442	0.1373	1.4735
chr19	59128983	6565847	0.111	0.7217
chr20	63025520	10079231	0.1599	0.541
chr21	48129895	4626786	0.0961	0.4771
chr22	51304566	3393422	0.0661	0.3354
chrMT	16571	111668	6.7388	4.7929
chrX	155270560	20360823	0.1311	0.6597

chrY	59373566	826063	0.0139	0.7308
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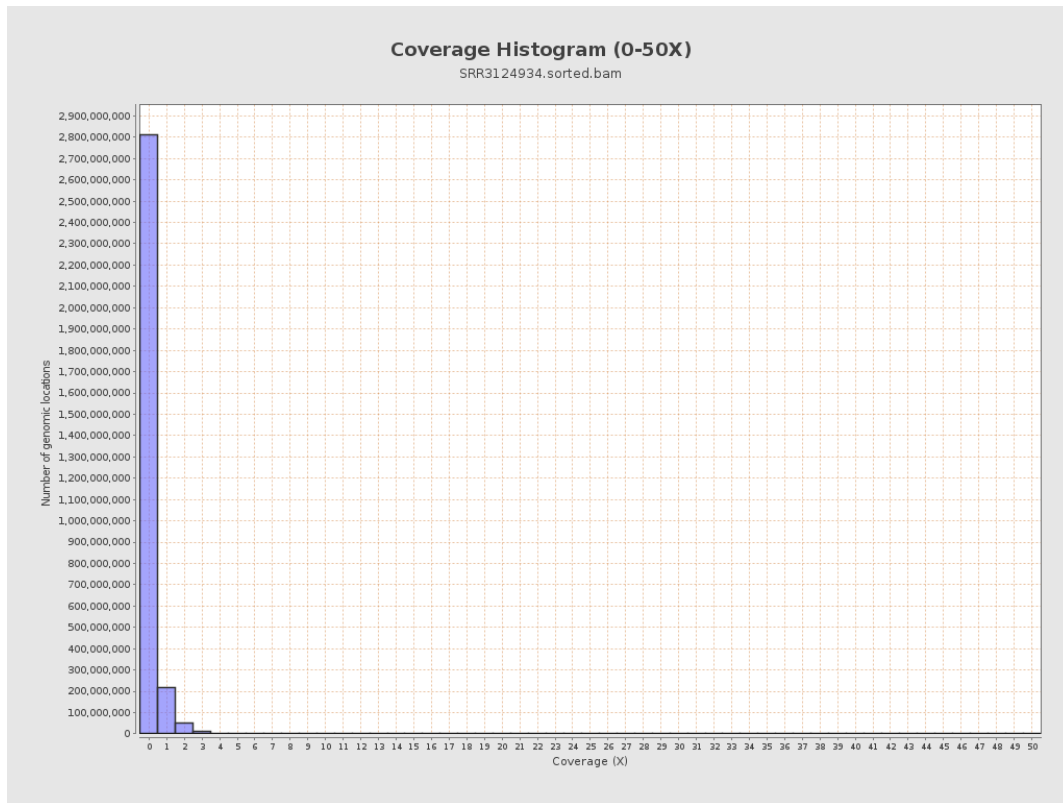
3. Results : Coverage across reference



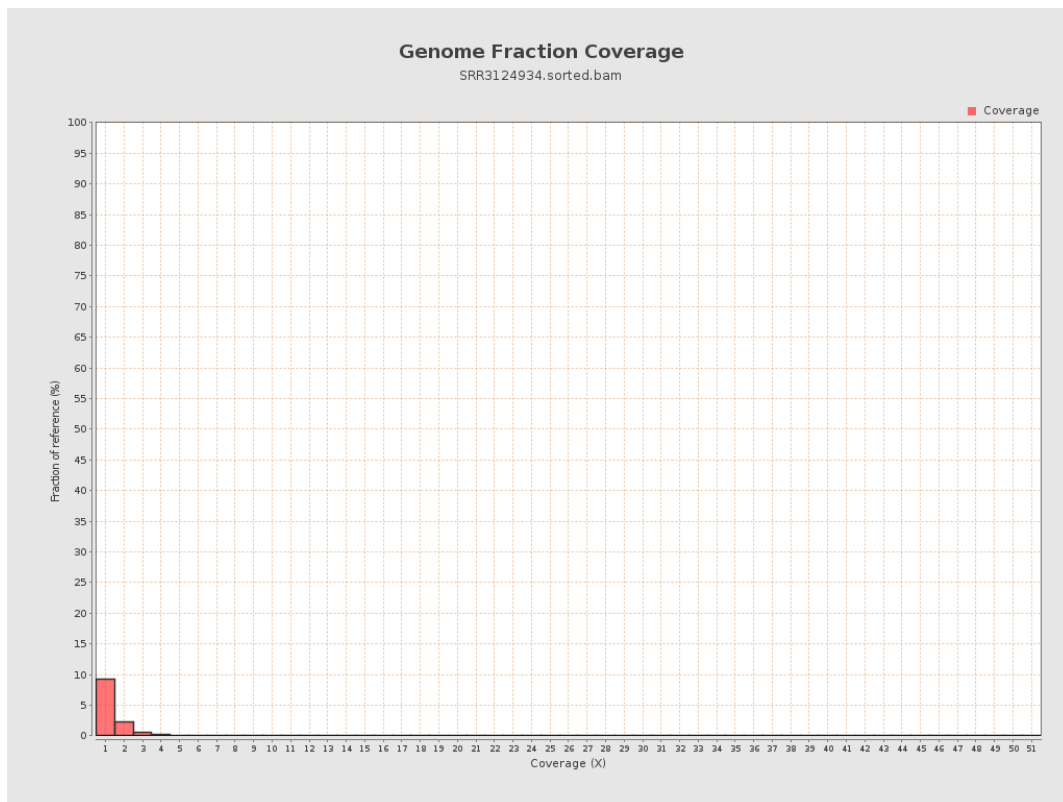
4. Results : Coverage Histogram



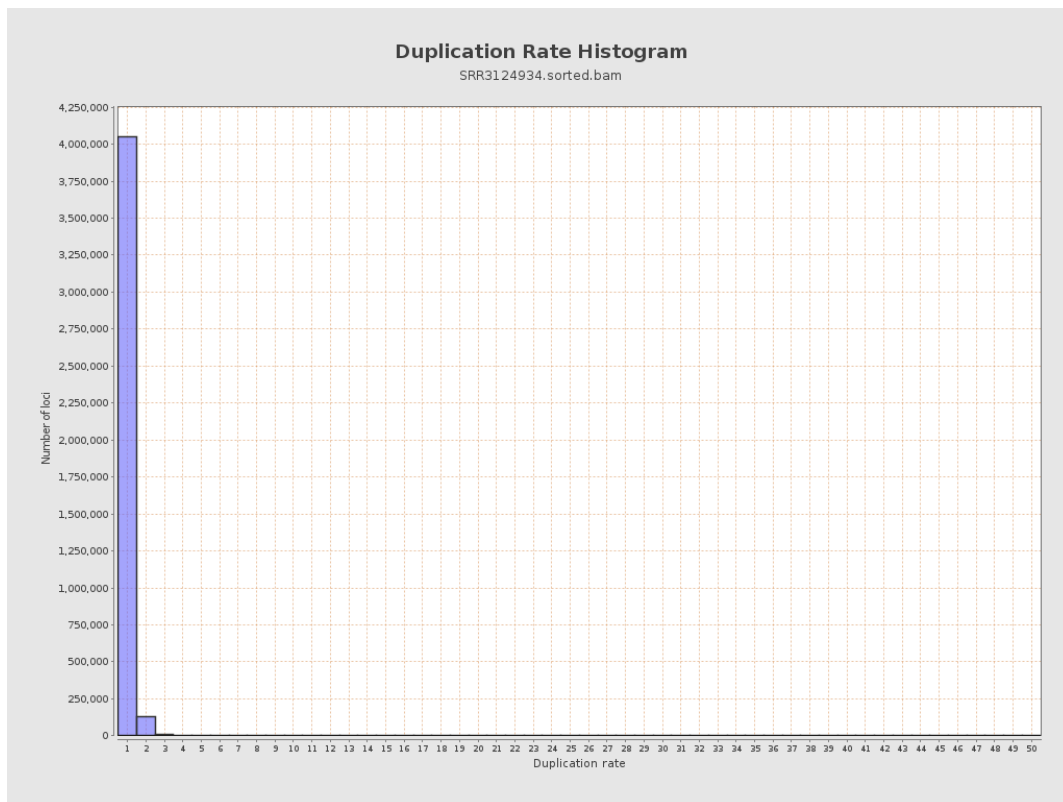
5. Results : Coverage Histogram (0-50X)



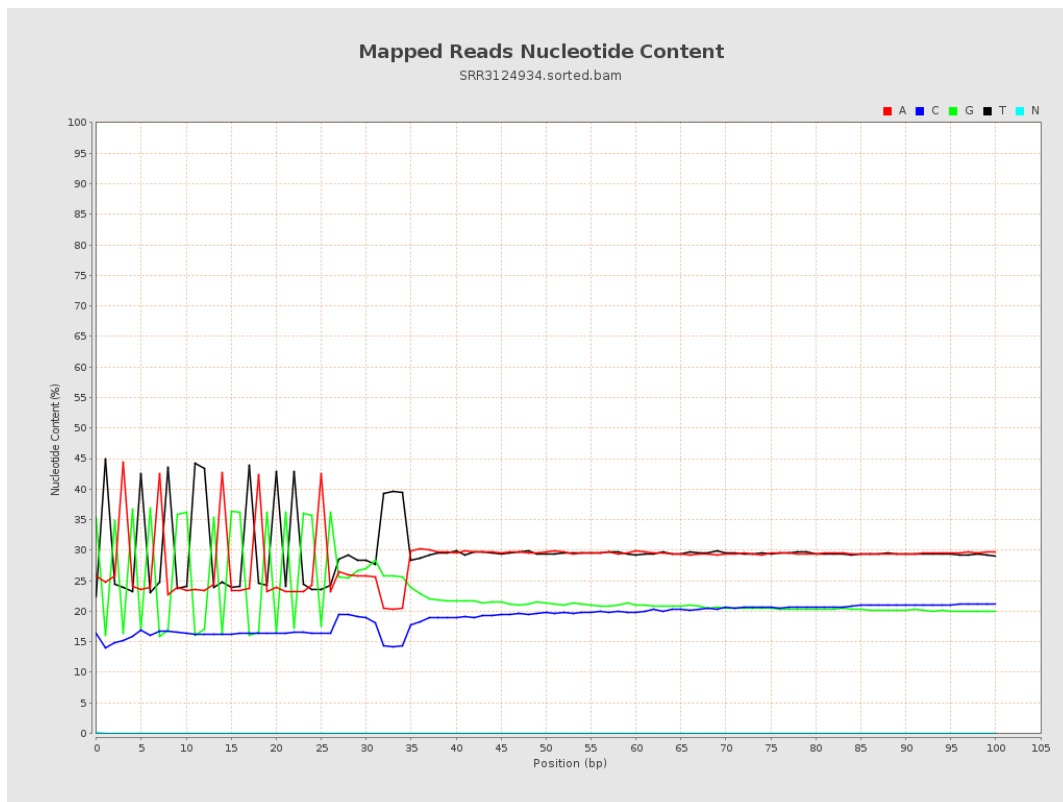
6. Results : Genome Fraction Coverage



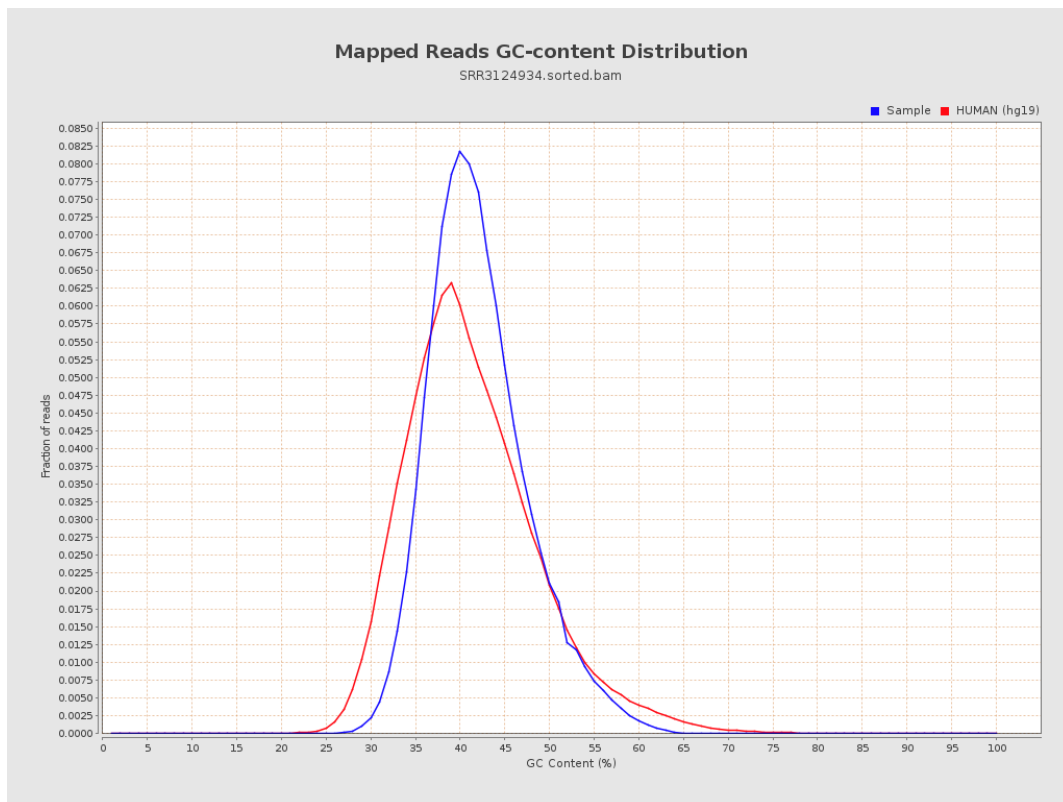
7. Results : Duplication Rate Histogram



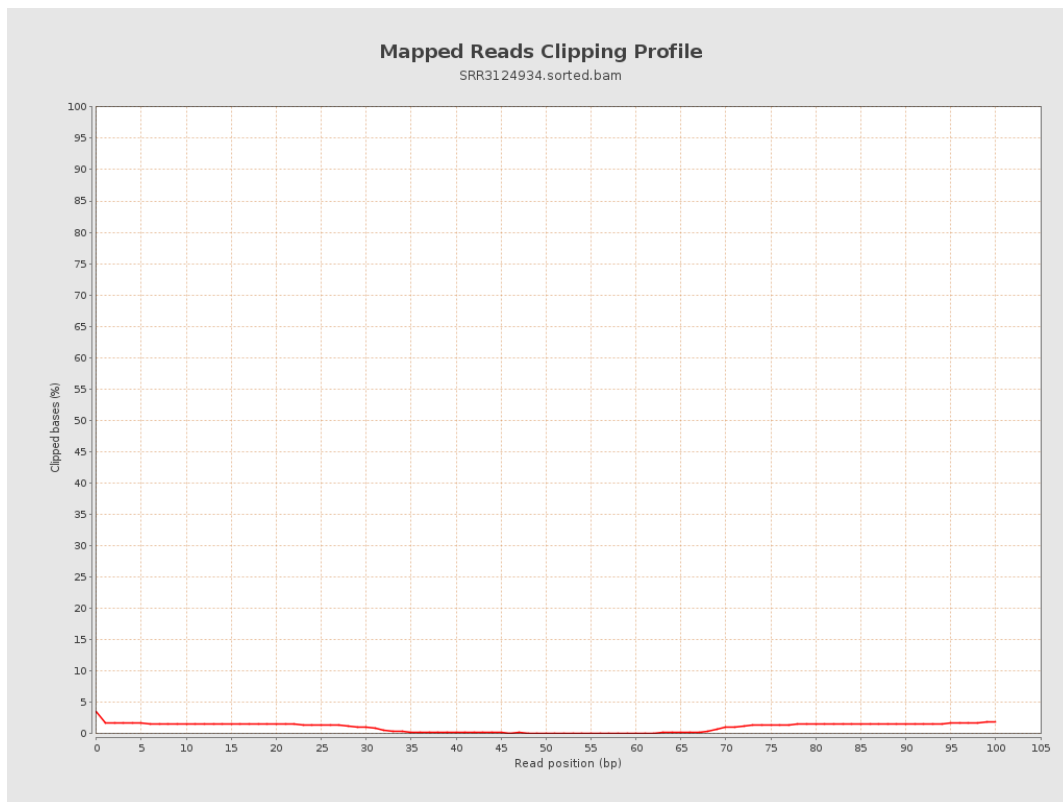
8. Results : Mapped Reads Nucleotide Content



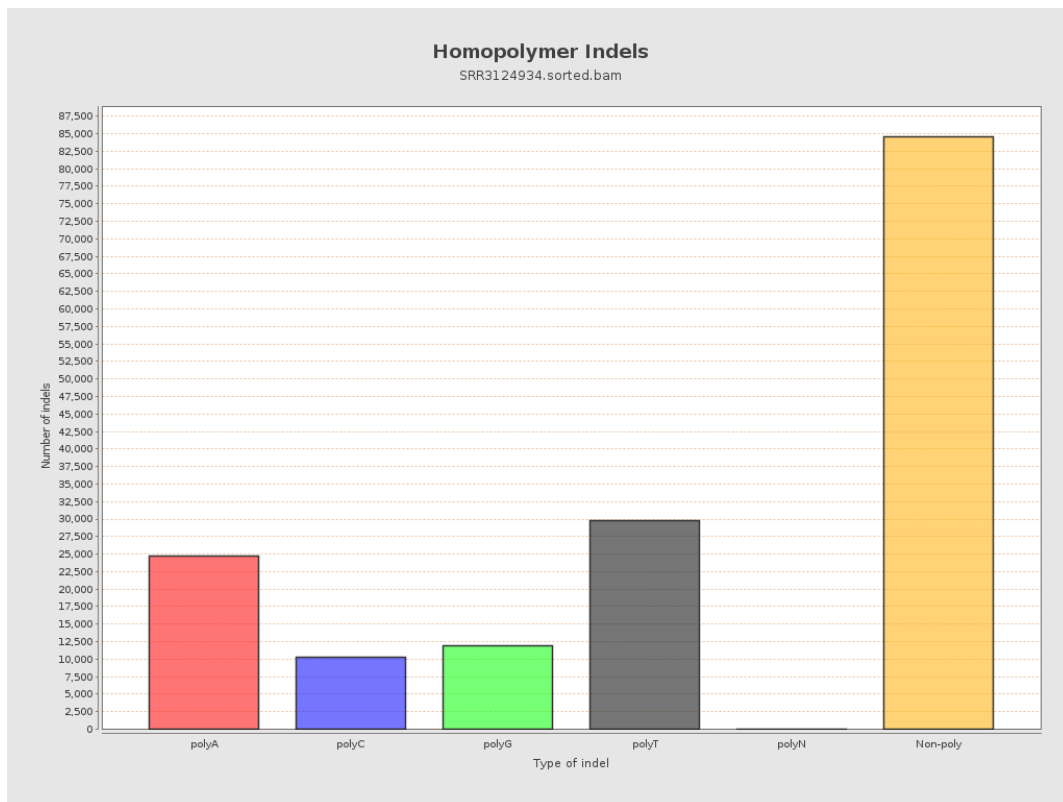
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



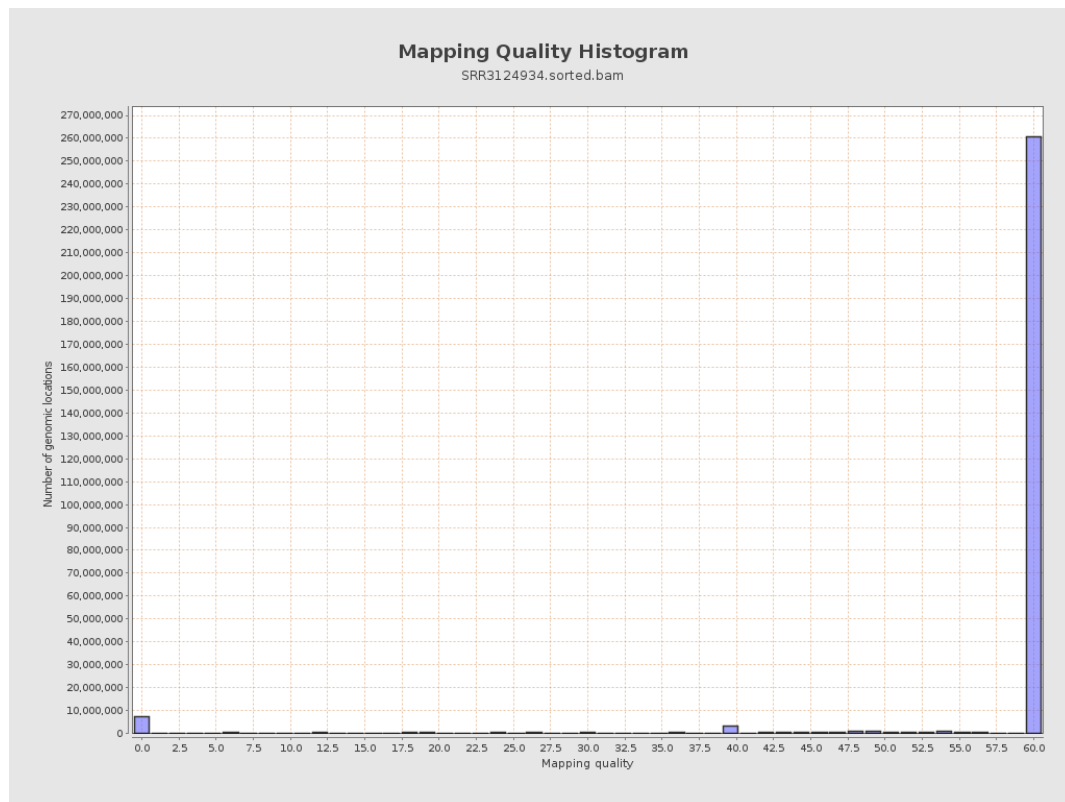
11. Results : Homopolymer Indels



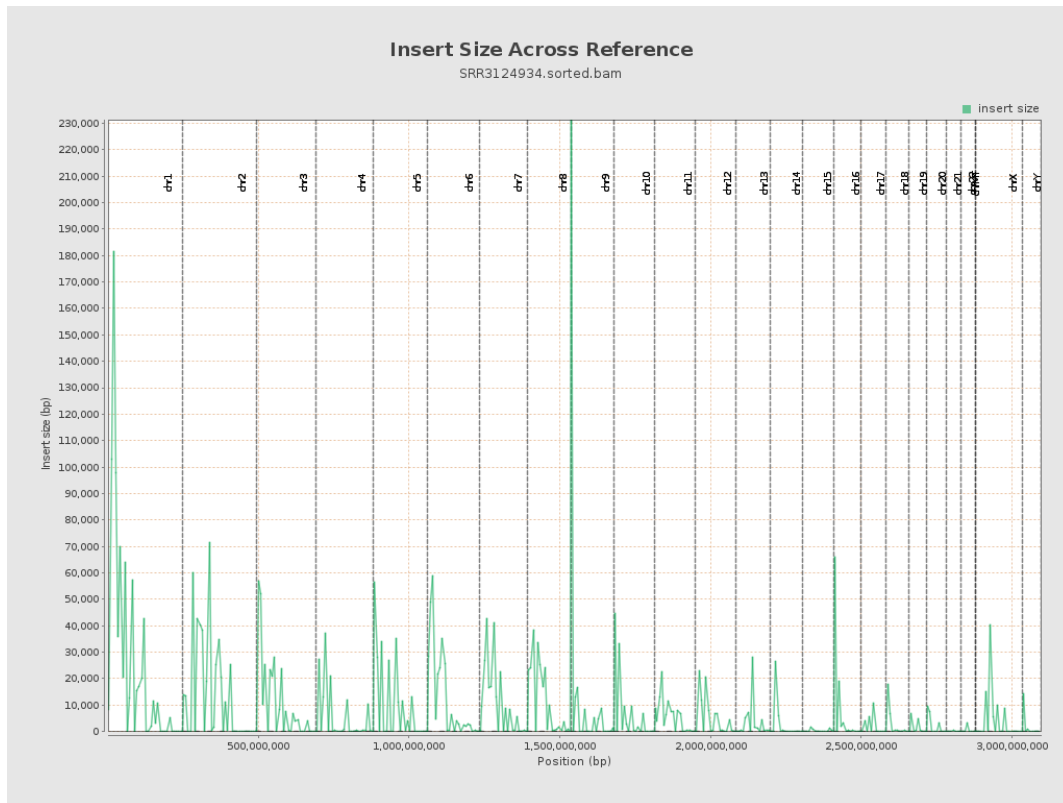
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

