

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/08 18:43:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124853.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_SRR3124853 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124853_1.fastq.gz SRR3124853_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 08 18:42:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124853.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	113,104,862
Mapped reads	109,101,875 / 96.46%
Unmapped reads	4,002,987 / 3.54%
Mapped paired reads	109,101,875 / 96.46%
Mapped reads, first in pair	55,010,160 / 48.64%
Mapped reads, second in pair	54,091,715 / 47.82%
Mapped reads, both in pair	107,916,754 / 95.41%
Mapped reads, singletons	1,185,121 / 1.05%
Secondary alignments	0
Supplementary alignments	2,912,929 / 2.58%
Read min/max/mean length	30 / 150 / 151.25
Duplicated reads (estimated)	46,547,865 / 41.15%
Duplication rate	23.93%
Clipped reads	63,944,270 / 56.54%

2.2. ACGT Content

Number/percentage of A's	4,098,621,518 / 28.68%
Number/percentage of C's	2,751,616,658 / 19.26%
Number/percentage of T's	4,258,991,491 / 29.8%
Number/percentage of G's	3,180,243,183 / 22.26%
Number/percentage of N's	321,337 / 0%

GC Percentage	41.51%
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2.3. Coverage

Mean	4.6199
Standard Deviation	76.3668

2.4. Mapping Quality

Mean Mapping Quality	53.18
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2.5. Insert size

Mean	141,329.81
Standard Deviation	3,527,034.1
P25/Median/P75	190 / 252 / 333

2.6. Mismatches and indels

General error rate	1.28%
Mismatches	172,502,333
Insertions	2,983,352
Mapped reads with at least one insertion	2.52%
Deletions	5,147,527
Mapped reads with at least one deletion	4.49%
Homopolymer indels	43.96%

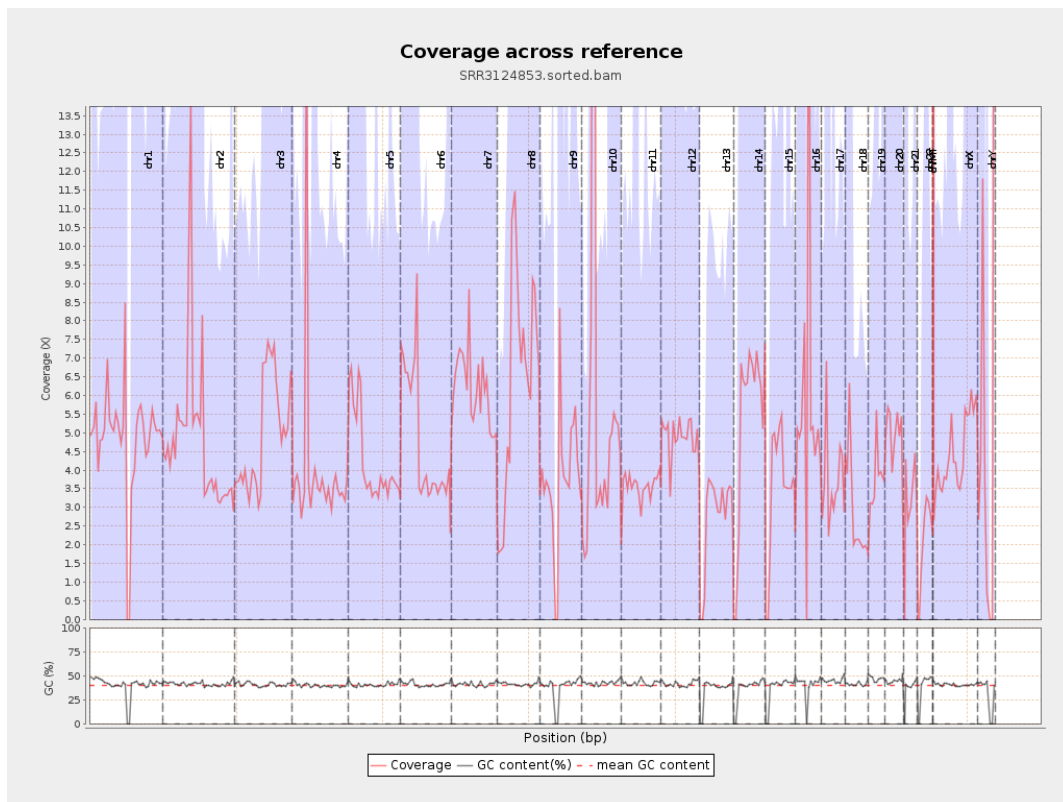
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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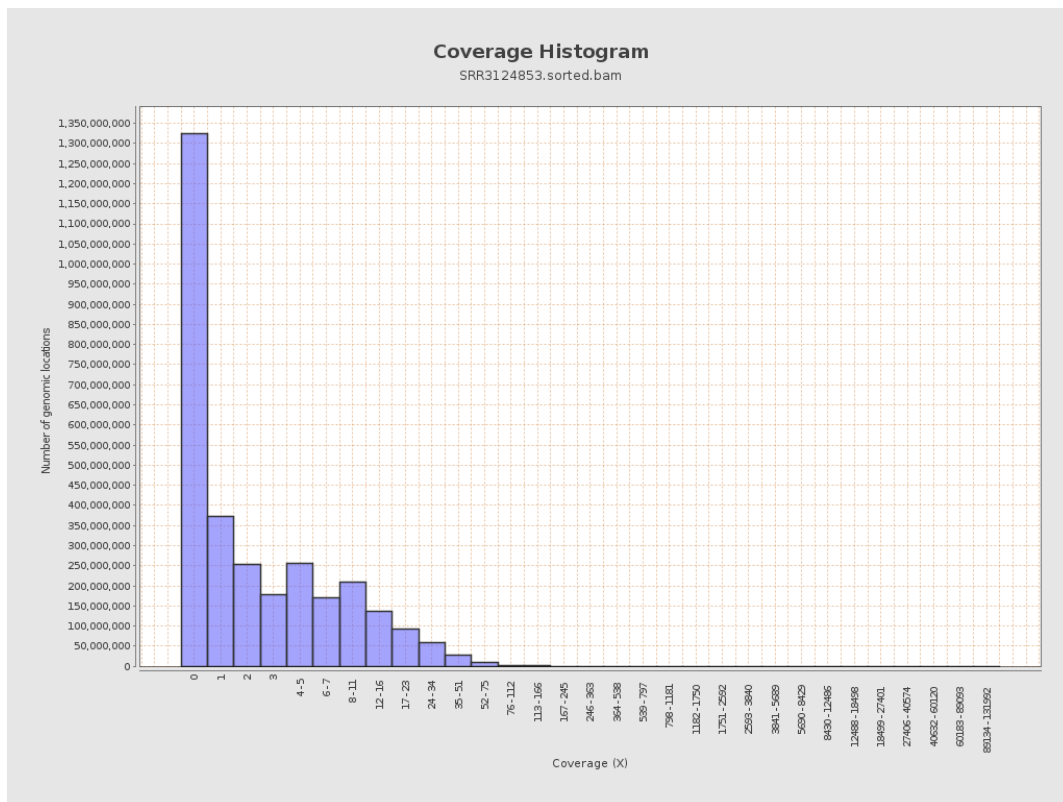
		bases	coverage	deviation
chr1	249250621	1213654328	4.8692	65.6208
chr2	243199373	1179643403	4.8505	73.6388
chr3	198022430	986064692	4.9796	10.6576
chr4	191154276	766091871	4.0077	90.2484
chr5	180915260	772468732	4.2698	10.269
chr6	171115067	816388780	4.771	30.3713
chr7	159138663	982638980	6.1747	57.3316
chr8	146364022	952798422	6.5098	20.8958
chr9	141213431	536144341	3.7967	86.8293
chr10	135534747	782258589	5.7716	250.3377
chr11	135006516	481245074	3.5646	21.9049
chr12	133851895	656743206	4.9065	23.5583
chr13	115169878	317242868	2.7546	6.0574
chr14	107349540	578002445	5.3843	11.9537
chr15	102531392	358916597	3.5006	13.0672
chr16	90354753	542381917	6.0028	113.3778
chr17	81195210	302707019	3.7281	59.1179
chr18	78077248	229426748	2.9385	68.2526
chr19	59128983	220226101	3.7245	34.0132
chr20	63025520	314999935	4.998	28.4662
chr21	48129895	153660298	3.1926	43.802
chr22	51304566	107991793	2.1049	8.487
chrMT	16571	17469750	1,054.2363	508.6046
chrX	155270560	693002207	4.4632	15.5881

chrY	59373566	339500599	5.718	158.7291
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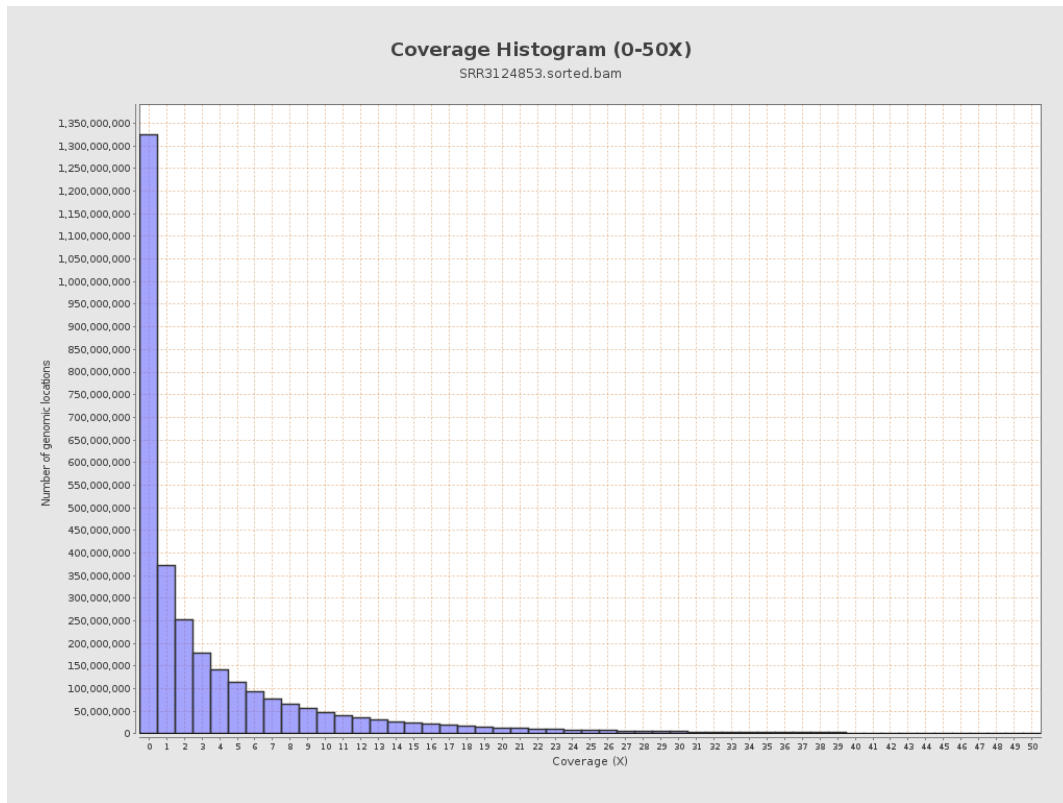
3. Results : Coverage across reference



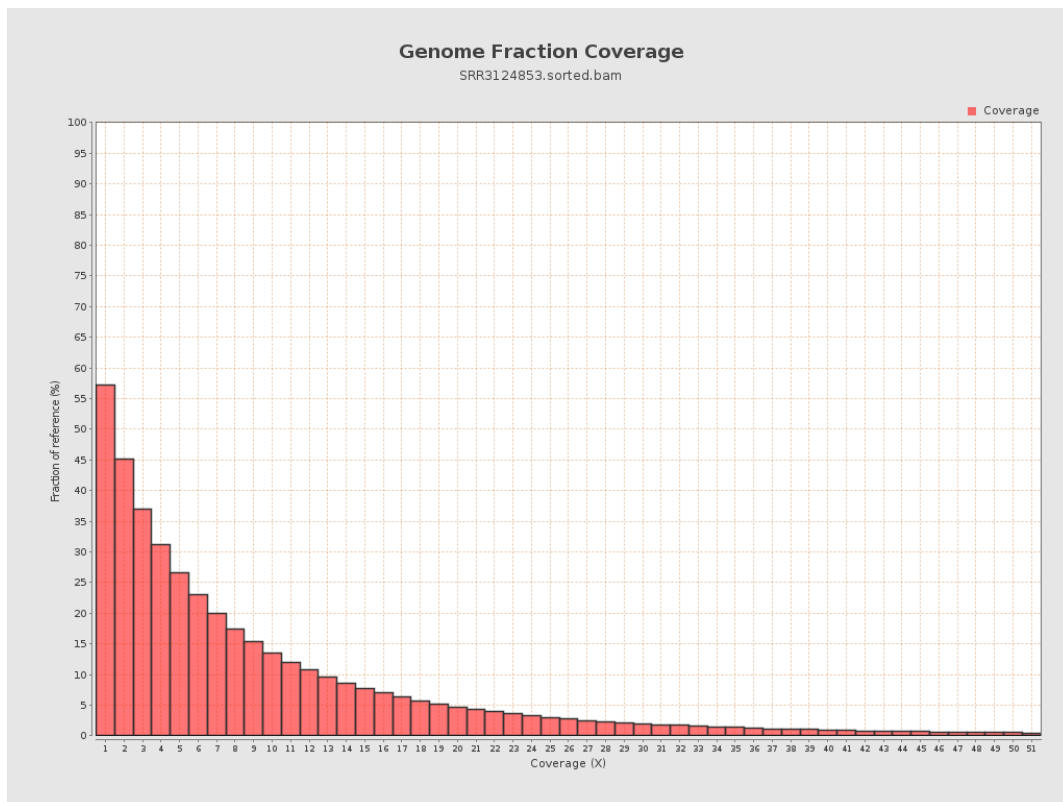
4. Results : Coverage Histogram



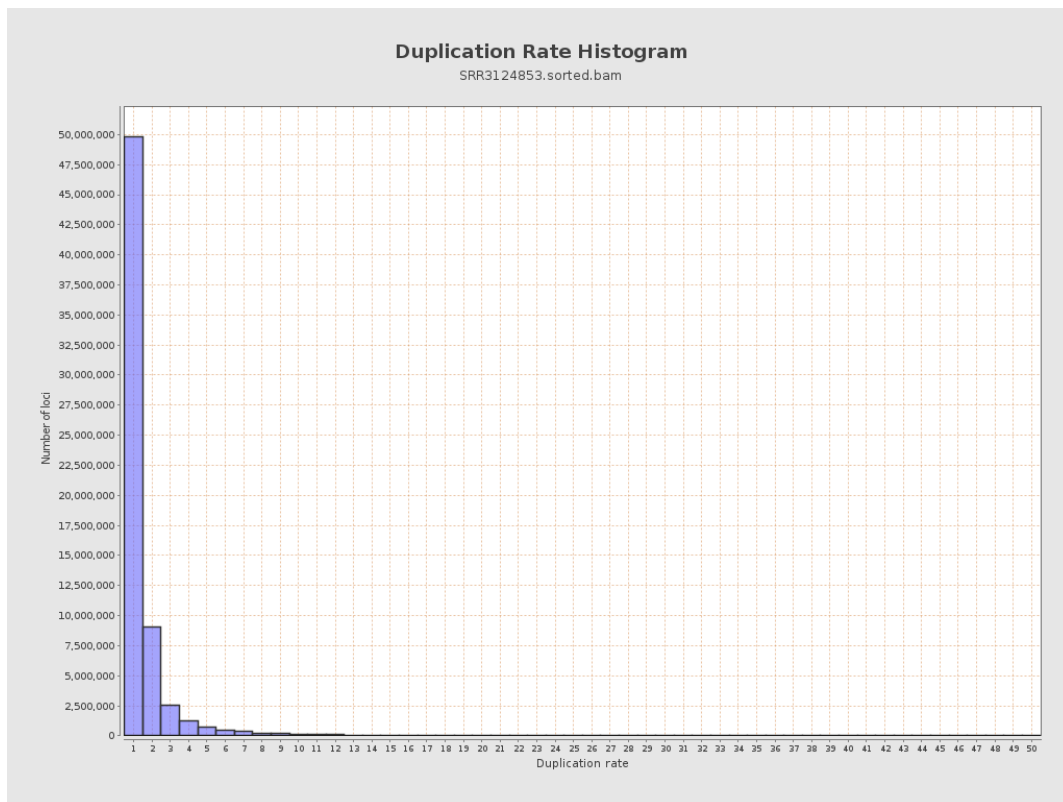
5. Results : Coverage Histogram (0-50X)



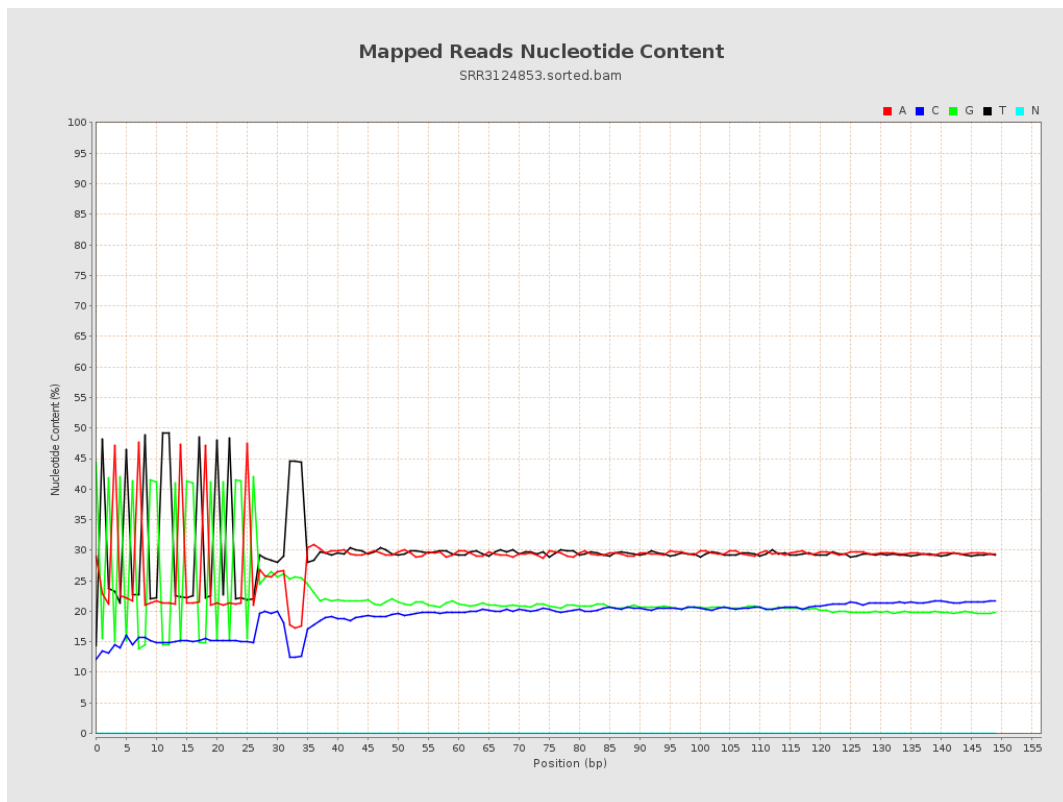
6. Results : Genome Fraction Coverage



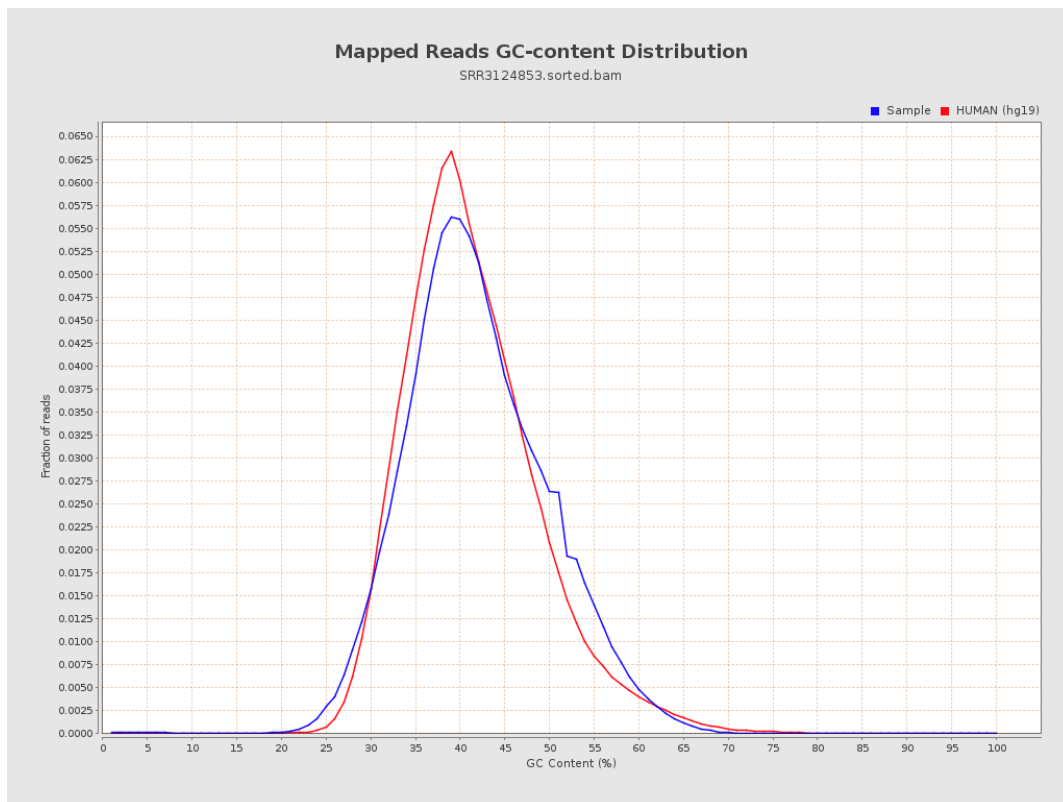
7. Results : Duplication Rate Histogram



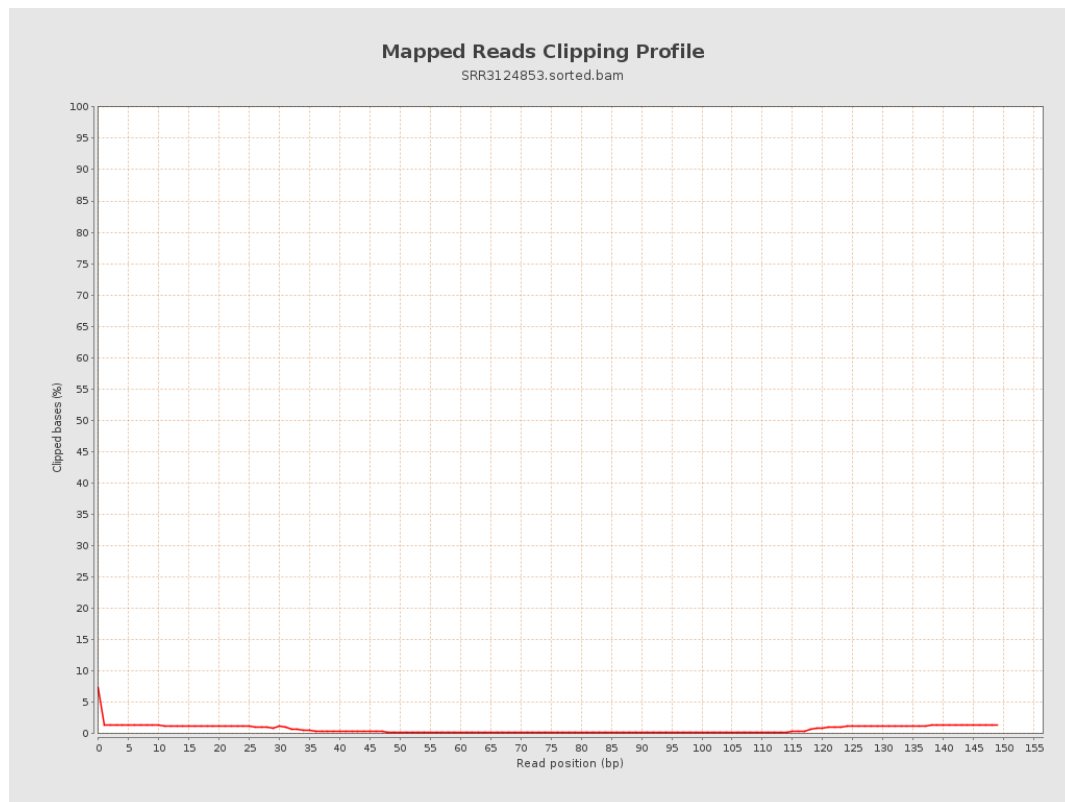
8. Results : Mapped Reads Nucleotide Content



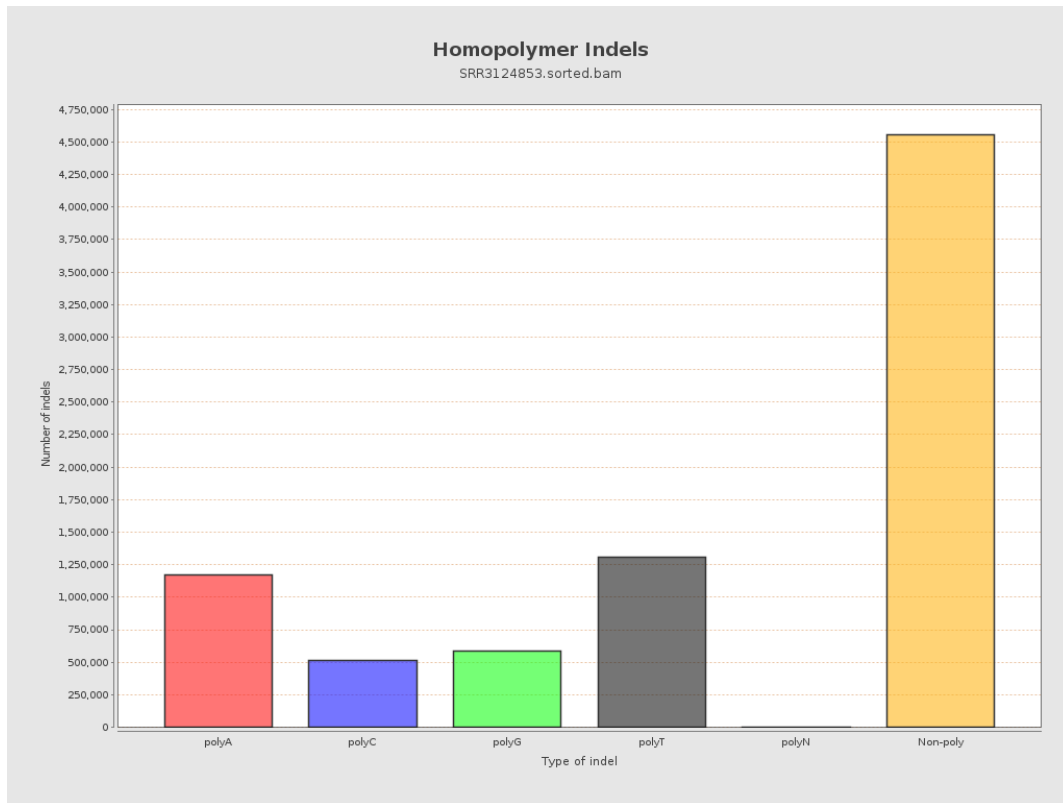
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



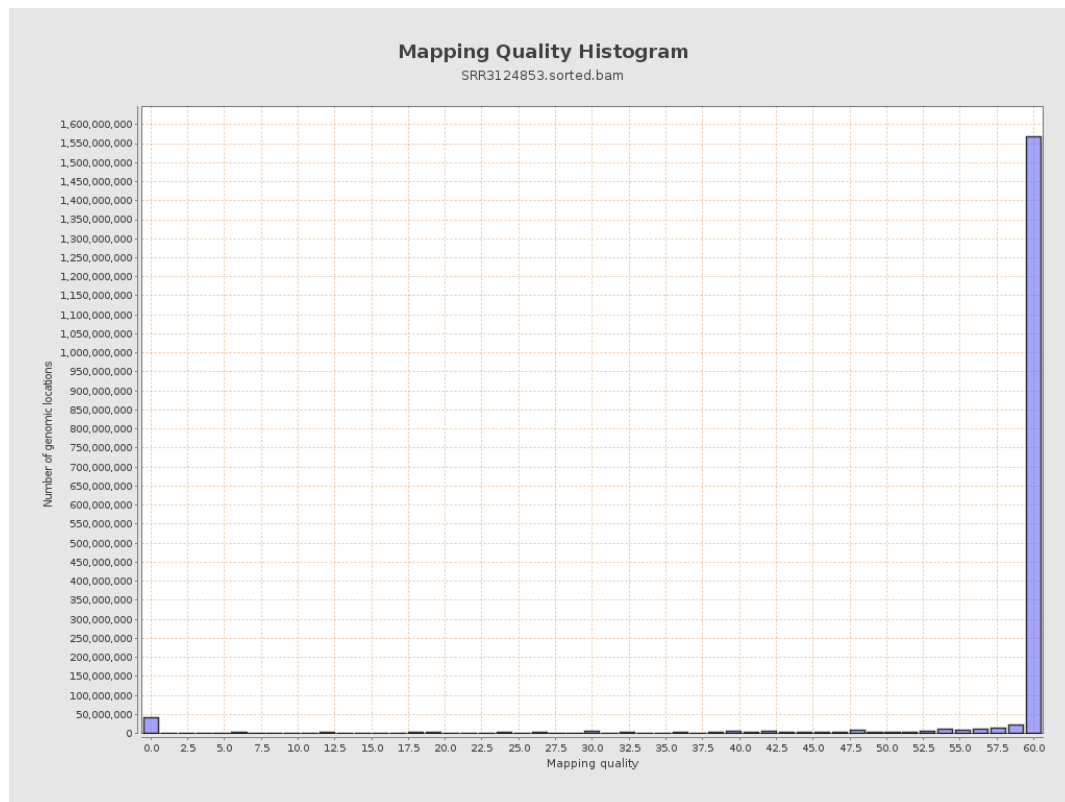
11. Results : Homopolymer Indels



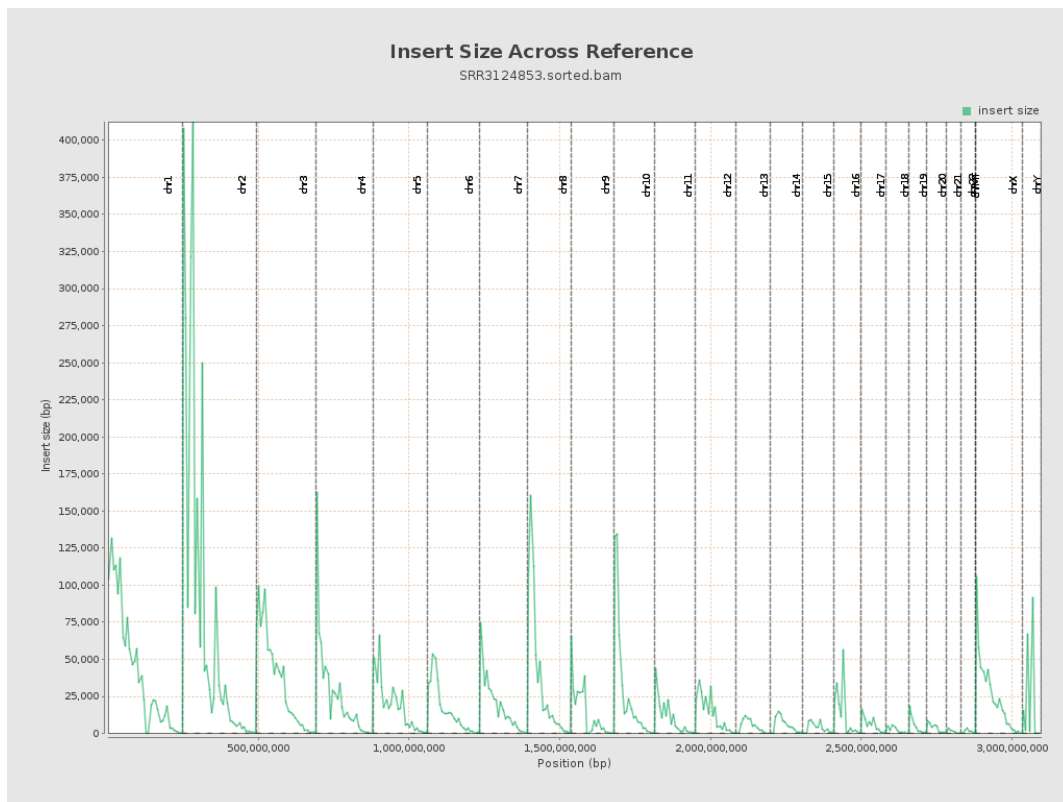
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

