

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/31 09:49:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504631.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_SRR504631 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504631_1.fastq.gz SRR504631_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 31 09:49:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504631.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	566,538,364
Mapped reads	481,718,823 / 85.03%
Unmapped reads	84,819,541 / 14.97%
Mapped paired reads	481,718,823 / 85.03%
Mapped reads, first in pair	247,278,238 / 43.65%
Mapped reads, second in pair	234,440,585 / 41.38%
Mapped reads, both in pair	456,062,266 / 80.5%
Mapped reads, singletons	25,656,557 / 4.53%
Secondary alignments	0
Supplementary alignments	4,165,015 / 0.74%
Read min/max/mean length	30 / 100 / 100.29
Duplicated reads (estimated)	166,602,519 / 29.41%
Duplication rate	22.87%
Clipped reads	114,716,615 / 20.25%

2.2. ACGT Content

Number/percentage of A's	12,337,919,234 / 27.28%
Number/percentage of C's	10,239,525,264 / 22.64%
Number/percentage of T's	12,431,949,087 / 27.49%
Number/percentage of G's	10,184,662,597 / 22.52%
Number/percentage of N's	30,476,198 / 0.07%

GC Percentage	45.16%
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2.3. Coverage

Mean	14.6207
Standard Deviation	309.1136

2.4. Mapping Quality

Mean Mapping Quality	51.49
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2.5. Insert size

Mean	103,323.57
Standard Deviation	2,990,313.81
P25/Median/P75	308 / 353 / 406

2.6. Mismatches and indels

General error rate	2.61%
Mismatches	1,135,455,157
Insertions	12,409,141
Mapped reads with at least one insertion	2.4%
Deletions	11,380,351
Mapped reads with at least one deletion	2.21%
Homopolymer indels	33.16%

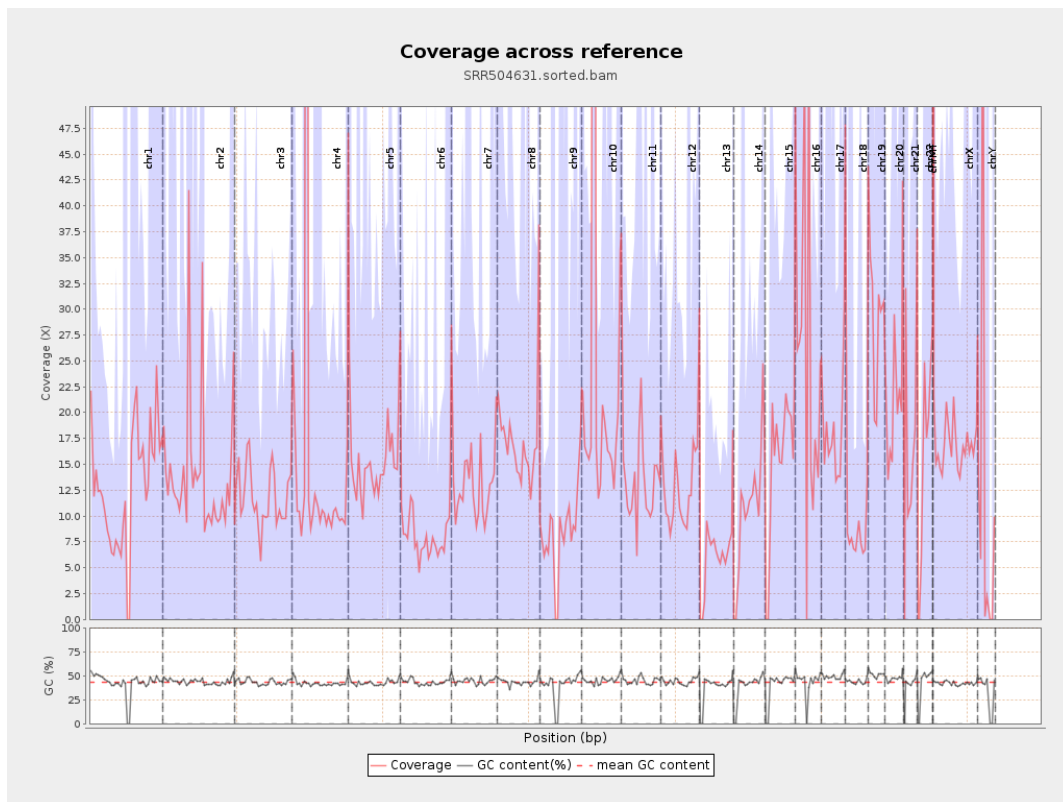
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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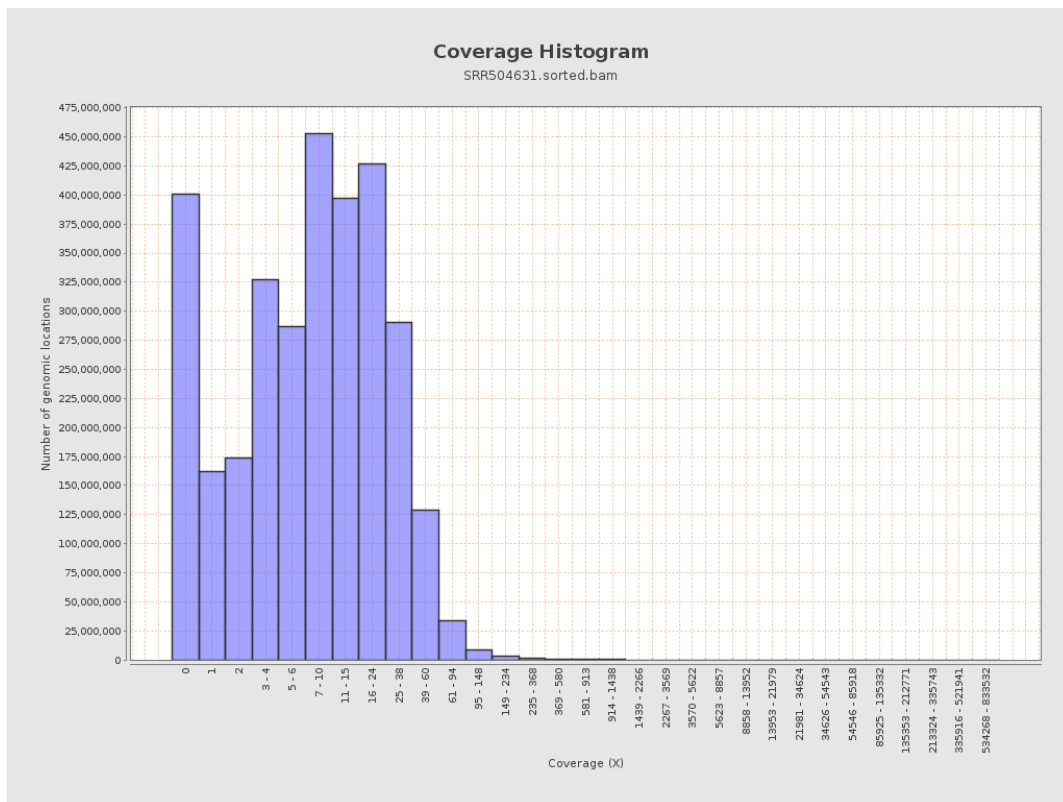
		bases	coverage	deviation
chr1	249250621	3198123369	12.831	103.7676
chr2	243199373	3424228967	14.0799	317.8151
chr3	198022430	2343273620	11.8334	36.2346
chr4	191154276	3281315351	17.1658	780.7011
chr5	180915260	2815143325	15.5606	44.3265
chr6	171115067	1357548731	7.9335	31.9441
chr7	159138663	2131225539	13.3923	50.0413
chr8	146364022	2526835614	17.264	234.2398
chr9	141213431	1185883464	8.3978	148.7351
chr10	135534747	3381681764	24.9507	762.8426
chr11	135006516	1840403702	13.632	36.6574
chr12	133851895	1717706329	12.8329	32.0941
chr13	115169878	708304465	6.1501	15.4458
chr14	107349540	1167303233	10.8739	37.7999
chr15	102531392	1541923454	15.0385	25.2349
chr16	90354753	2384607882	26.3916	312.0225
chr17	81195210	1433613956	17.6564	99.844
chr18	78077248	753337805	9.6486	391.77
chr19	59128983	1710303648	28.925	63.0436
chr20	63025520	1320916032	20.9584	213.1337
chr21	48129895	859560694	17.8592	283.1104
chr22	51304566	778774291	15.1794	40.5633
chrMT	16571	15158411	914.7554	423.2752
chrX	155270560	2641386040	17.0115	34.6311

chrY	59373566	742776340	12.5102	726.6934
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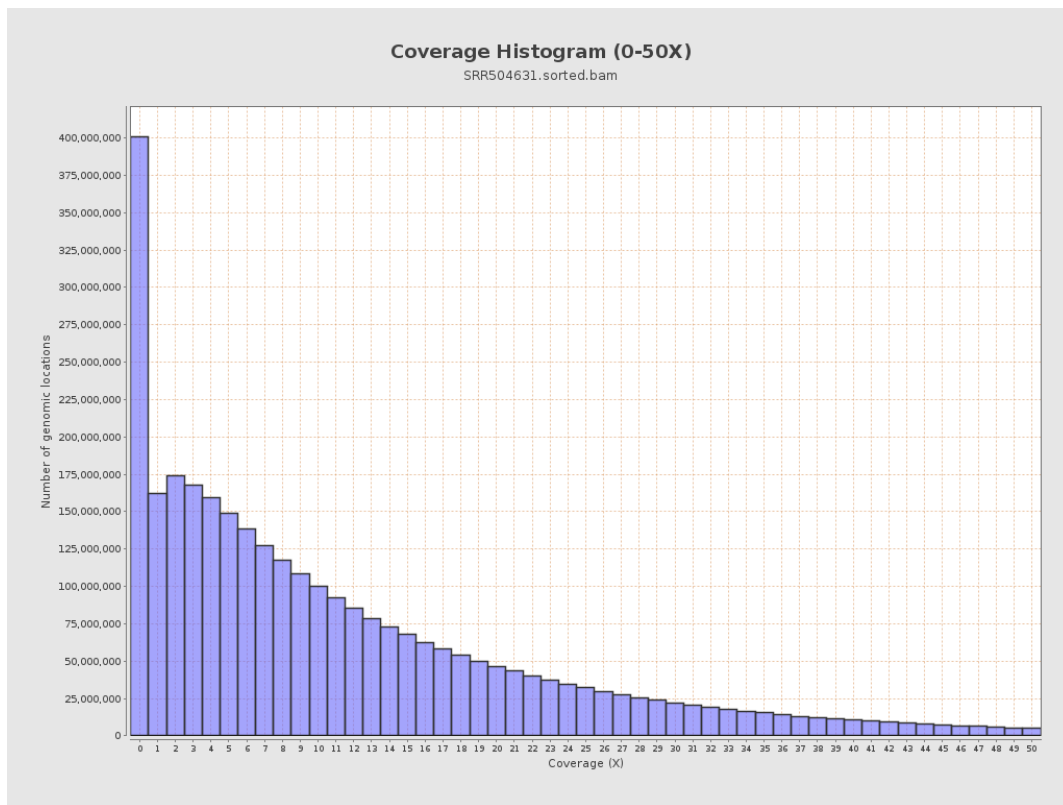
3. Results : Coverage across reference



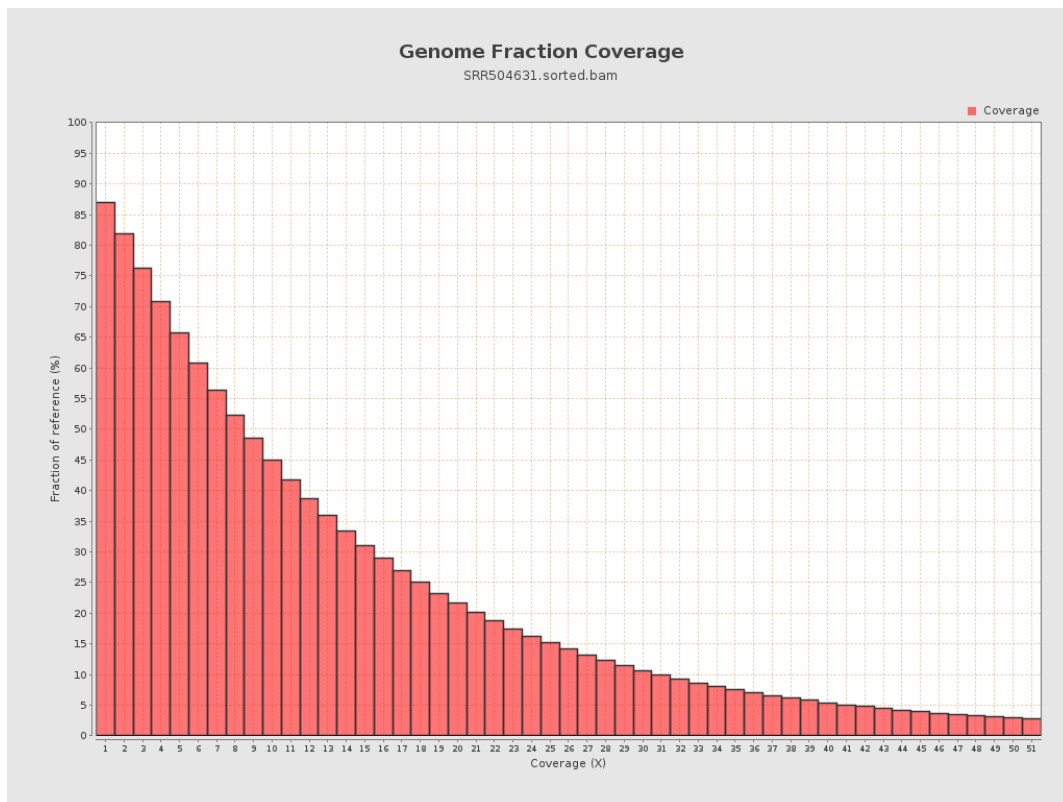
4. Results : Coverage Histogram



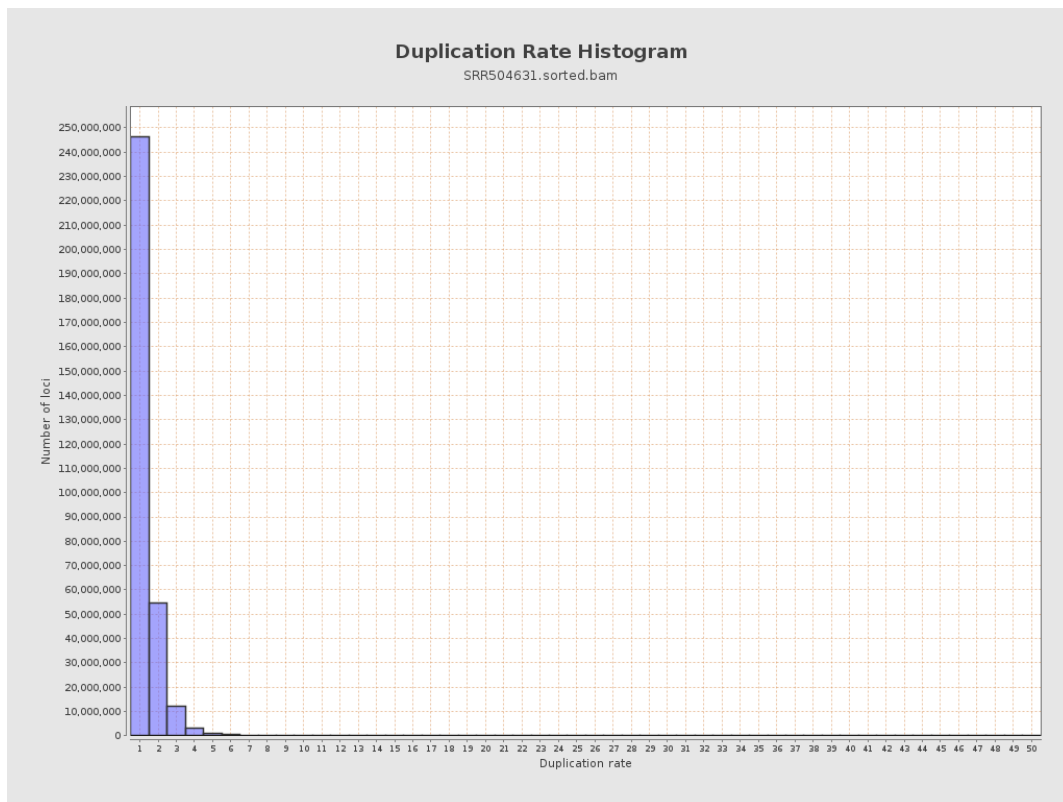
5. Results : Coverage Histogram (0-50X)



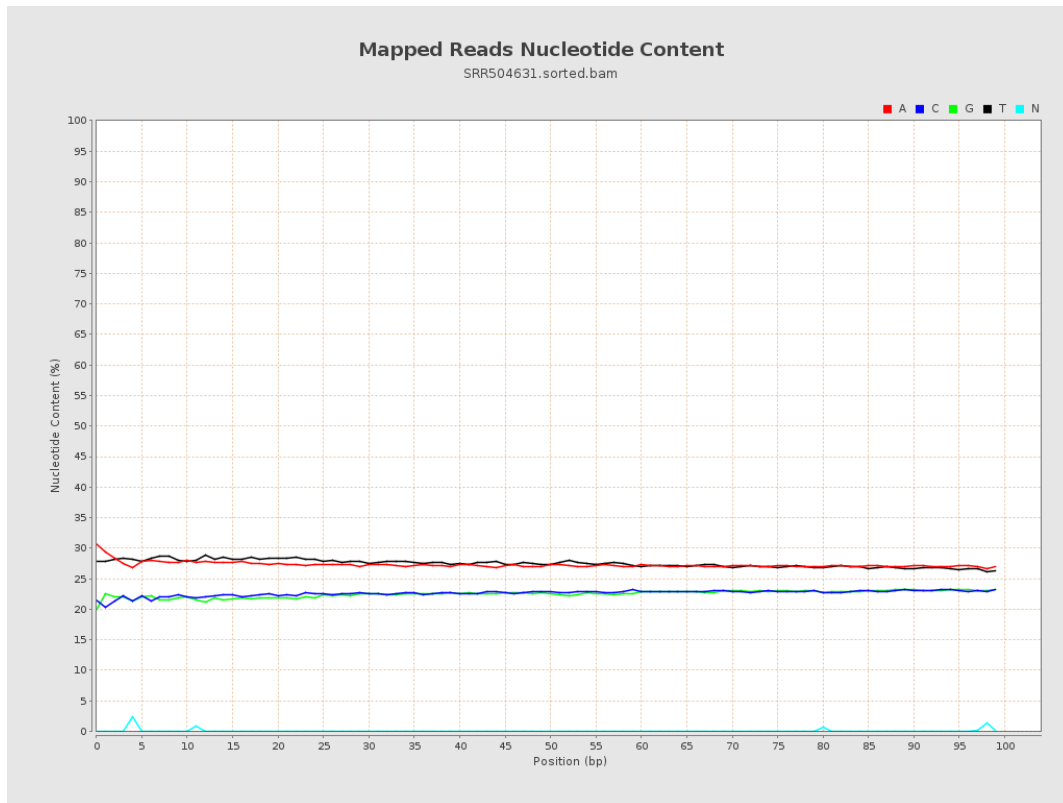
6. Results : Genome Fraction Coverage



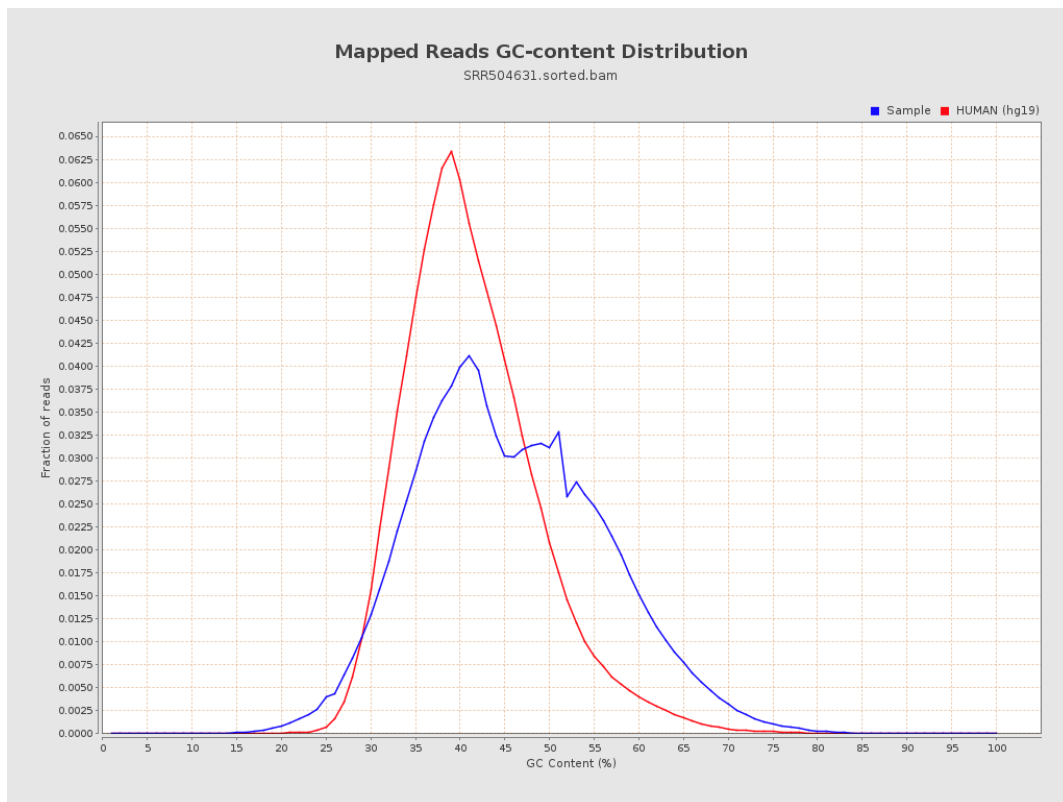
7. Results : Duplication Rate Histogram



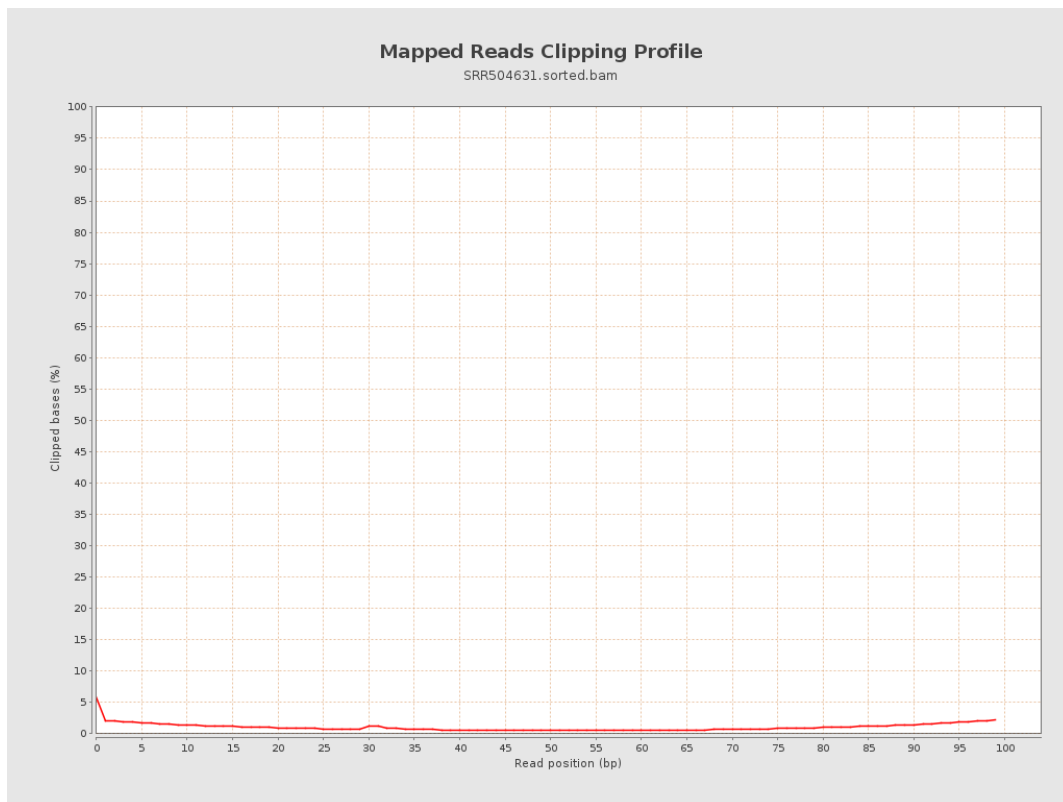
8. Results : Mapped Reads Nucleotide Content



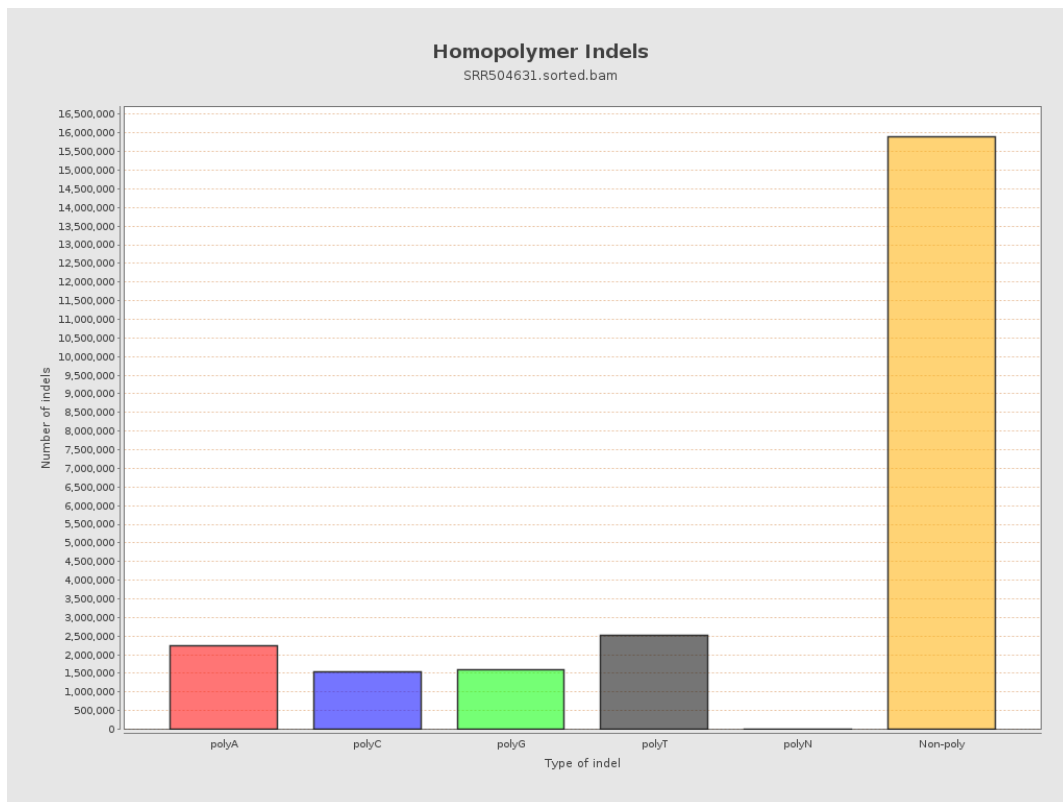
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



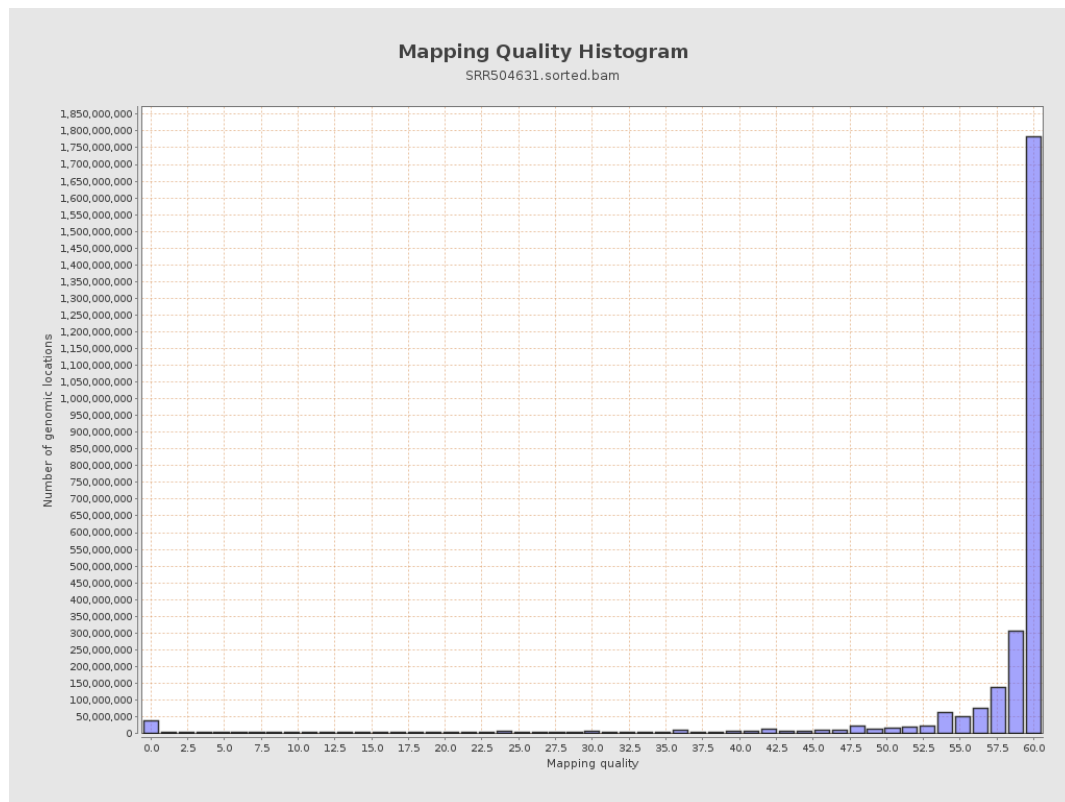
11. Results : Homopolymer Indels



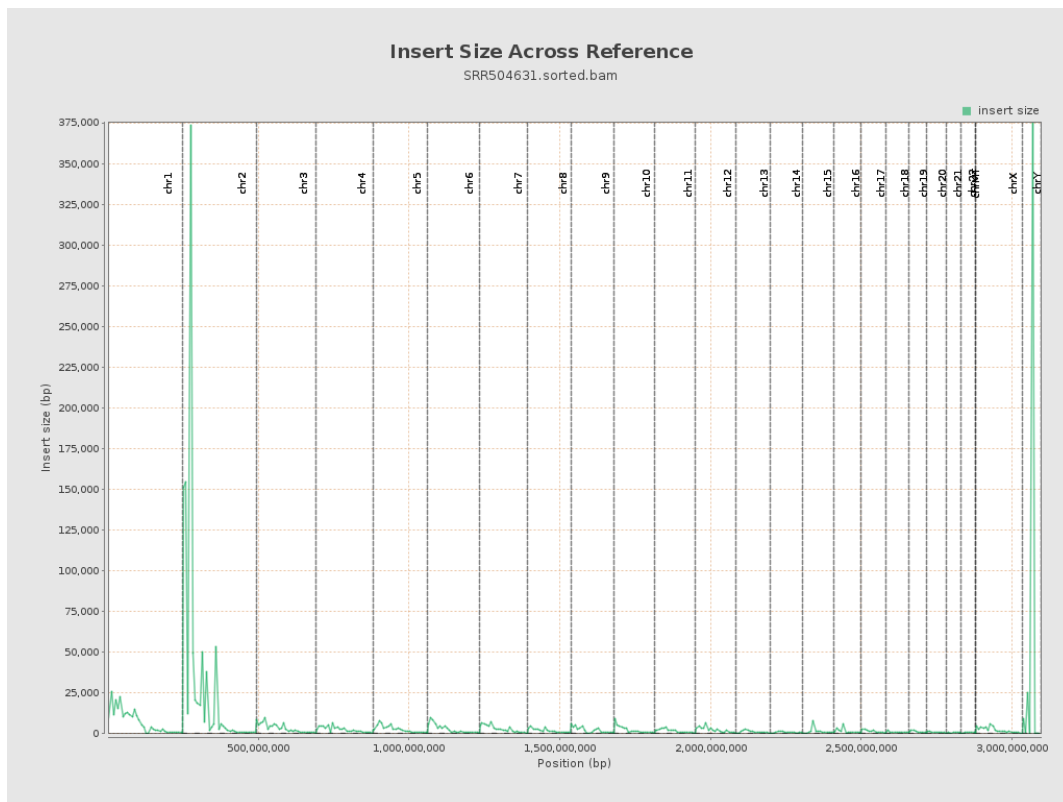
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

