

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 01:46:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124891.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_SRR3124891 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124891_1.fastq.gz SRR3124891_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 01:46:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124891.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,823,212
Mapped reads	4,788,561 / 99.28%
Unmapped reads	34,651 / 0.72%
Mapped paired reads	4,788,561 / 99.28%
Mapped reads, first in pair	2,398,212 / 49.72%
Mapped reads, second in pair	2,390,349 / 49.56%
Mapped reads, both in pair	4,777,658 / 99.06%
Mapped reads, singletons	10,903 / 0.23%
Secondary alignments	0
Supplementary alignments	65,514 / 1.36%
Read min/max/mean length	30 / 151 / 151.7
Duplicated reads (estimated)	755,990 / 15.67%
Duplication rate	13.69%
Clipped reads	2,011,406 / 41.7%

2.2. ACGT Content

Number/percentage of A's	203,882,522 / 29.98%
Number/percentage of C's	134,929,165 / 19.84%
Number/percentage of T's	202,377,544 / 29.76%
Number/percentage of G's	138,799,733 / 20.41%
Number/percentage of N's	40,020 / 0.01%

GC Percentage	40.25%
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2.3. Coverage

Mean	0.2198
Standard Deviation	2.7968

2.4. Mapping Quality

Mean Mapping Quality	53.6
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2.5. Insert size

Mean	40,976.13
Standard Deviation	1,894,561.28
P25/Median/P75	143 / 172 / 214

2.6. Mismatches and indels

General error rate	1.15%
Mismatches	7,548,805
Insertions	123,780
Mapped reads with at least one insertion	2.47%
Deletions	278,951
Mapped reads with at least one deletion	5.61%
Homopolymer indels	49.06%

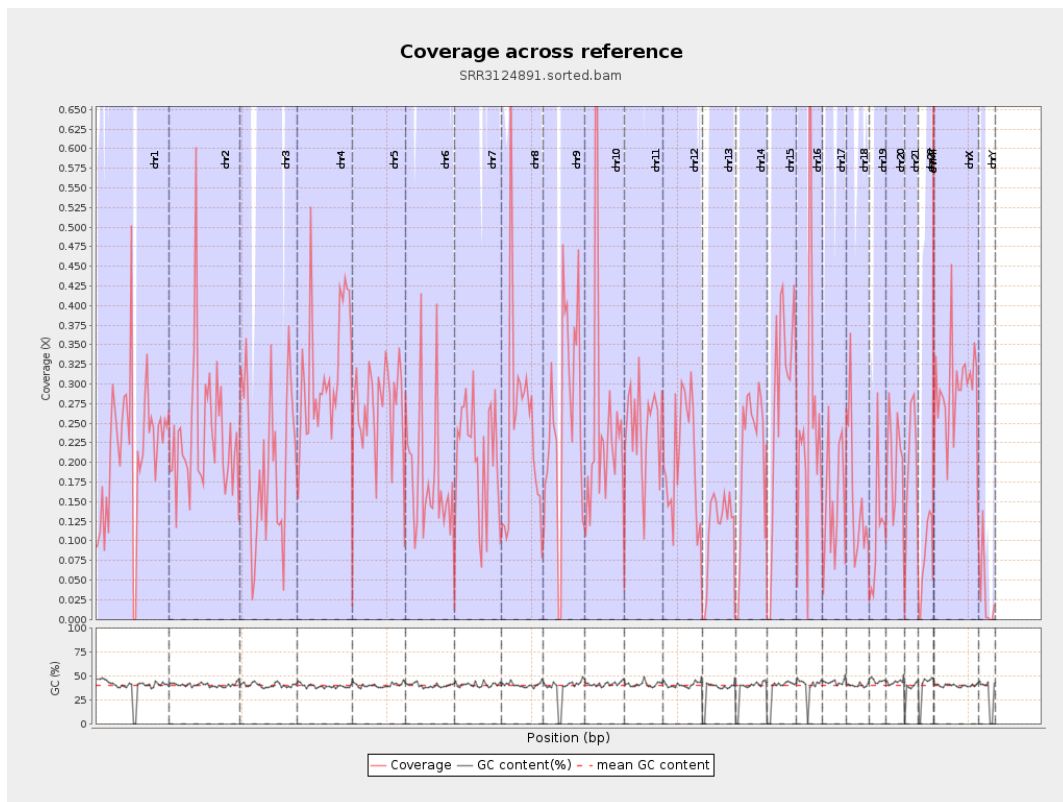
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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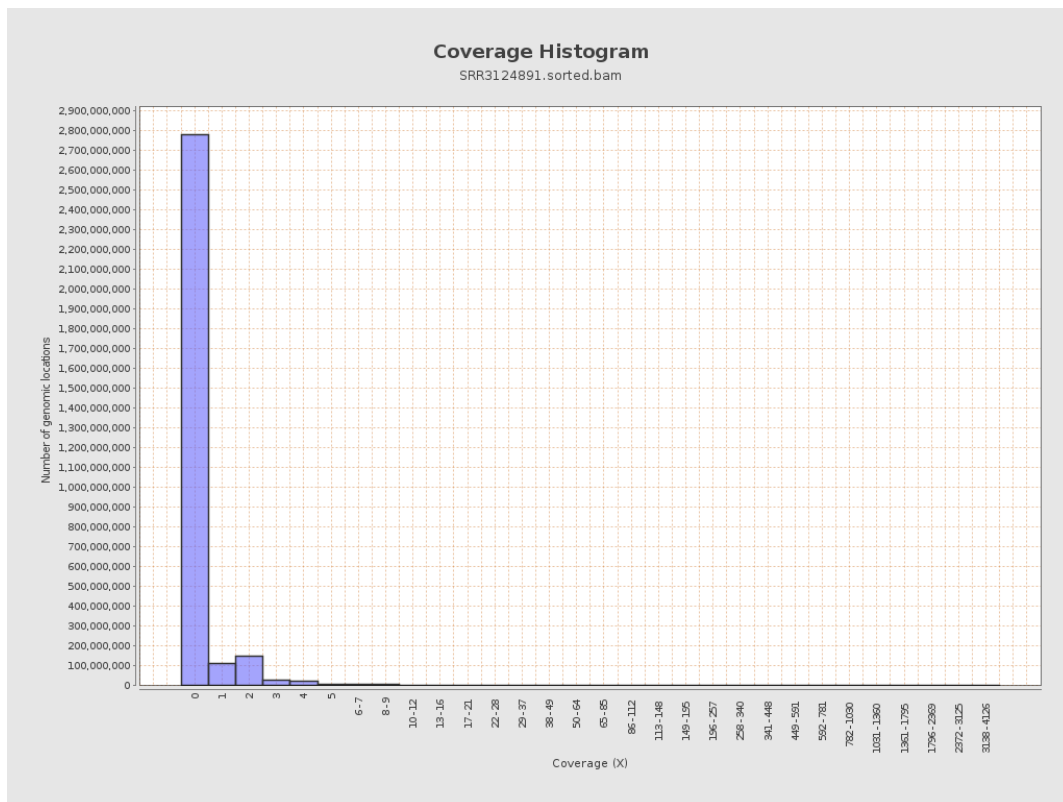
		bases	coverage	deviation
chr1	249250621	53568382	0.2149	4.2151
chr2	243199373	57259601	0.2354	2.5569
chr3	198022430	40173493	0.2029	0.7818
chr4	191154276	60240696	0.3151	2.0017
chr5	180915260	48619577	0.2687	0.8201
chr6	171115067	31224849	0.1825	1.9792
chr7	159138663	33919397	0.2131	2.5555
chr8	146364022	34803219	0.2378	1.2234
chr9	141213431	37001472	0.262	4.8419
chr10	135534747	33317571	0.2458	6.7591
chr11	135006516	32627489	0.2417	2.2018
chr12	133851895	27448089	0.2051	0.7164
chr13	115169878	13043642	0.1133	0.5064
chr14	107349540	22346715	0.2082	0.7508
chr15	102531392	28554403	0.2785	0.8645
chr16	90354753	22664815	0.2508	4.1121
chr17	81195210	11570394	0.1425	3.4959
chr18	78077248	12411636	0.159	4.0847
chr19	59128983	6471867	0.1095	2.3541
chr20	63025520	12773833	0.2027	0.9598
chr21	48129895	9123018	0.1895	1.1754
chr22	51304566	4184970	0.0816	0.4458
chrMT	16571	25891	1.5624	1.8586
chrX	155270560	45454140	0.2927	1.4116

chrY	59373566	1696784	0.0286	2.1014
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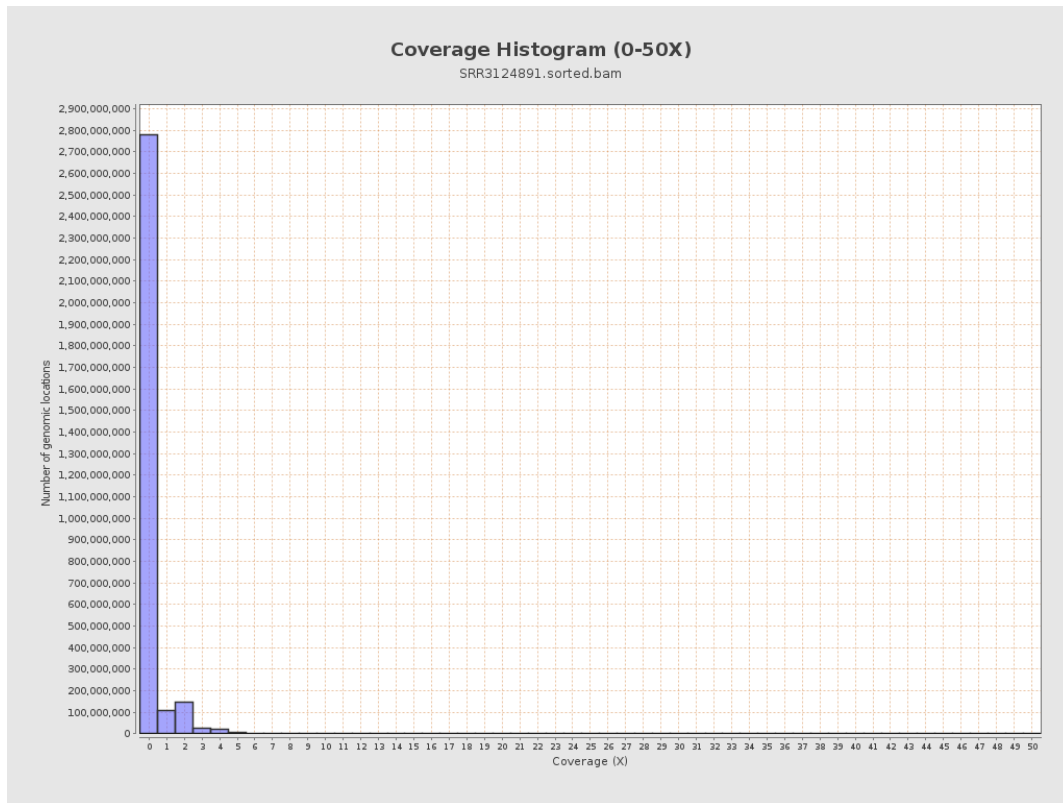
3. Results : Coverage across reference



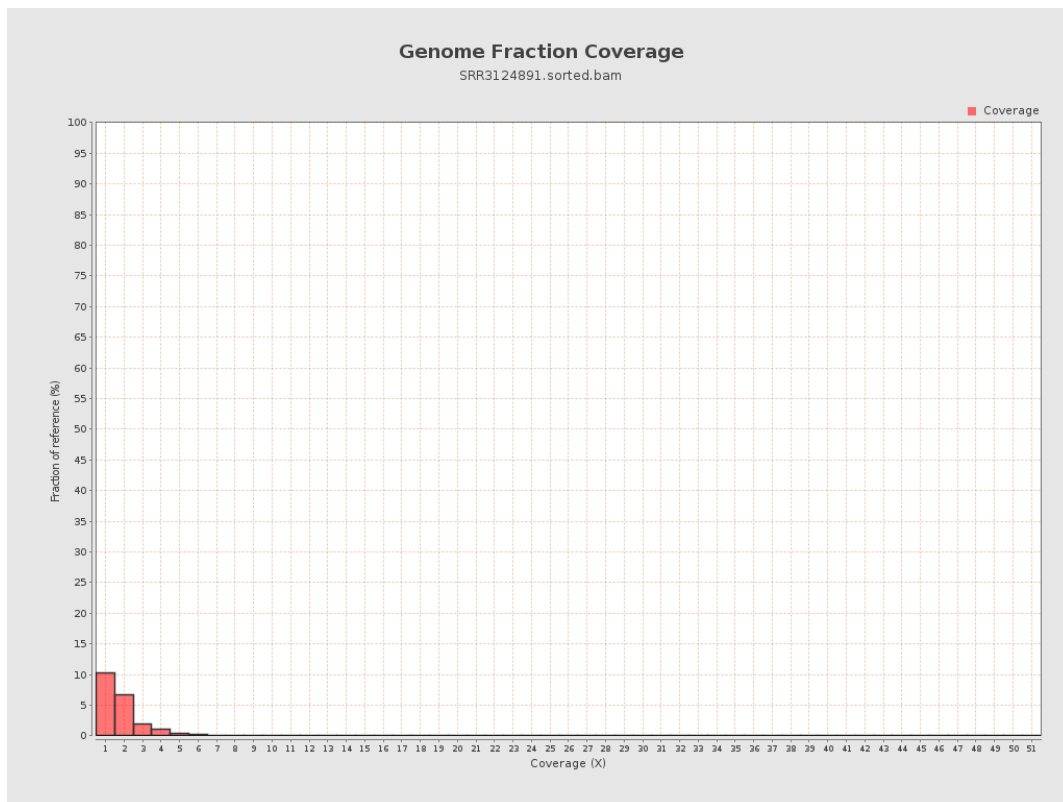
4. Results : Coverage Histogram



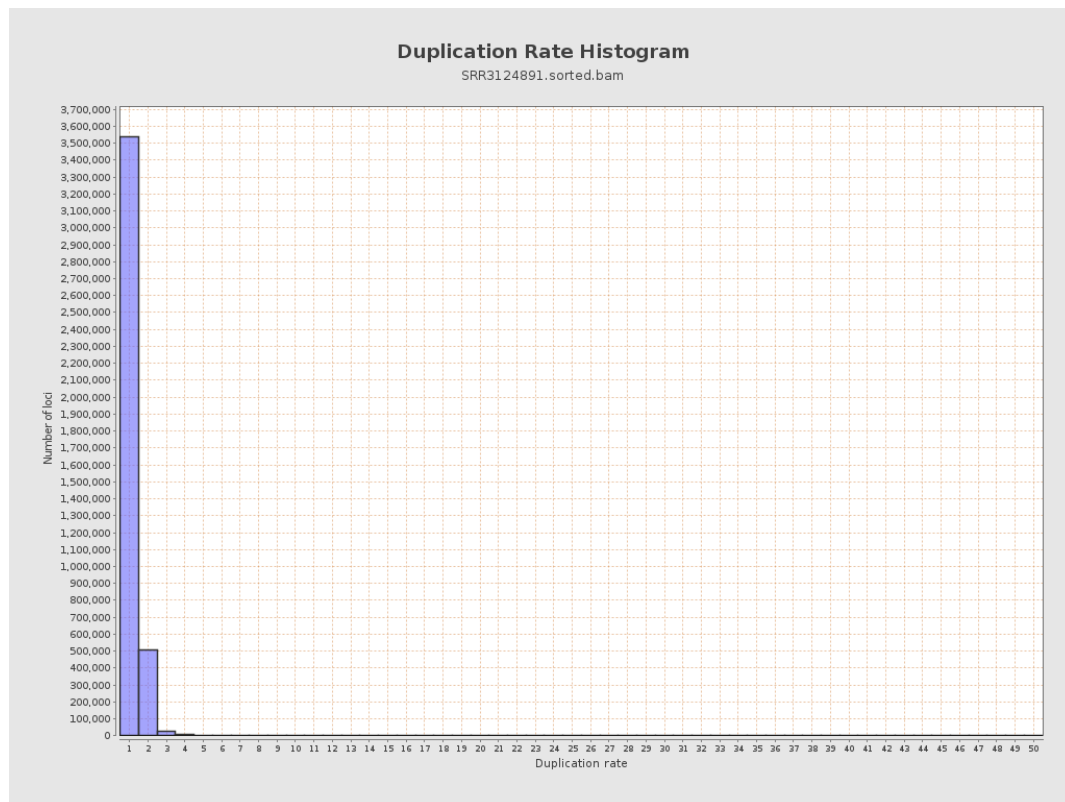
5. Results : Coverage Histogram (0-50X)



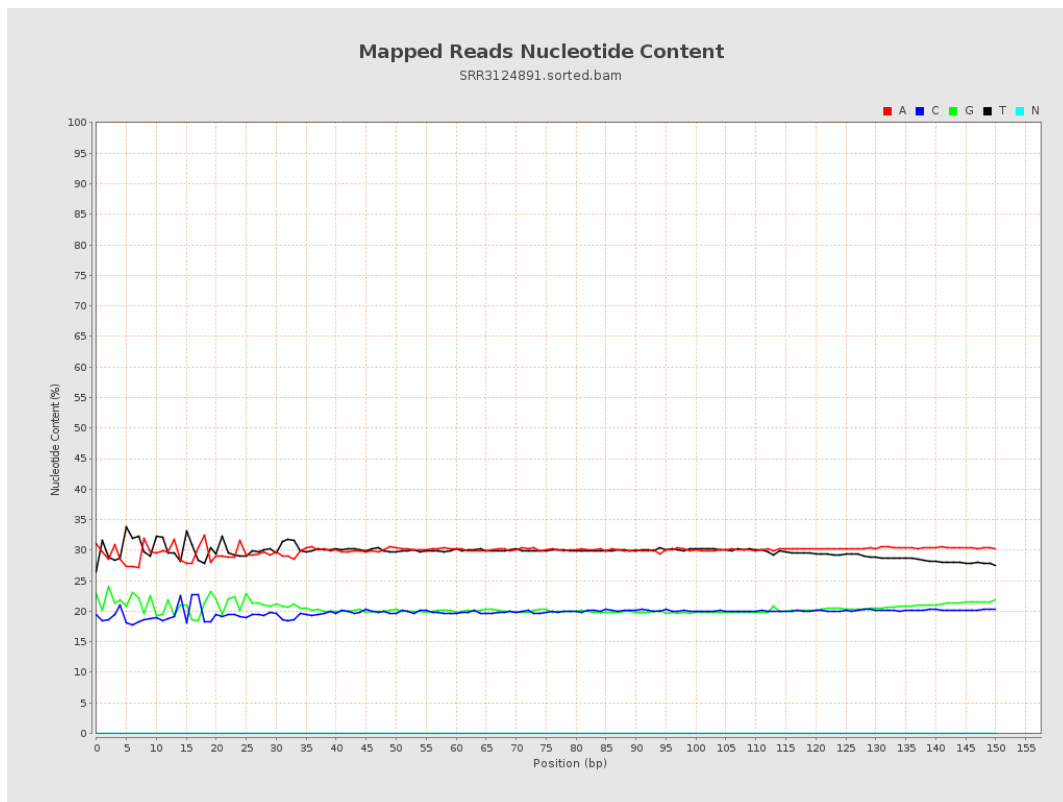
6. Results : Genome Fraction Coverage



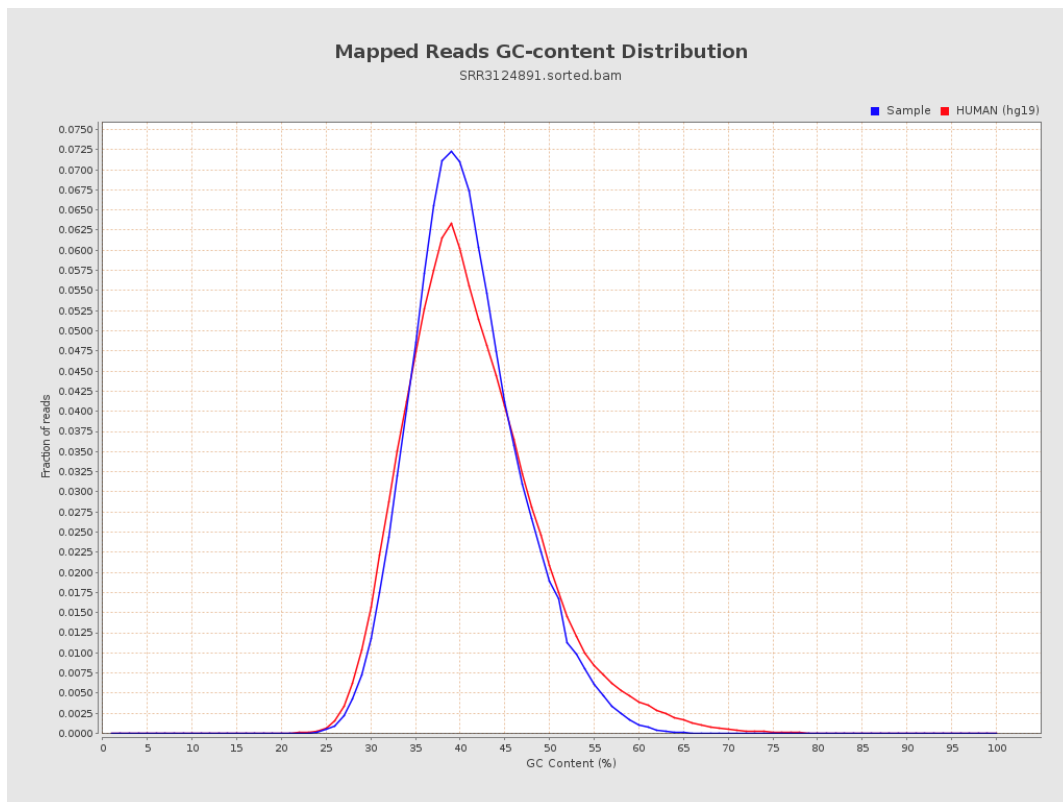
7. Results : Duplication Rate Histogram



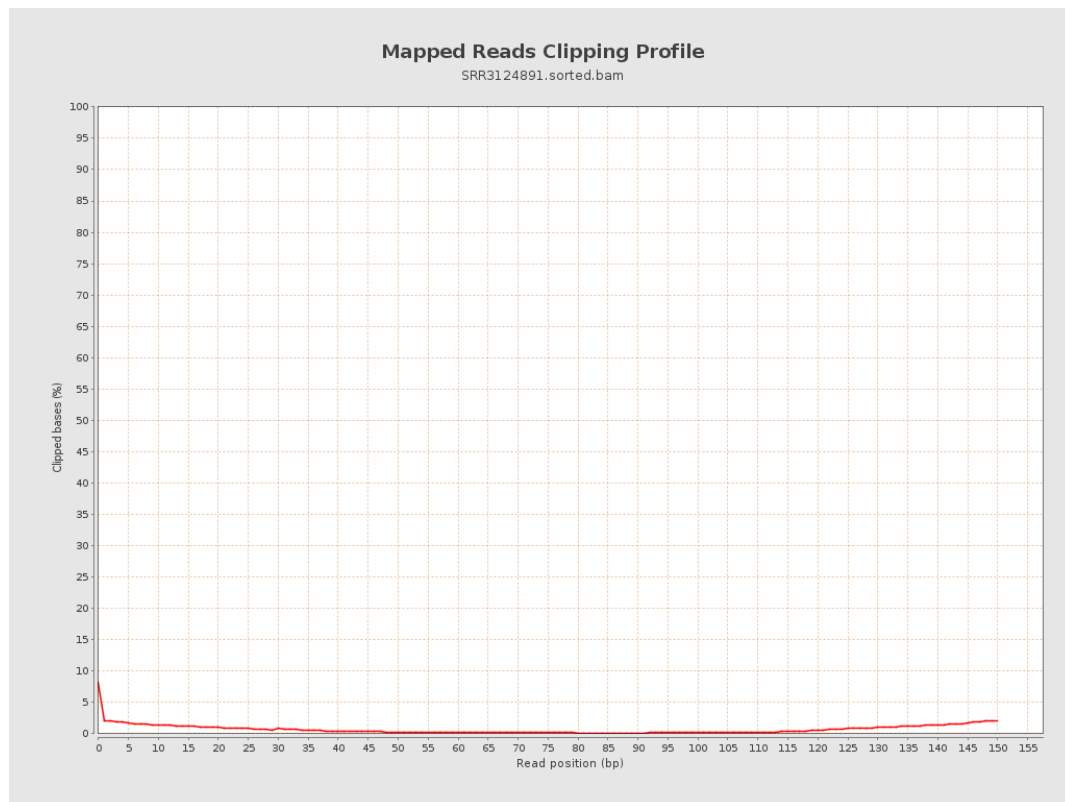
8. Results : Mapped Reads Nucleotide Content



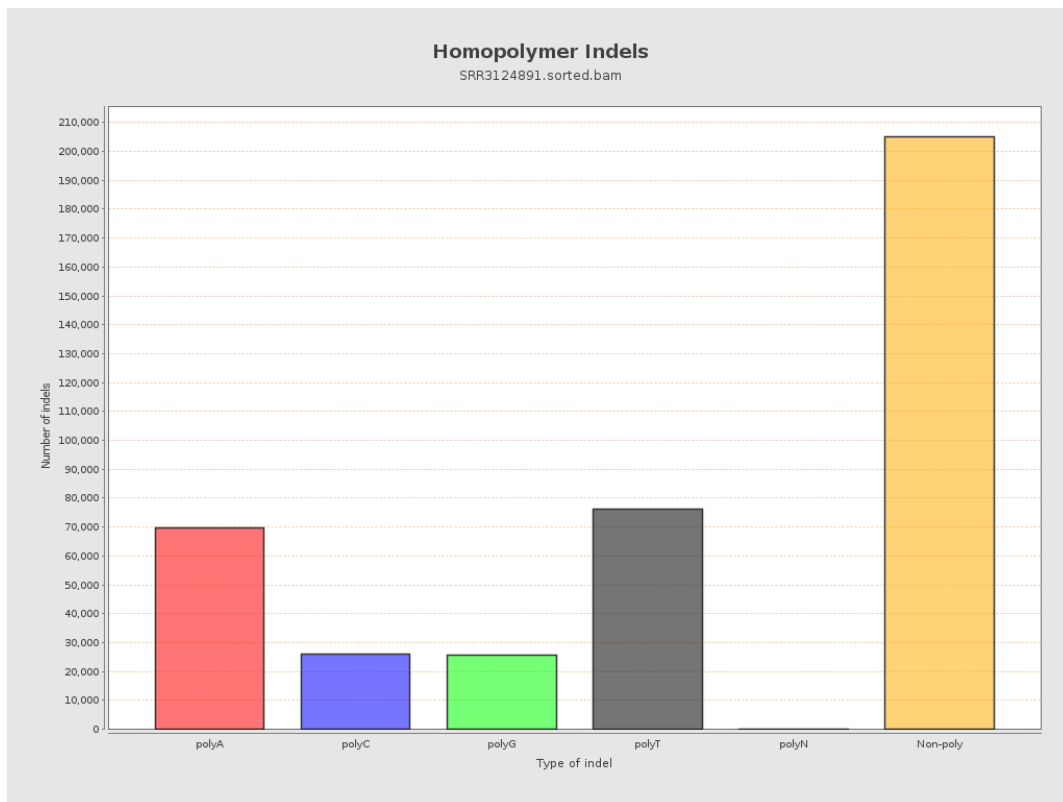
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



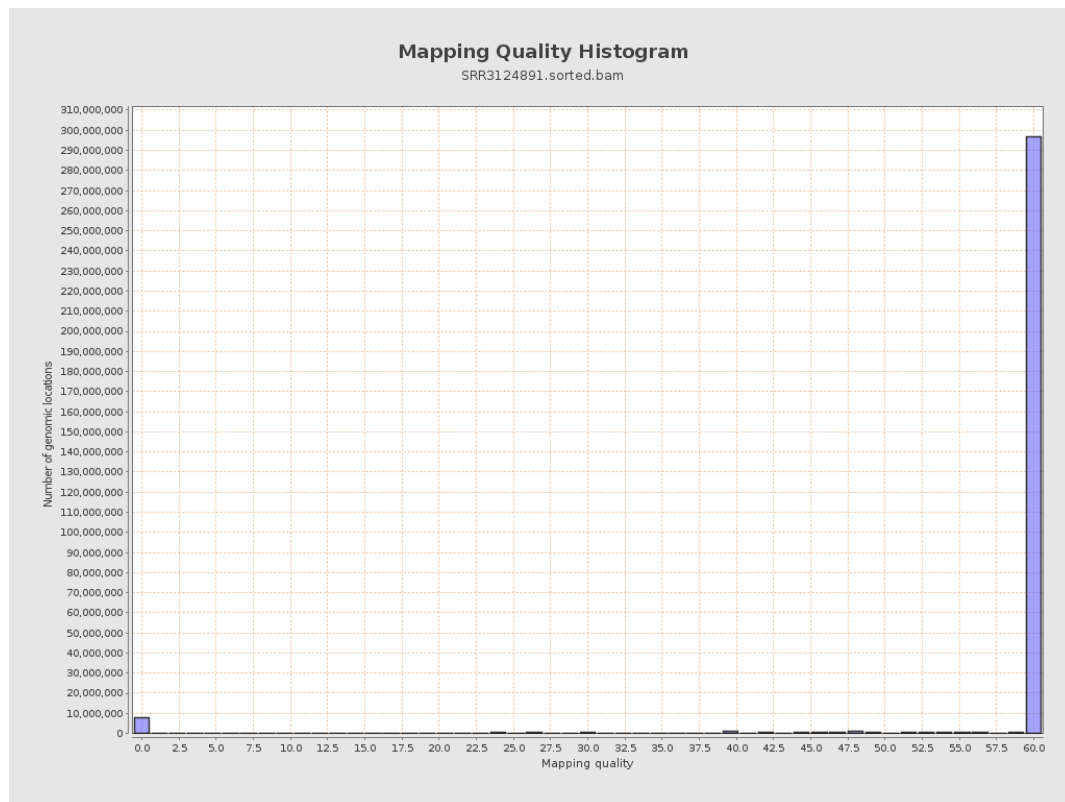
11. Results : Homopolymer Indels



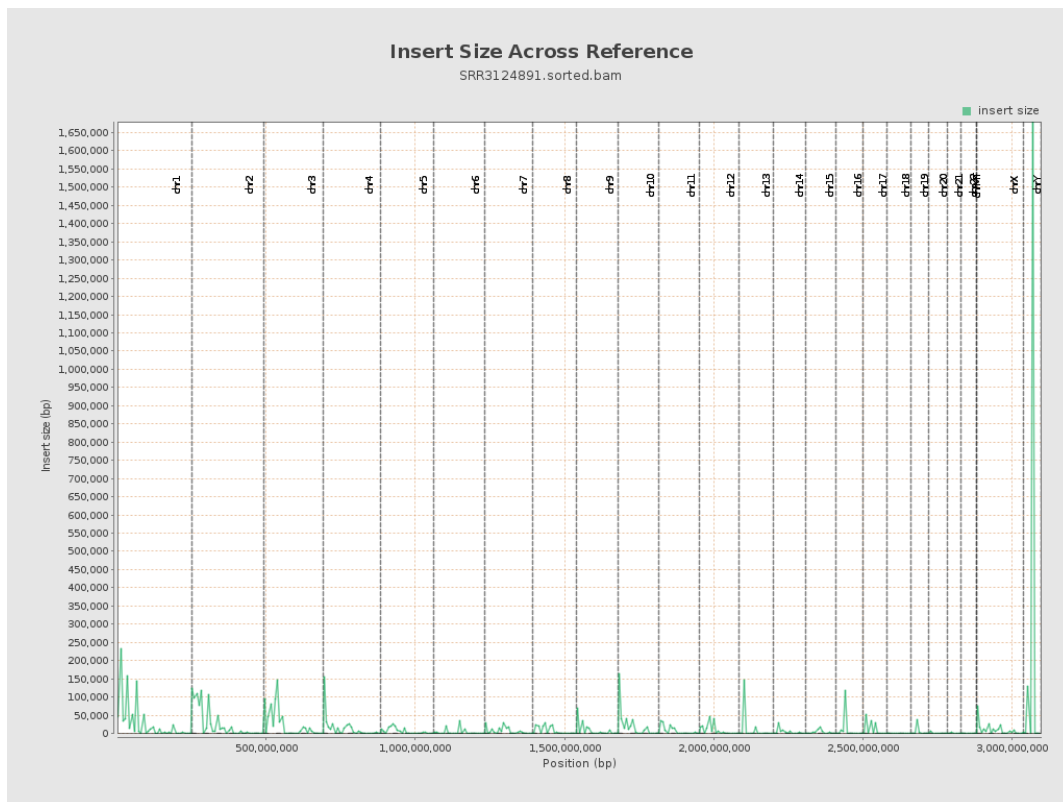
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

