

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 10:00:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038491.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_SRR5038491 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038491_1.fastq.gz SRR5038491_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 10:00:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038491.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,300,066
Mapped reads	10,620,151 / 93.98%
Unmapped reads	679,915 / 6.02%
Mapped paired reads	10,620,151 / 93.98%
Mapped reads, first in pair	5,386,033 / 47.66%
Mapped reads, second in pair	5,234,118 / 46.32%
Mapped reads, both in pair	10,449,312 / 92.47%
Mapped reads, singletons	170,839 / 1.51%
Secondary alignments	0
Supplementary alignments	196,662 / 1.74%
Read min/max/mean length	30 / 150 / 150.88
Duplicated reads (estimated)	1,507,543 / 13.34%
Duplication rate	8.78%
Clipped reads	2,760,184 / 24.43%

2.2. ACGT Content

Number/percentage of A's	437,140,764 / 28.99%
Number/percentage of C's	308,698,759 / 20.48%
Number/percentage of T's	438,753,646 / 29.1%
Number/percentage of G's	323,021,414 / 21.43%
Number/percentage of N's	33,737 / 0%

GC Percentage	41.9%
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2.3. Coverage

Mean	0.4874
Standard Deviation	6.8698

2.4. Mapping Quality

Mean Mapping Quality	53.69
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2.5. Insert size

Mean	84,540.92
Standard Deviation	2,712,849.7
P25/Median/P75	221 / 261 / 313

2.6. Mismatches and indels

General error rate	1.49%
Mismatches	21,600,410
Insertions	292,545
Mapped reads with at least one insertion	2.55%
Deletions	558,534
Mapped reads with at least one deletion	5.02%
Homopolymer indels	45.73%

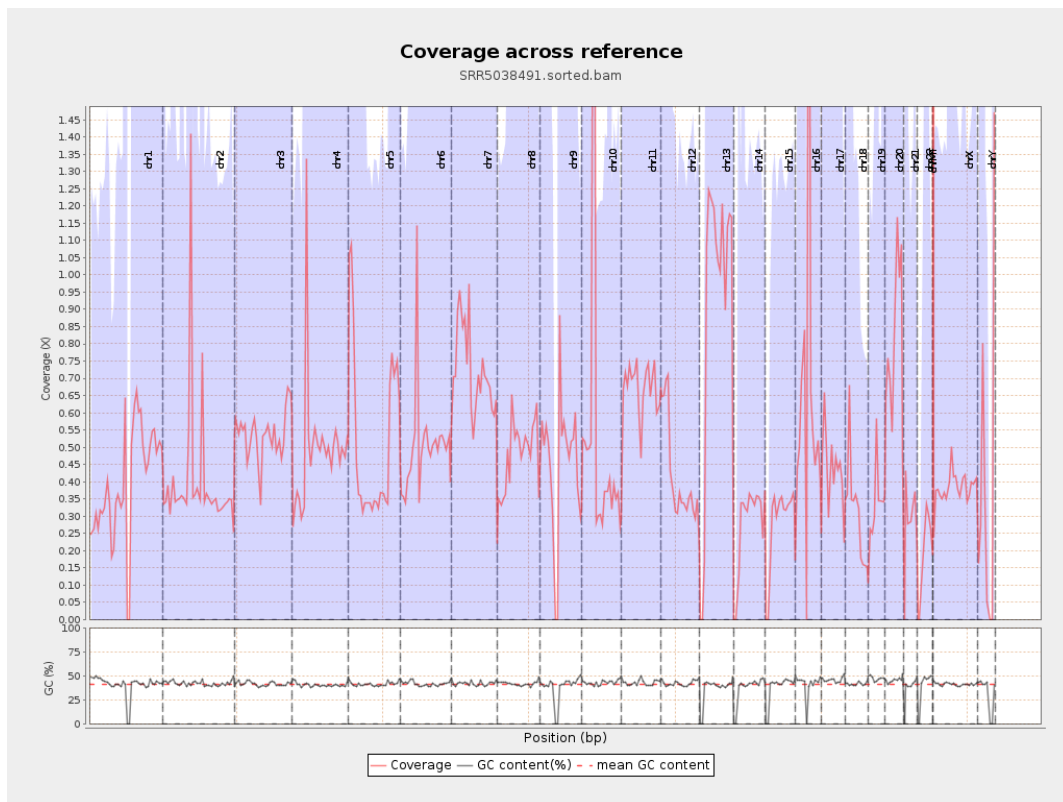
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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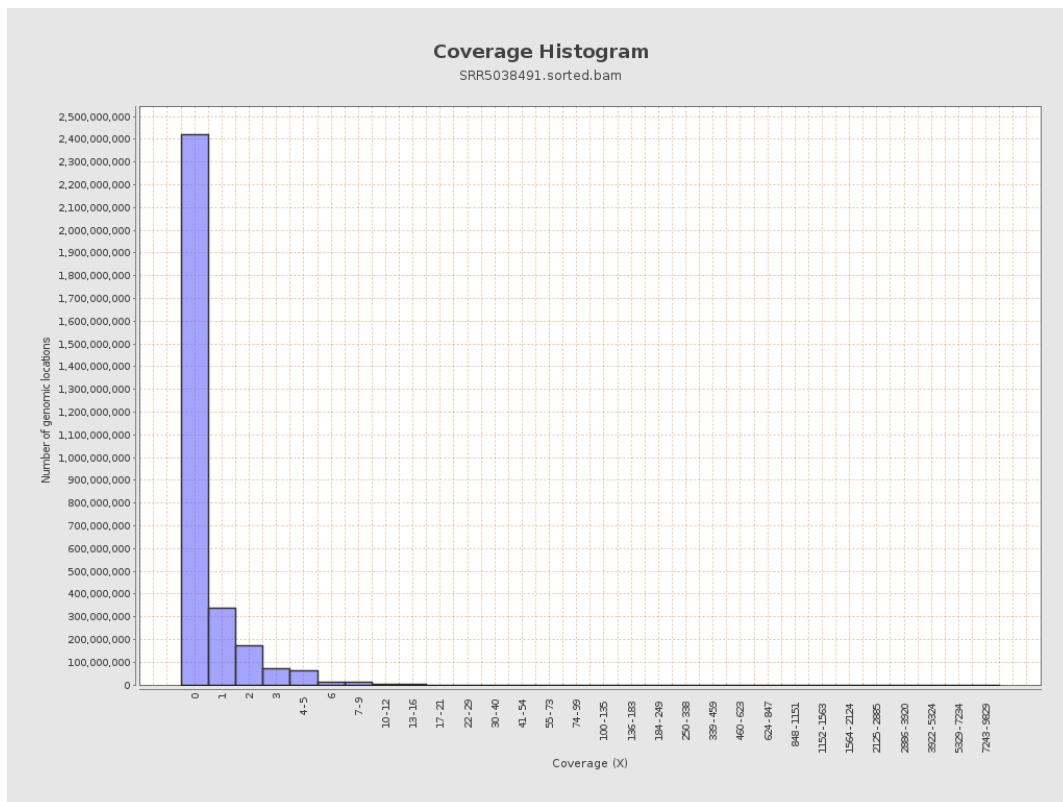
		bases	coverage	deviation
chr1	249250621	98900112	0.3968	5.0286
chr2	243199373	97285300	0.4	7.5113
chr3	198022430	105818160	0.5344	1.2893
chr4	191154276	94395336	0.4938	6.3858
chr5	180915260	92968985	0.5139	1.3856
chr6	171115067	86275840	0.5042	6.9154
chr7	159138663	114809279	0.7214	7.1499
chr8	146364022	70365228	0.4808	1.7805
chr9	141213431	64405184	0.4561	8.8773
chr10	135534747	71064740	0.5243	19.9045
chr11	135006516	90166855	0.6679	4.1169
chr12	133851895	55646539	0.4157	1.1377
chr13	115169878	106798000	0.9273	1.8551
chr14	107349540	29615017	0.2759	1.0502
chr15	102531392	28266835	0.2757	0.8474
chr16	90354753	60938480	0.6744	13.7671
chr17	81195210	36296805	0.447	3.467
chr18	78077248	24540714	0.3143	7.6194
chr19	59128983	19786077	0.3346	2.9946
chr20	63025520	52046618	0.8258	2.5575
chr21	48129895	14114664	0.2933	3.0953
chr22	51304566	9993937	0.1948	0.9572
chrMT	16571	1393152	84.0717	35.4981
chrX	155270560	59232015	0.3815	1.4324

chrY	59373566	23717929	0.3995	11.8461
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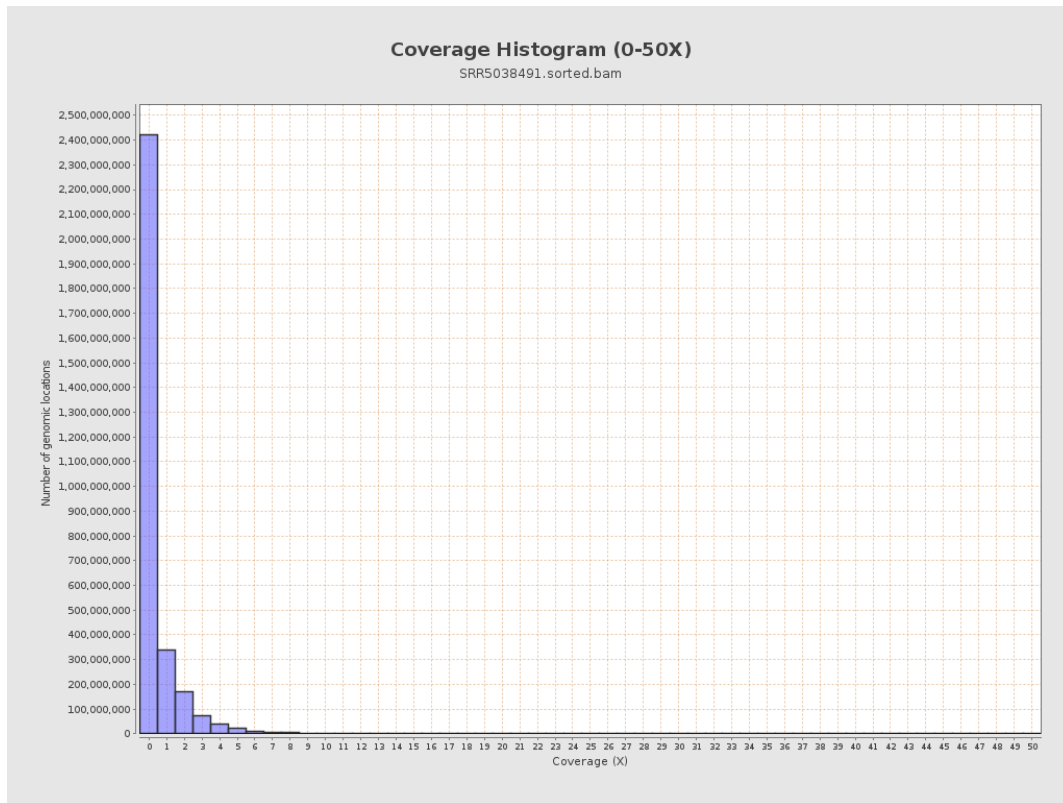
3. Results : Coverage across reference



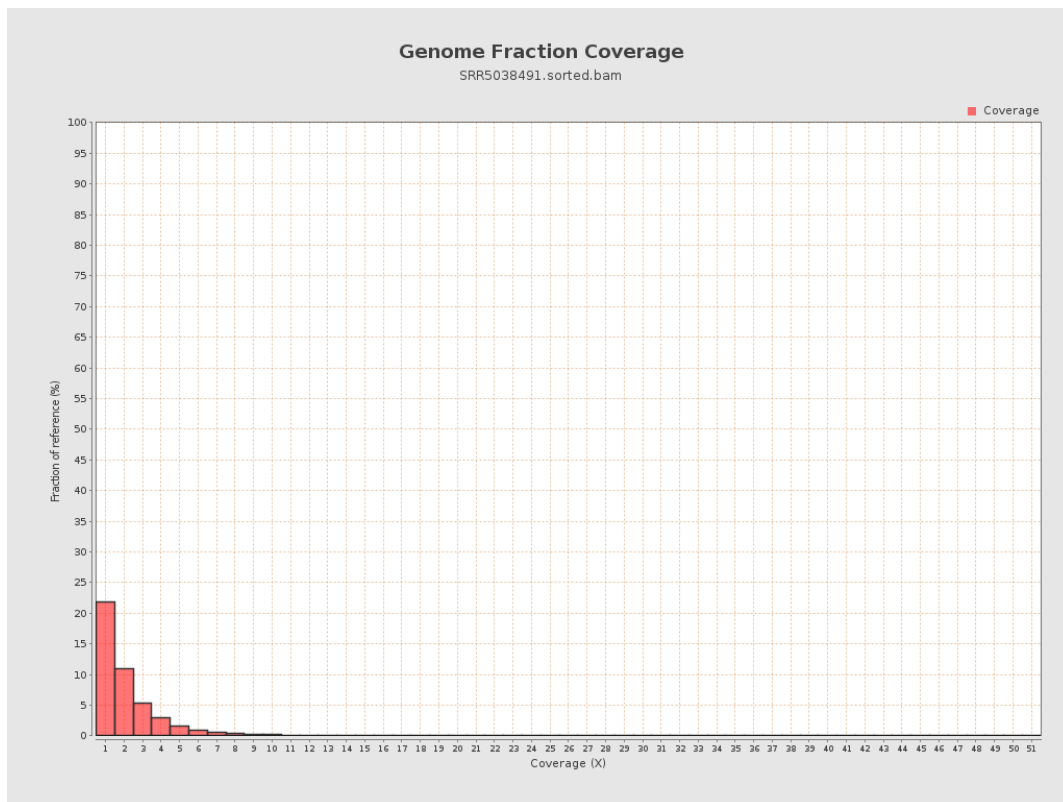
4. Results : Coverage Histogram



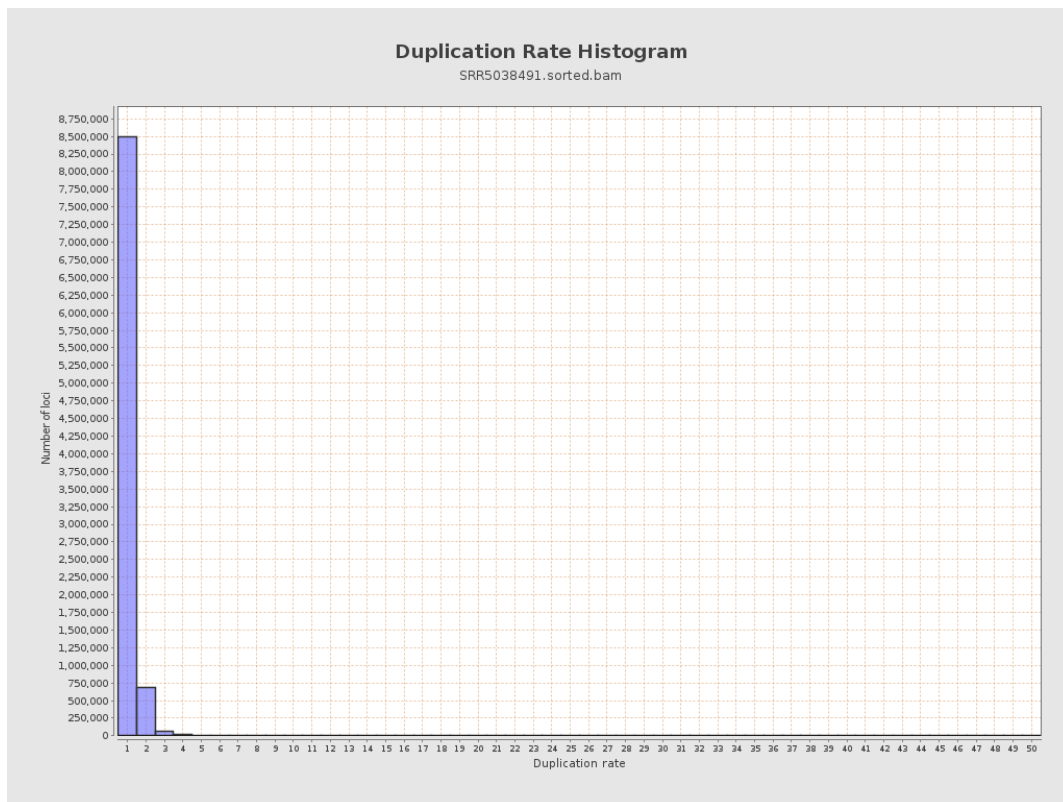
5. Results : Coverage Histogram (0-50X)



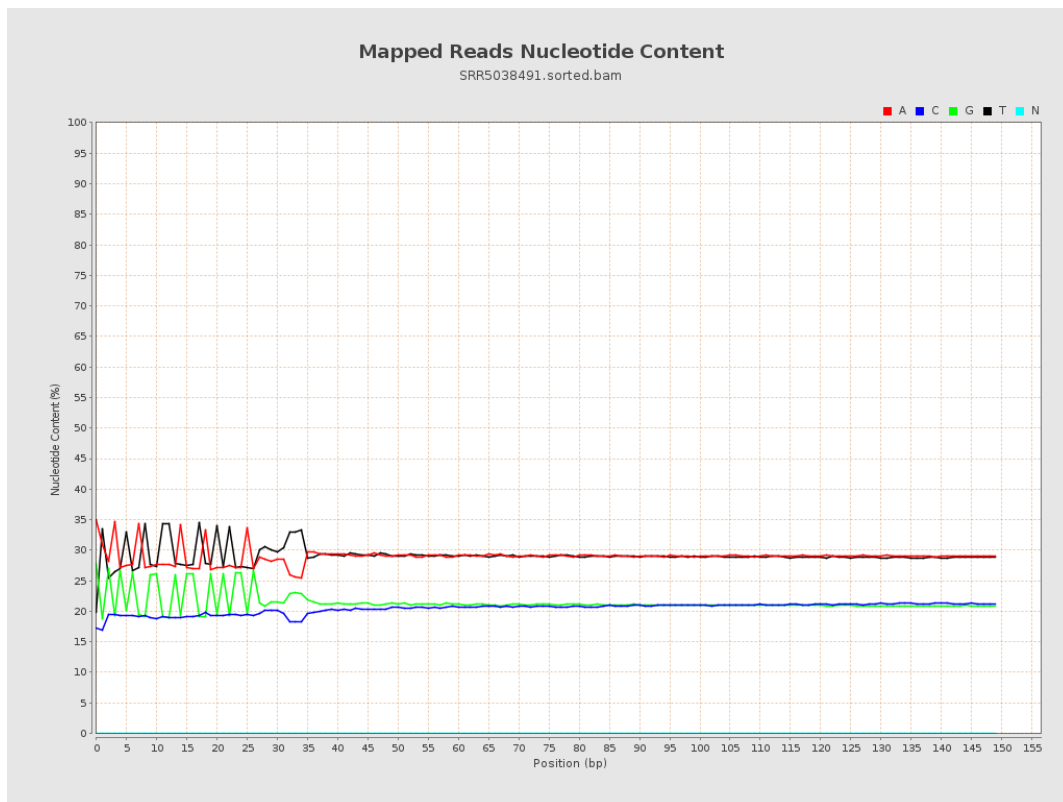
6. Results : Genome Fraction Coverage



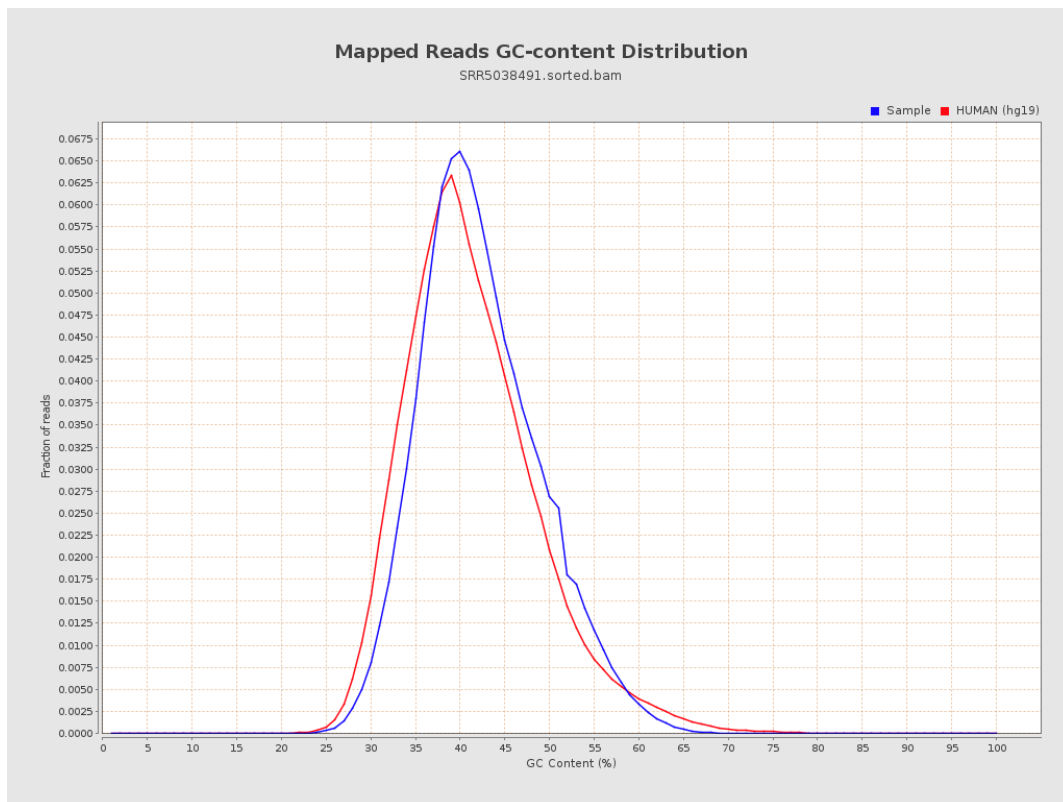
7. Results : Duplication Rate Histogram



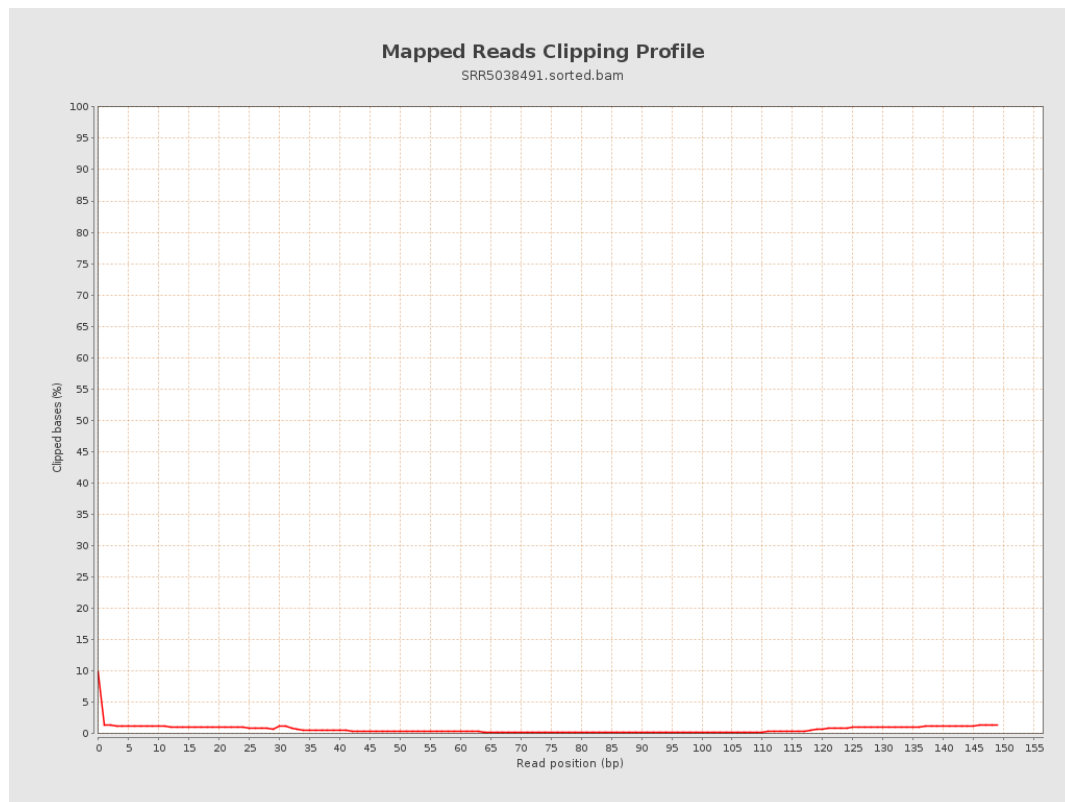
8. Results : Mapped Reads Nucleotide Content



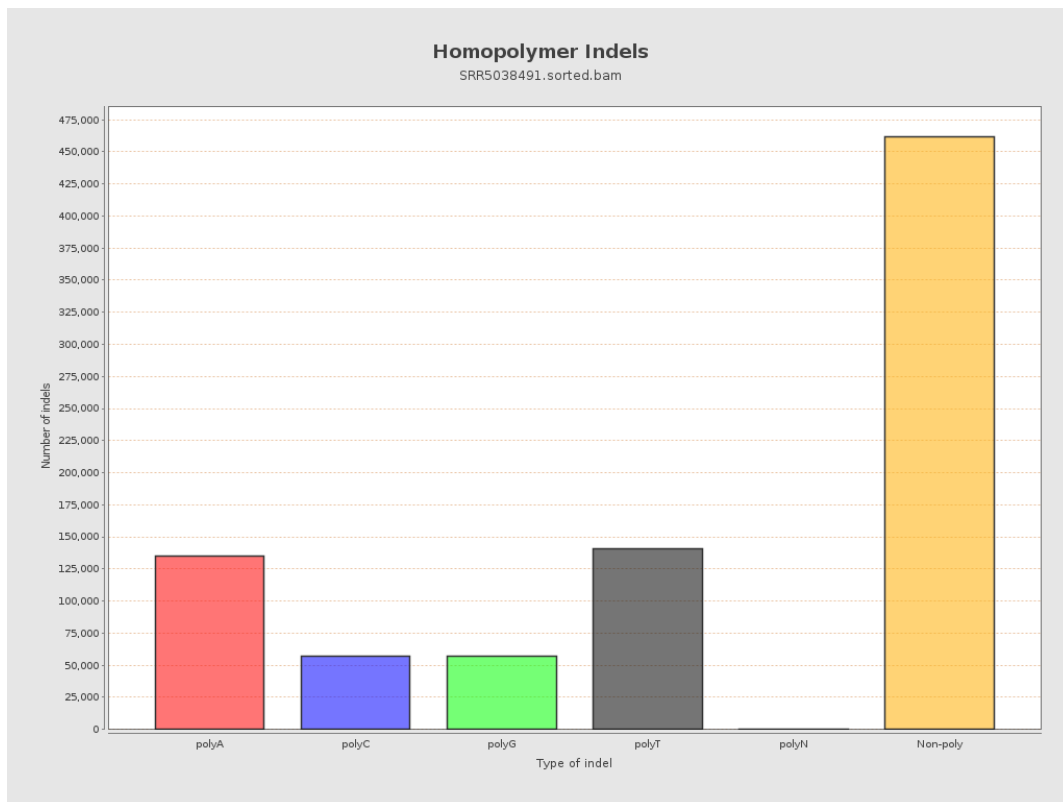
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



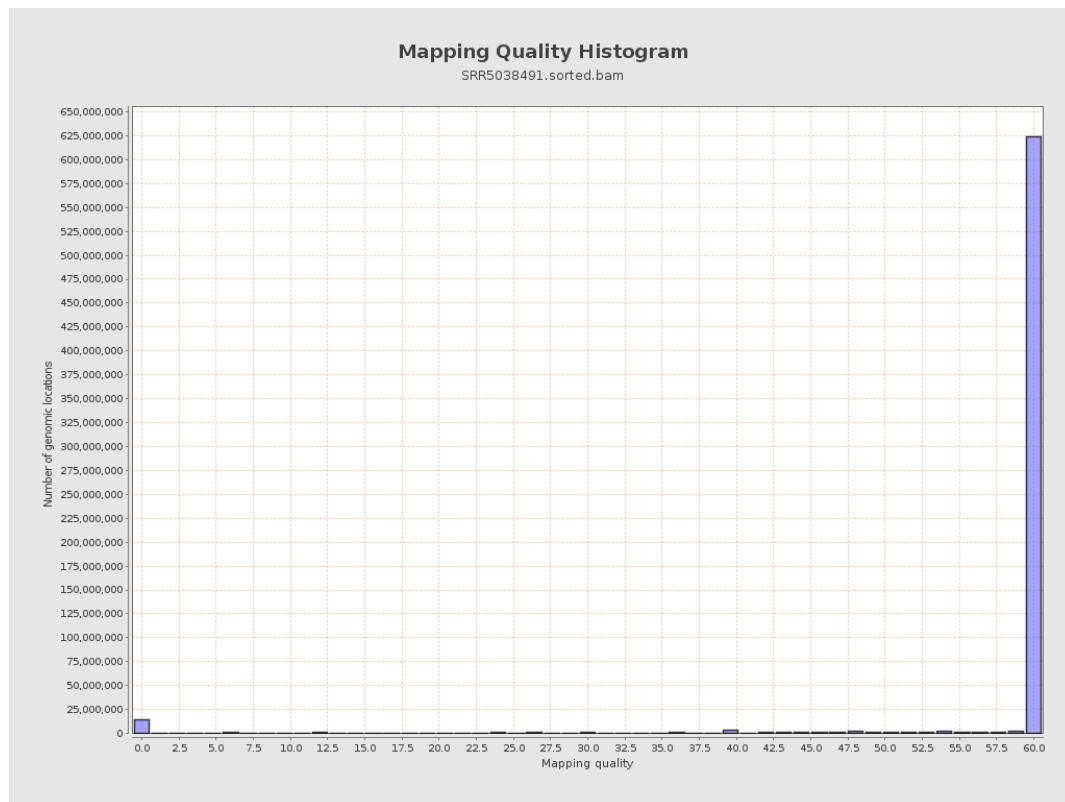
11. Results : Homopolymer Indels



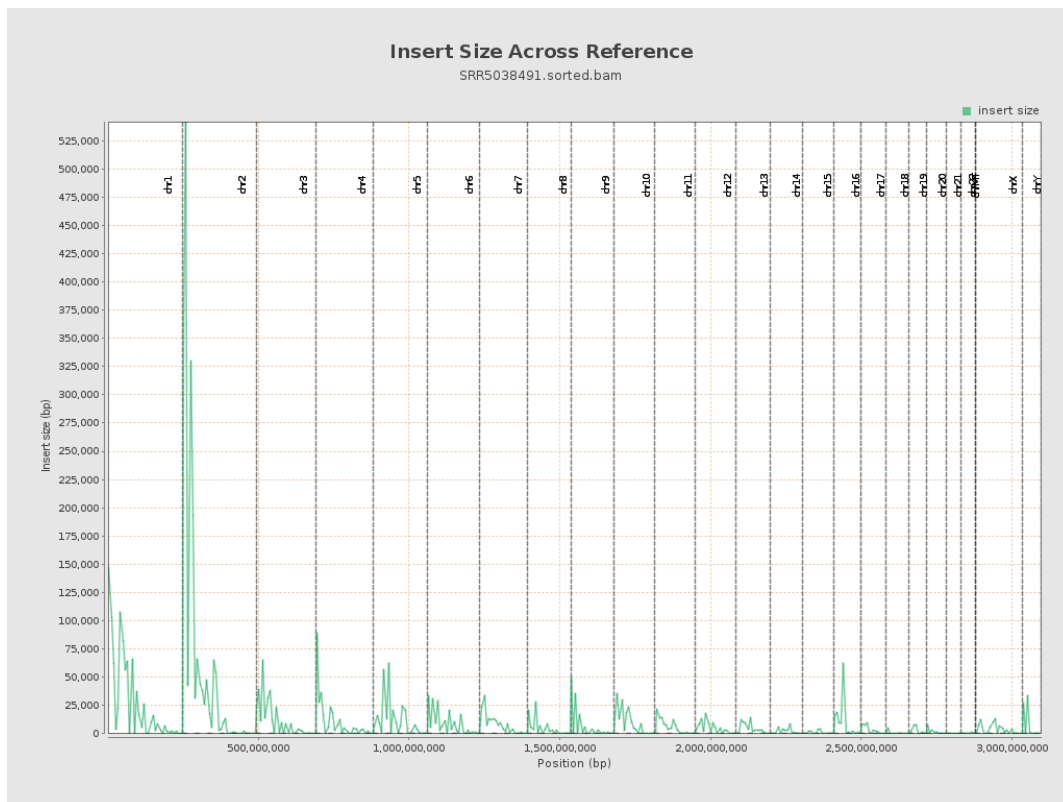
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

