

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 14:19:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038399.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_SRR5038399 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038399_1.fastq.gz SRR5038399_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 14:19:18 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038399.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,698,730
Mapped reads	17,874,388 / 95.59%
Unmapped reads	824,342 / 4.41%
Mapped paired reads	17,874,388 / 95.59%
Mapped reads, first in pair	9,035,503 / 48.32%
Mapped reads, second in pair	8,838,885 / 47.27%
Mapped reads, both in pair	17,622,956 / 94.25%
Mapped reads, singletons	251,432 / 1.34%
Secondary alignments	0
Supplementary alignments	309,401 / 1.65%
Read min/max/mean length	30 / 150 / 150.83
Duplicated reads (estimated)	3,712,761 / 19.86%
Duplication rate	14.52%
Clipped reads	8,317,001 / 44.48%

2.2. ACGT Content

Number/percentage of A's	690,486,529 / 28.6%
Number/percentage of C's	480,336,481 / 19.9%
Number/percentage of T's	703,025,473 / 29.12%
Number/percentage of G's	540,104,870 / 22.37%
Number/percentage of N's	200,802 / 0.01%

GC Percentage	42.27%
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2.3. Coverage

Mean	0.7804
Standard Deviation	11.7919

2.4. Mapping Quality

Mean Mapping Quality	53.53
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2.5. Insert size

Mean	94,746.19
Standard Deviation	2,934,937.36
P25/Median/P75	195 / 243 / 305

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	30,184,908
Insertions	427,868
Mapped reads with at least one insertion	2.27%
Deletions	829,405
Mapped reads with at least one deletion	4.46%
Homopolymer indels	46.83%

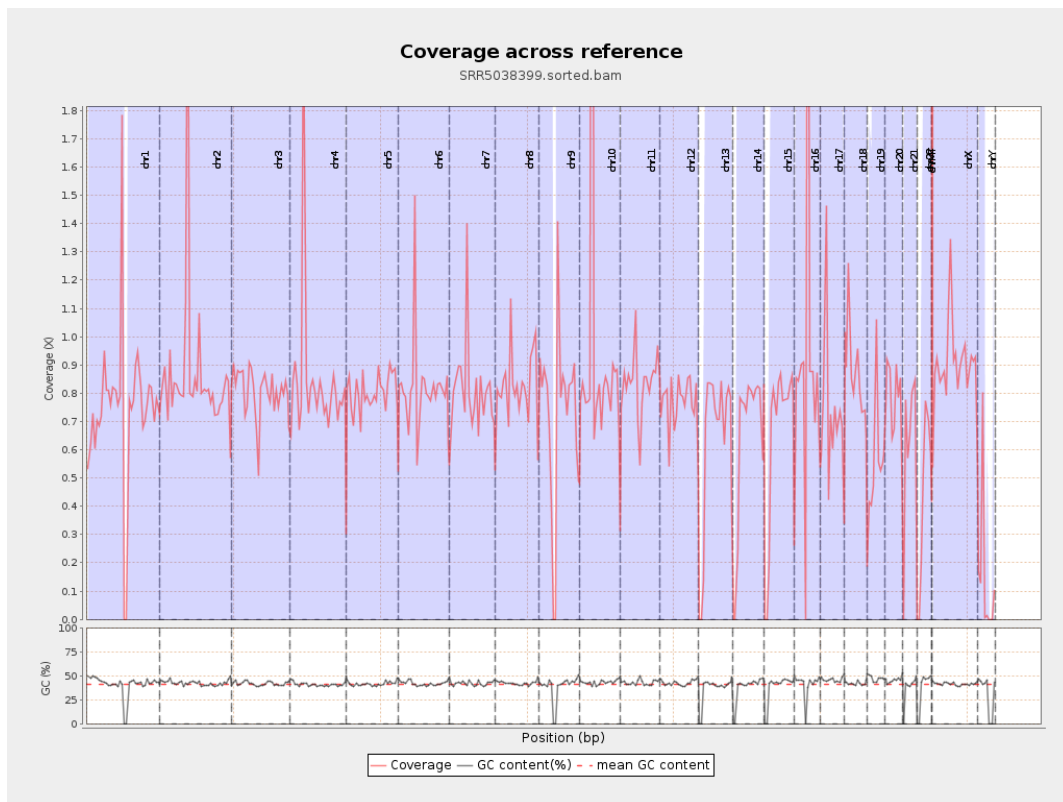
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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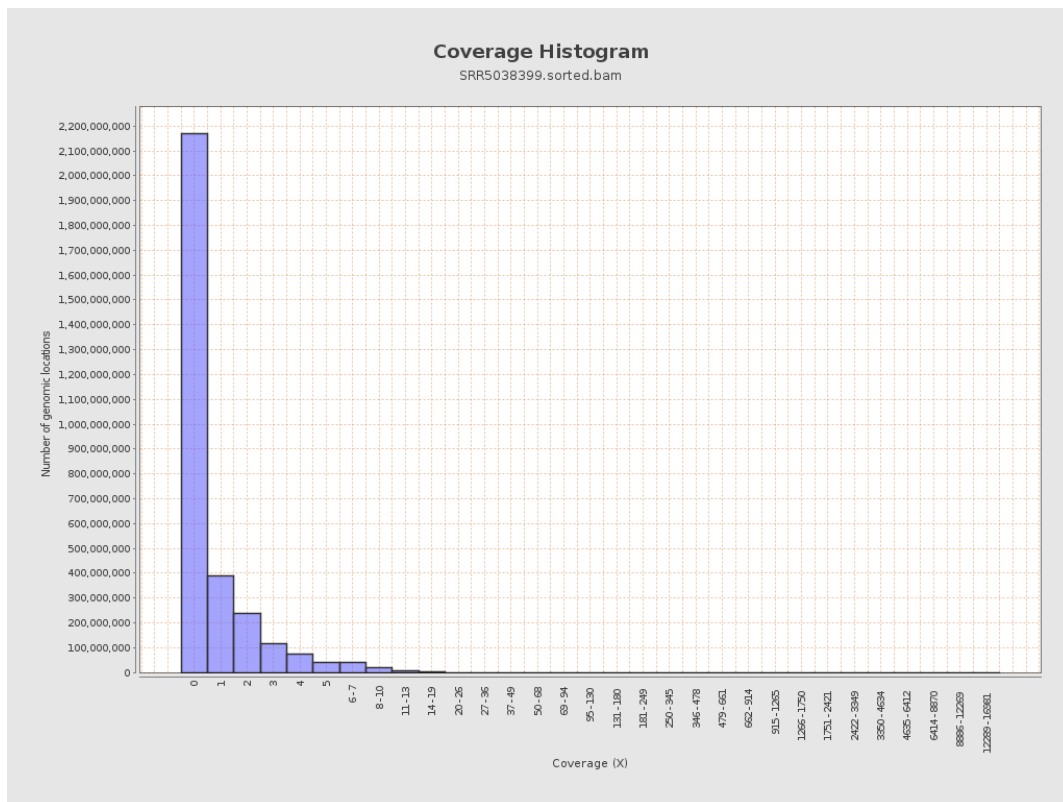
		bases	coverage	deviation
chr1	249250621	185935174	0.746	17.0268
chr2	243199373	212399610	0.8734	11.0654
chr3	198022430	159718199	0.8066	1.8192
chr4	191154276	160440518	0.8393	9.2561
chr5	180915260	144652078	0.7996	1.6718
chr6	171115067	140590339	0.8216	7.8427
chr7	159138663	128180418	0.8055	10.8109
chr8	146364022	121387843	0.8294	3.6147
chr9	141213431	100405701	0.711	16.0416
chr10	135534747	139649342	1.0304	34.692
chr11	135006516	111194434	0.8236	7.2895
chr12	133851895	102656951	0.7669	1.7568
chr13	115169878	73261582	0.6361	1.4587
chr14	107349540	68375941	0.6369	1.654
chr15	102531392	65955067	0.6433	1.4912
chr16	90354753	87147286	0.9645	18.334
chr17	81195210	58679206	0.7227	12.1442
chr18	78077248	68094799	0.8721	12.9441
chr19	59128983	32604372	0.5514	8.2418
chr20	63025520	49150624	0.7799	3.0605
chr21	48129895	30552408	0.6348	4.5003
chr22	51304566	22608171	0.4407	1.3005
chrMT	16571	2924154	176.4621	97.9689
chrX	155270560	140231494	0.9031	3.8788

chrY	59373566	9051295	0.1524	11.5066
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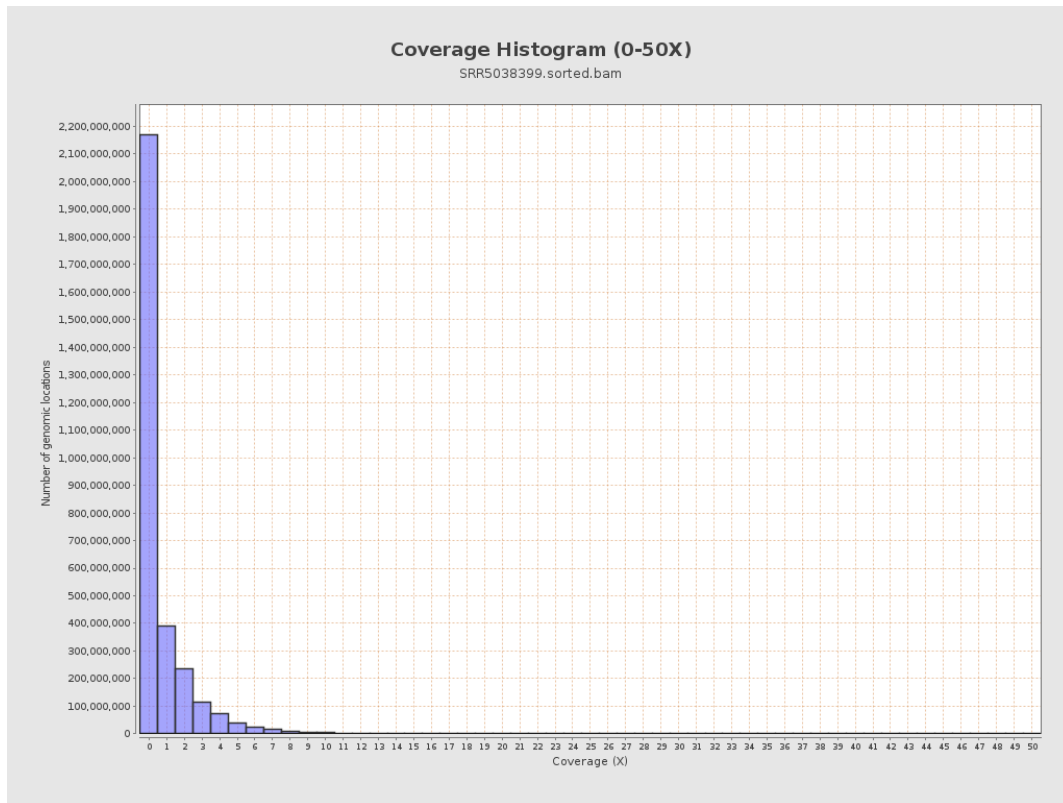
3. Results : Coverage across reference



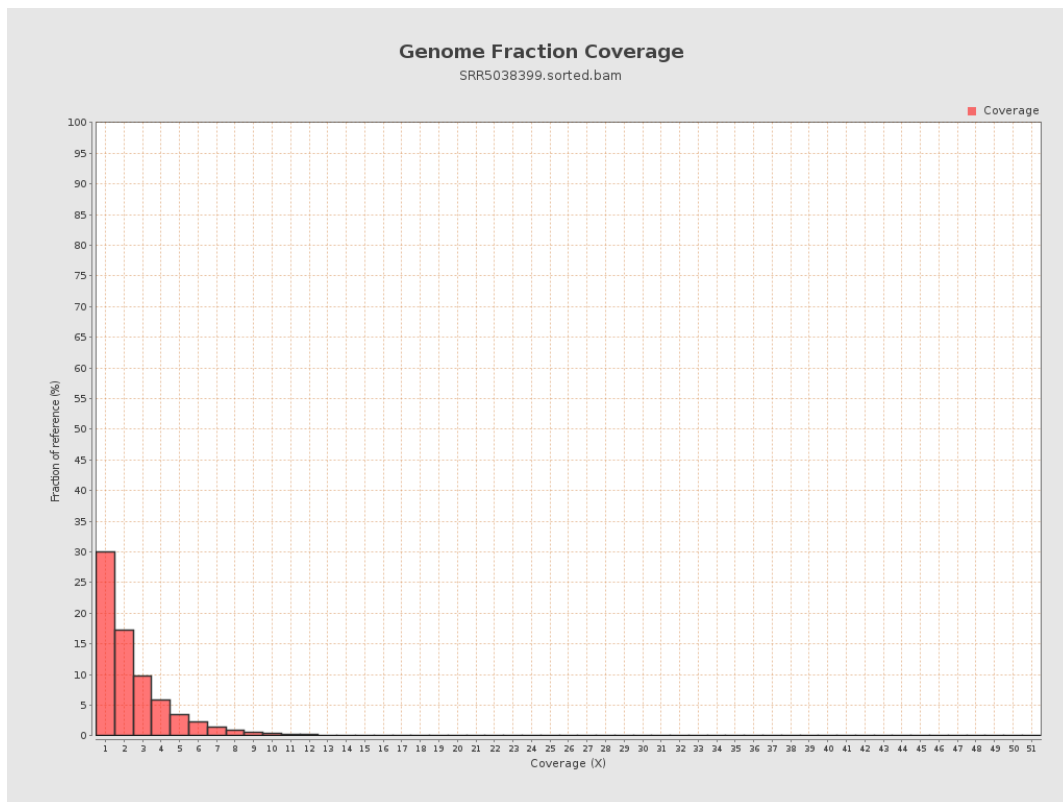
4. Results : Coverage Histogram



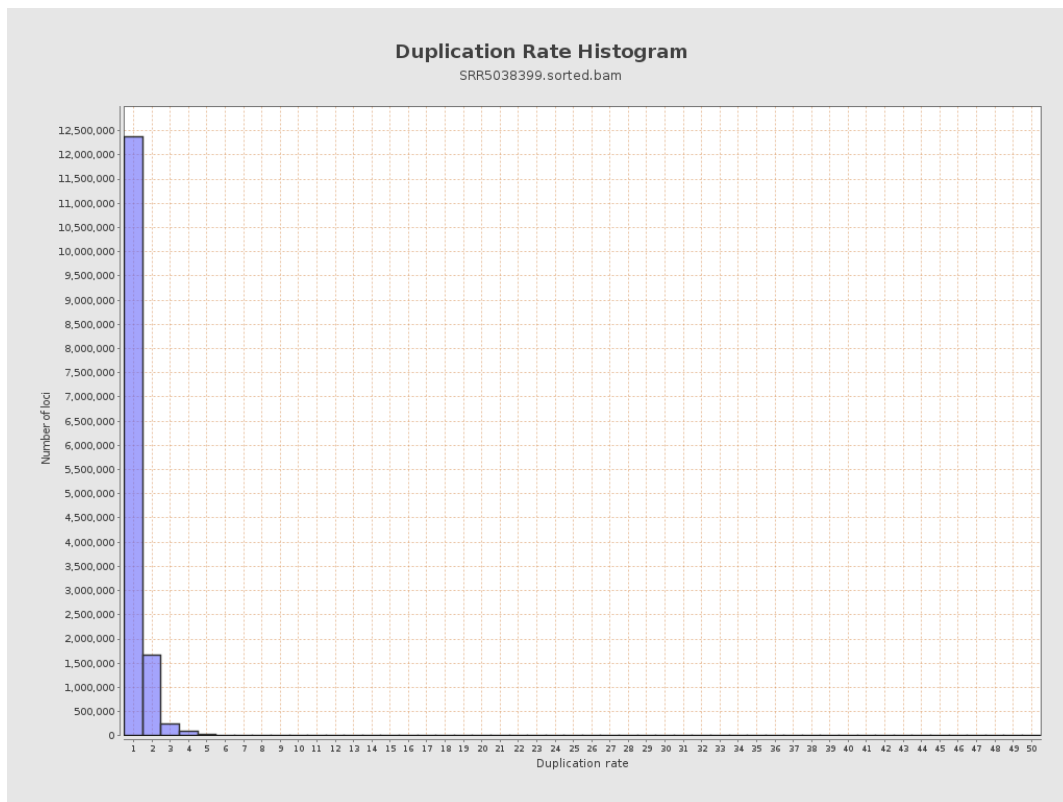
5. Results : Coverage Histogram (0-50X)



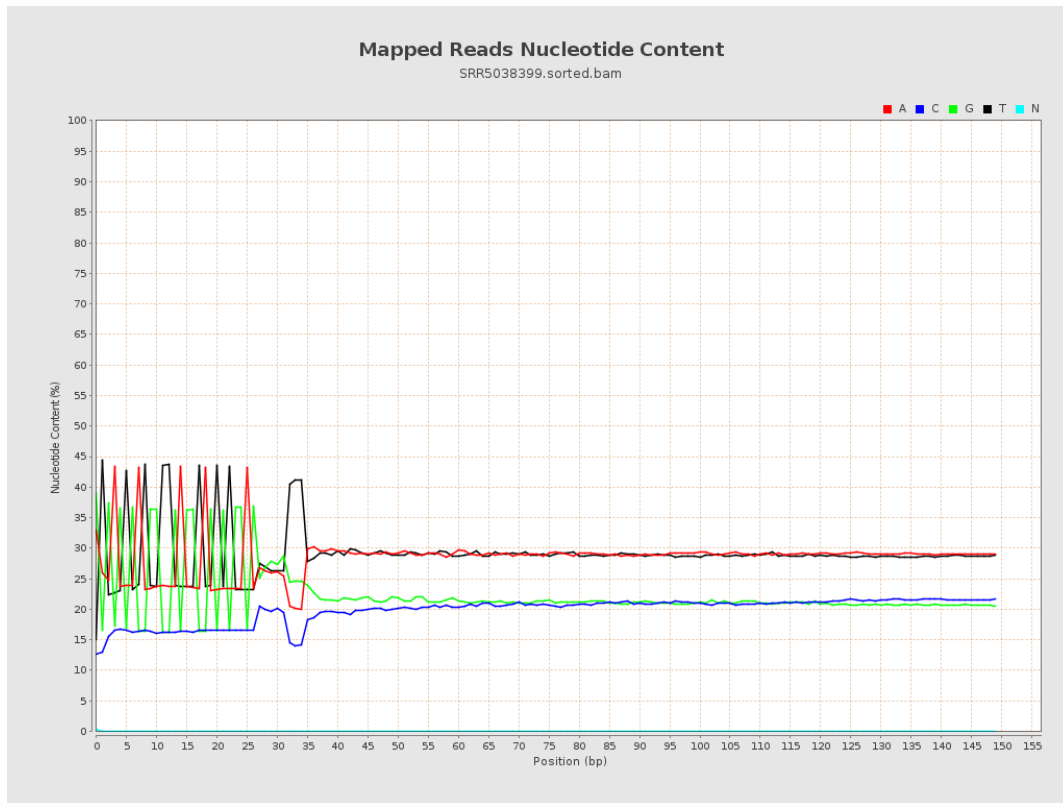
6. Results : Genome Fraction Coverage



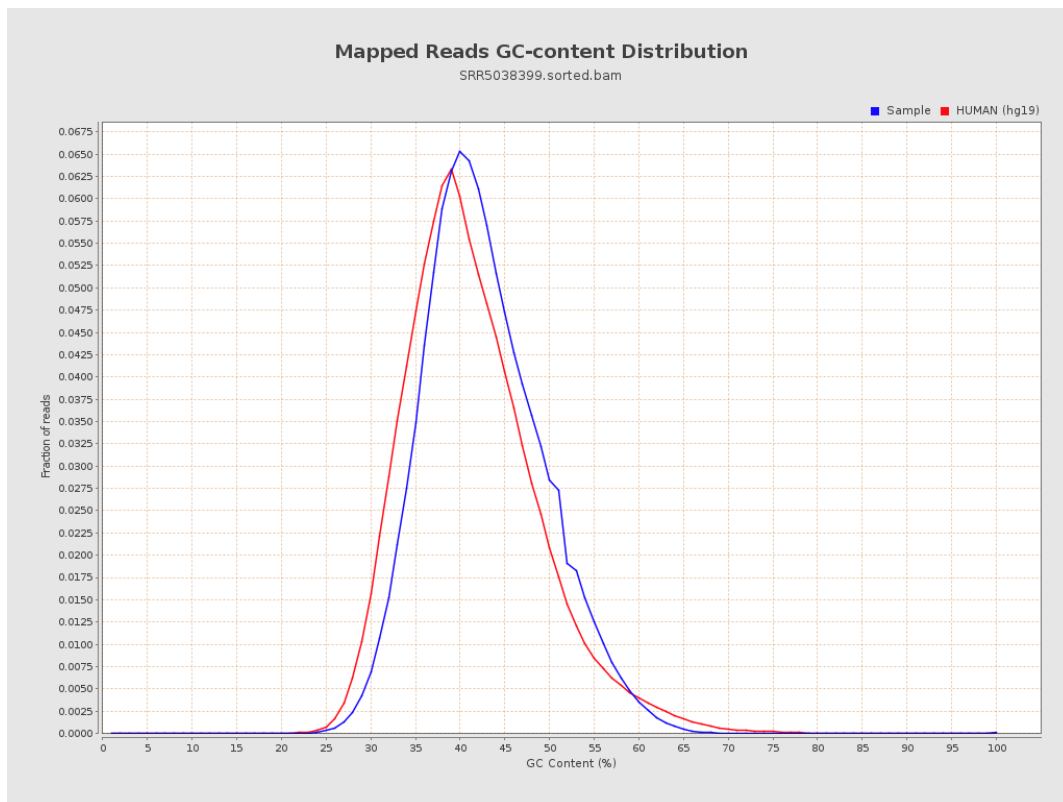
7. Results : Duplication Rate Histogram



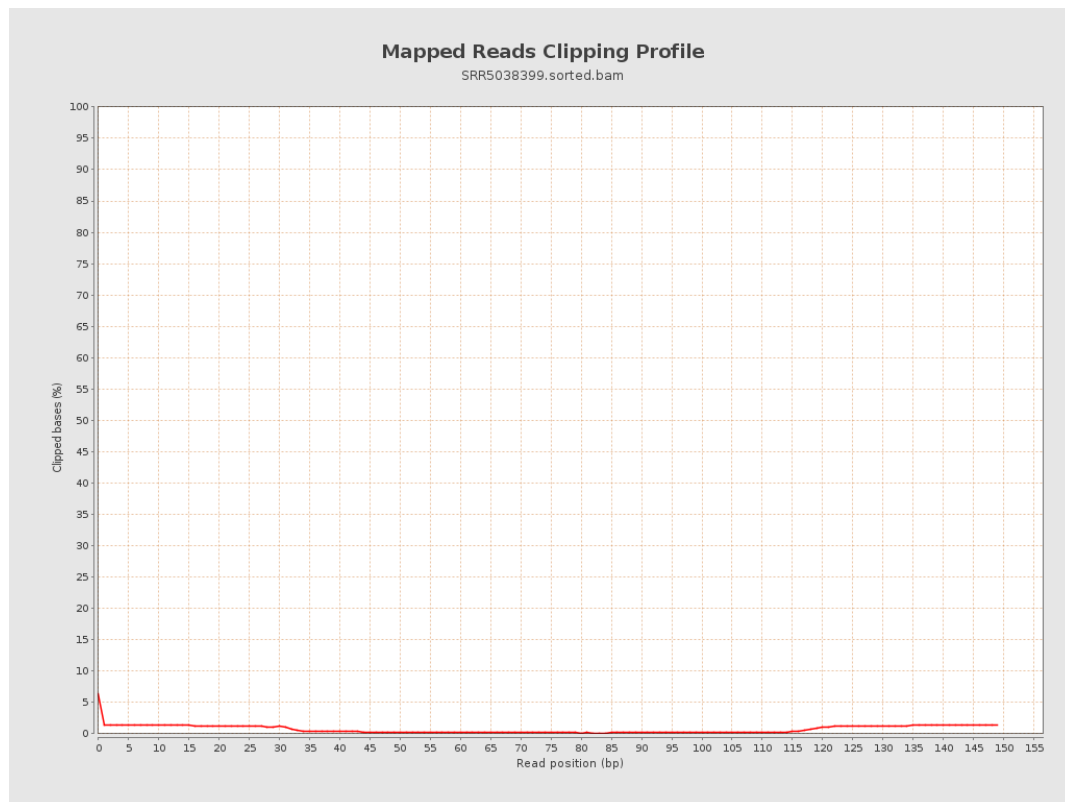
8. Results : Mapped Reads Nucleotide Content



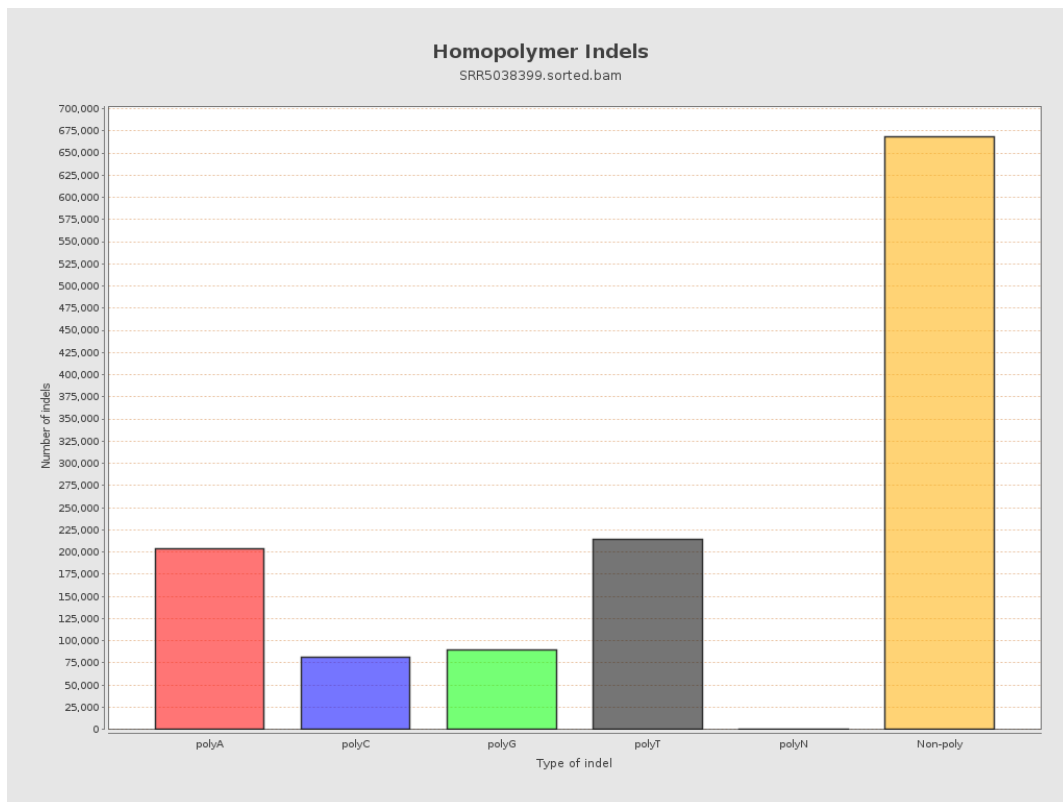
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



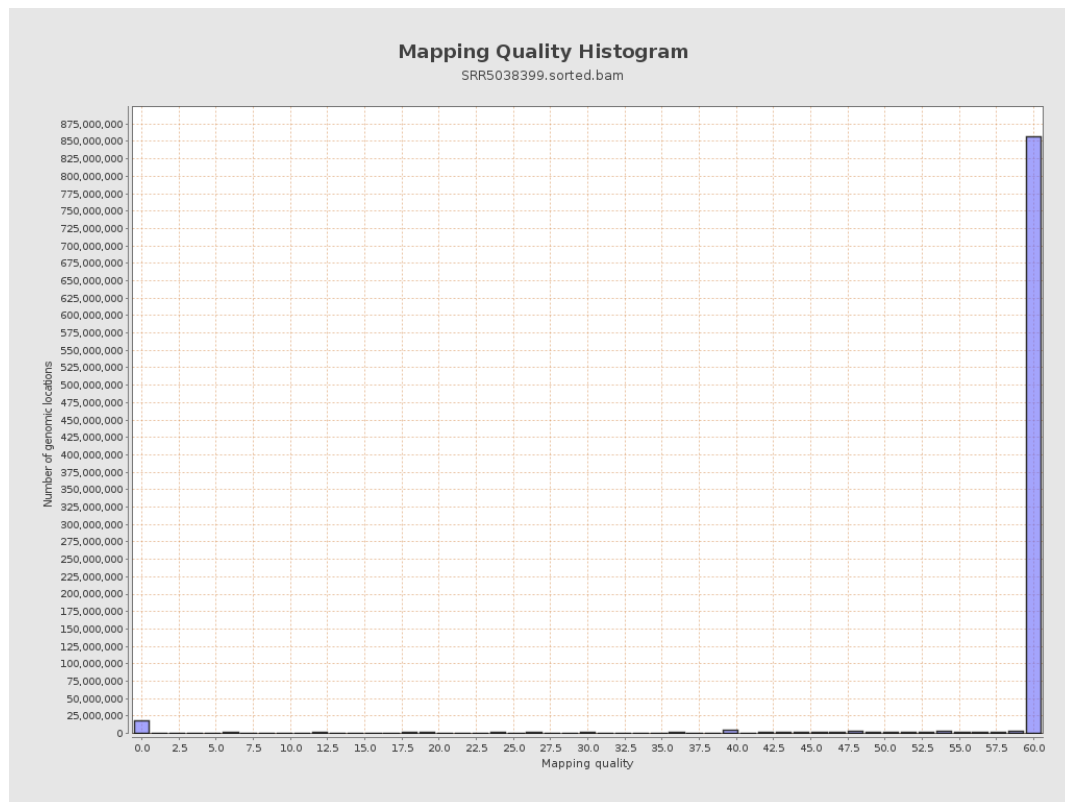
11. Results : Homopolymer Indels



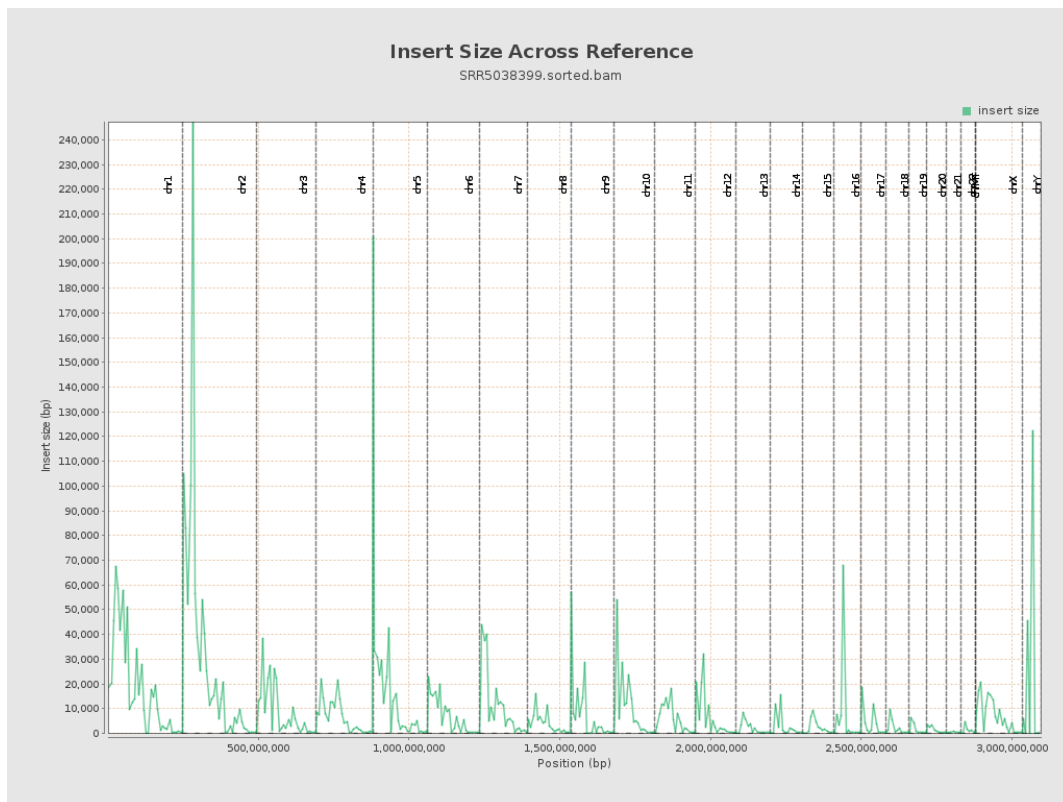
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

