

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 02:48:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438280.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_SRR8438280 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438280_1.fastq.gz SRR8438280_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 02:48:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438280.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	705,171,500
Mapped reads	702,961,073 / 99.69%
Unmapped reads	2,210,427 / 0.31%
Mapped paired reads	702,961,073 / 99.69%
Mapped reads, first in pair	351,500,433 / 49.85%
Mapped reads, second in pair	351,460,640 / 49.84%
Mapped reads, both in pair	701,421,586 / 99.47%
Mapped reads, singletons	1,539,487 / 0.22%
Secondary alignments	0
Supplementary alignments	11,009,744 / 1.56%
Read min/max/mean length	28 / 151 / 144.8
Duplicated reads (estimated)	377,075,734 / 53.47%
Duplication rate	50.81%
Clipped reads	132,104,100 / 18.73%

2.2. ACGT Content

Number/percentage of A's	30,518,178,542 / 30.26%
Number/percentage of C's	20,146,070,644 / 19.98%
Number/percentage of T's	29,222,445,984 / 28.98%
Number/percentage of G's	20,965,879,826 / 20.79%
Number/percentage of N's	623,193 / 0%

GC Percentage	40.76%
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2.3. Coverage

Mean	32.5872
Standard Deviation	72.7164

2.4. Mapping Quality

Mean Mapping Quality	55.07
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2.5. Insert size

Mean	37,435.1
Standard Deviation	1,874,937.15
P25/Median/P75	175 / 225 / 294

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	513,691,917
Insertions	12,411,716
Mapped reads with at least one insertion	1.74%
Deletions	11,048,265
Mapped reads with at least one deletion	1.55%
Homopolymer indels	48.24%

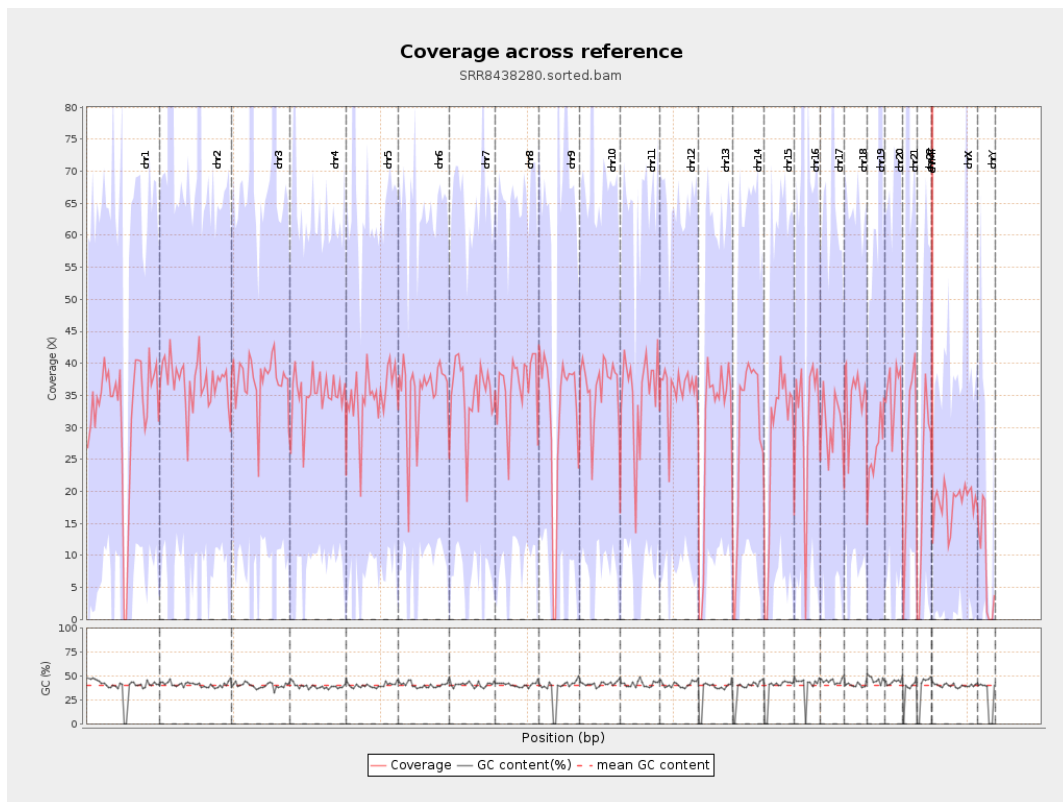
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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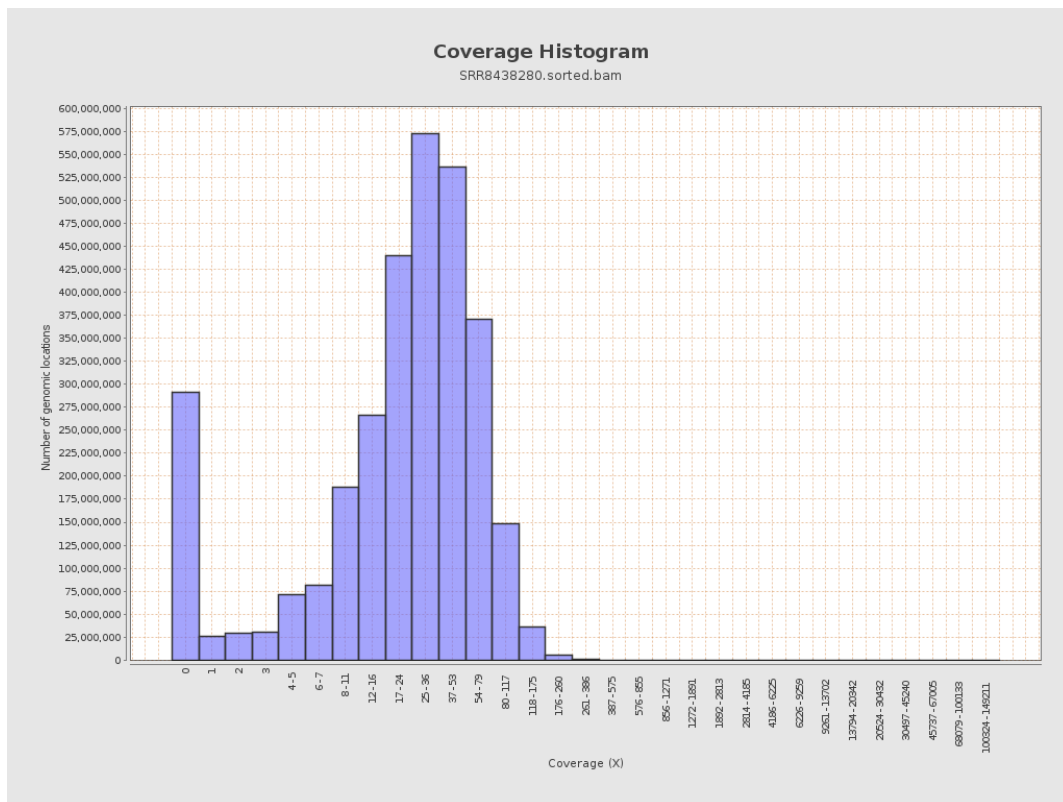
		bases	coverage	deviation
chr1	249250621	8120434657	32.5794	31.12
chr2	243199373	9025421816	37.1112	132.8651
chr3	198022430	7440355800	37.5733	162.7871
chr4	191154276	6736878902	35.2432	28.075
chr5	180915260	6298568598	34.815	32.4336
chr6	171115067	6119514190	35.7626	28.5521
chr7	159138663	5599037229	35.1834	29.8172
chr8	146364022	5347161917	36.5333	28.3554
chr9	141213431	4500870965	31.8728	34.899
chr10	135534747	4936135004	36.4197	36.3404
chr11	135006516	4763784151	35.2856	28.8455
chr12	133851895	4811359016	35.9454	28.277
chr13	115169878	3477380606	30.1935	27.4872
chr14	107349540	3197027962	29.7815	29.811
chr15	102531392	2884505116	28.1329	30.2946
chr16	90354753	2787585344	30.8516	51.2213
chr17	81195210	2441833933	30.0736	37.0472
chr18	78077248	2756176937	35.3006	28.727
chr19	59128983	1564120164	26.4527	241.9113
chr20	63025520	2199735102	34.9023	31.7451
chr21	48129895	1342499179	27.8932	72.4461
chr22	51304566	1106254771	21.5625	28.7473
chrMT	16571	86524259	5,221.4265	2,065.9709
chrX	155270560	2847004308	18.3358	26.4552

chrY	59373566	489853635	8.2504	25.9471
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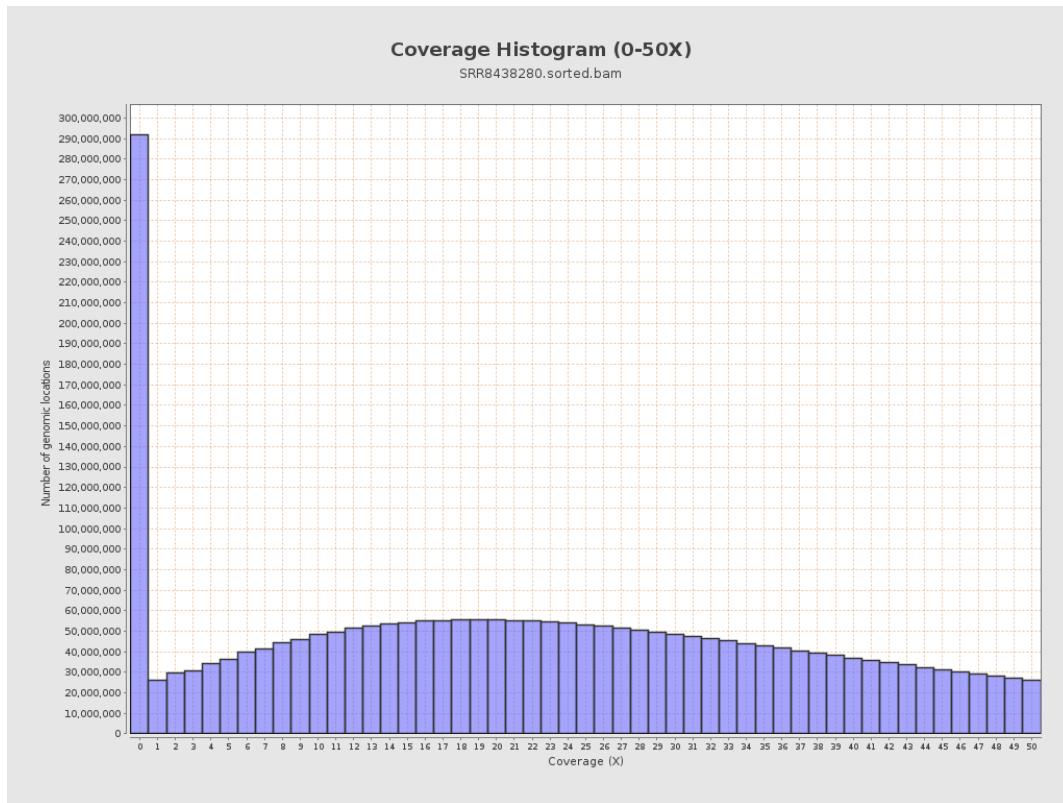
3. Results : Coverage across reference



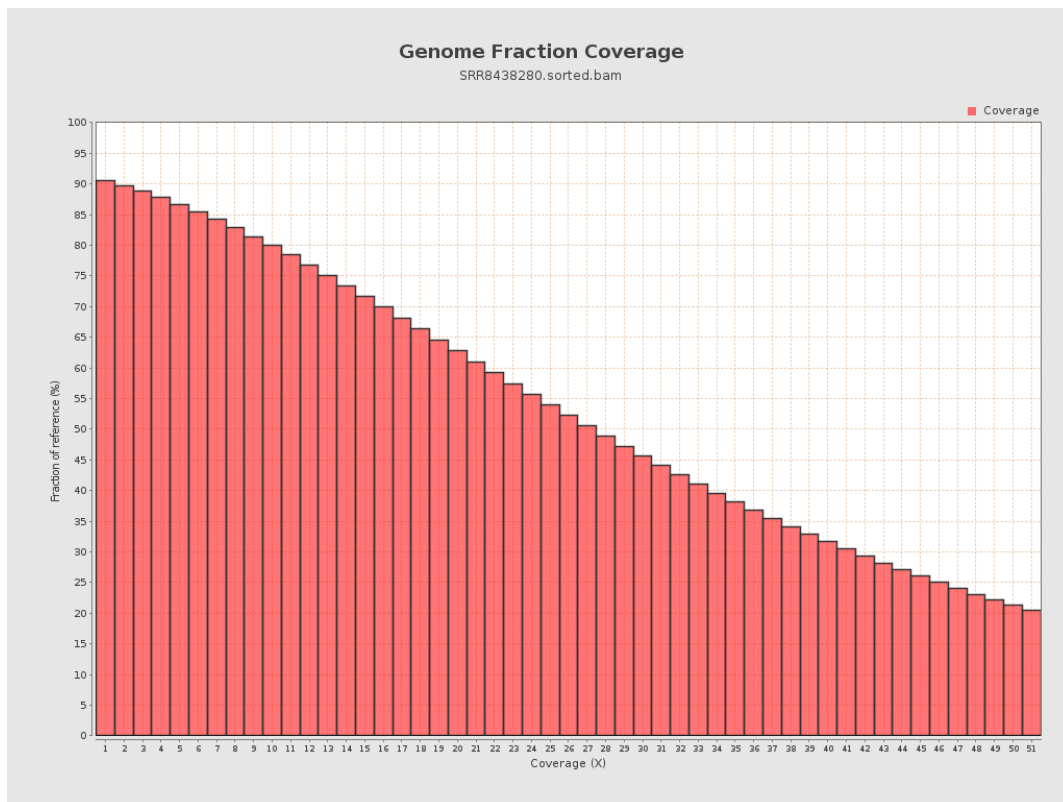
4. Results : Coverage Histogram



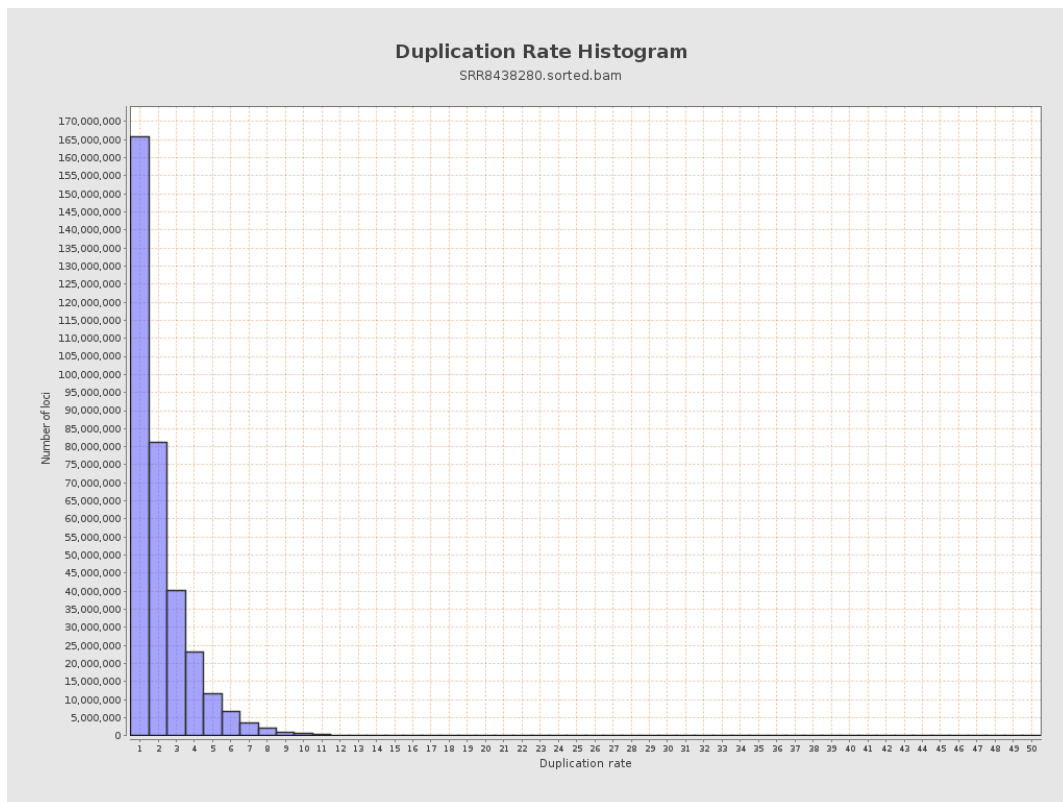
5. Results : Coverage Histogram (0-50X)



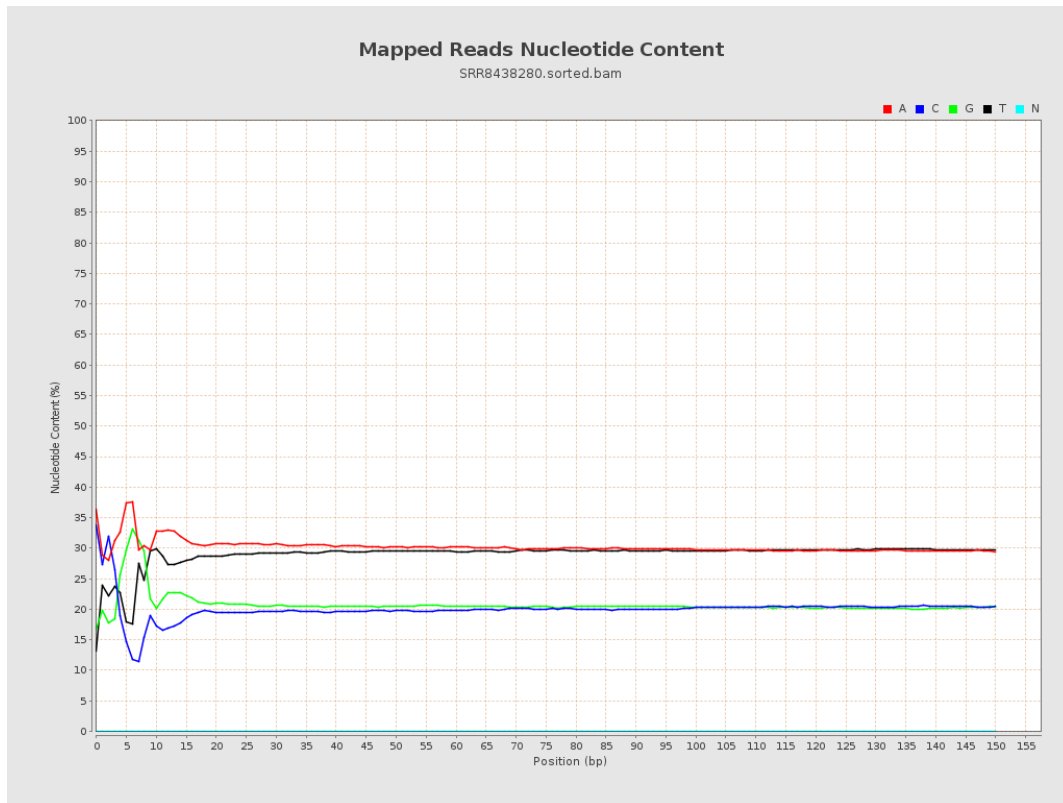
6. Results : Genome Fraction Coverage



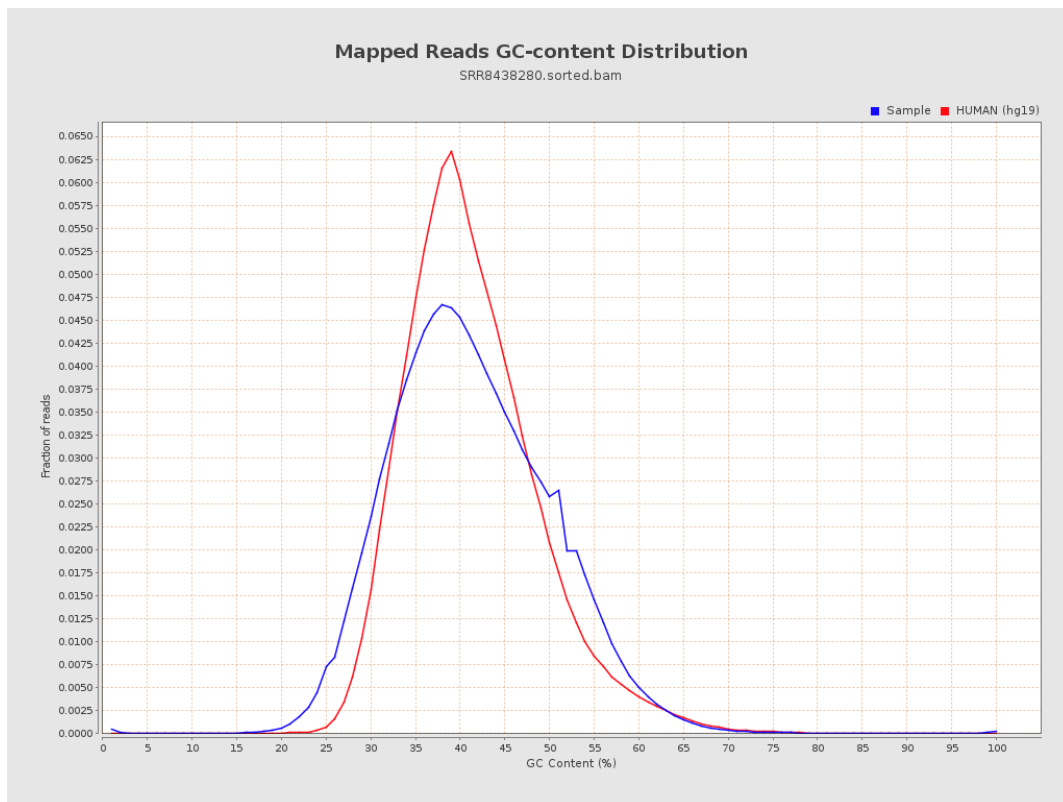
7. Results : Duplication Rate Histogram



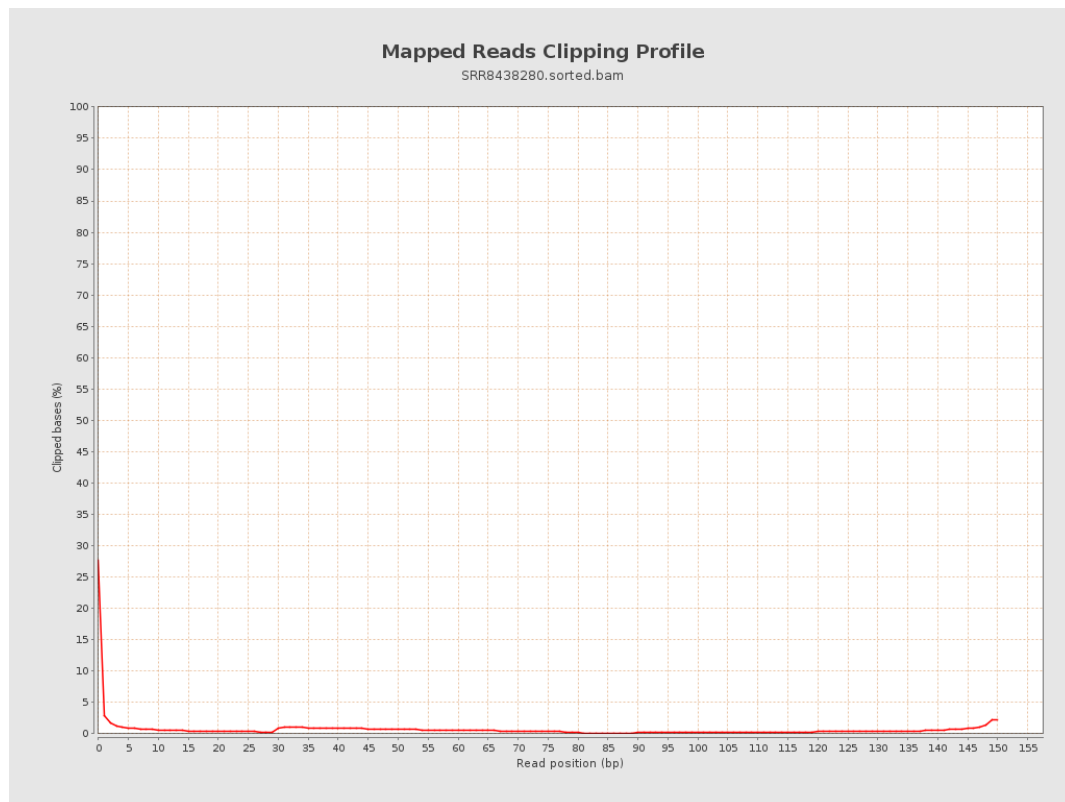
8. Results : Mapped Reads Nucleotide Content



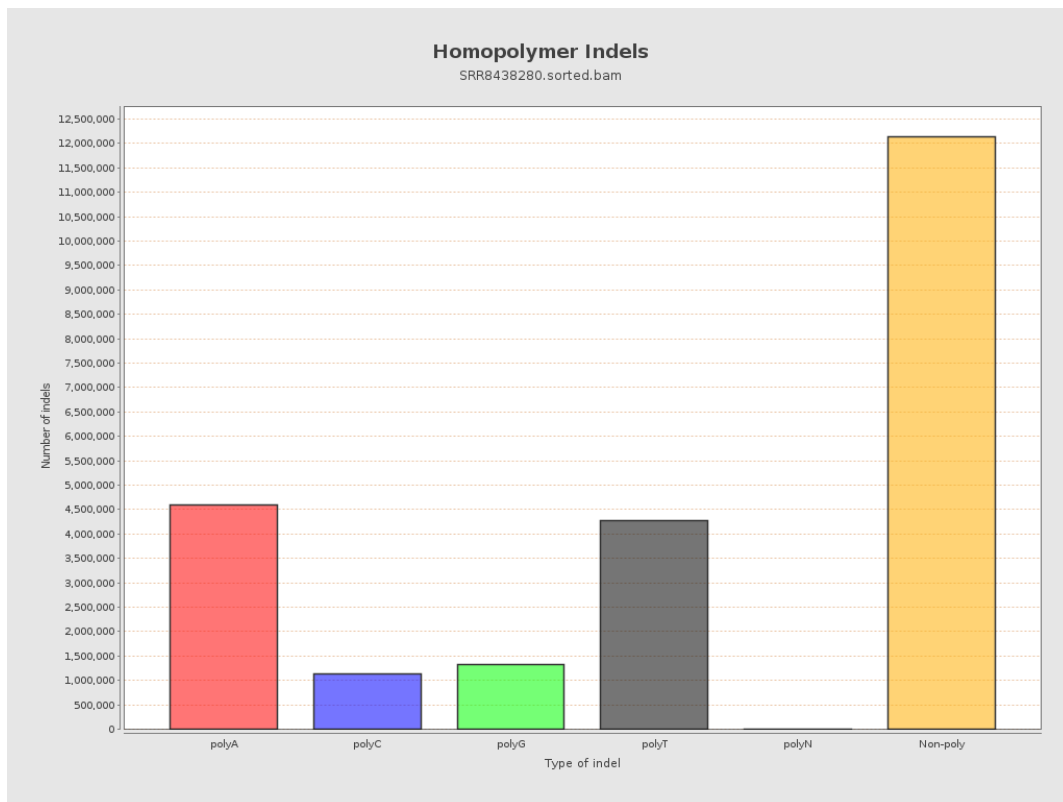
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



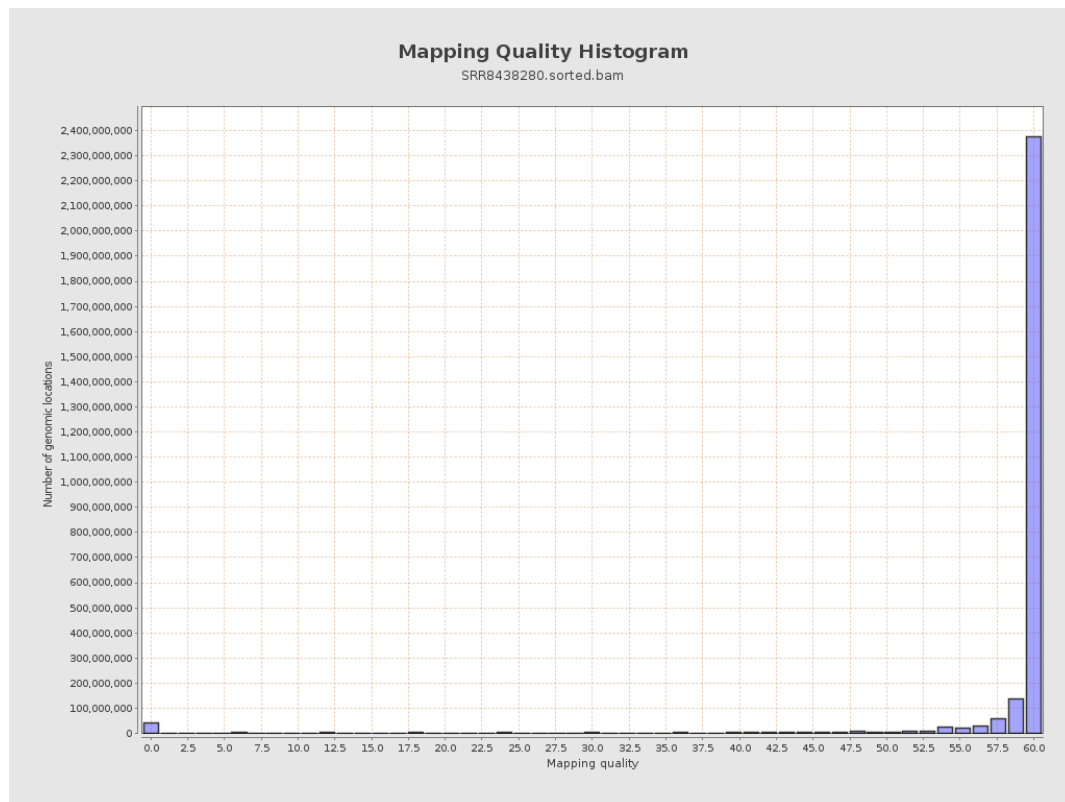
11. Results : Homopolymer Indels



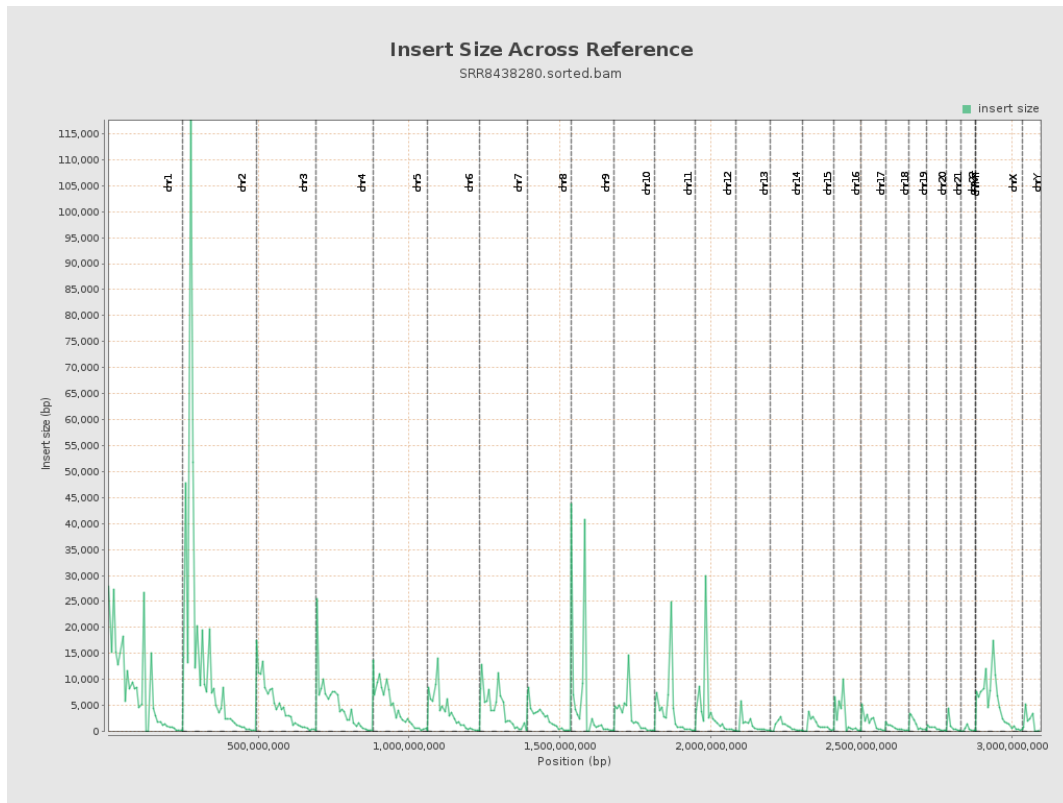
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

