

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 03:59:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438282.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_SRR8438282 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438282_1.fastq.gz SRR8438282_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 03:59:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438282.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	640,533,988
Mapped reads	638,512,766 / 99.68%
Unmapped reads	2,021,222 / 0.32%
Mapped paired reads	638,512,766 / 99.68%
Mapped reads, first in pair	319,480,812 / 49.88%
Mapped reads, second in pair	319,031,954 / 49.81%
Mapped reads, both in pair	637,092,372 / 99.46%
Mapped reads, singletons	1,420,394 / 0.22%
Secondary alignments	0
Supplementary alignments	11,179,827 / 1.75%
Read min/max/mean length	28 / 151 / 144.91
Duplicated reads (estimated)	210,380,889 / 32.84%
Duplication rate	30.41%
Clipped reads	113,130,616 / 17.66%

2.2. ACGT Content

Number/percentage of A's	27,603,725,798 / 30.11%
Number/percentage of C's	18,468,555,622 / 20.14%
Number/percentage of T's	26,298,858,766 / 28.68%
Number/percentage of G's	19,318,678,165 / 21.07%
Number/percentage of N's	688,912 / 0%

GC Percentage	41.21%
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2.3. Coverage

Mean	29.6264
Standard Deviation	38.7346

2.4. Mapping Quality

Mean Mapping Quality	55.23
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2.5. Insert size

Mean	38,166.88
Standard Deviation	1,909,169.25
P25/Median/P75	193 / 265 / 386

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	468,591,438
Insertions	10,852,469
Mapped reads with at least one insertion	1.67%
Deletions	9,586,568
Mapped reads with at least one deletion	1.48%
Homopolymer indels	48.29%

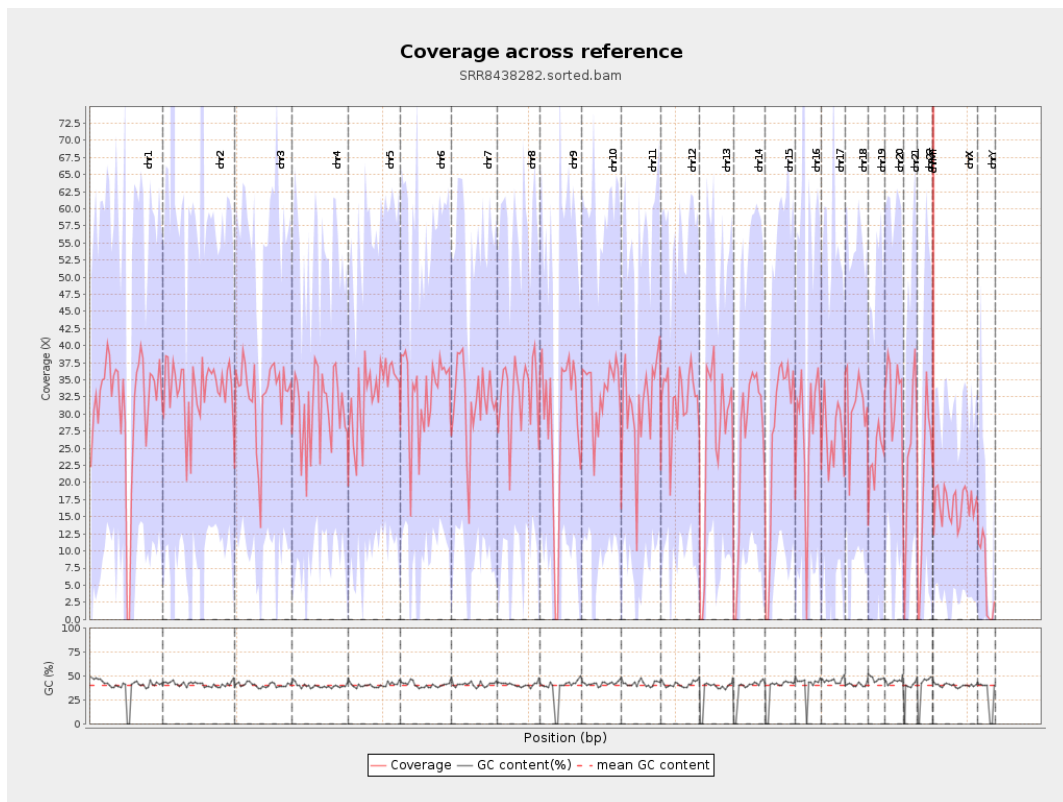
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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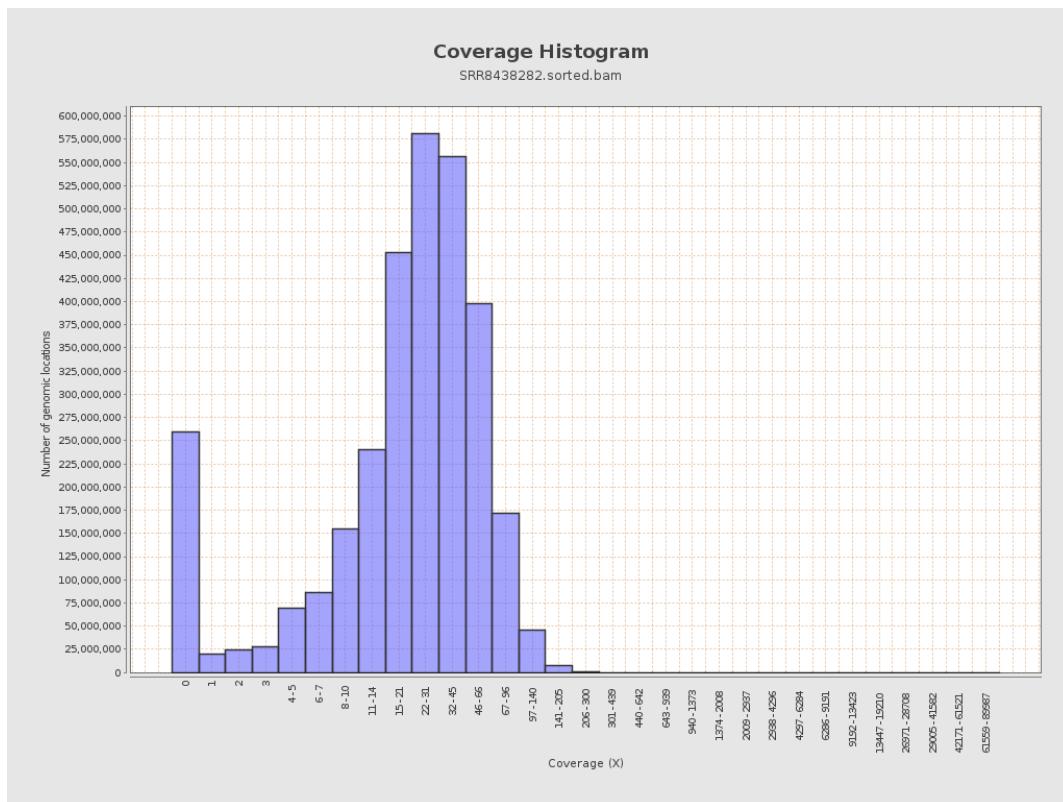
		bases	coverage	deviation
chr1	249250621	7761923322	31.141	26.9761
chr2	243199373	8196112824	33.7012	87.3175
chr3	198022430	6486623857	32.757	23.8816
chr4	191154276	5881877171	30.7703	22.3425
chr5	180915260	5970313582	33.0006	23.4325
chr6	171115067	5700929254	33.3163	24.5872
chr7	159138663	5062724827	31.8133	23.349
chr8	146364022	4827720508	32.9843	24.5692
chr9	141213431	4042761036	28.6287	28.0606
chr10	135534747	4555407333	33.6106	26.7409
chr11	135006516	4242902984	31.4274	24.446
chr12	133851895	4359492811	32.5695	23.4258
chr13	115169878	3057044985	26.5438	23.9251
chr14	107349540	2847551795	26.526	24.5412
chr15	102531392	2789133278	27.2027	26.4612
chr16	90354753	2481325437	27.462	36.1946
chr17	81195210	2224550556	27.3976	29.7744
chr18	78077248	2439458650	31.2442	24.2517
chr19	59128983	1422212637	24.0527	25.6049
chr20	63025520	2101634397	33.3458	26.2647
chr21	48129895	1155967468	24.0177	26.7689
chr22	51304566	1024438791	19.9678	24.9904
chrMT	16571	117949262	7,117.812	2,503.8044
chrX	155270560	2608661384	16.8007	13.631

chrY	59373566	355625523	5.9896	17.9325
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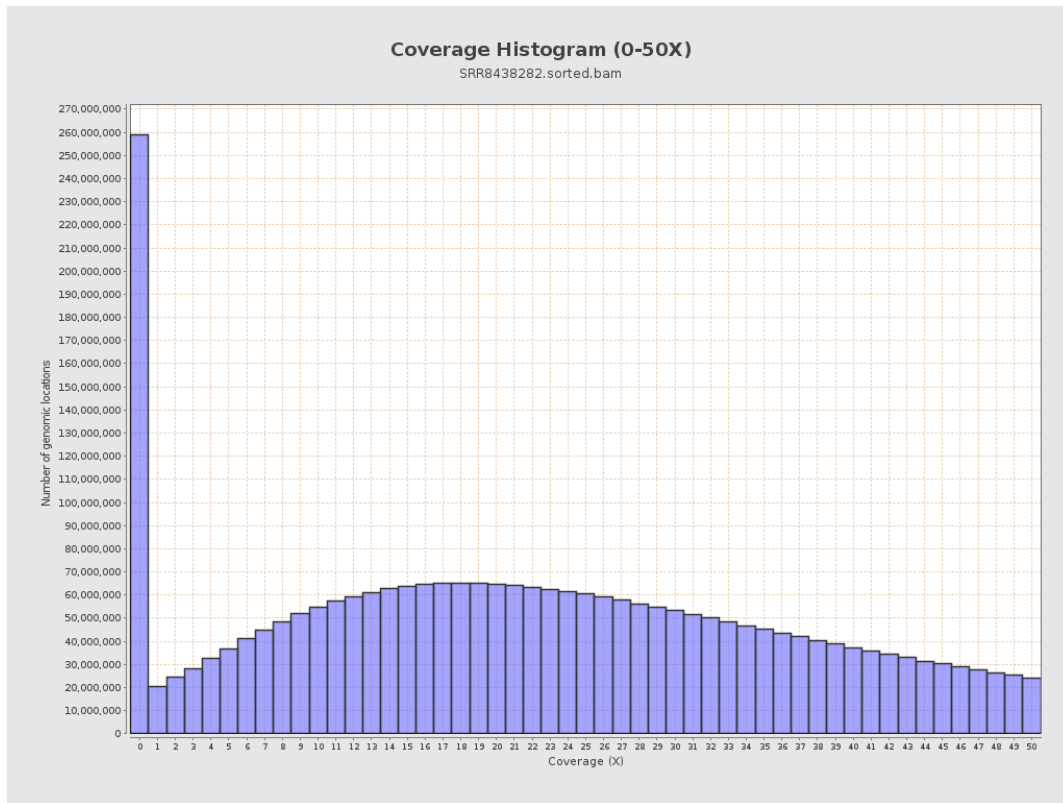
3. Results : Coverage across reference



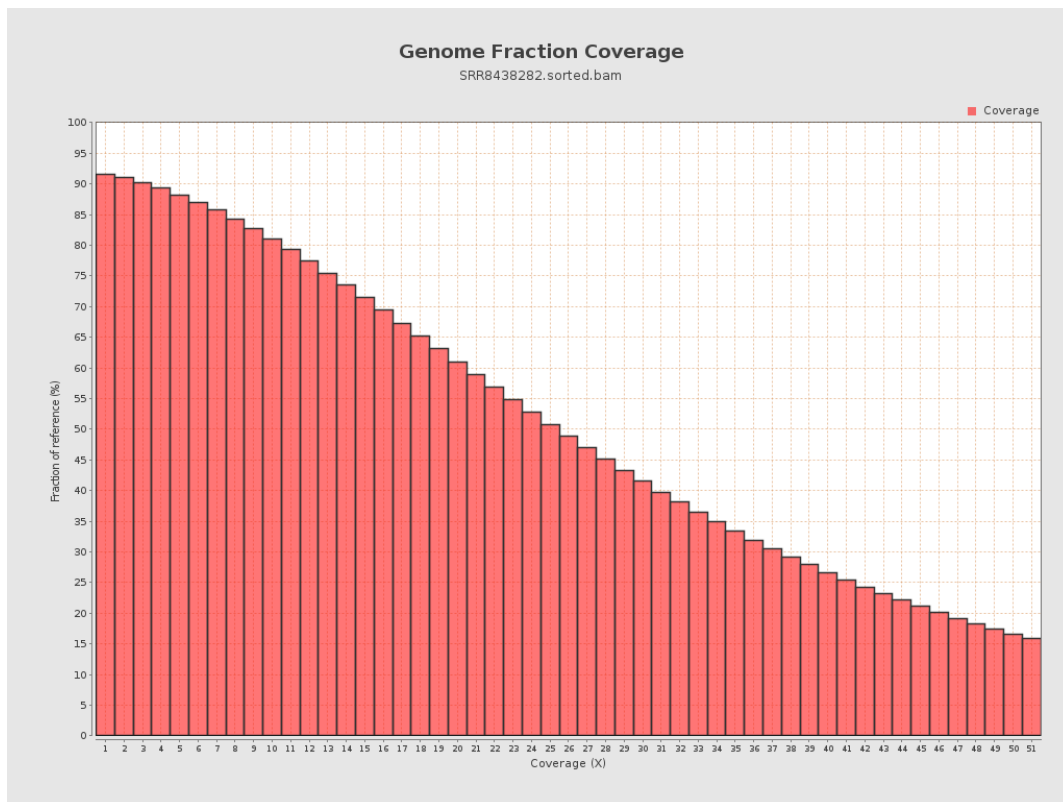
4. Results : Coverage Histogram



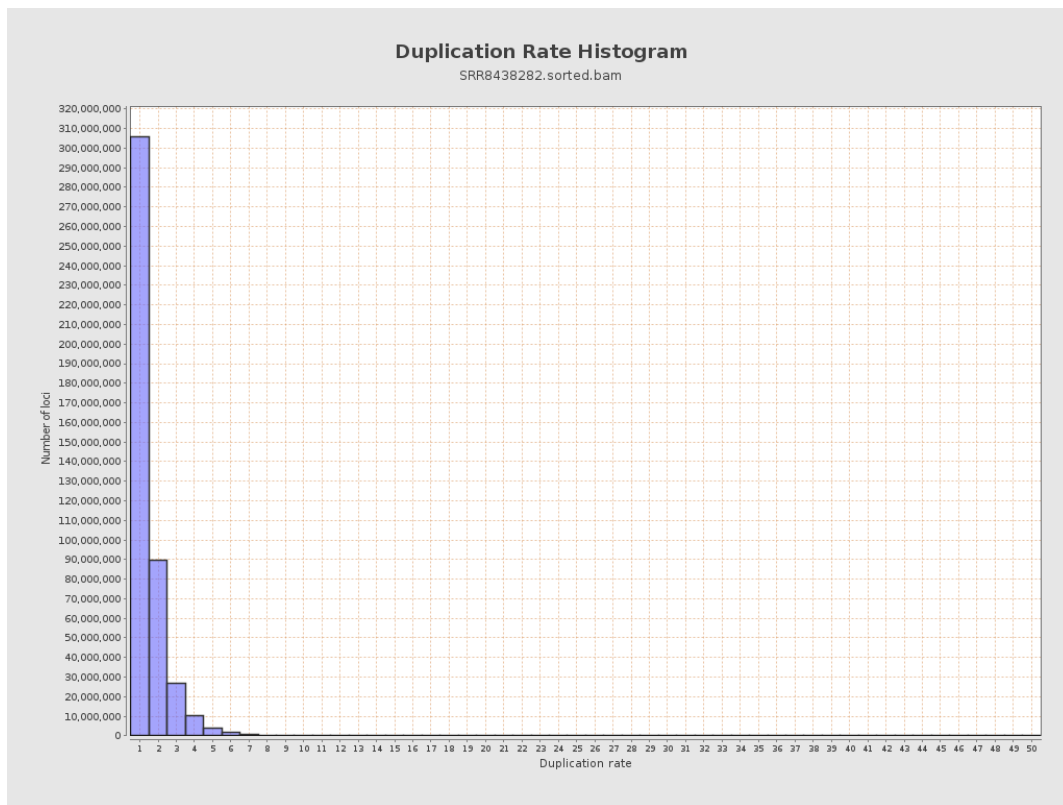
5. Results : Coverage Histogram (0-50X)



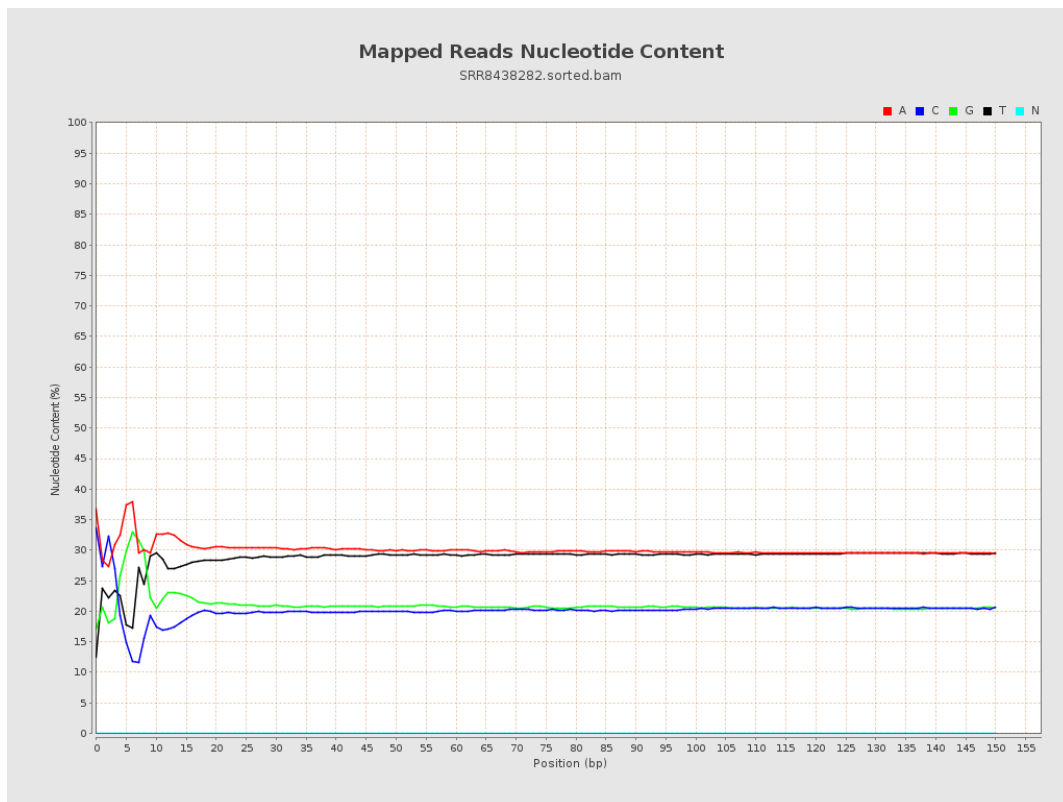
6. Results : Genome Fraction Coverage



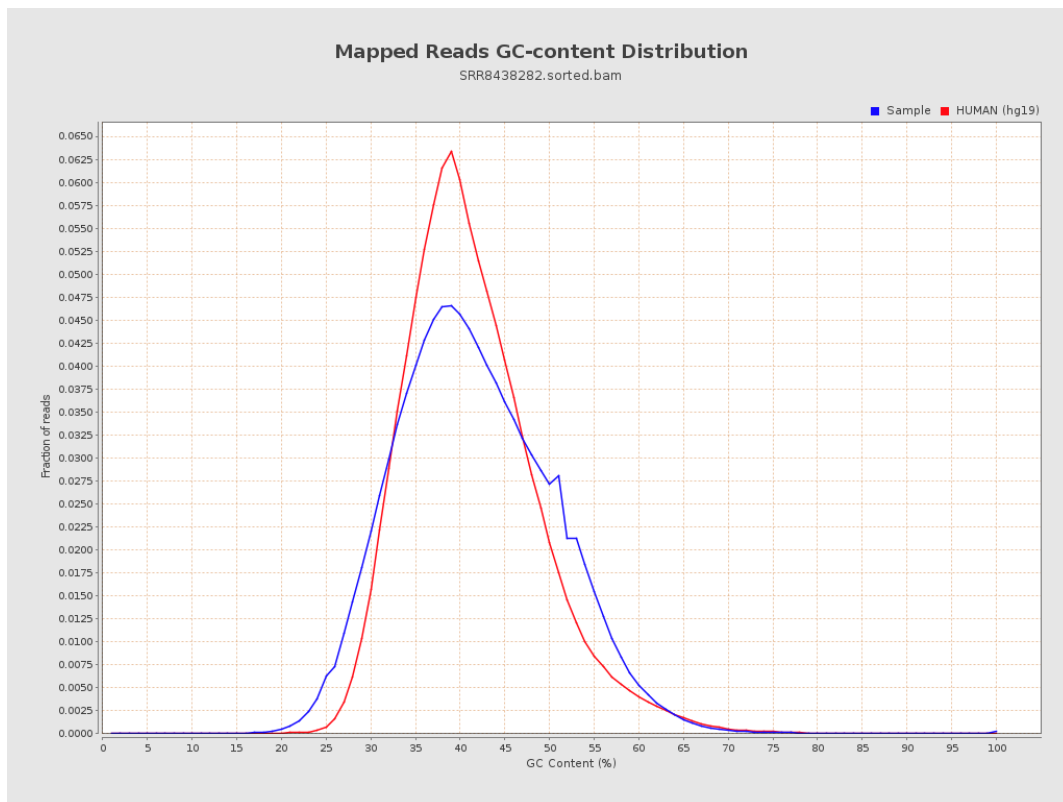
7. Results : Duplication Rate Histogram



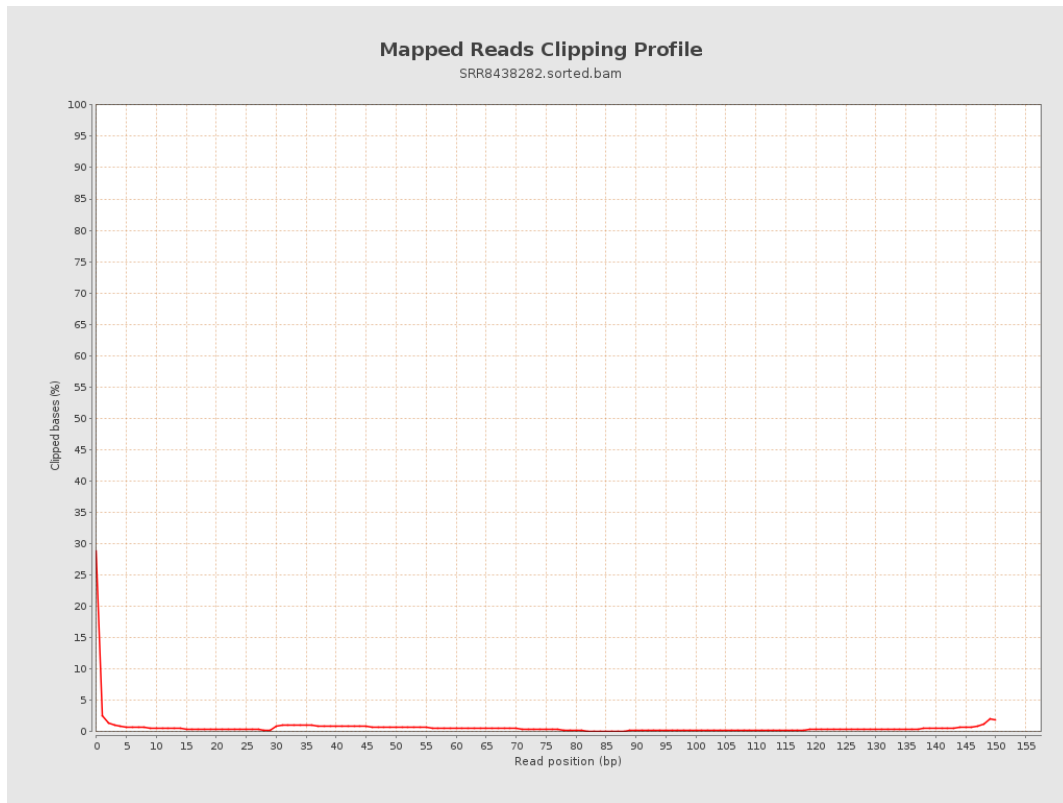
8. Results : Mapped Reads Nucleotide Content



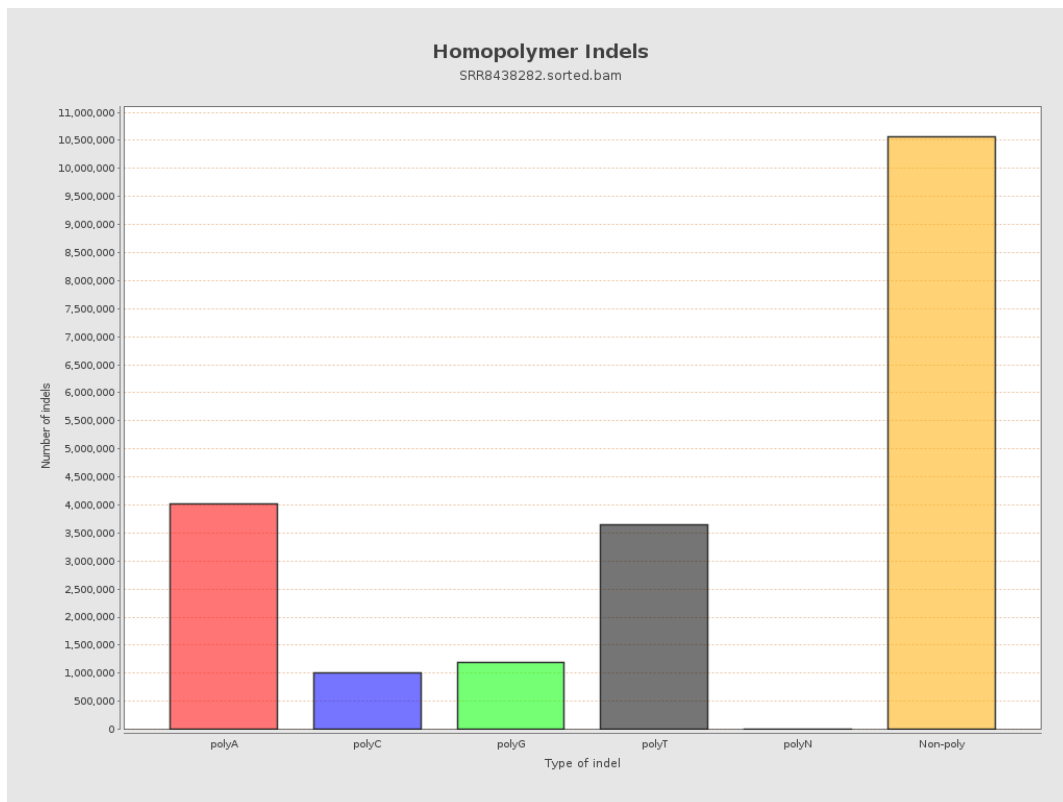
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



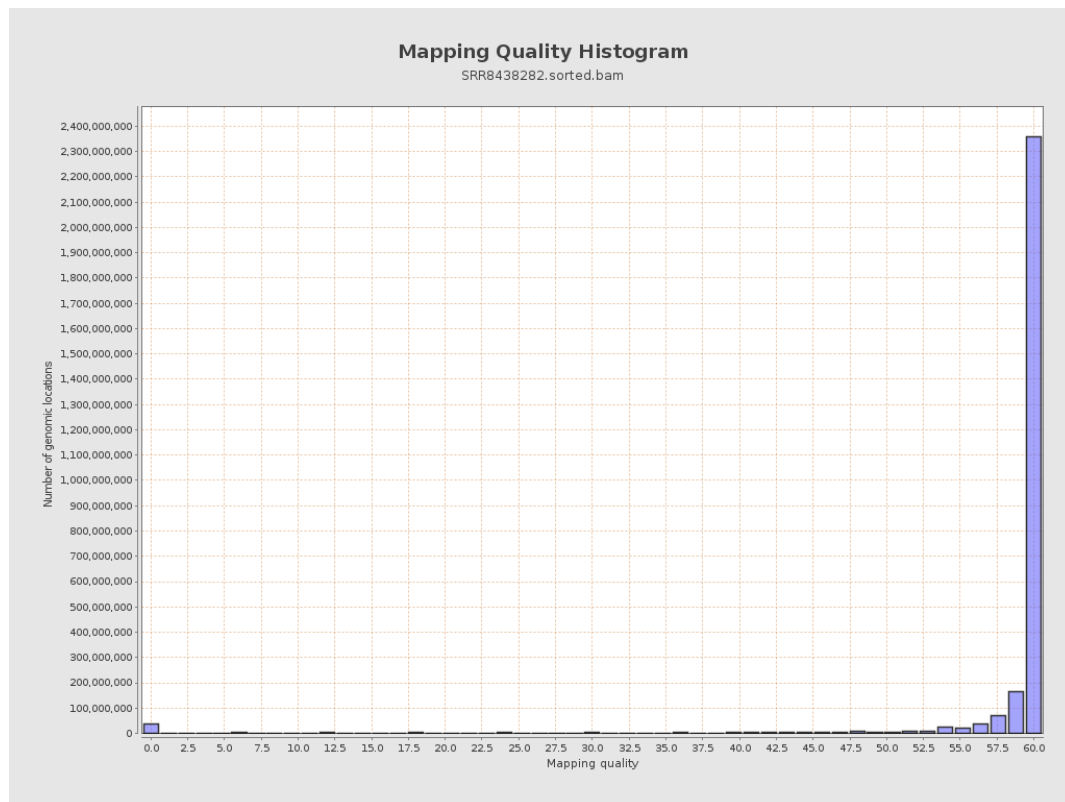
11. Results : Homopolymer Indels



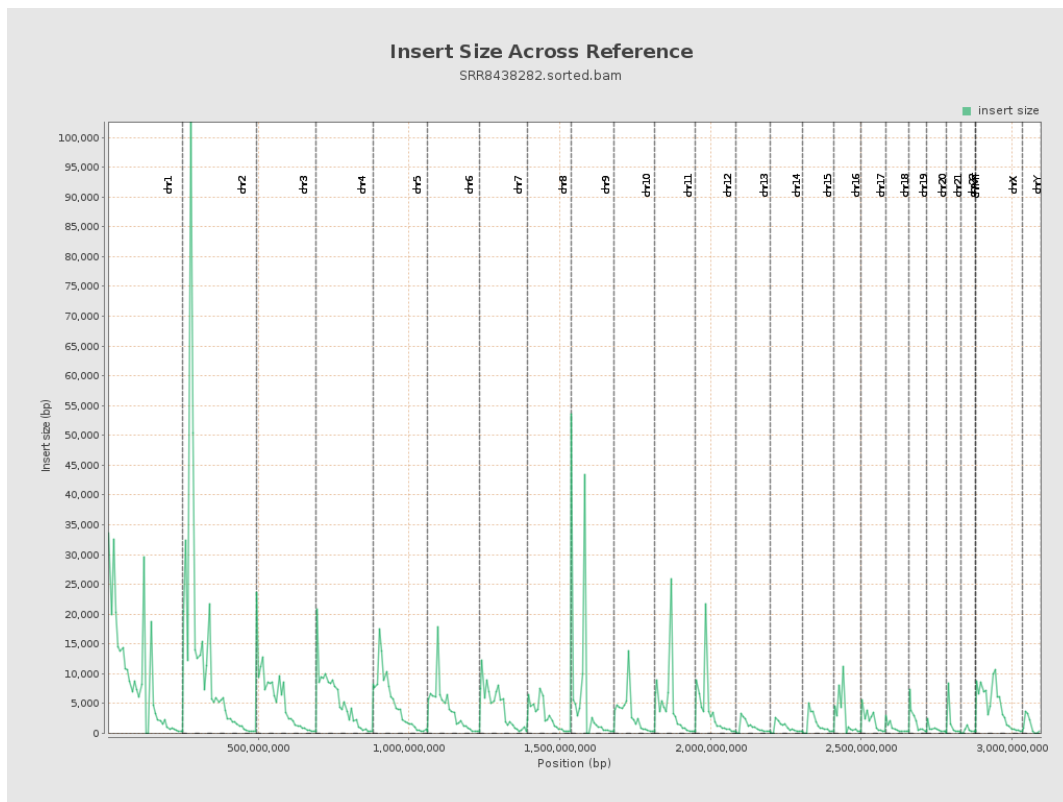
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

