

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 07:56:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038435.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_SRR5038435 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038435_1.fastq.gz SRR5038435_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 07:56:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038435.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,340,820
Mapped reads	14,943,533 / 91.45%
Unmapped reads	1,397,287 / 8.55%
Mapped paired reads	14,943,533 / 91.45%
Mapped reads, first in pair	7,613,616 / 46.59%
Mapped reads, second in pair	7,329,917 / 44.86%
Mapped reads, both in pair	14,607,808 / 89.39%
Mapped reads, singletons	335,725 / 2.05%
Secondary alignments	0
Supplementary alignments	218,853 / 1.34%
Read min/max/mean length	30 / 150 / 150.67
Duplicated reads (estimated)	2,770,762 / 16.96%
Duplication rate	12.88%
Clipped reads	6,893,420 / 42.19%

2.2. ACGT Content

Number/percentage of A's	577,809,552 / 28.66%
Number/percentage of C's	401,371,277 / 19.91%
Number/percentage of T's	588,396,988 / 29.19%
Number/percentage of G's	448,311,371 / 22.24%
Number/percentage of N's	155,935 / 0.01%

GC Percentage	42.15%
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2.3. Coverage

Mean	0.6517
Standard Deviation	9.0835

2.4. Mapping Quality

Mean Mapping Quality	53.35
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2.5. Insert size

Mean	91,552.68
Standard Deviation	2,958,585.89
P25/Median/P75	199 / 251 / 318

2.6. Mismatches and indels

General error rate	1.4%
Mismatches	27,415,538
Insertions	348,044
Mapped reads with at least one insertion	2.21%
Deletions	723,362
Mapped reads with at least one deletion	4.67%
Homopolymer indels	47.26%

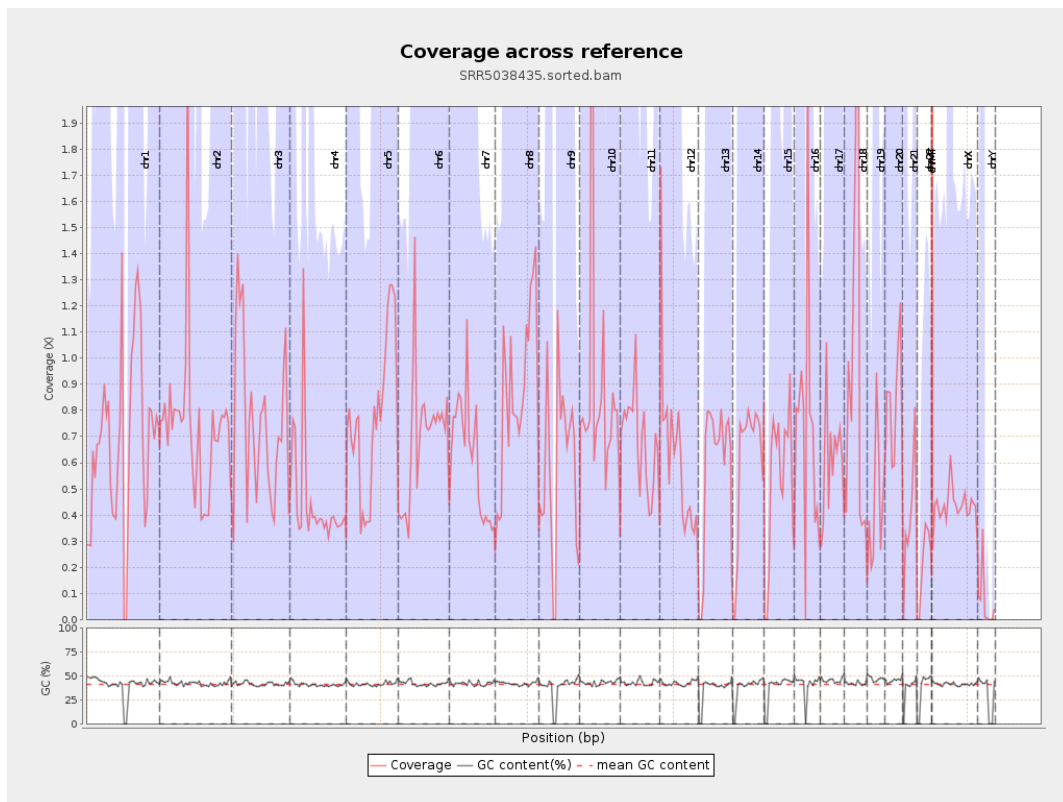
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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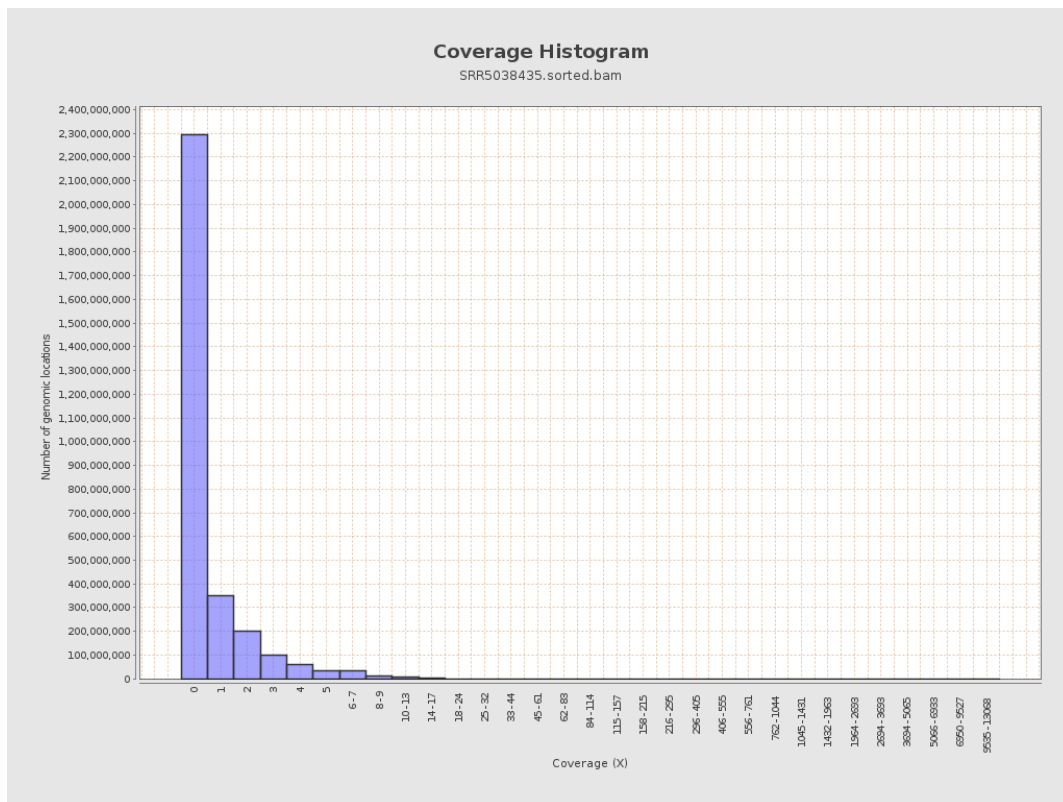
		bases	coverage	deviation
chr1	249250621	173120155	0.6946	12.8276
chr2	243199373	180982511	0.7442	9.629
chr3	198022430	148633023	0.7506	1.7156
chr4	191154276	86236211	0.4511	7.905
chr5	180915260	138907466	0.7678	1.6293
chr6	171115067	120130835	0.702	7.5061
chr7	159138663	97691813	0.6139	9.1264
chr8	146364022	129147973	0.8824	3.5845
chr9	141213431	79693358	0.5643	14.202
chr10	135534747	124696252	0.92	24.783
chr11	135006516	91334130	0.6765	7.9268
chr12	133851895	83196104	0.6216	1.5913
chr13	115169878	68163856	0.5919	1.3889
chr14	107349540	64862635	0.6042	1.5076
chr15	102531392	54297895	0.5296	1.3443
chr16	90354753	64507170	0.7139	9.8916
chr17	81195210	48794651	0.601	10.8721
chr18	78077248	80345073	1.029	9.6712
chr19	59128983	25873360	0.4376	5.3113
chr20	63025520	52646945	0.8353	2.9885
chr21	48129895	19594417	0.4071	3.632
chr22	51304566	11040595	0.2152	0.8441
chrMT	16571	2047230	123.5429	61.6504
chrX	155270560	67413355	0.4342	2.0506

chrY	59373566	4089579	0.0689	7.3155
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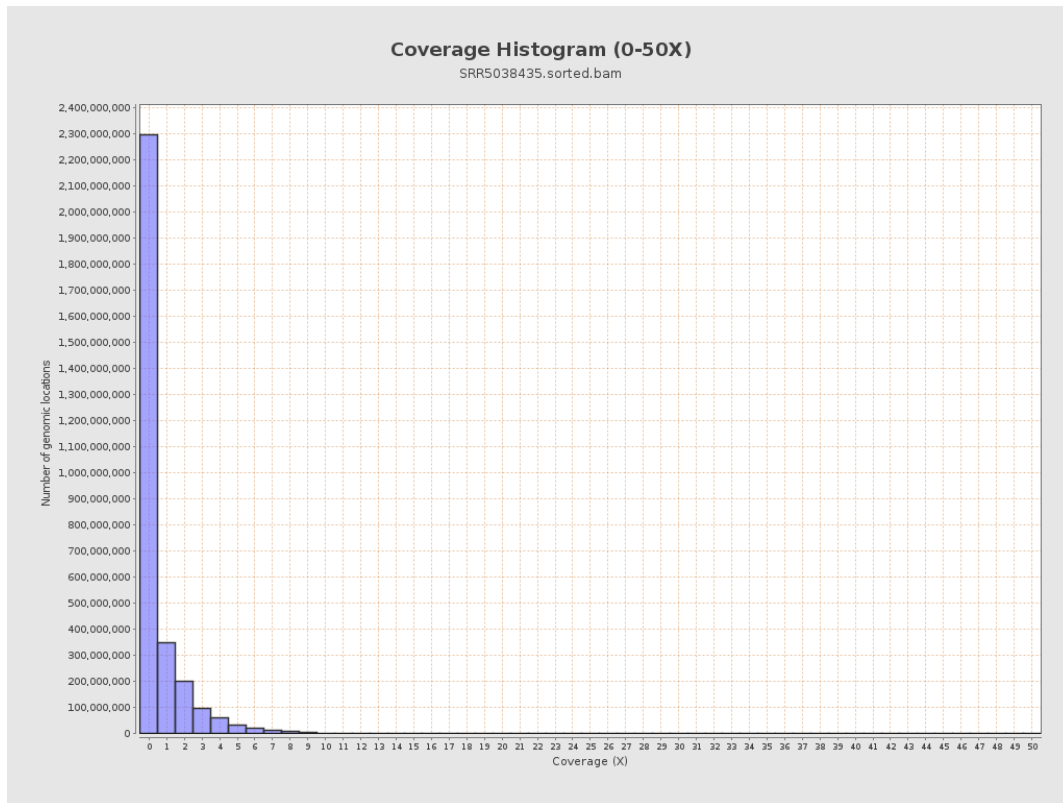
3. Results : Coverage across reference



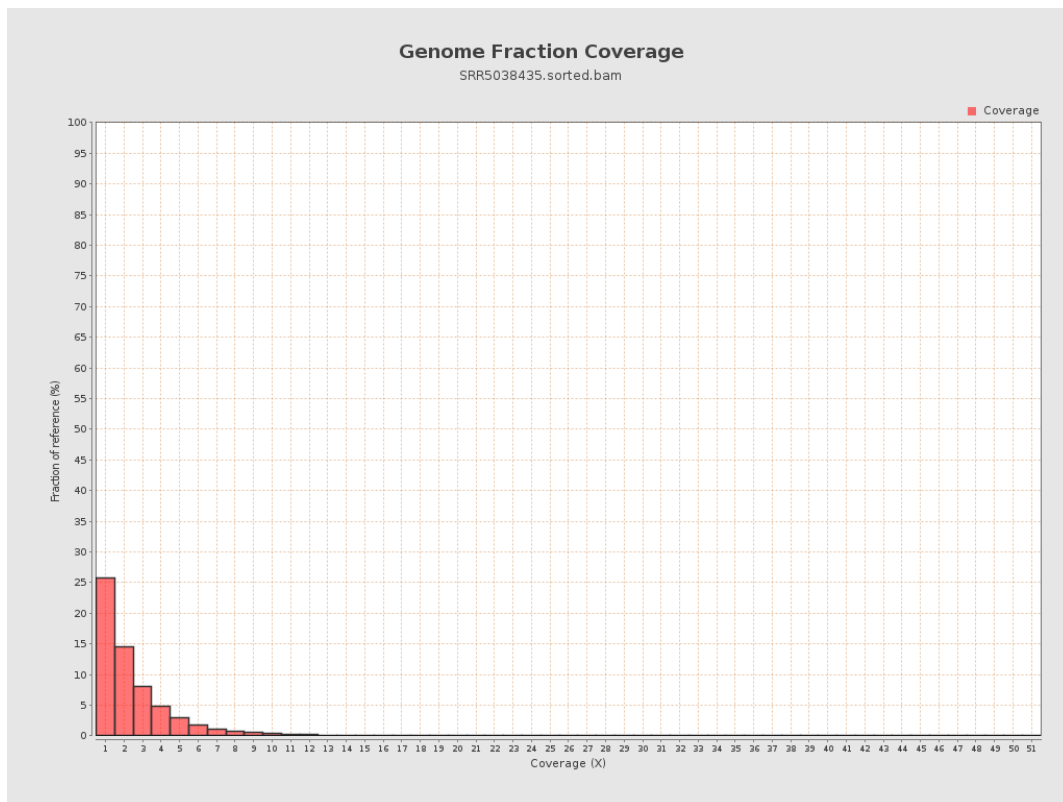
4. Results : Coverage Histogram



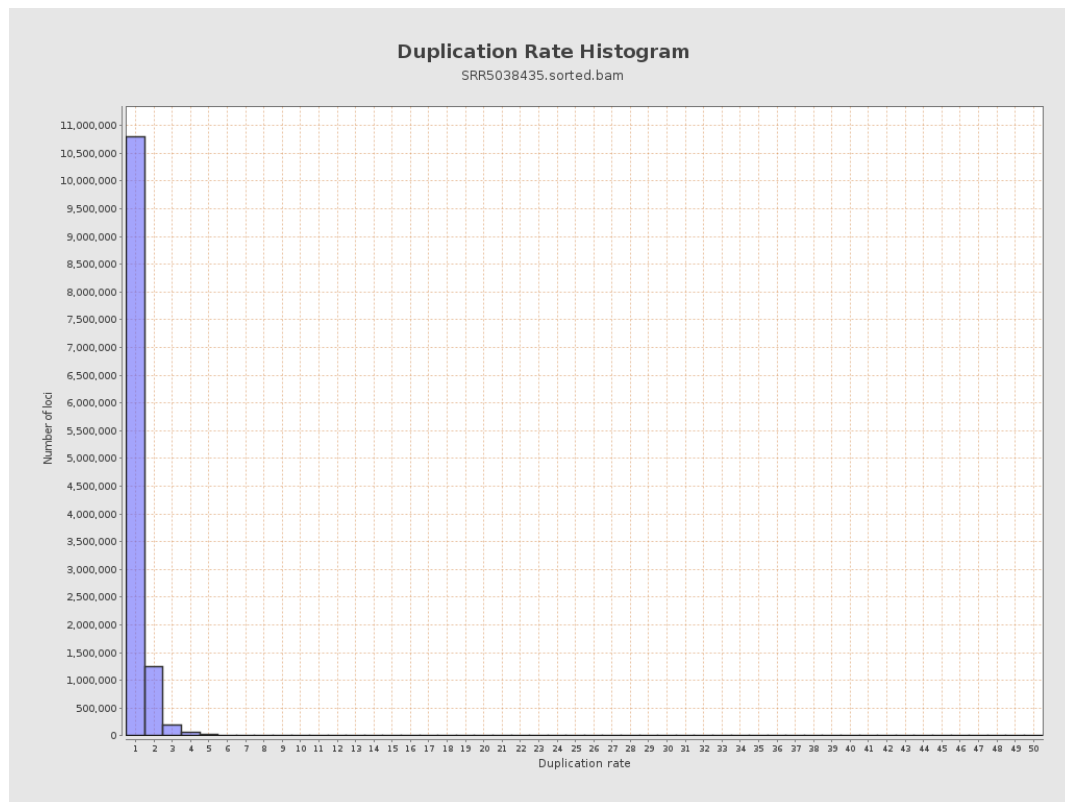
5. Results : Coverage Histogram (0-50X)



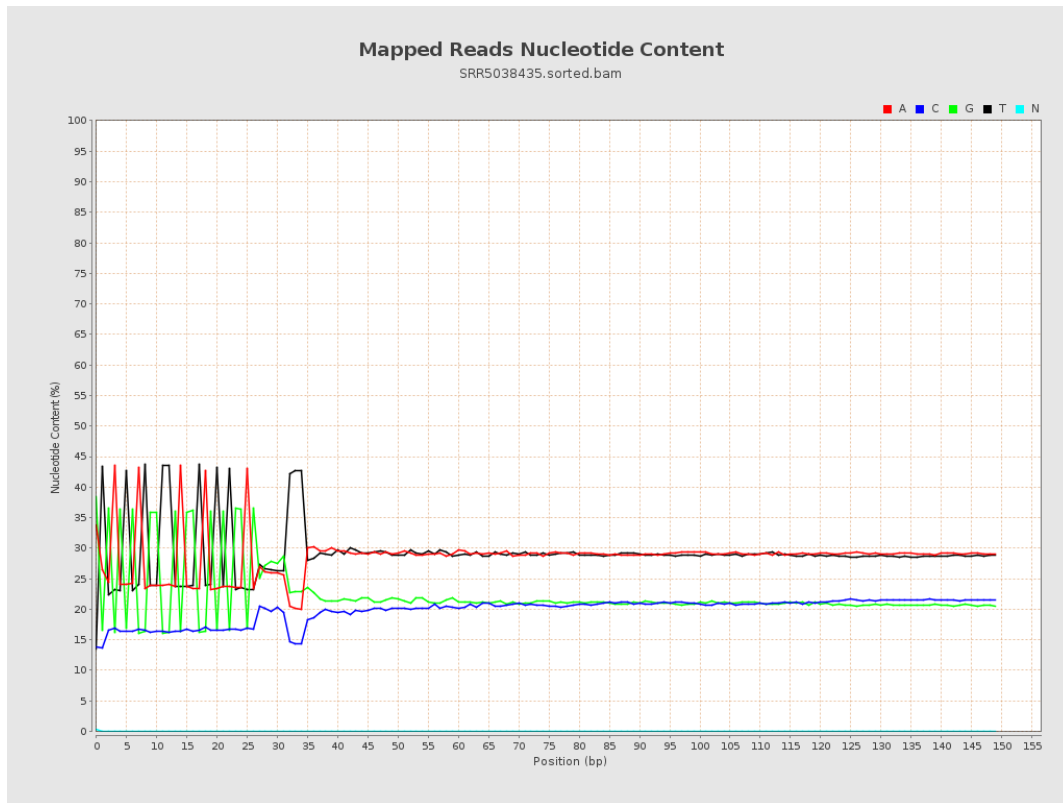
6. Results : Genome Fraction Coverage



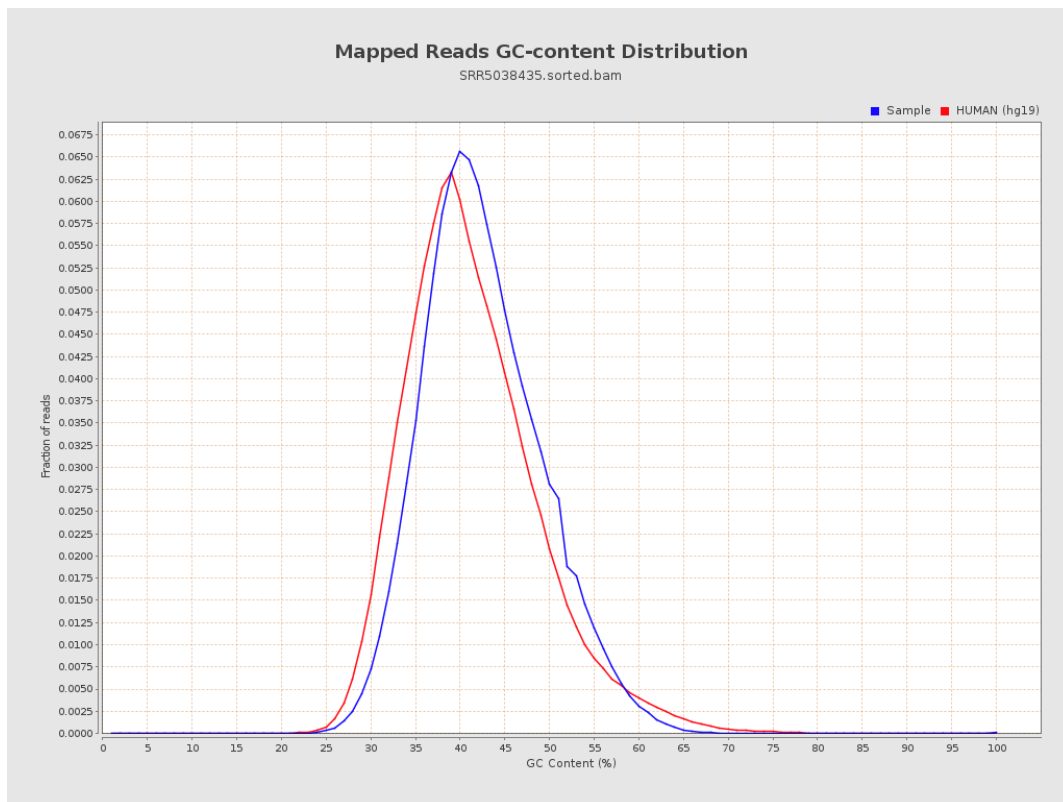
7. Results : Duplication Rate Histogram



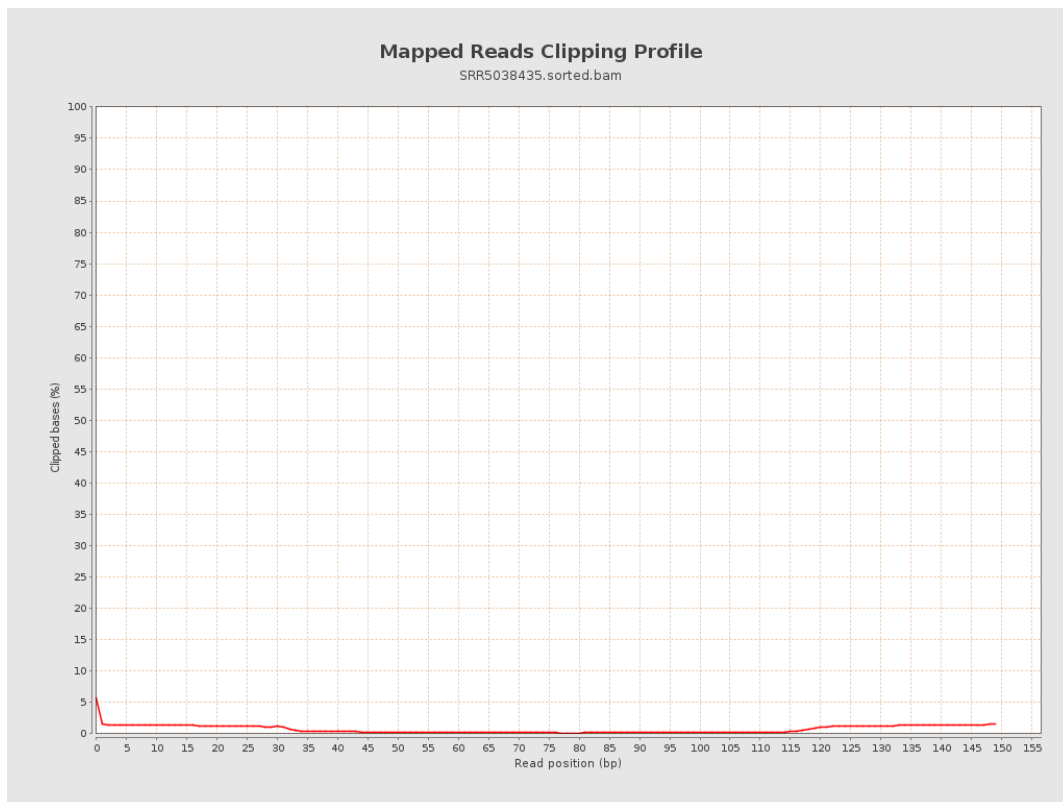
8. Results : Mapped Reads Nucleotide Content



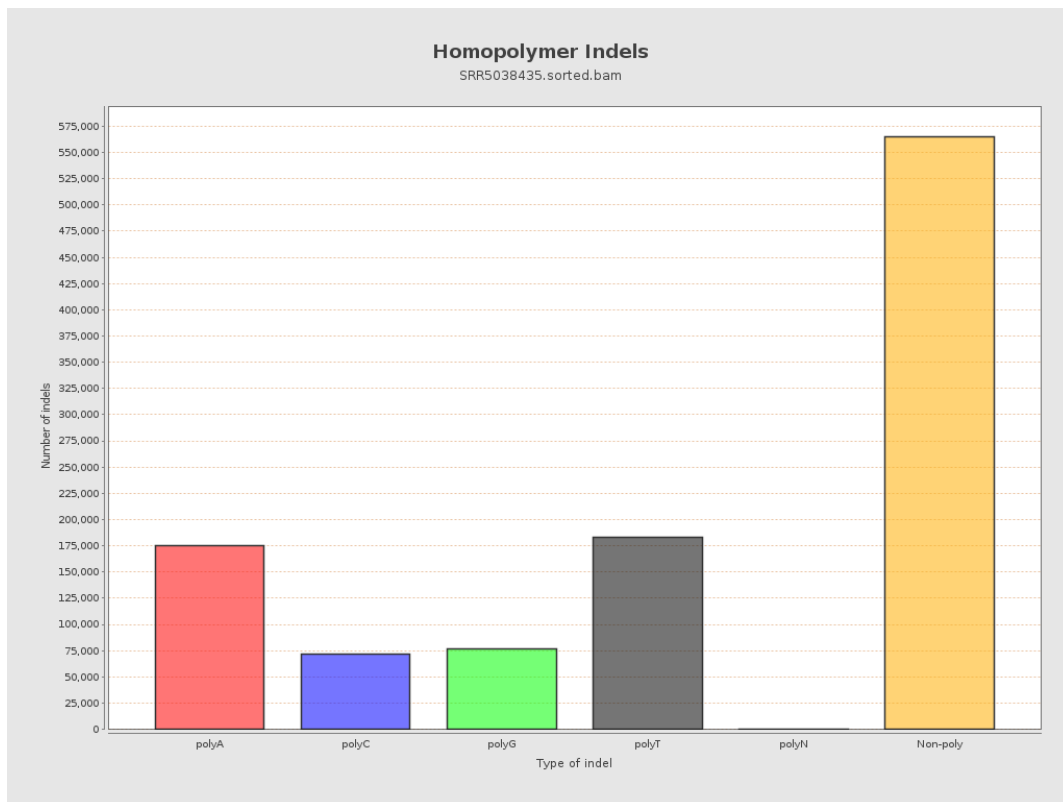
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



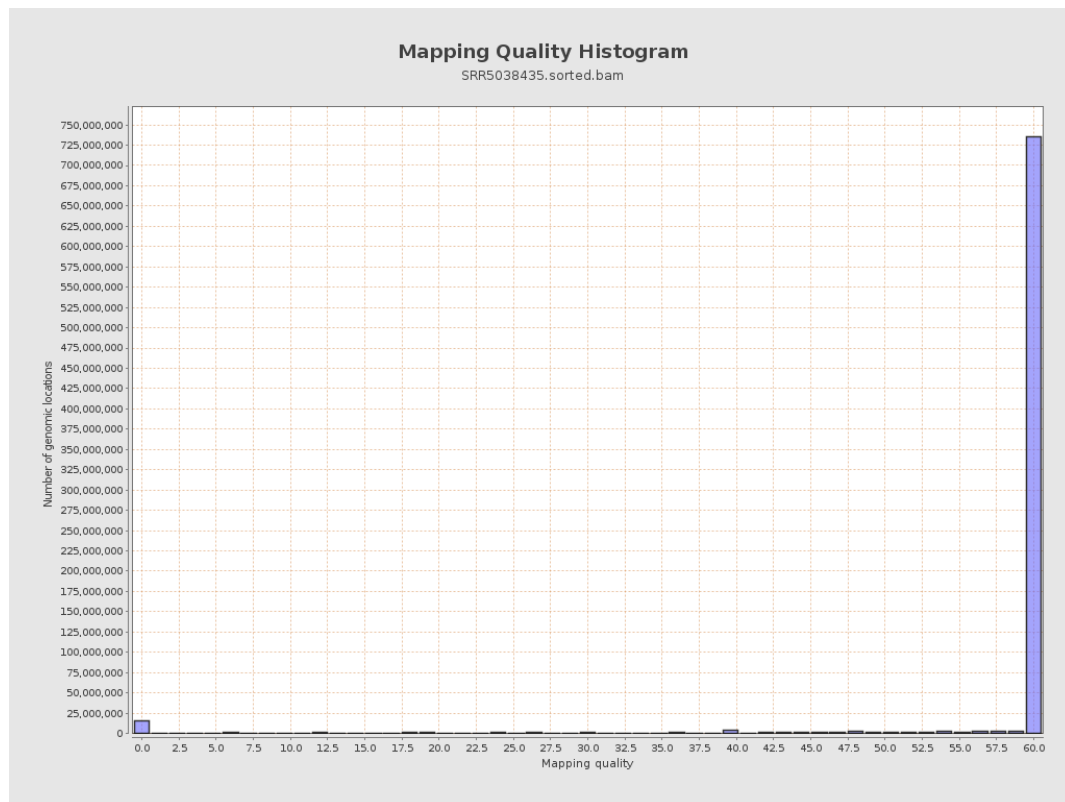
11. Results : Homopolymer Indels



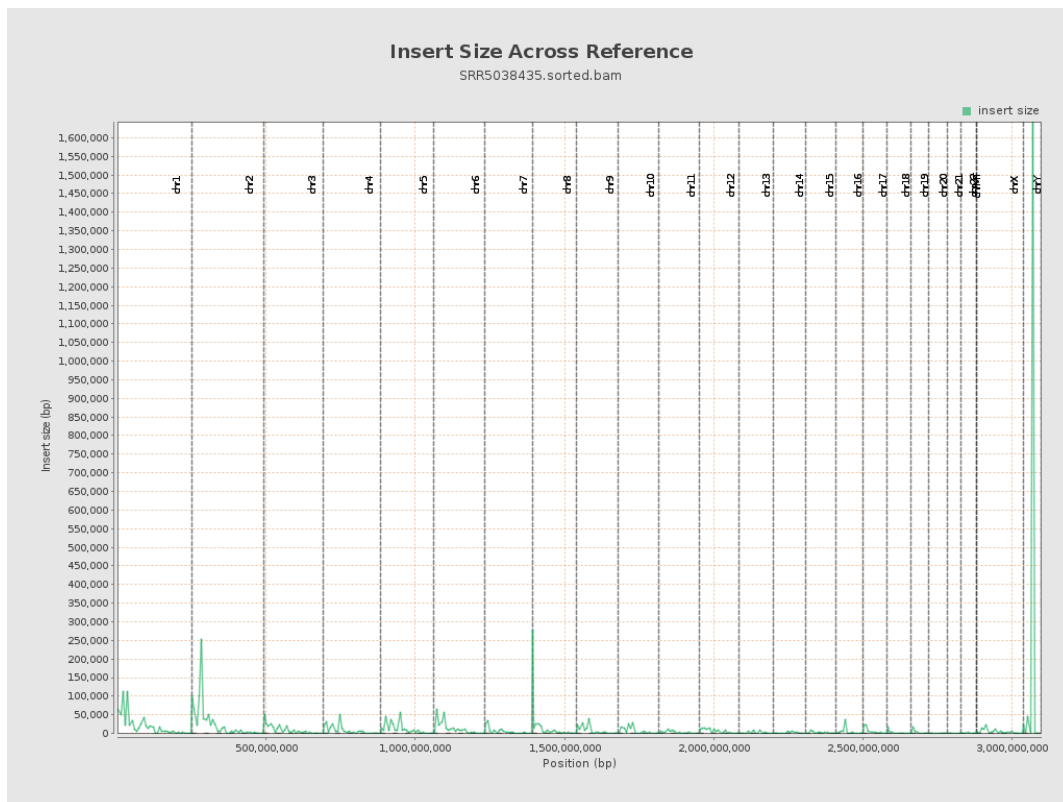
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

