

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 04:03:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038428.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_SRR5038428 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038428_1.fastq.gz SRR5038428_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 04:03:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038428.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,193,458
Mapped reads	17,624,917 / 91.83%
Unmapped reads	1,568,541 / 8.17%
Mapped paired reads	17,624,917 / 91.83%
Mapped reads, first in pair	8,948,498 / 46.62%
Mapped reads, second in pair	8,676,419 / 45.21%
Mapped reads, both in pair	17,296,550 / 90.12%
Mapped reads, singletons	328,367 / 1.71%
Secondary alignments	0
Supplementary alignments	254,060 / 1.32%
Read min/max/mean length	30 / 150 / 150.67
Duplicated reads (estimated)	3,567,956 / 18.59%
Duplication rate	14.36%
Clipped reads	8,000,476 / 41.68%

2.2. ACGT Content

Number/percentage of A's	679,775,638 / 28.52%
Number/percentage of C's	476,452,802 / 19.99%
Number/percentage of T's	689,937,069 / 28.95%
Number/percentage of G's	536,986,066 / 22.53%
Number/percentage of N's	189,219 / 0.01%

GC Percentage	42.52%
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2.3. Coverage

Mean	0.7704
Standard Deviation	9.2083

2.4. Mapping Quality

Mean Mapping Quality	53.57
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2.5. Insert size

Mean	90,411.05
Standard Deviation	2,918,585.99
P25/Median/P75	204 / 256 / 323

2.6. Mismatches and indels

General error rate	1.34%
Mismatches	30,901,763
Insertions	411,815
Mapped reads with at least one insertion	2.23%
Deletions	874,730
Mapped reads with at least one deletion	4.79%
Homopolymer indels	47.93%

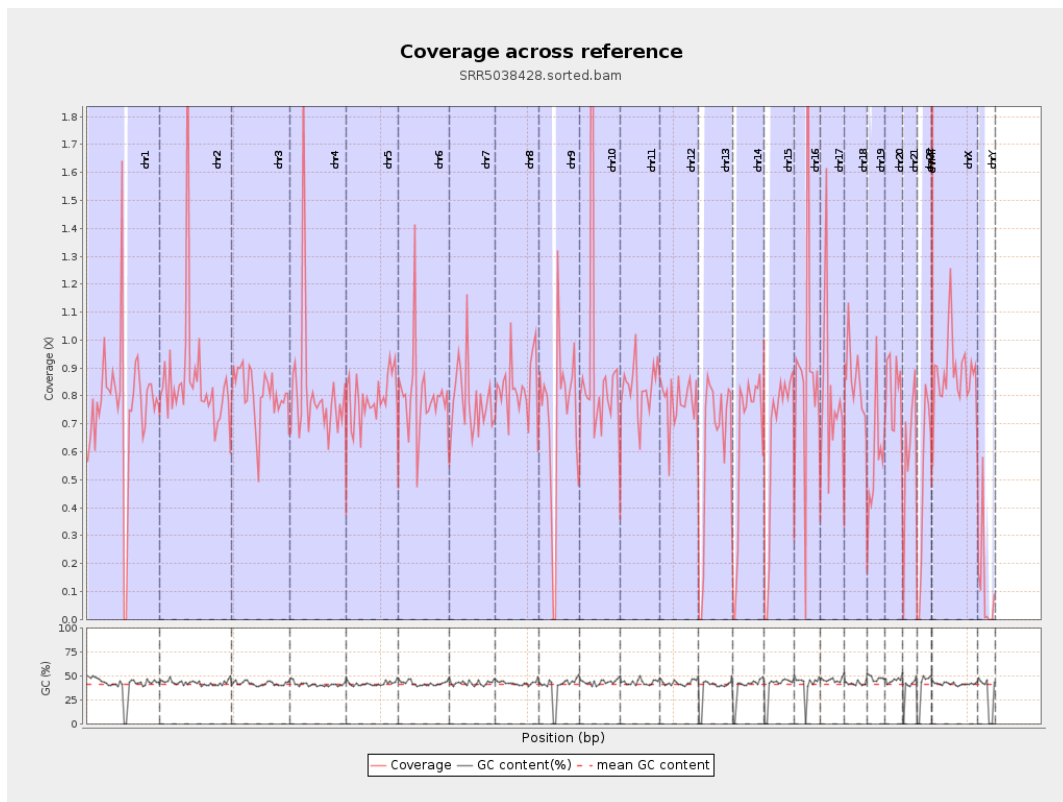
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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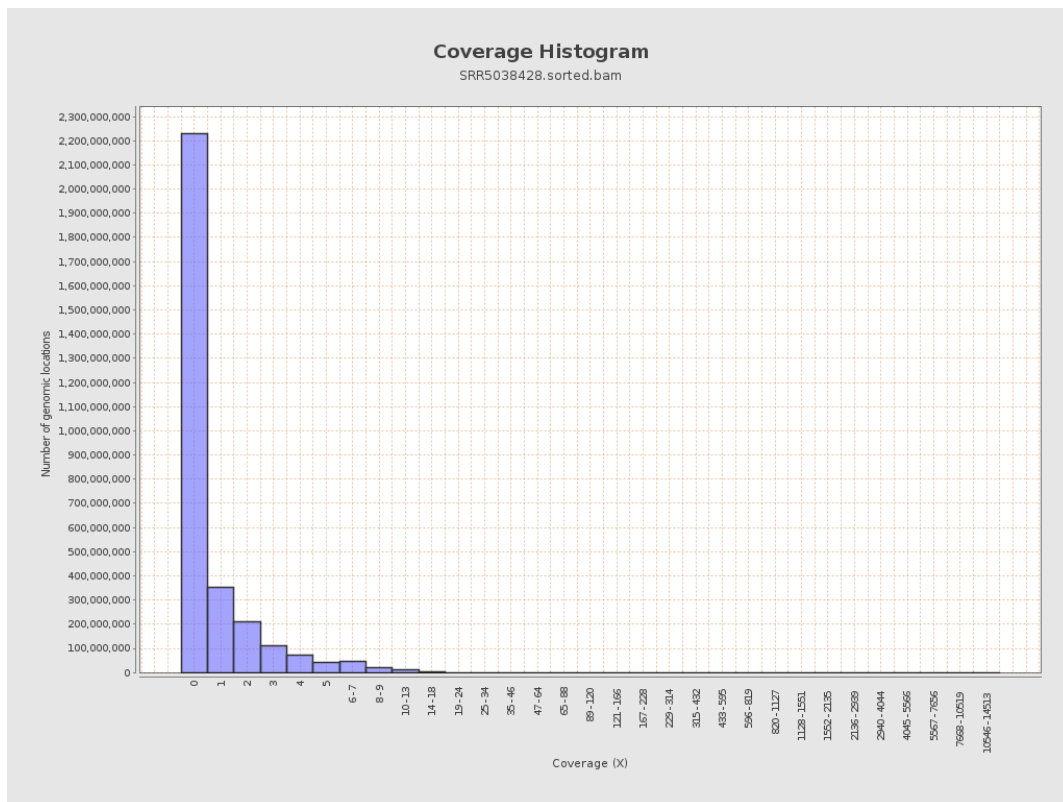
		bases	coverage	deviation
chr1	249250621	190187469	0.763	14.7332
chr2	243199373	208760777	0.8584	9.784
chr3	198022430	160101288	0.8085	1.7861
chr4	191154276	155227600	0.8121	8.7867
chr5	180915260	142417010	0.7872	1.7498
chr6	171115067	137199925	0.8018	6.9709
chr7	159138663	123616411	0.7768	8.8705
chr8	146364022	121448947	0.8298	3.1796
chr9	141213431	99693464	0.706	15.5515
chr10	135534747	127079629	0.9376	20.0679
chr11	135006516	110722204	0.8201	6.9284
chr12	133851895	103956466	0.7767	1.8493
chr13	115169878	72457634	0.6291	1.5396
chr14	107349540	70002376	0.6521	1.7042
chr15	102531392	66062277	0.6443	1.5923
chr16	90354753	80334684	0.8891	11.592
chr17	81195210	62945204	0.7752	13.1827
chr18	78077248	66585998	0.8528	11.973
chr19	59128983	33412341	0.5651	7.1
chr20	63025520	51153838	0.8116	3.0864
chr21	48129895	29811871	0.6194	4.4438
chr22	51304566	24679974	0.481	1.4396
chrMT	16571	3798773	229.2422	145.1477
chrX	155270560	136402057	0.8785	3.5204

chrY	59373566	6948215	0.117	9.2313
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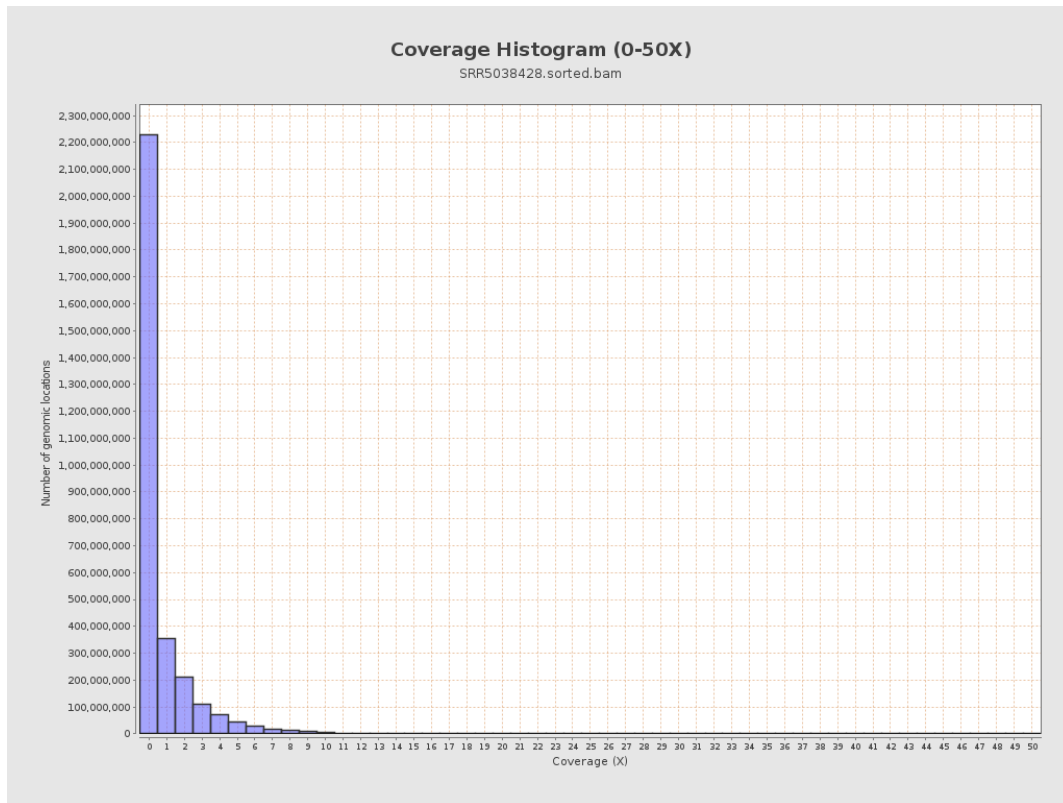
3. Results : Coverage across reference



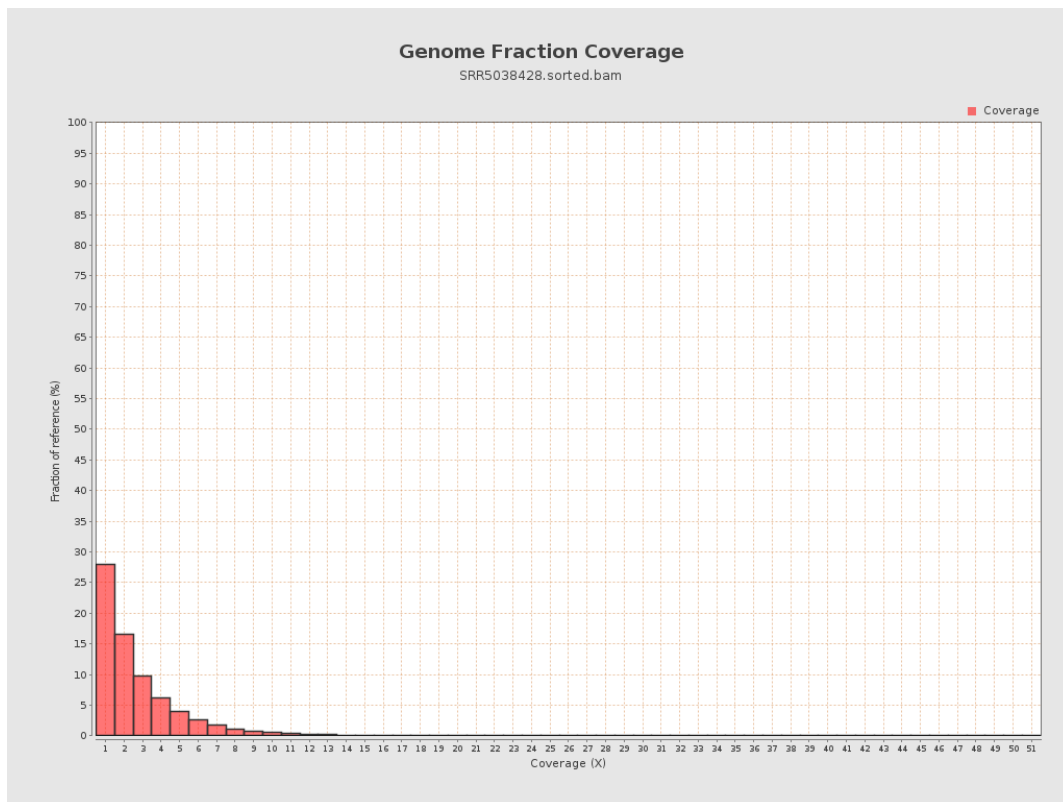
4. Results : Coverage Histogram



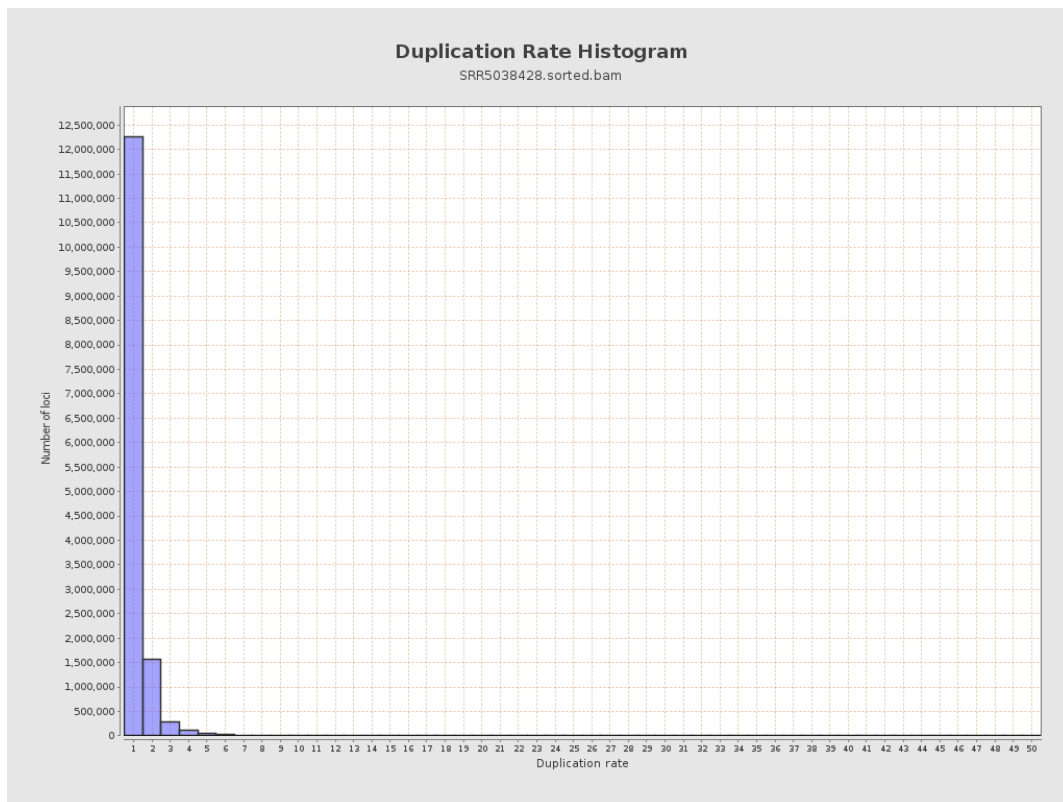
5. Results : Coverage Histogram (0-50X)



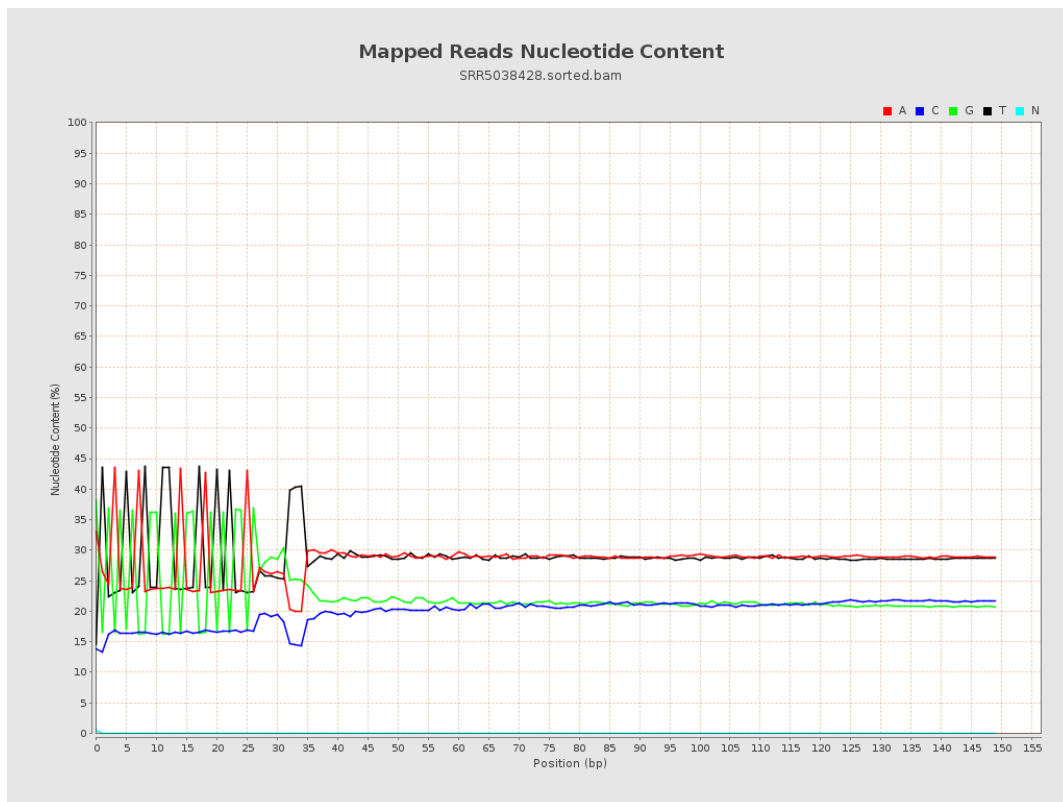
6. Results : Genome Fraction Coverage



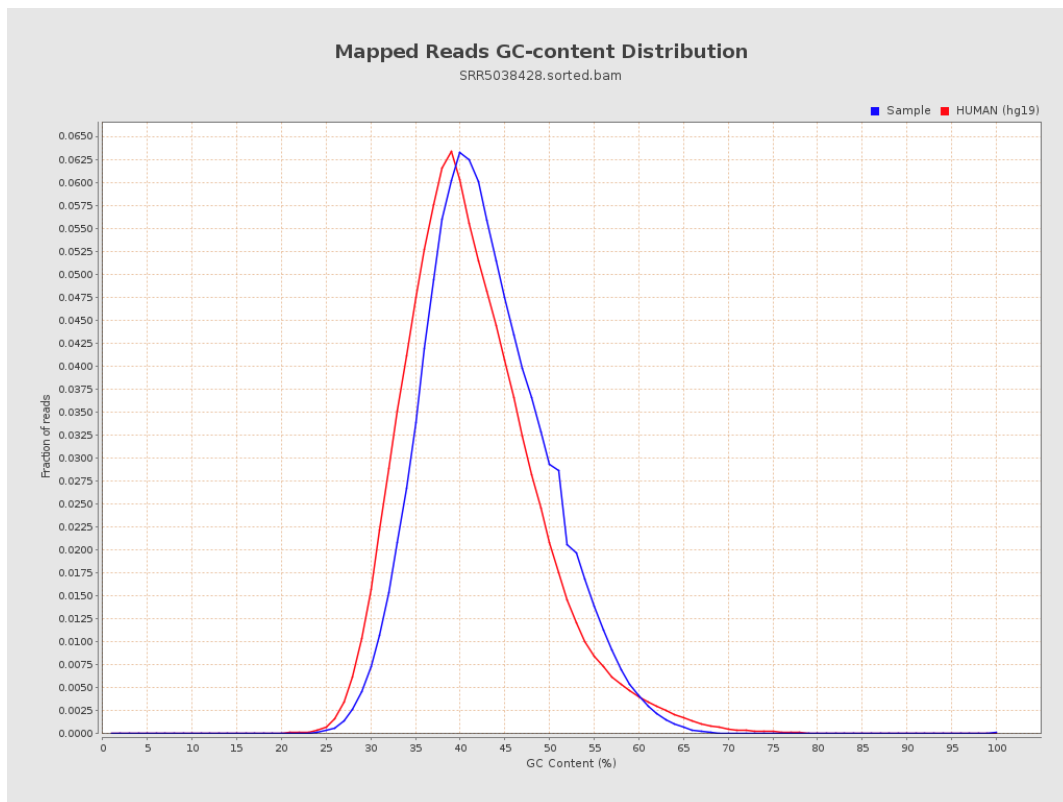
7. Results : Duplication Rate Histogram



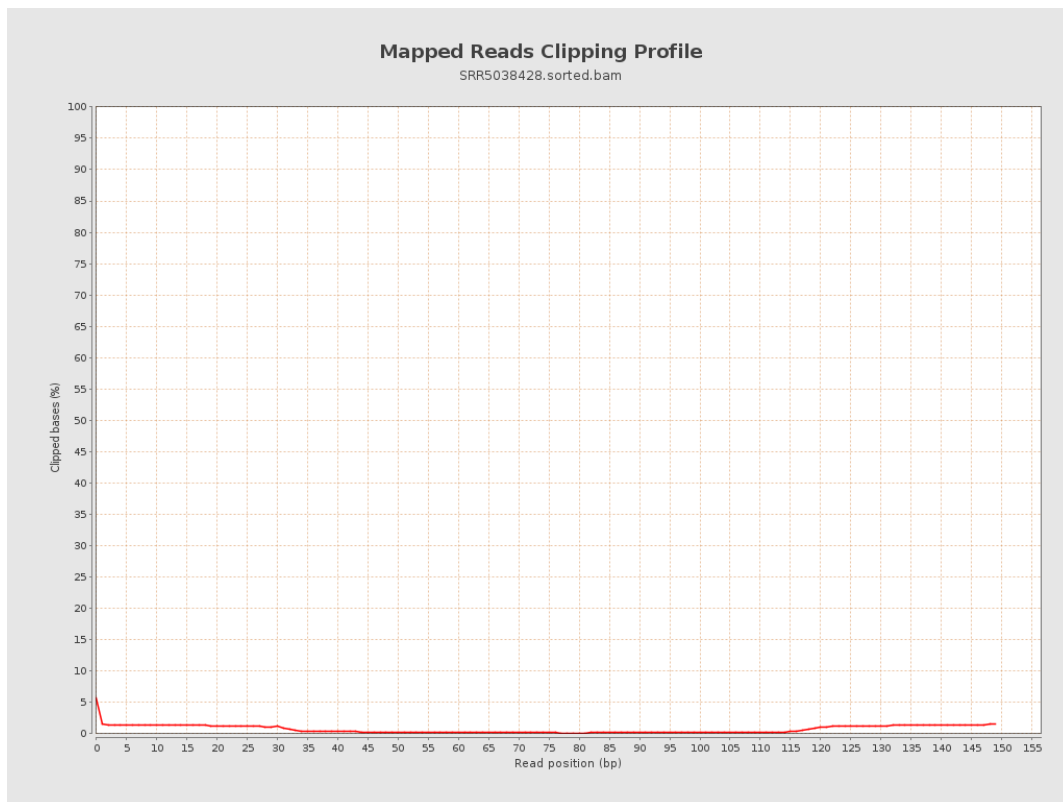
8. Results : Mapped Reads Nucleotide Content



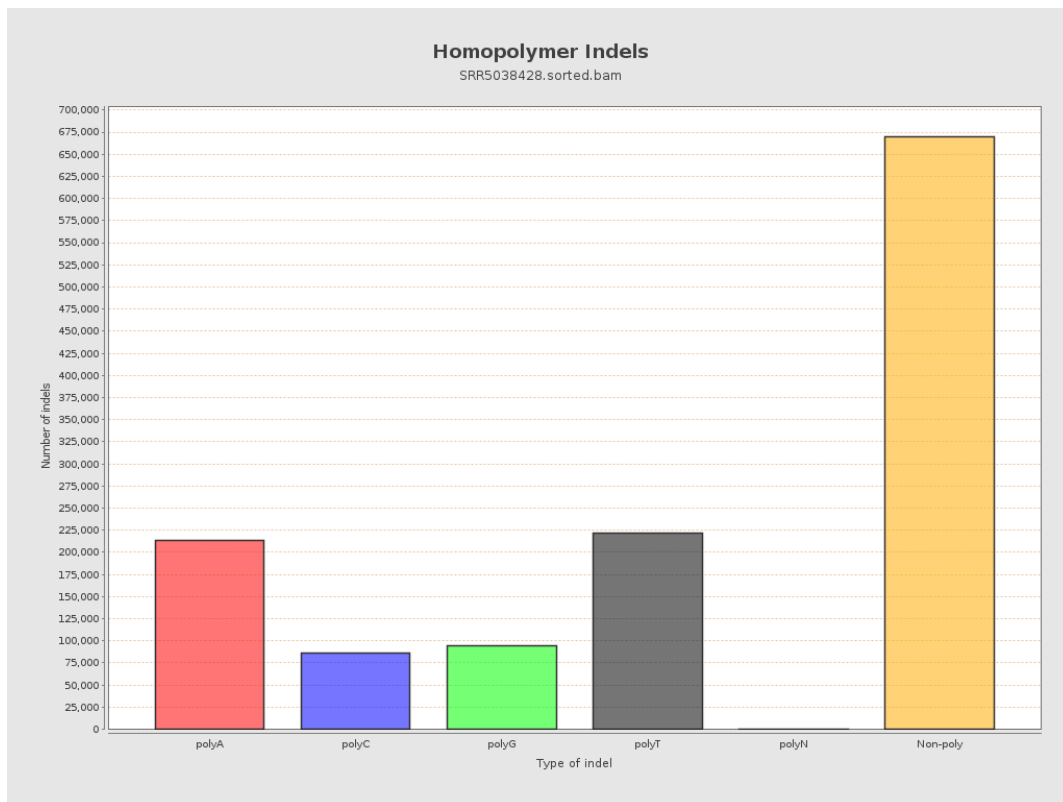
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



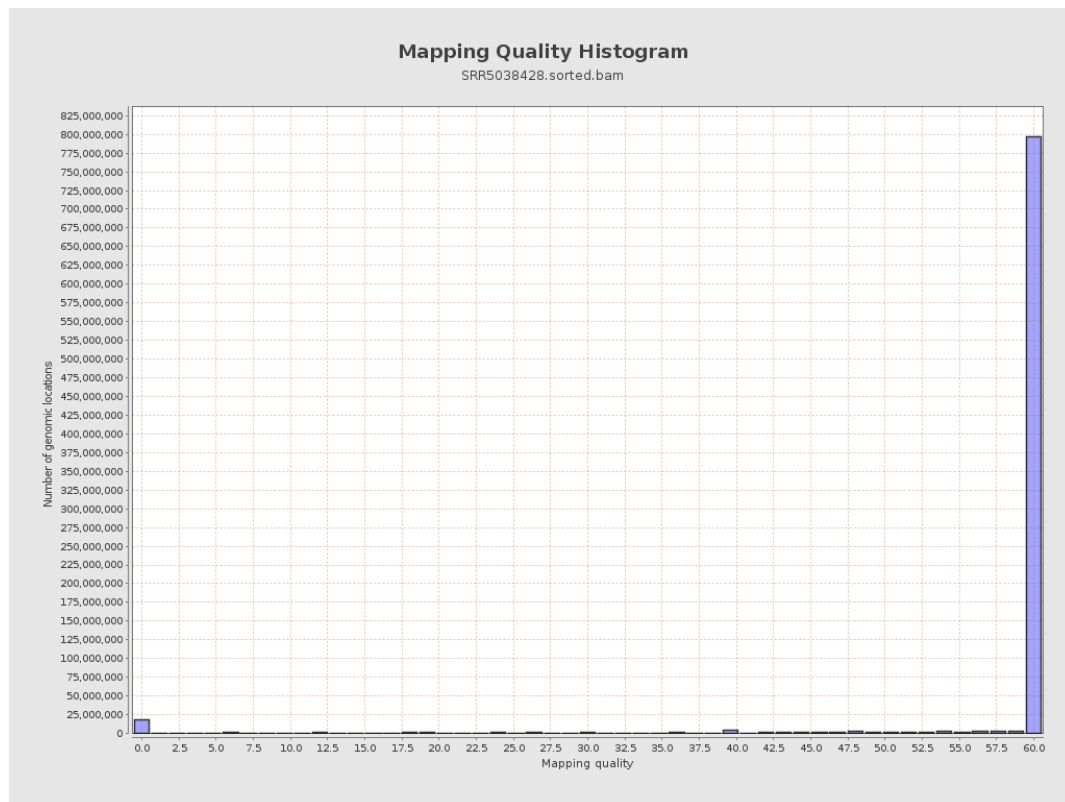
11. Results : Homopolymer Indels



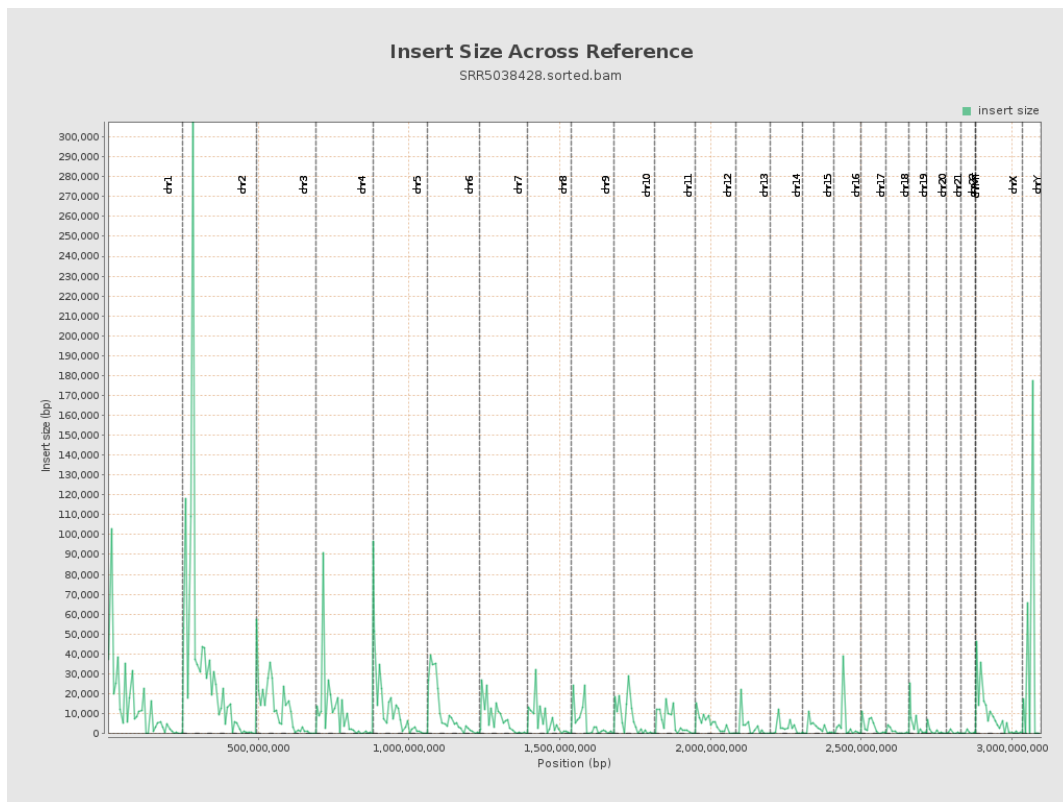
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

