

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 13:06:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038396.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_SRR5038396 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038396_1.fastq.gz SRR5038396_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 13:06:25 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038396.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,497,024
Mapped reads	18,730,269 / 91.38%
Unmapped reads	1,766,755 / 8.62%
Mapped paired reads	18,730,269 / 91.38%
Mapped reads, first in pair	9,489,672 / 46.3%
Mapped reads, second in pair	9,240,597 / 45.08%
Mapped reads, both in pair	18,408,346 / 89.81%
Mapped reads, singletons	321,923 / 1.57%
Secondary alignments	0
Supplementary alignments	389,018 / 1.9%
Read min/max/mean length	30 / 150 / 150.93
Duplicated reads (estimated)	4,423,800 / 21.58%
Duplication rate	15.79%
Clipped reads	9,366,817 / 45.7%

2.2. ACGT Content

Number/percentage of A's	712,661,079 / 28.53%
Number/percentage of C's	499,216,227 / 19.98%
Number/percentage of T's	727,410,852 / 29.12%
Number/percentage of G's	558,855,512 / 22.37%
Number/percentage of N's	195,705 / 0.01%

GC Percentage	42.35%
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2.3. Coverage

Mean	0.8077
Standard Deviation	11.6981

2.4. Mapping Quality

Mean Mapping Quality	53.34
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2.5. Insert size

Mean	92,712.44
Standard Deviation	2,889,258.91
P25/Median/P75	187 / 239 / 304

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	33,183,067
Insertions	534,943
Mapped reads with at least one insertion	2.66%
Deletions	969,153
Mapped reads with at least one deletion	4.94%
Homopolymer indels	45.76%

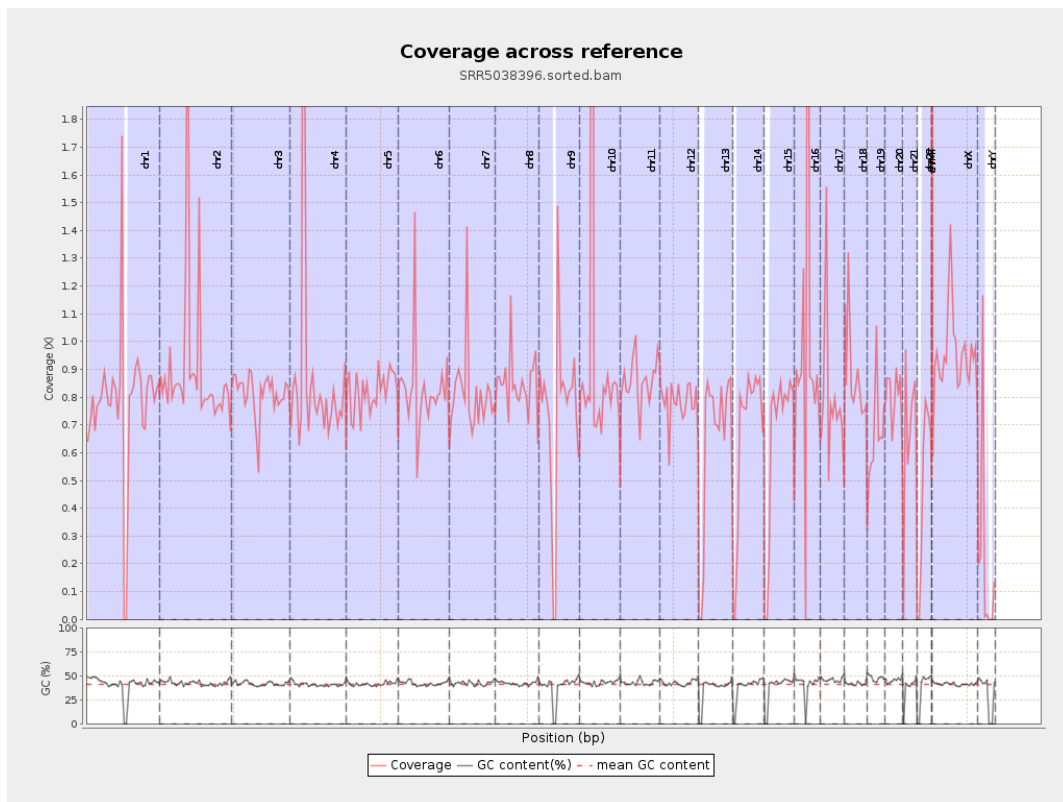
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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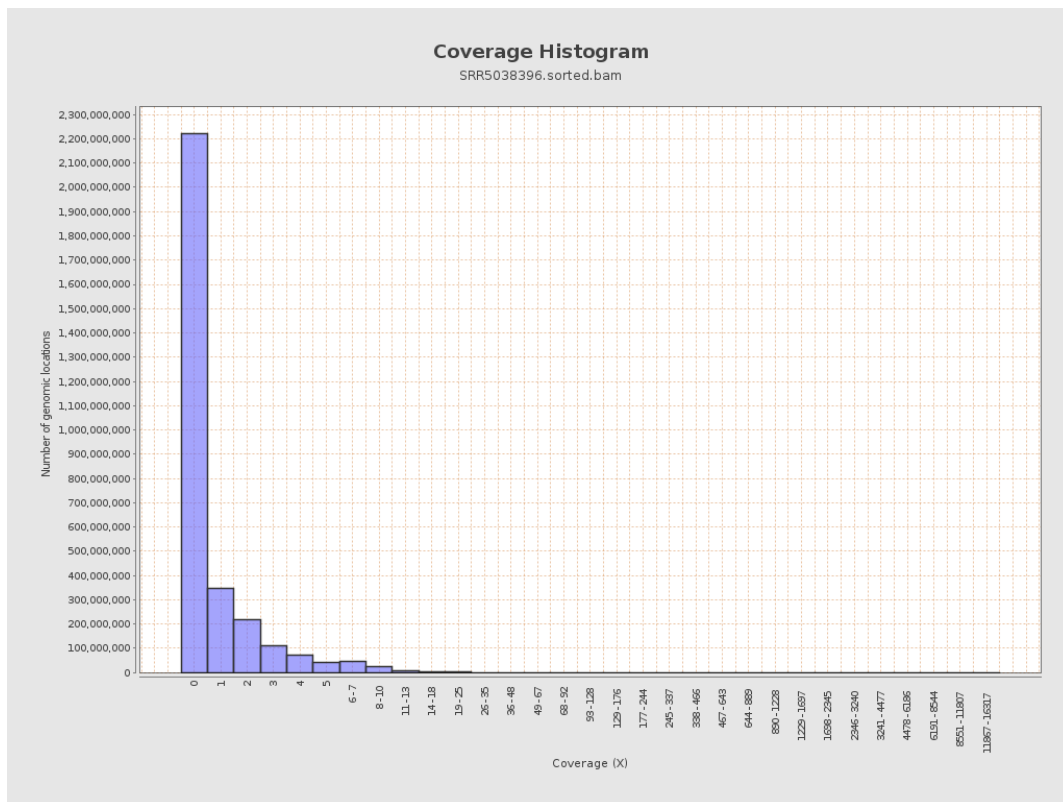
		bases	coverage	deviation
chr1	249250621	195244517	0.7833	16.1633
chr2	243199373	221071648	0.909	12.9348
chr3	198022430	161009894	0.8131	1.9112
chr4	191154276	164531675	0.8607	14.0391
chr5	180915260	148243809	0.8194	1.9149
chr6	171115067	141966131	0.8297	7.6315
chr7	159138663	129003331	0.8106	10.6014
chr8	146364022	123927887	0.8467	3.7061
chr9	141213431	102994255	0.7294	16.6518
chr10	135534747	136476477	1.0069	27.5892
chr11	135006516	114687720	0.8495	6.7625
chr12	133851895	104456886	0.7804	1.9134
chr13	115169878	74750584	0.649	1.6473
chr14	107349540	71751321	0.6684	1.9269
chr15	102531392	66215008	0.6458	1.5952
chr16	90354753	91242443	1.0098	18.0287
chr17	81195210	63495303	0.782	12.6201
chr18	78077248	68246467	0.8741	13.6922
chr19	59128983	38697237	0.6545	7.8456
chr20	63025520	50446573	0.8004	4.3866
chr21	48129895	32544049	0.6762	6.6363
chr22	51304566	24669581	0.4808	1.7375
chrMT	16571	14114624	851.7666	425.1825
chrX	155270560	147629959	0.9508	4.087

chrY	59373566	13045912	0.2197	17.0469
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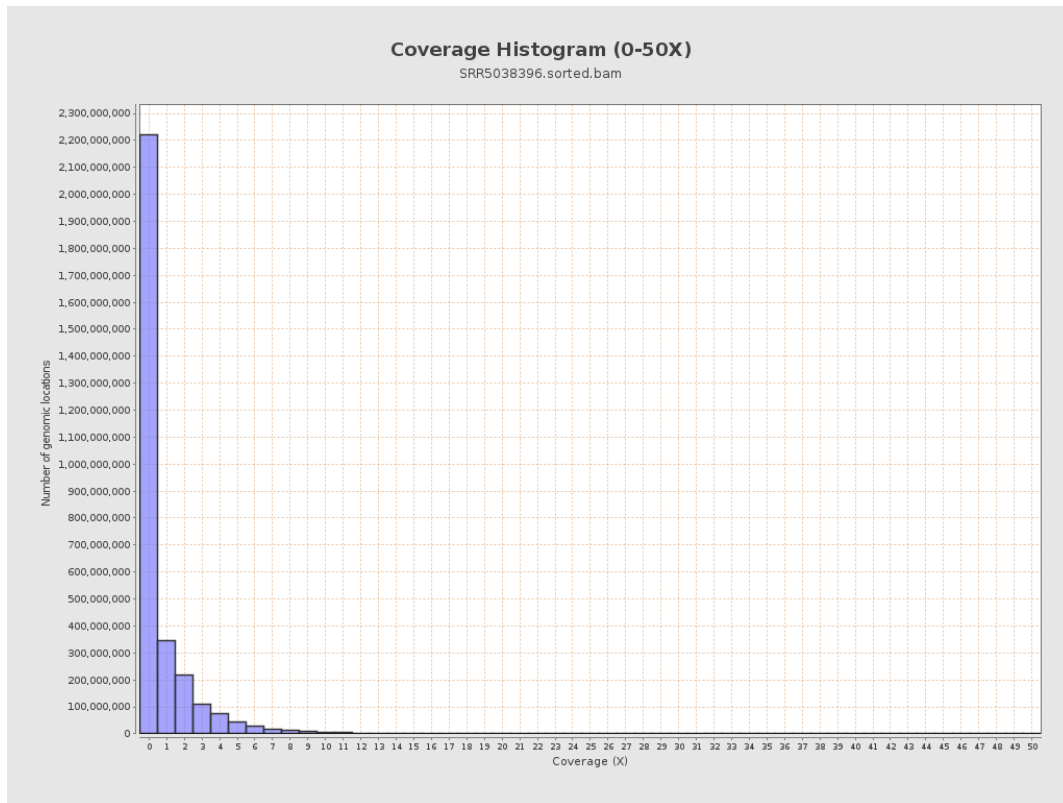
3. Results : Coverage across reference



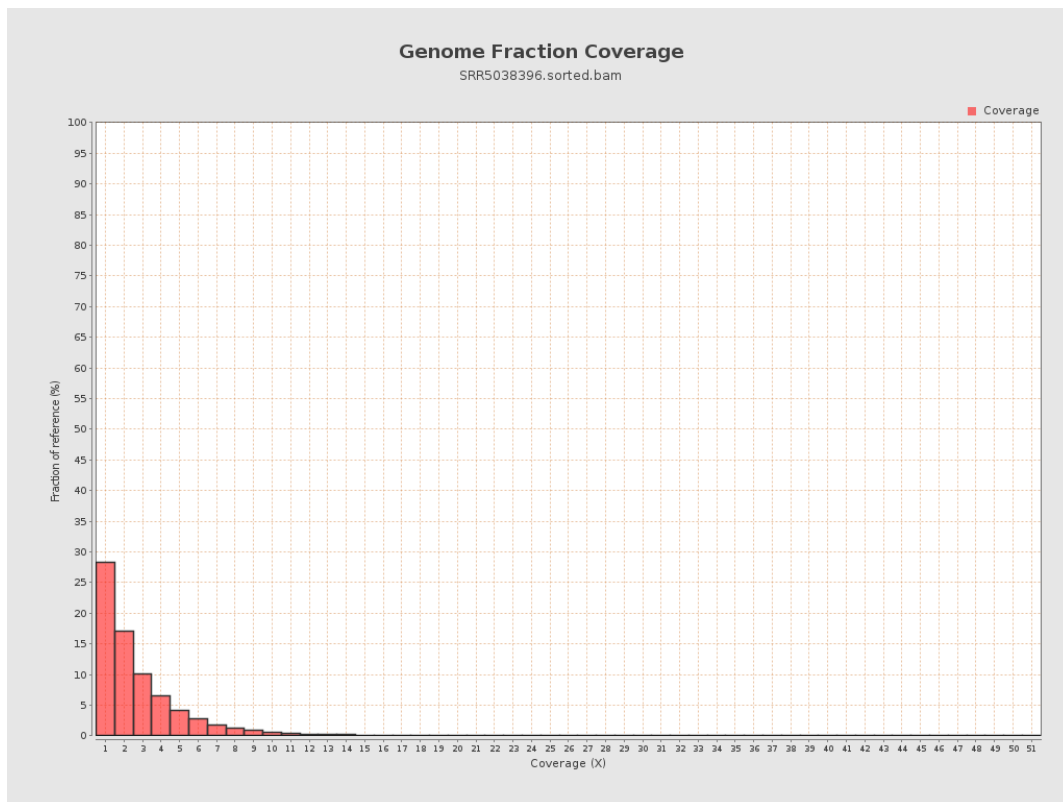
4. Results : Coverage Histogram



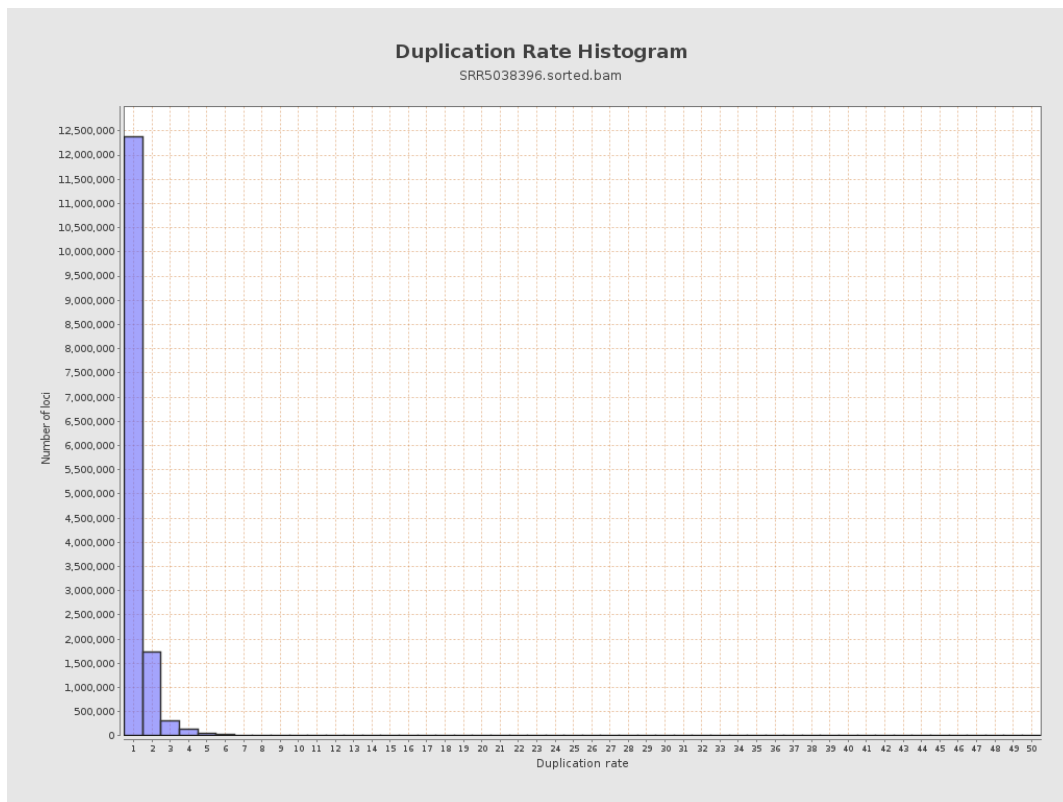
5. Results : Coverage Histogram (0-50X)



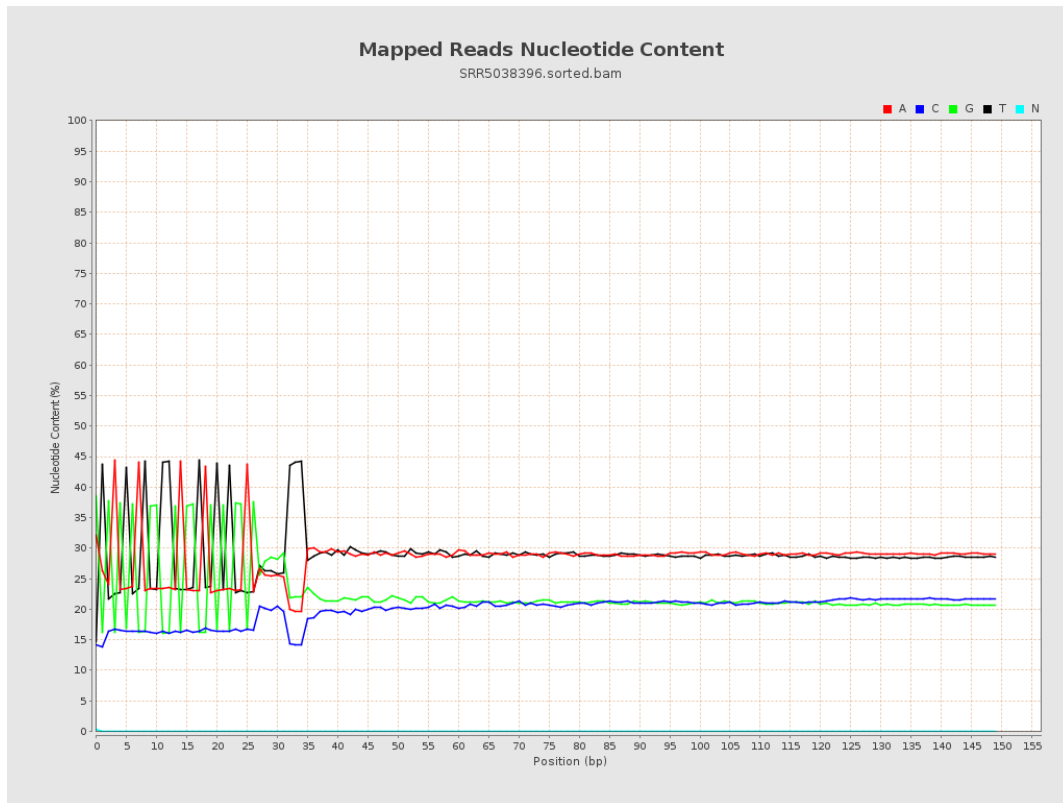
6. Results : Genome Fraction Coverage



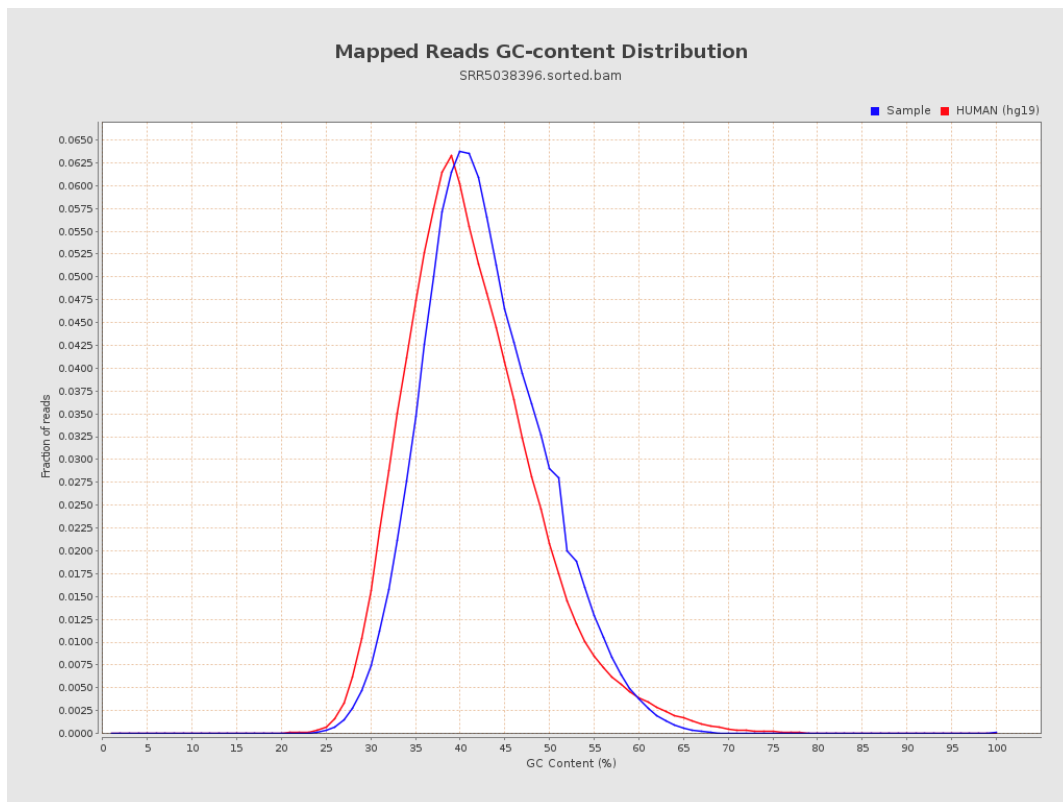
7. Results : Duplication Rate Histogram



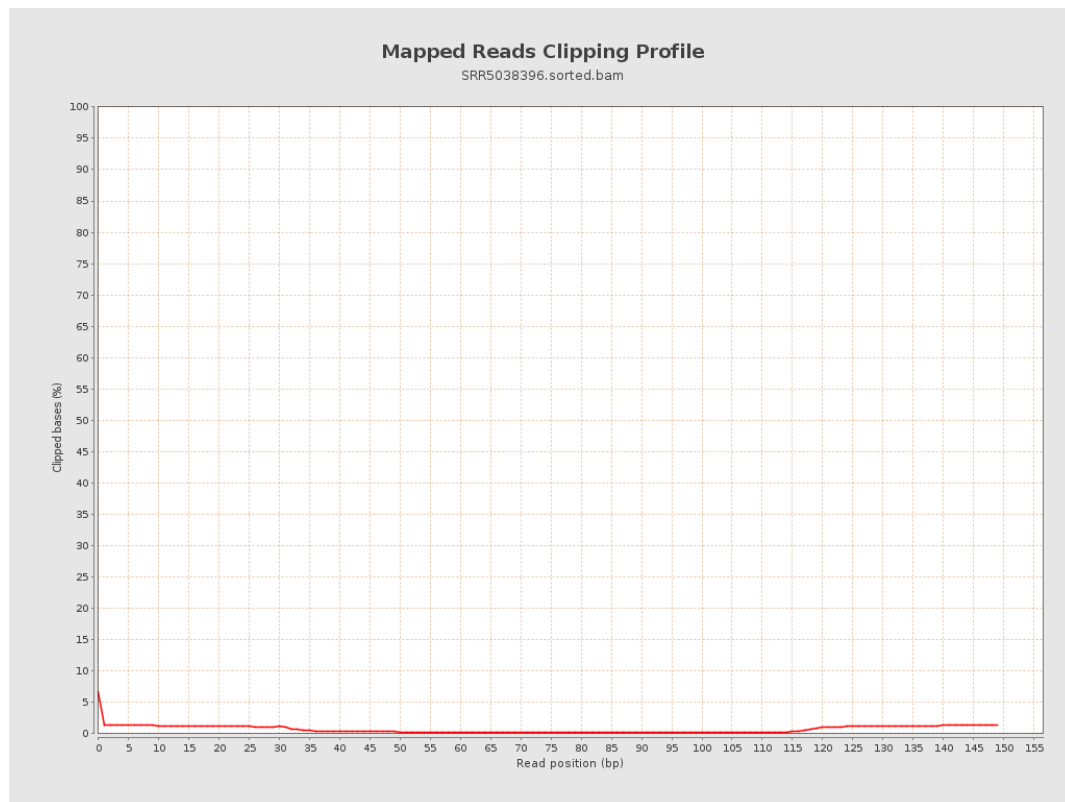
8. Results : Mapped Reads Nucleotide Content



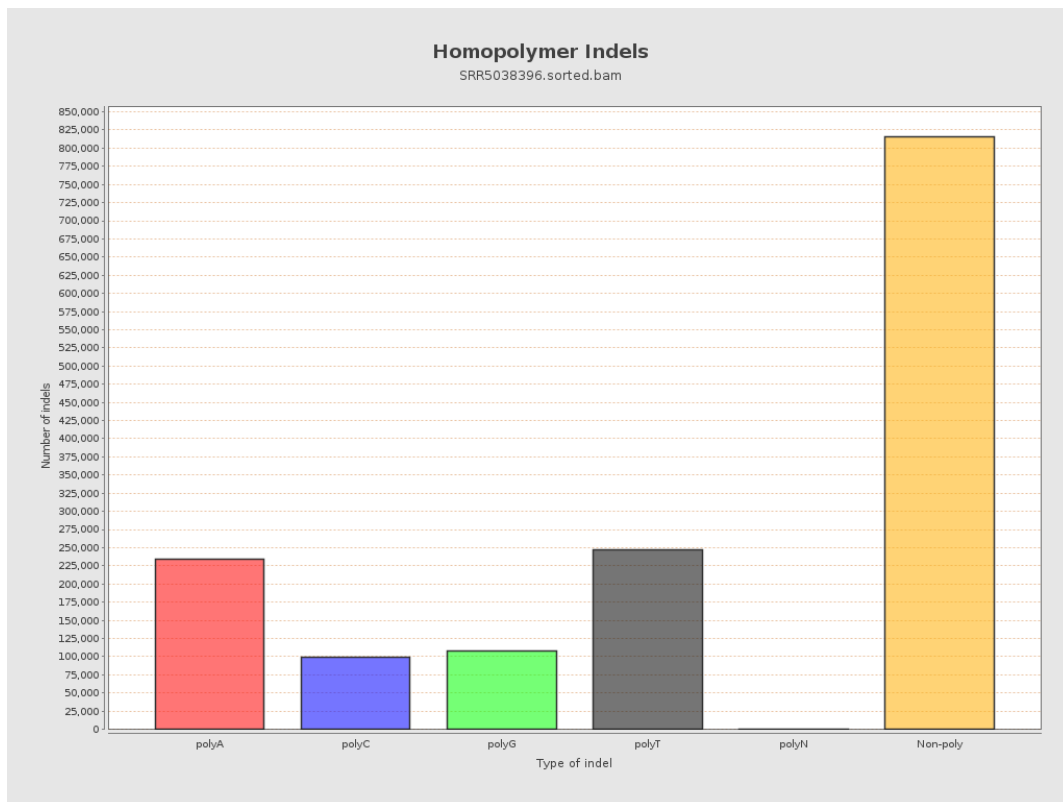
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



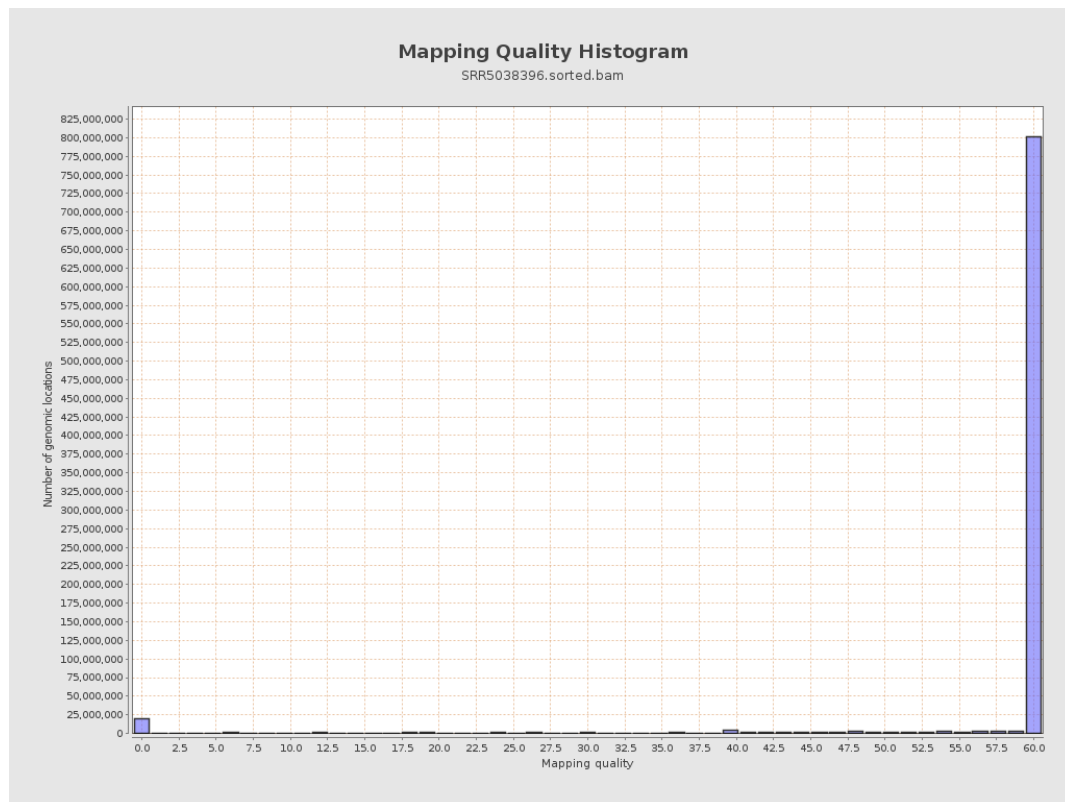
11. Results : Homopolymer Indels



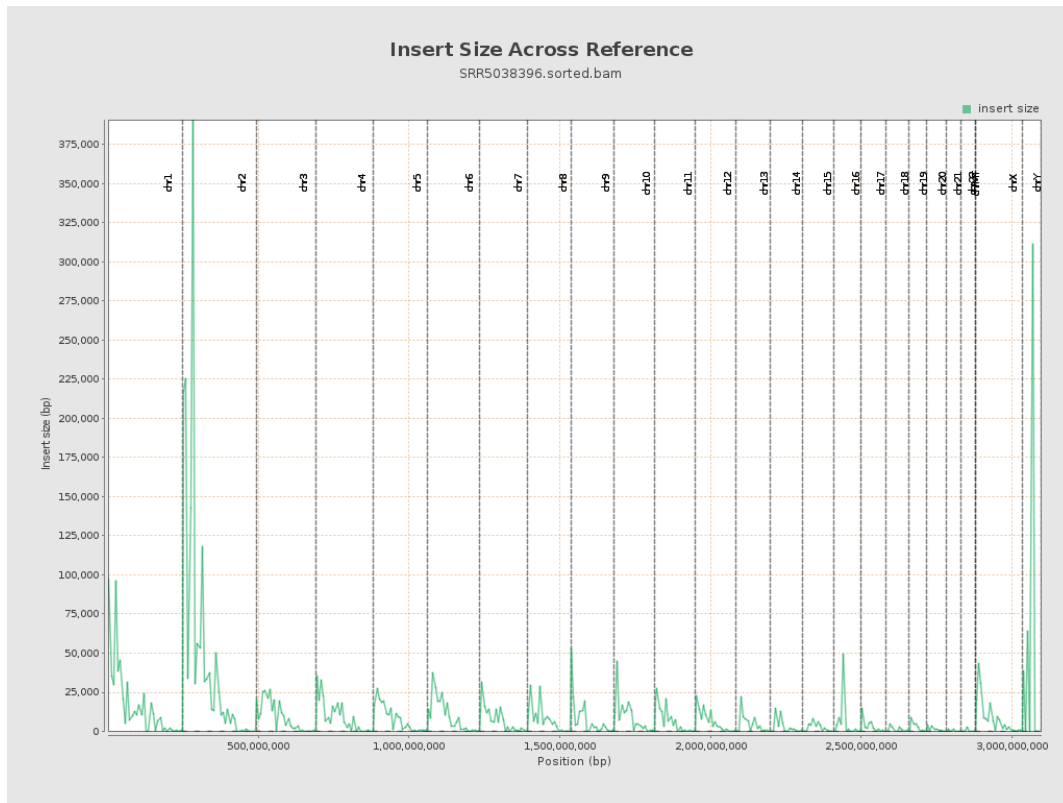
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

