

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/02 14:43:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432716.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_SRR6432716 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432716_1.fastq.gz SRR6432716_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 02 14:43:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432716.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	412,014,350
Mapped reads	411,856,618 / 99.96%
Unmapped reads	157,732 / 0.04%
Mapped paired reads	411,856,618 / 99.96%
Mapped reads, first in pair	205,932,948 / 49.98%
Mapped reads, second in pair	205,923,670 / 49.98%
Mapped reads, both in pair	411,797,230 / 99.95%
Mapped reads, singletons	59,388 / 0.01%
Secondary alignments	0
Supplementary alignments	197,495 / 0.05%
Read min/max/mean length	30 / 150 / 139.56
Duplicated reads (estimated)	197,565,973 / 47.95%
Duplication rate	32.07%
Clipped reads	116,725,412 / 28.33%

2.2. ACGT Content

Number/percentage of A's	15,526,954,655 / 27.55%
Number/percentage of C's	12,081,993,519 / 21.44%
Number/percentage of T's	15,338,554,587 / 27.22%
Number/percentage of G's	13,409,359,489 / 23.79%
Number/percentage of N's	907,626 / 0%

GC Percentage	45.23%
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2.3. Coverage

Mean	18.2225
Standard Deviation	49.8692

2.4. Mapping Quality

Mean Mapping Quality	55.41
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2.5. Insert size

Mean	71,909.13
Standard Deviation	2,693,953.32
P25/Median/P75	288 / 305 / 320

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	512,185,063
Insertions	11,439,638
Mapped reads with at least one insertion	2.71%
Deletions	36,785,908
Mapped reads with at least one deletion	8.53%
Homopolymer indels	51.47%

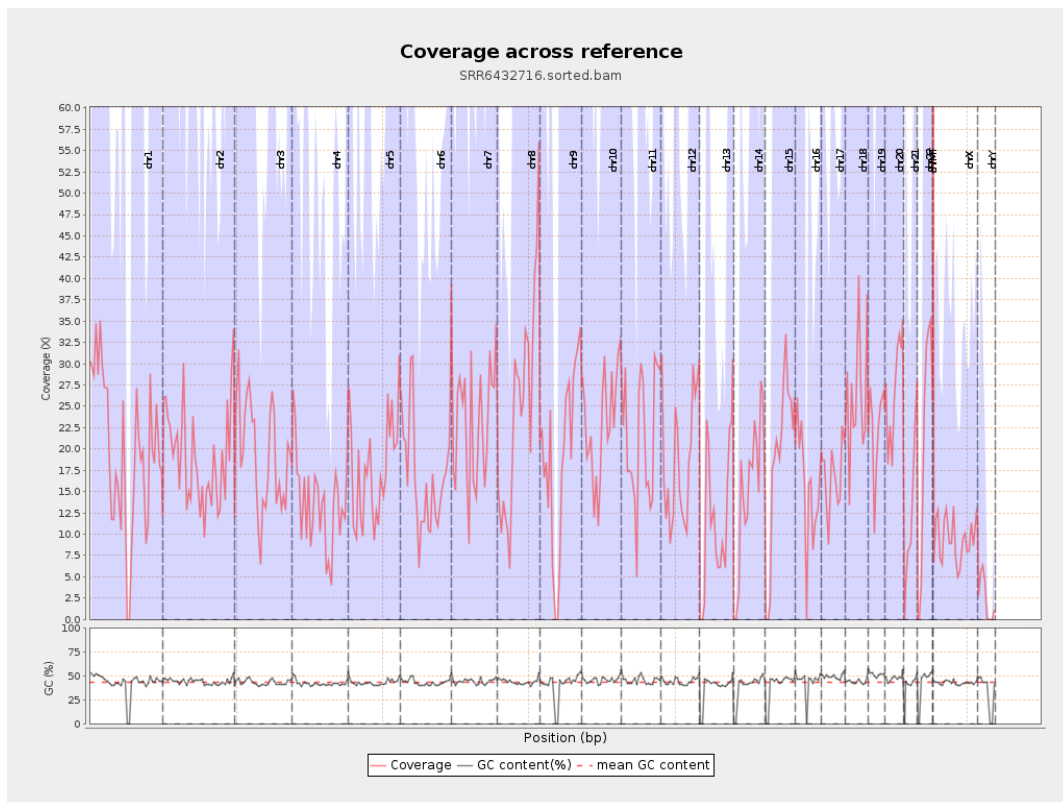
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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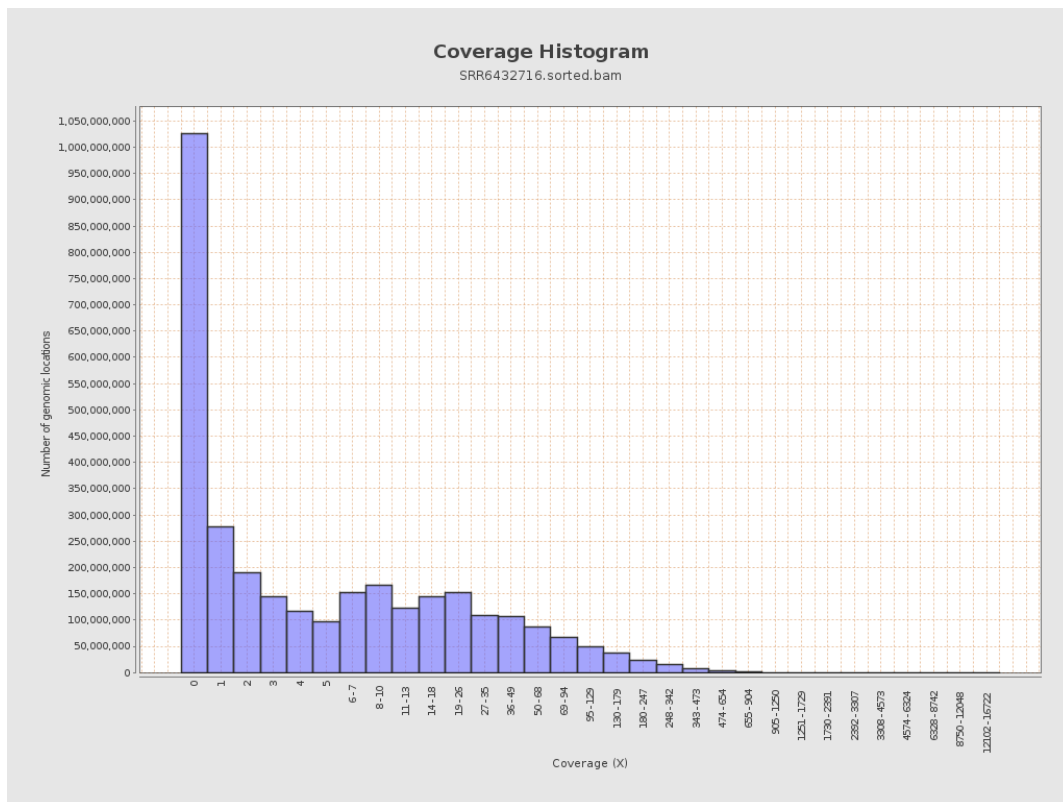
		bases	coverage	deviation
chr1	249250621	4862562003	19.5087	52.0972
chr2	243199373	4617675947	18.9872	53.8459
chr3	198022430	3772650766	19.0516	47.1284
chr4	191154276	2615516394	13.6828	38.4129
chr5	180915260	3230171271	17.8546	46.493
chr6	171115067	2837443987	16.5821	43.2748
chr7	159138663	3713620044	23.3357	58.1415
chr8	146364022	3663353593	25.0291	65.5747
chr9	141213431	2695921133	19.0911	56.6805
chr10	135534747	3080881279	22.7313	55.0018
chr11	135006516	2868041930	21.2437	52.1959
chr12	133851895	2515162486	18.7906	48.3286
chr13	115169878	1353777635	11.7546	36.5238
chr14	107349540	1635230446	15.2328	42.0703
chr15	102531392	1911237562	18.6405	50.2849
chr16	90354753	1405054335	15.5504	48.1734
chr17	81195210	1347101052	16.5909	41.6504
chr18	78077248	2013645282	25.7904	65.3914
chr19	59128983	1310181646	22.158	56.8048
chr20	63025520	1676339920	26.5978	61.0739
chr21	48129895	601193190	12.4911	43.6443
chr22	51304566	1066300962	20.7837	57.3239
chrMT	16571	5230513	315.6426	581.9682
chrX	155270560	1461019376	9.4095	25.8513

chrY	59373566	152120342	2.5621	19.6666
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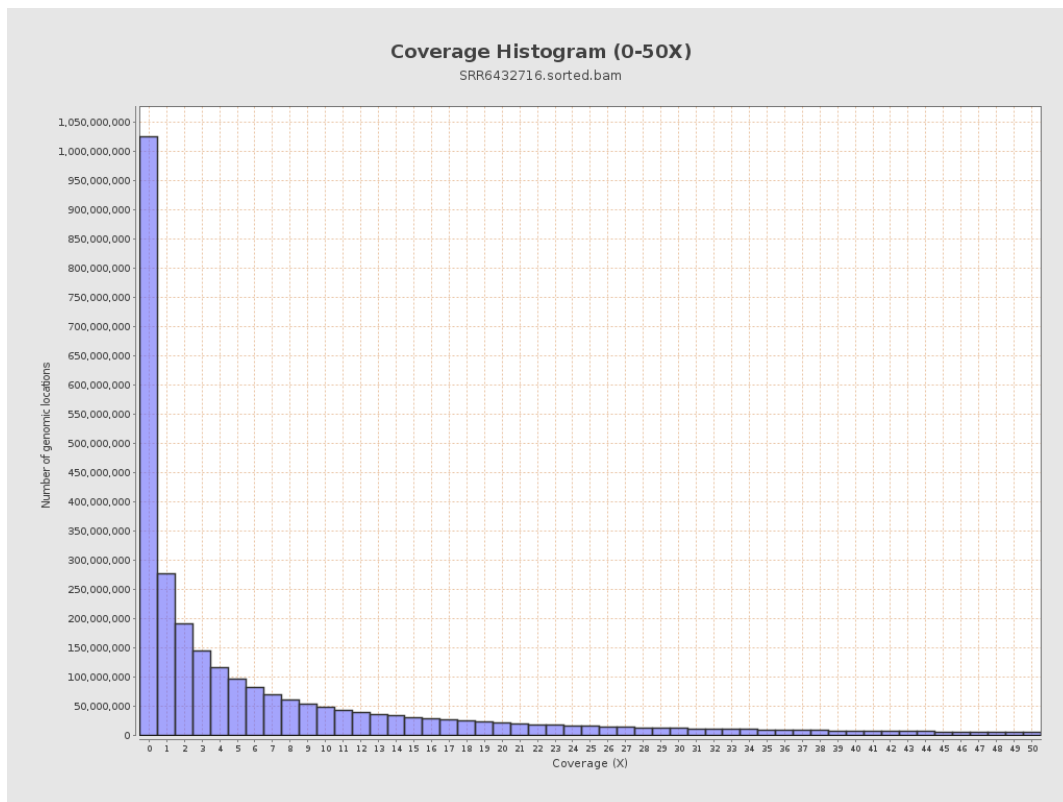
3. Results : Coverage across reference



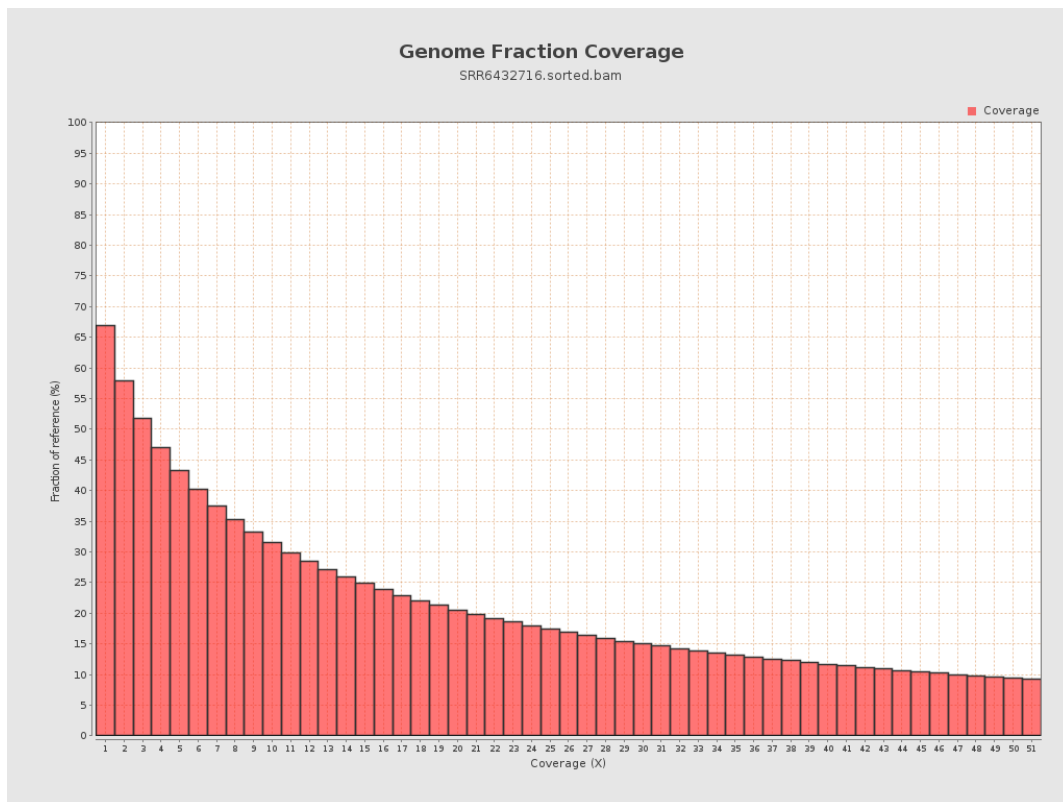
4. Results : Coverage Histogram



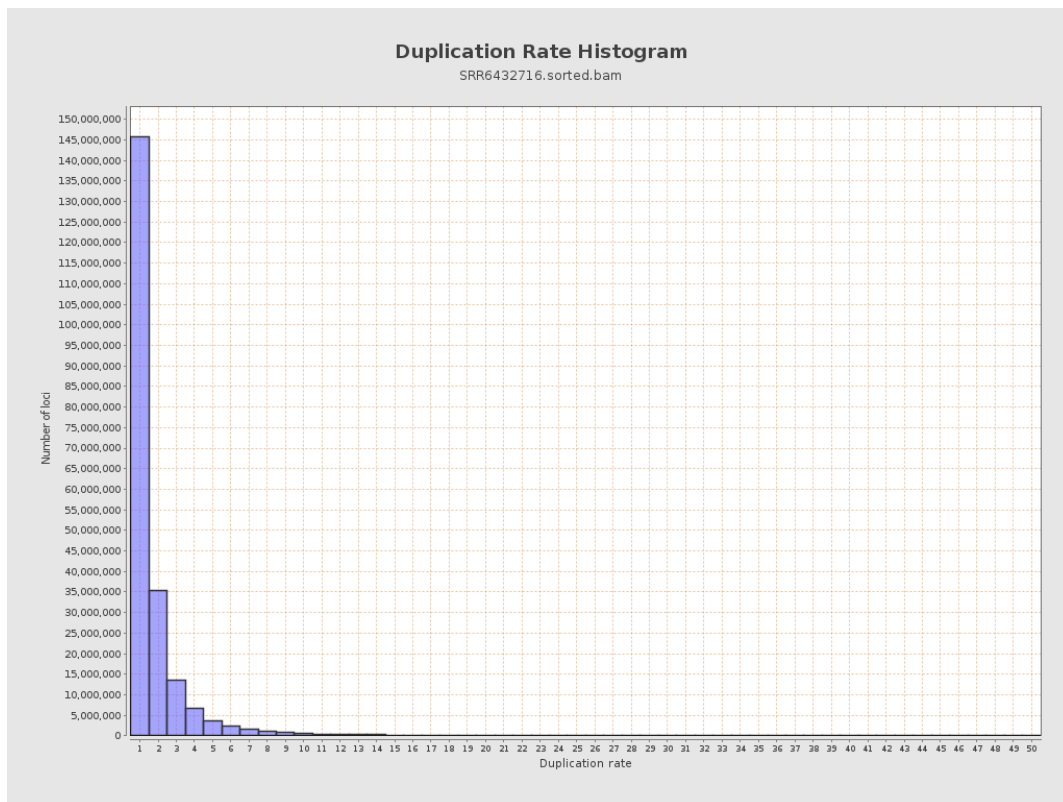
5. Results : Coverage Histogram (0-50X)



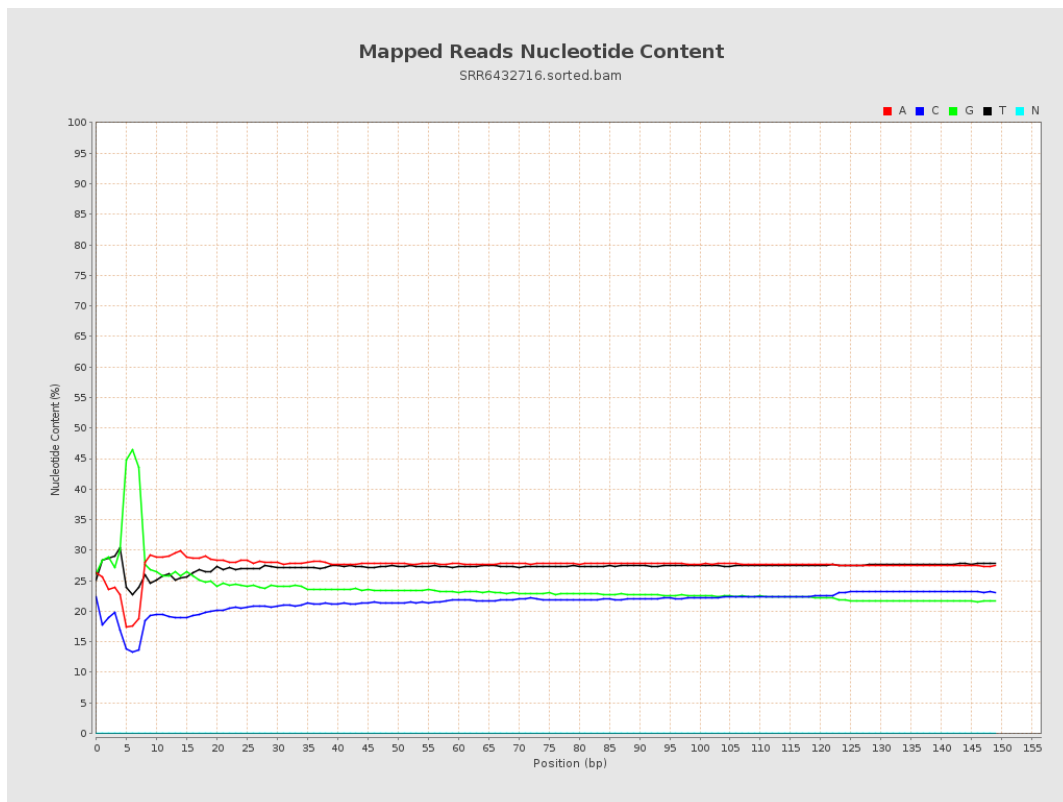
6. Results : Genome Fraction Coverage



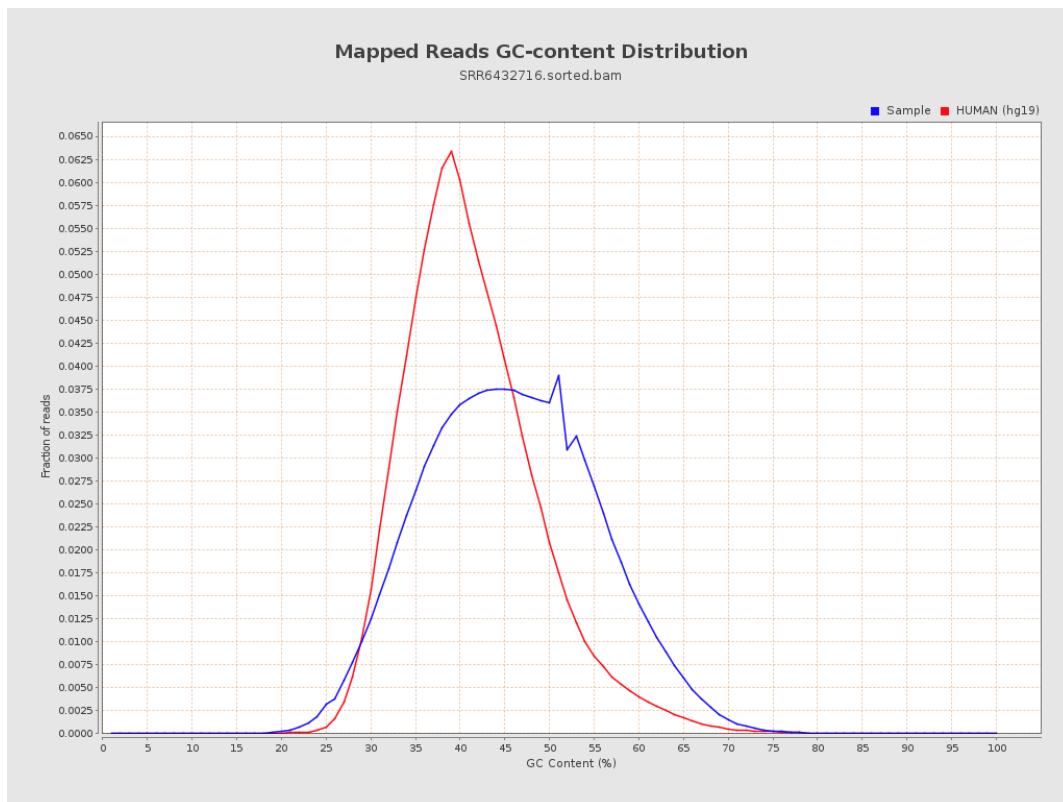
7. Results : Duplication Rate Histogram



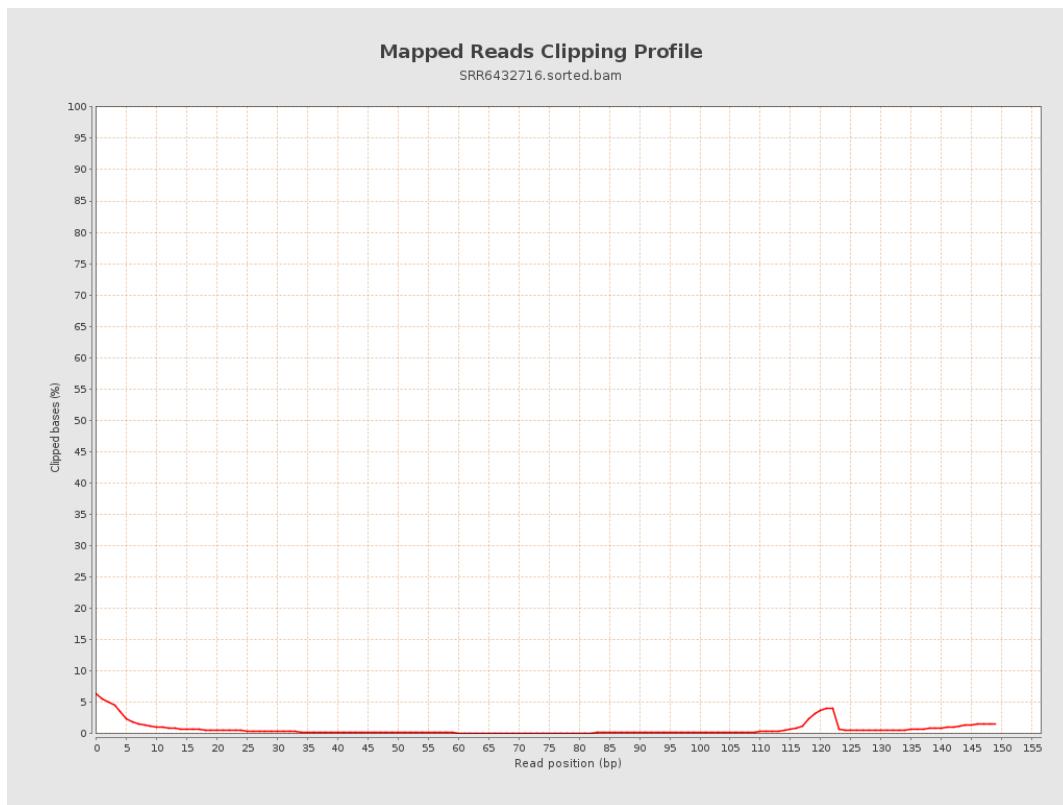
8. Results : Mapped Reads Nucleotide Content



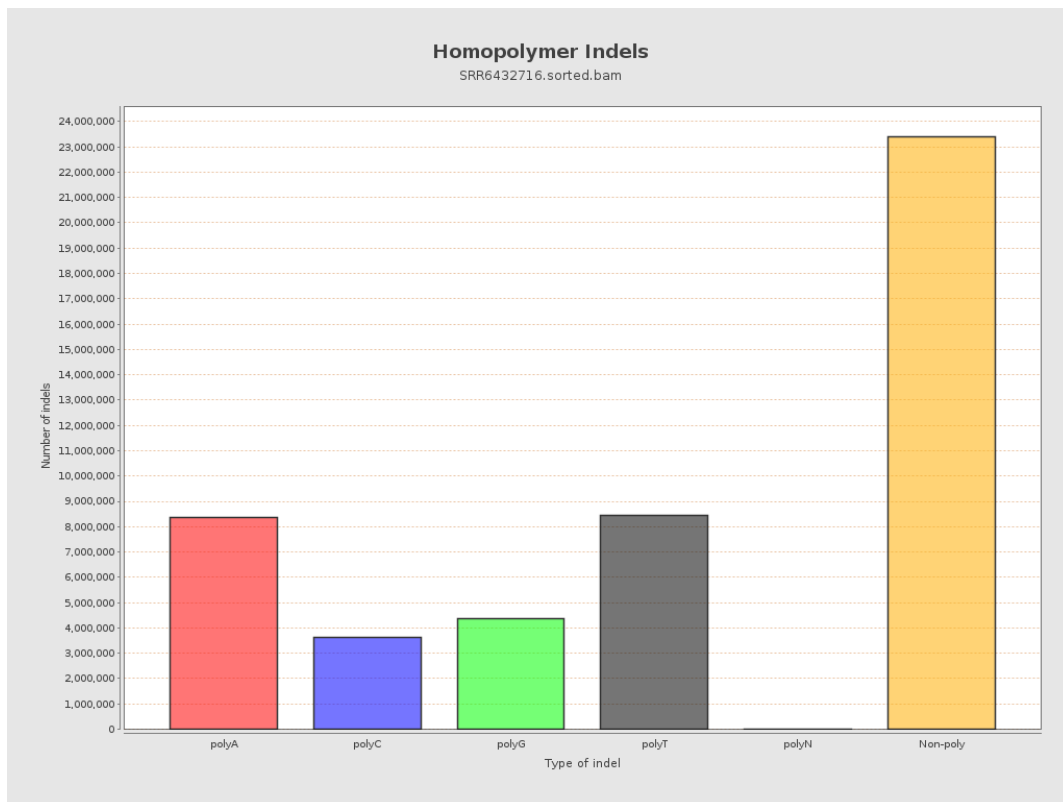
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



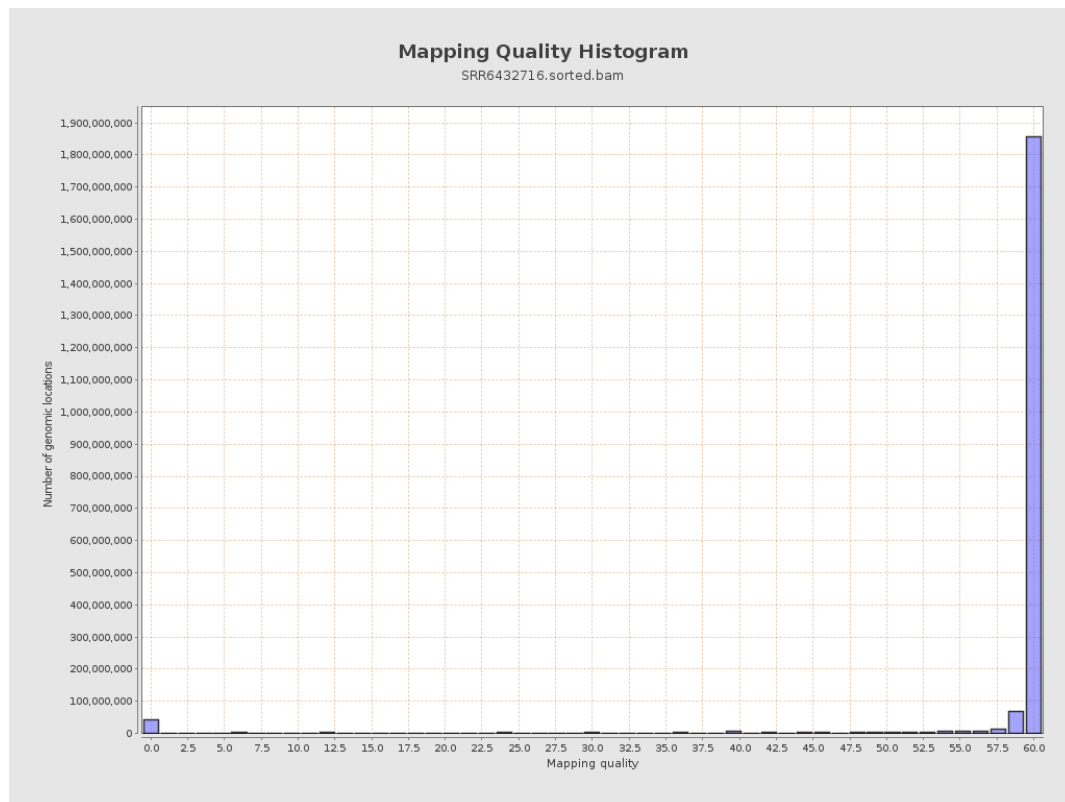
11. Results : Homopolymer Indels



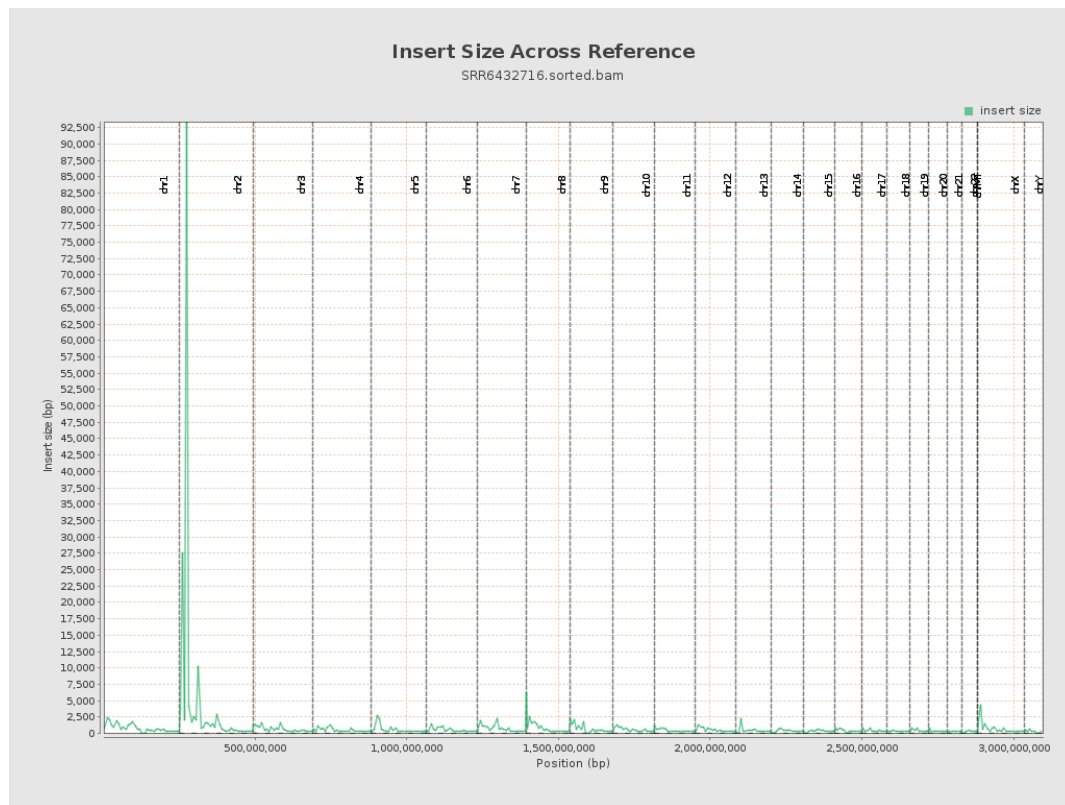
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

