

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/01 00:58:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432712.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_SRR6432712 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432712_1.fastq.gz SRR6432712_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 01 00:58:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432712.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	335,190,218
Mapped reads	335,047,863 / 99.96%
Unmapped reads	142,355 / 0.04%
Mapped paired reads	335,047,863 / 99.96%
Mapped reads, first in pair	167,528,607 / 49.98%
Mapped reads, second in pair	167,519,256 / 49.98%
Mapped reads, both in pair	334,994,926 / 99.94%
Mapped reads, singletons	52,937 / 0.02%
Secondary alignments	0
Supplementary alignments	1,168,997 / 0.35%
Read min/max/mean length	30 / 150 / 143.64
Duplicated reads (estimated)	167,969,732 / 50.11%
Duplication rate	35.3%
Clipped reads	57,942,018 / 17.29%

2.2. ACGT Content

Number/percentage of A's	13,282,893,622 / 27.95%
Number/percentage of C's	10,131,272,864 / 21.32%
Number/percentage of T's	13,120,911,023 / 27.61%
Number/percentage of G's	10,987,938,393 / 23.12%
Number/percentage of N's	6,036,637 / 0.01%

GC Percentage	44.43%
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2.3. Coverage

Mean	15.369
Standard Deviation	54.9752

2.4. Mapping Quality

Mean Mapping Quality	57.48
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2.5. Insert size

Mean	36,211.57
Standard Deviation	1,942,560.13
P25/Median/P75	311 / 330 / 349

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	416,639,811
Insertions	10,181,639
Mapped reads with at least one insertion	2.97%
Deletions	34,972,577
Mapped reads with at least one deletion	9.91%
Homopolymer indels	53.7%

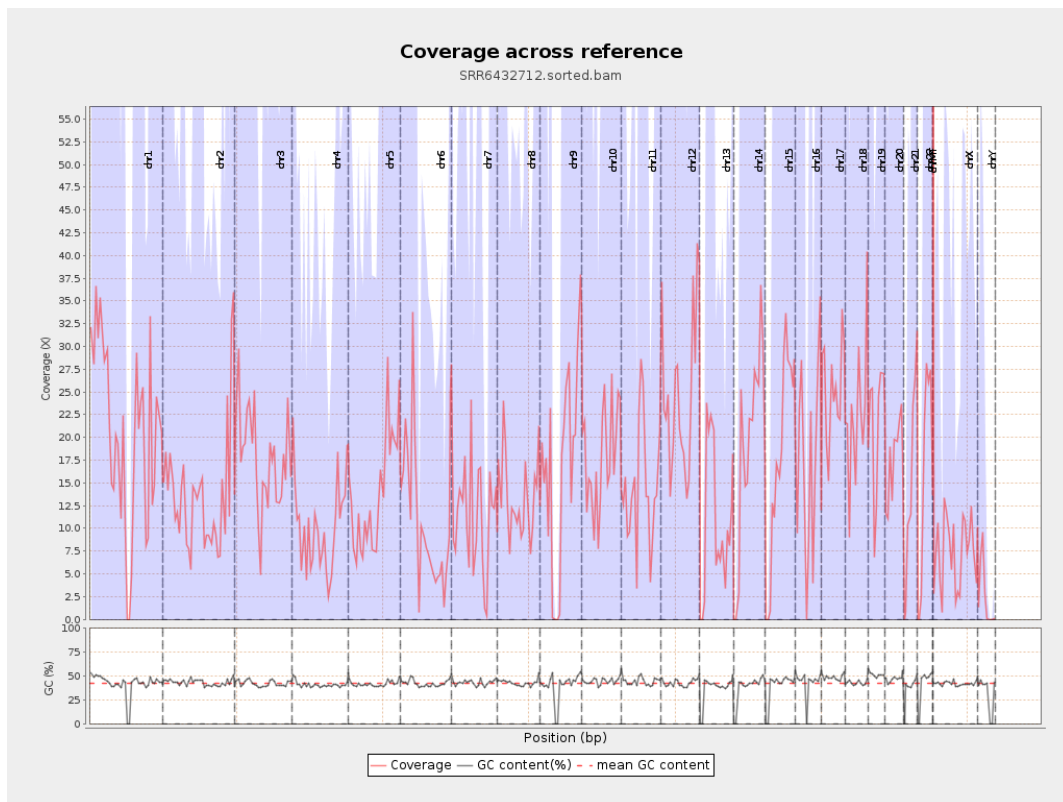
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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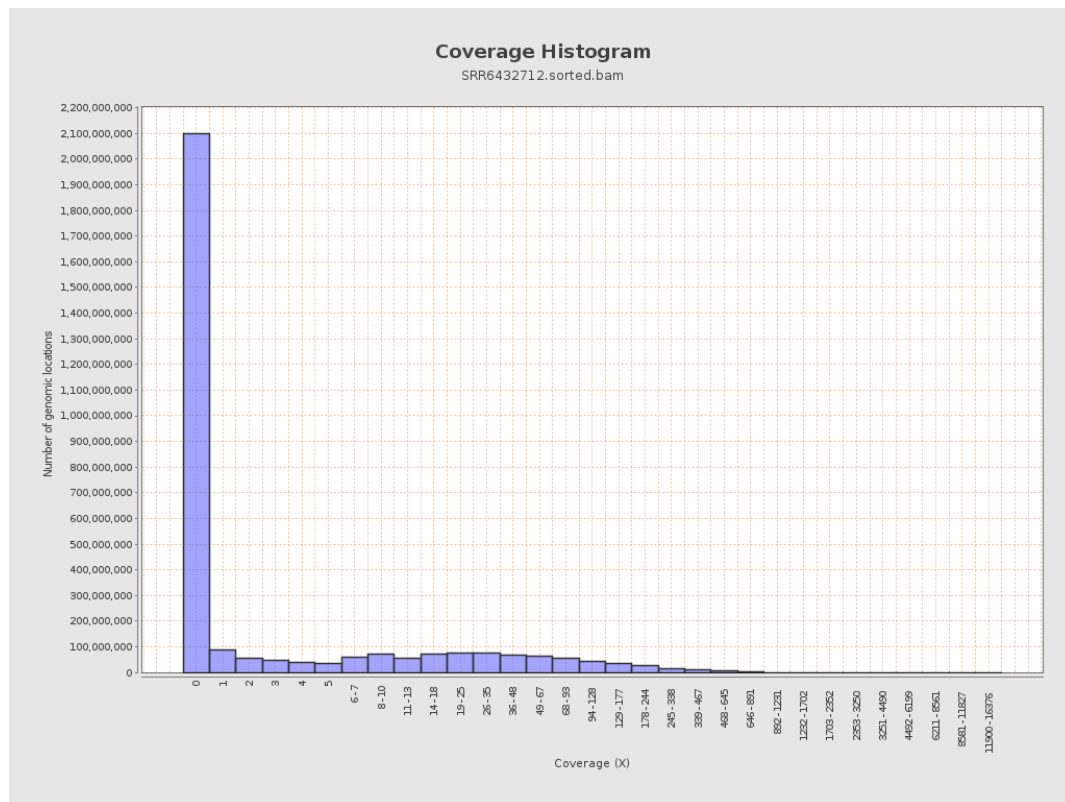
		bases	coverage	deviation
chr1	249250621	5097448633	20.4511	65.6288
chr2	243199373	3254356814	13.3814	51.7115
chr3	198022430	3475469913	17.5509	55.7254
chr4	191154276	1914966372	10.0179	38.9846
chr5	180915260	2511832872	13.884	48.7531
chr6	171115067	1830302898	10.6963	44.4208
chr7	159138663	1858058448	11.6757	44.5505
chr8	146364022	1963000550	13.4118	46.9209
chr9	141213431	2359974859	16.7121	59.4491
chr10	135534747	2403998556	17.7371	57.7348
chr11	135006516	1943541605	14.3959	51.1164
chr12	133851895	3294022941	24.6095	71.9981
chr13	115169878	1212071367	10.5242	42.8897
chr14	107349540	2088003382	19.4505	63.2187
chr15	102531392	1791141264	17.4692	61.0556
chr16	90354753	1572183838	17.4001	67.4369
chr17	81195210	2047273587	25.2142	72.8281
chr18	78077248	1708071405	21.8767	67.3574
chr19	59128983	1253317206	21.1963	68.0116
chr20	63025520	1116323939	17.7123	58.9242
chr21	48129895	718389067	14.926	54.169
chr22	51304566	847661442	16.5221	59.1472
chrMT	16571	5258213	317.3142	483.2809
chrX	155270560	1151897063	7.4186	33.6545

chrY	59373566	159255669	2.6823	25.5967
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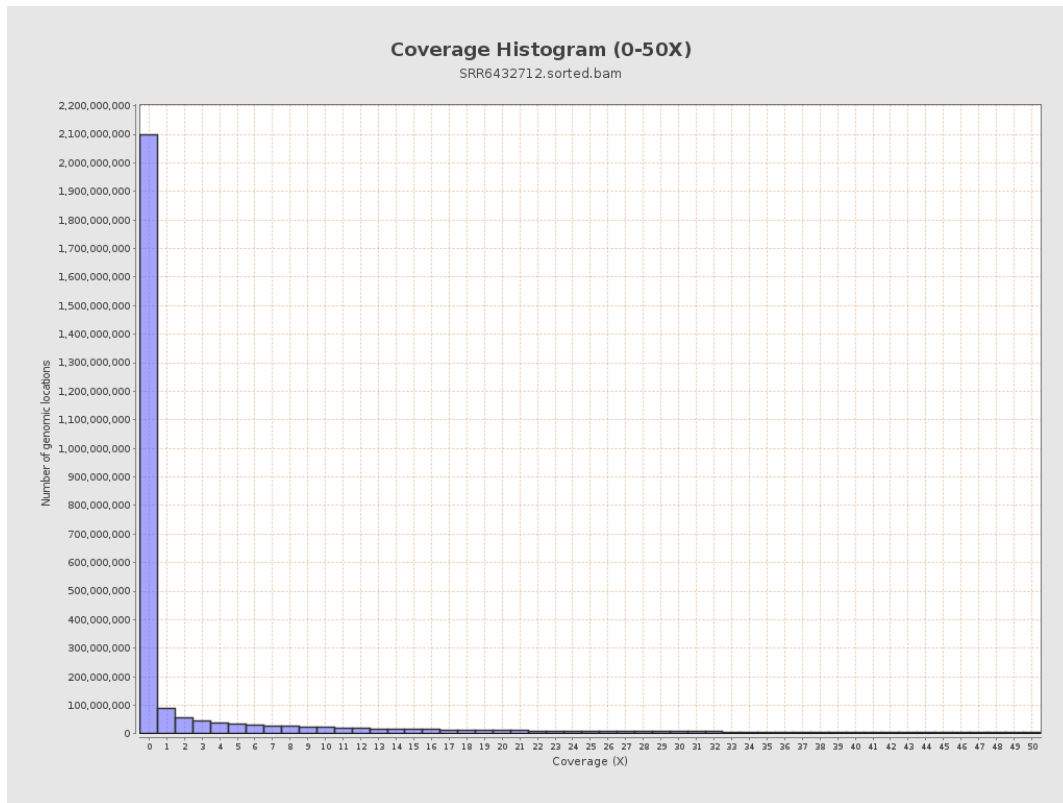
3. Results : Coverage across reference



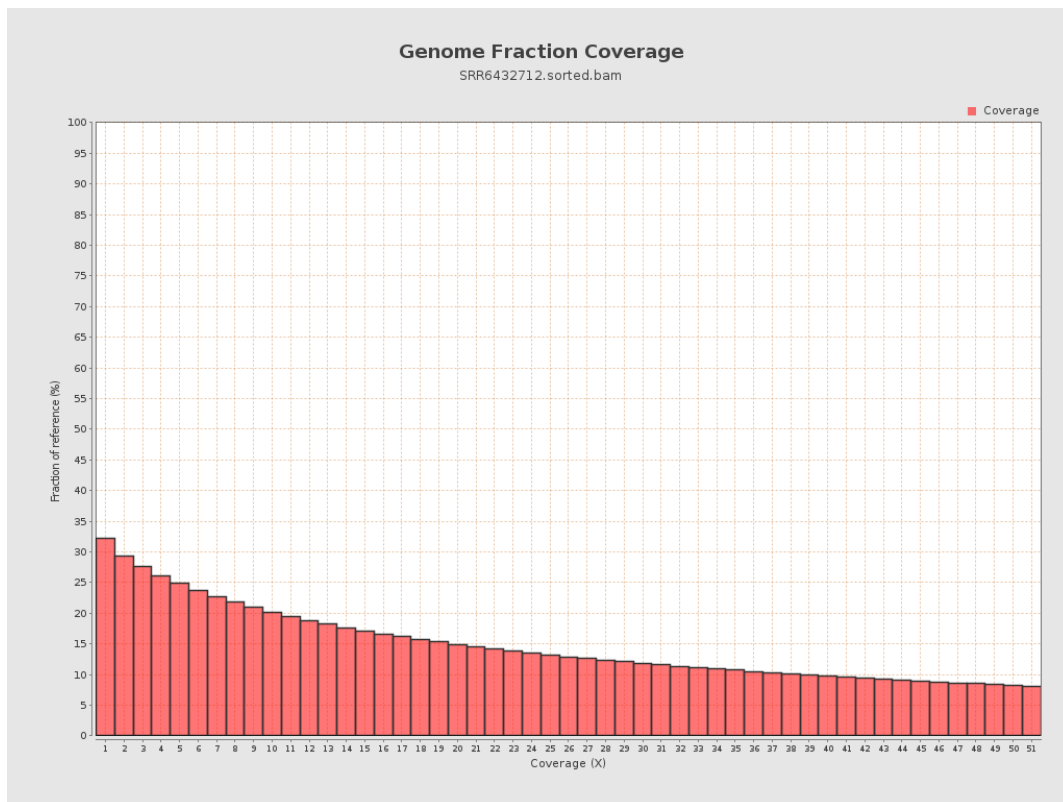
4. Results : Coverage Histogram



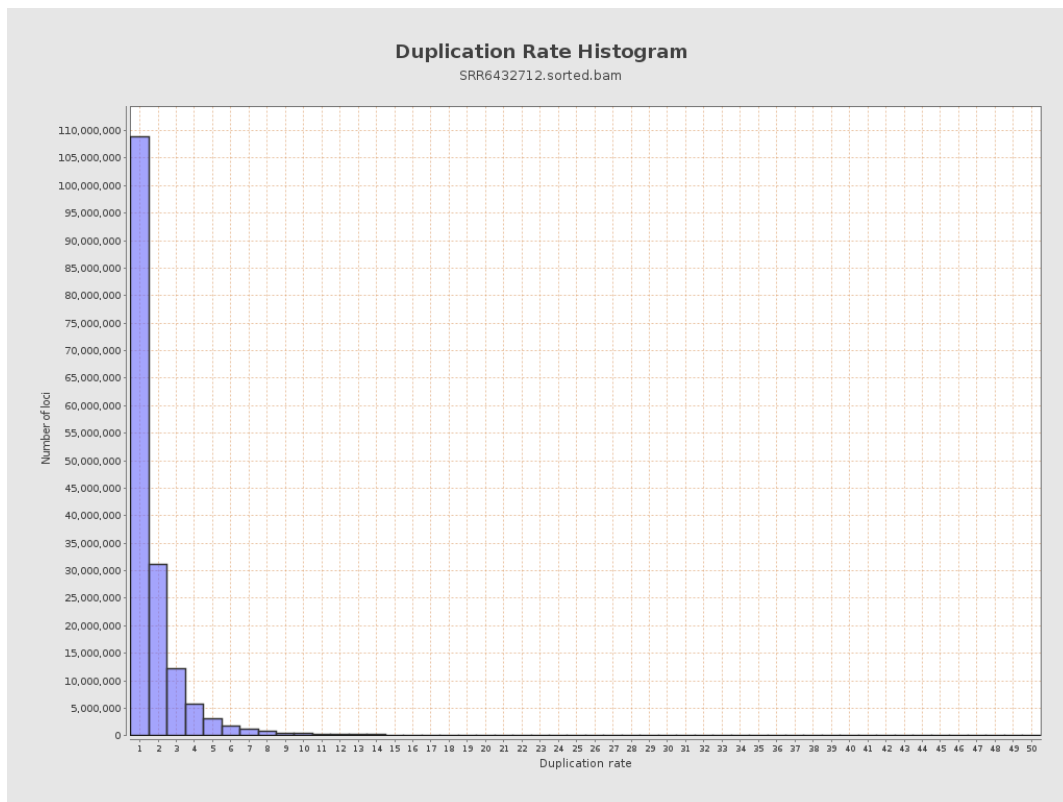
5. Results : Coverage Histogram (0-50X)



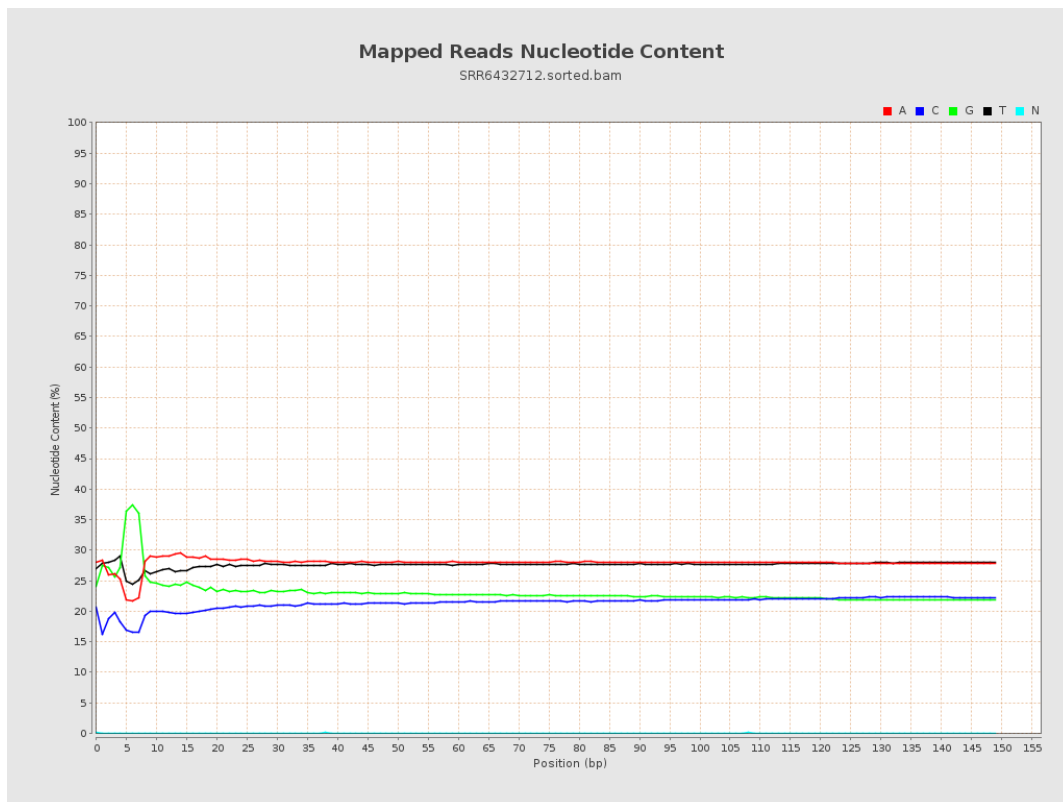
6. Results : Genome Fraction Coverage



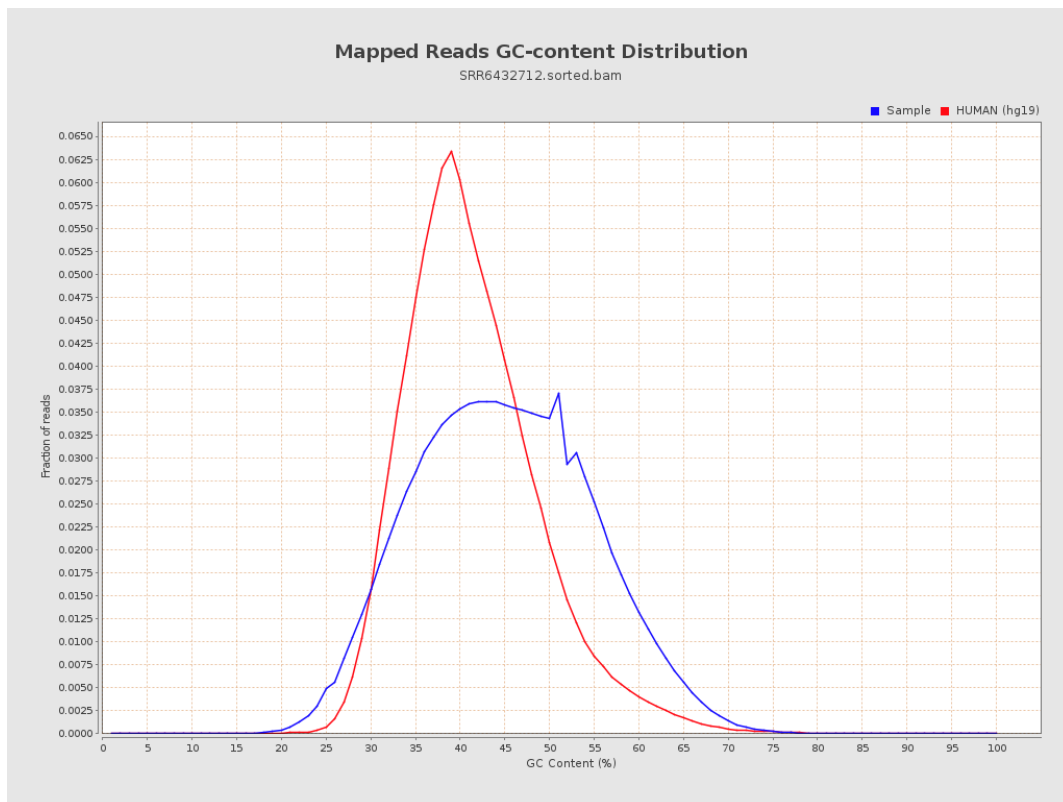
7. Results : Duplication Rate Histogram



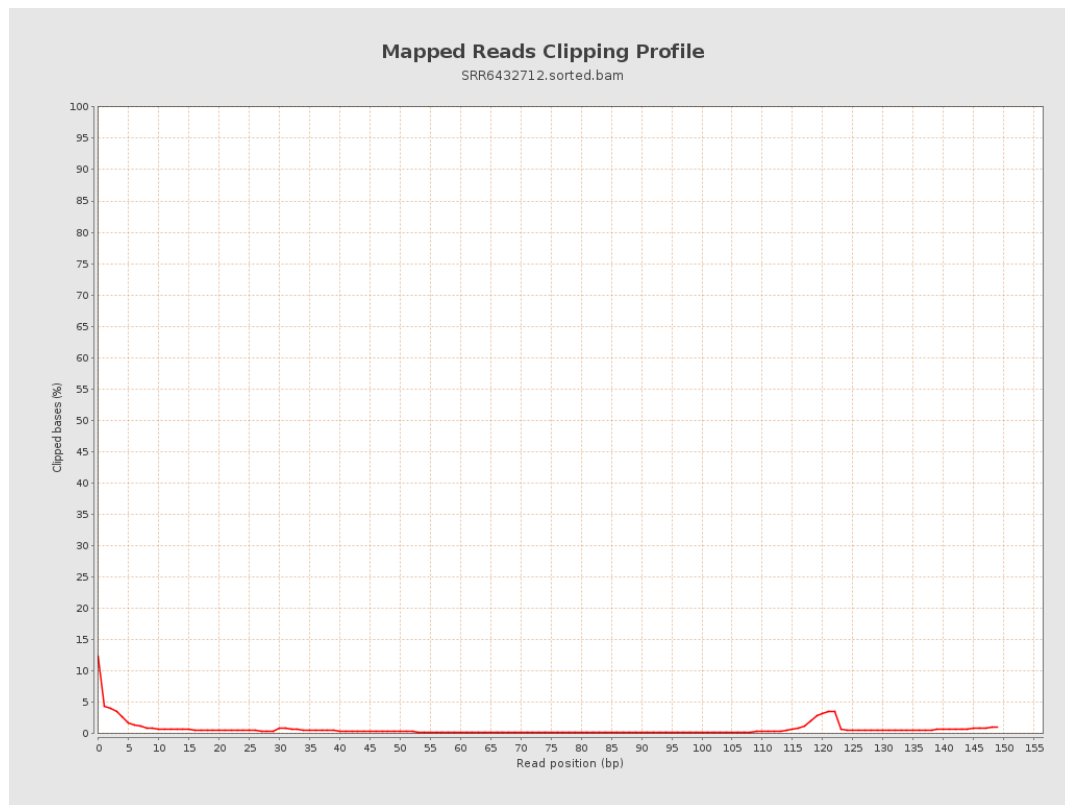
8. Results : Mapped Reads Nucleotide Content



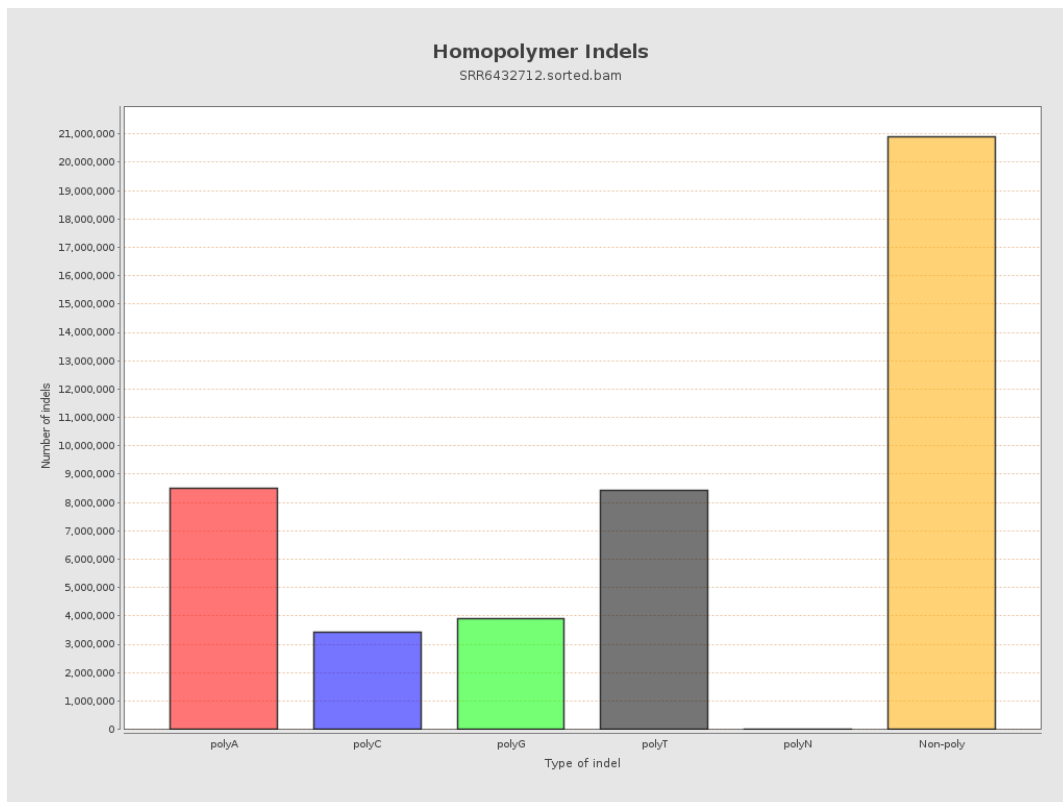
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



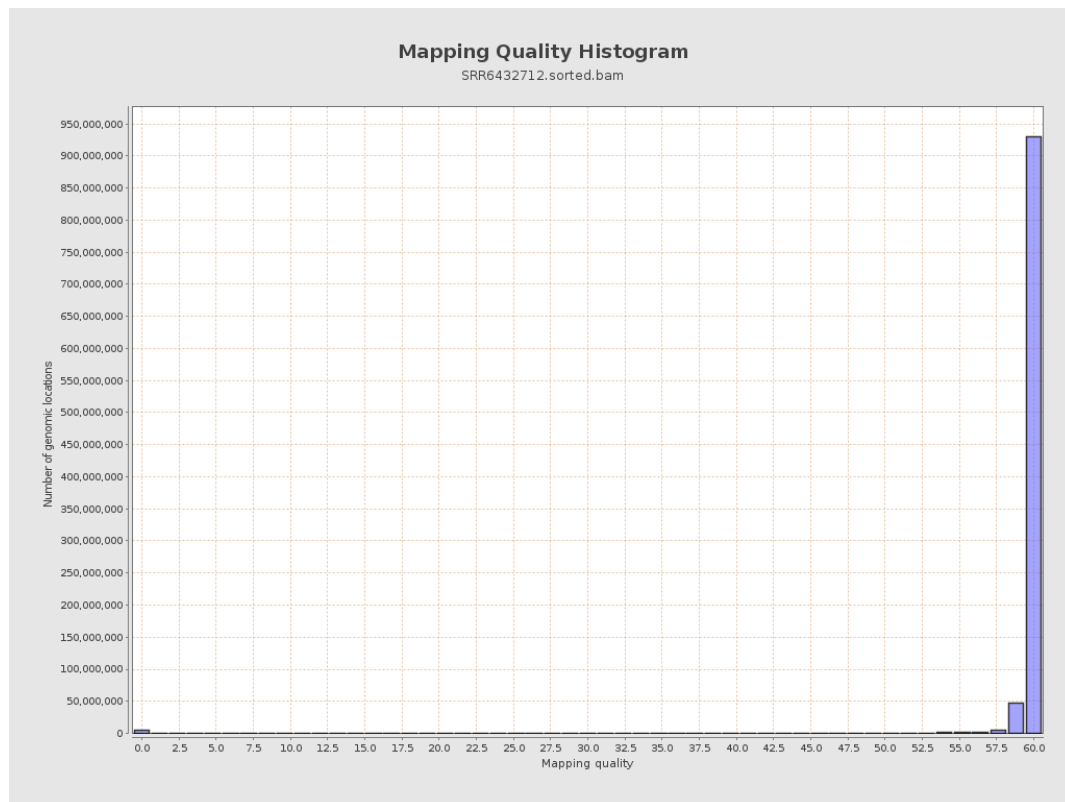
11. Results : Homopolymer Indels



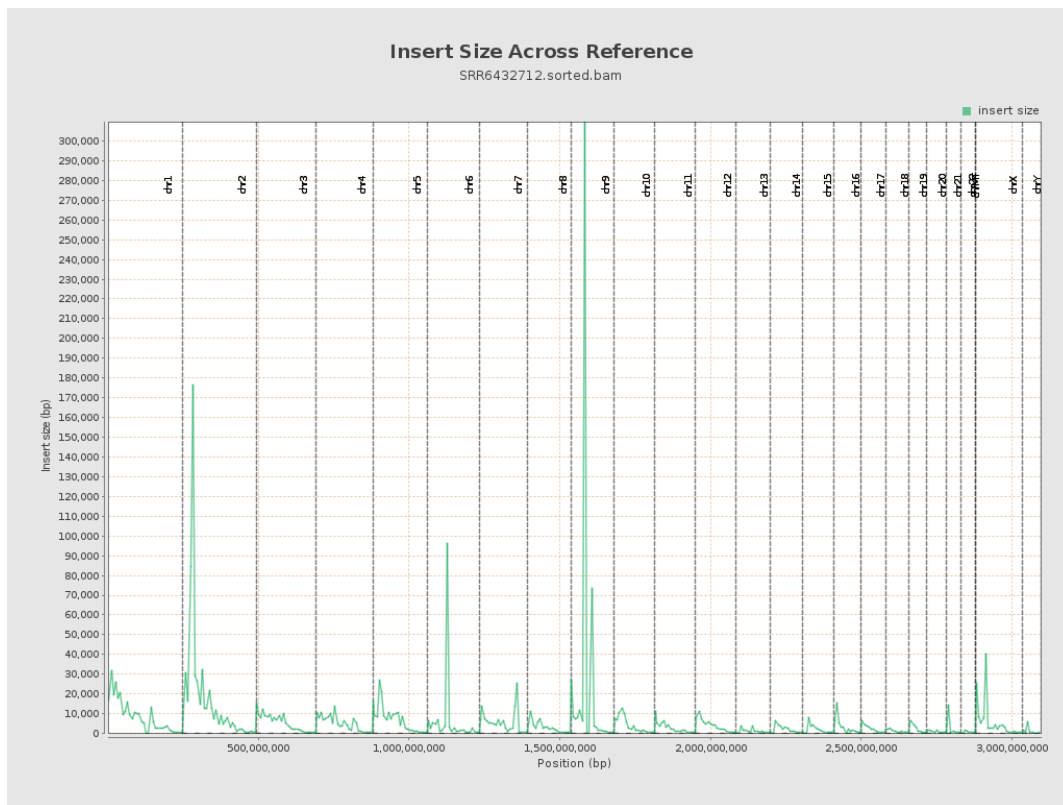
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

