

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/24 19:26:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504669.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_SRR504669 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504669_1.fastq.gz SRR504669_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jun 24 19:26:45 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504669.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	98,706,562
Mapped reads	98,195,689 / 99.48%
Unmapped reads	510,873 / 0.52%
Mapped paired reads	98,195,689 / 99.48%
Mapped reads, first in pair	49,203,782 / 49.85%
Mapped reads, second in pair	48,991,907 / 49.63%
Mapped reads, both in pair	97,942,576 / 99.23%
Mapped reads, singletons	253,113 / 0.26%
Secondary alignments	0
Supplementary alignments	1,003,052 / 1.02%
Read min/max/mean length	30 / 101 / 101.42
Duplicated reads (estimated)	52,698,422 / 53.39%
Duplication rate	24.57%
Clipped reads	24,811,772 / 25.14%

2.2. ACGT Content

Number/percentage of A's	2,853,497,268 / 30.65%
Number/percentage of C's	1,796,664,769 / 19.3%
Number/percentage of T's	2,876,392,624 / 30.89%
Number/percentage of G's	1,779,207,260 / 19.11%
Number/percentage of N's	5,235,905 / 0.06%

GC Percentage	38.4%
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2.3. Coverage

Mean	3.0104
Standard Deviation	157.876

2.4. Mapping Quality

Mean Mapping Quality	51.13
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2.5. Insert size

Mean	34,904.58
Standard Deviation	1,833,314.76
P25/Median/P75	110 / 168 / 239

2.6. Mismatches and indels

General error rate	1.14%
Mismatches	98,129,540
Insertions	3,143,917
Mapped reads with at least one insertion	3.13%
Deletions	3,188,877
Mapped reads with at least one deletion	3.17%
Homopolymer indels	38.37%

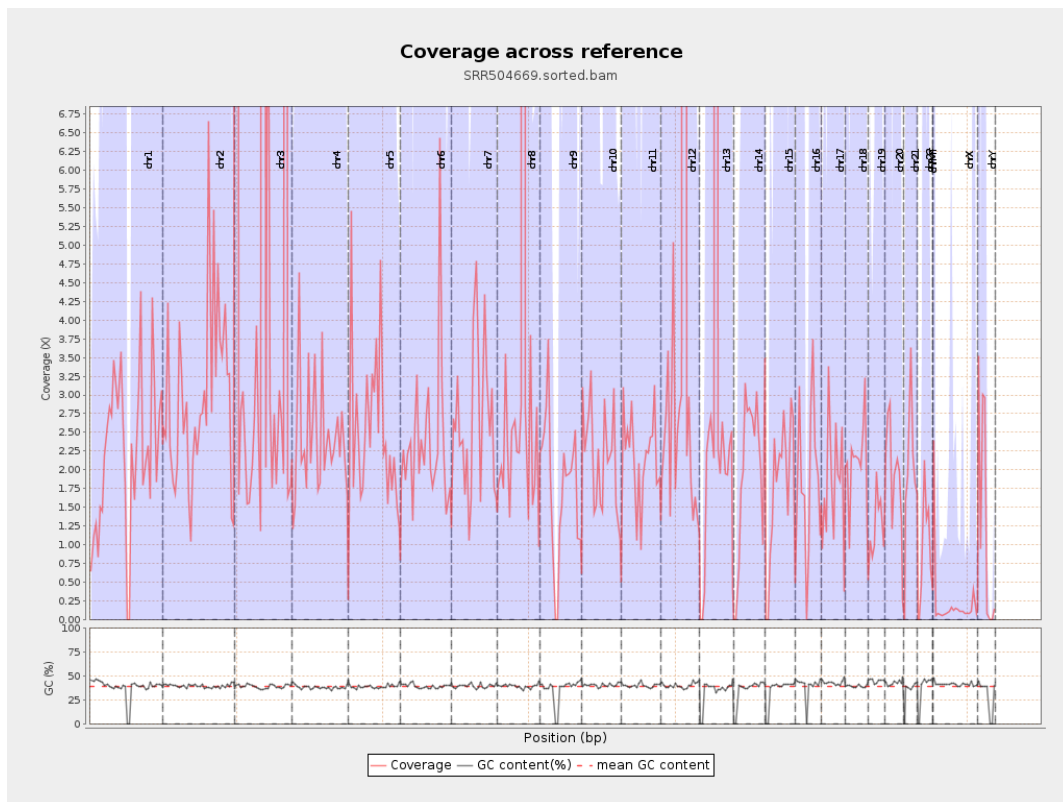
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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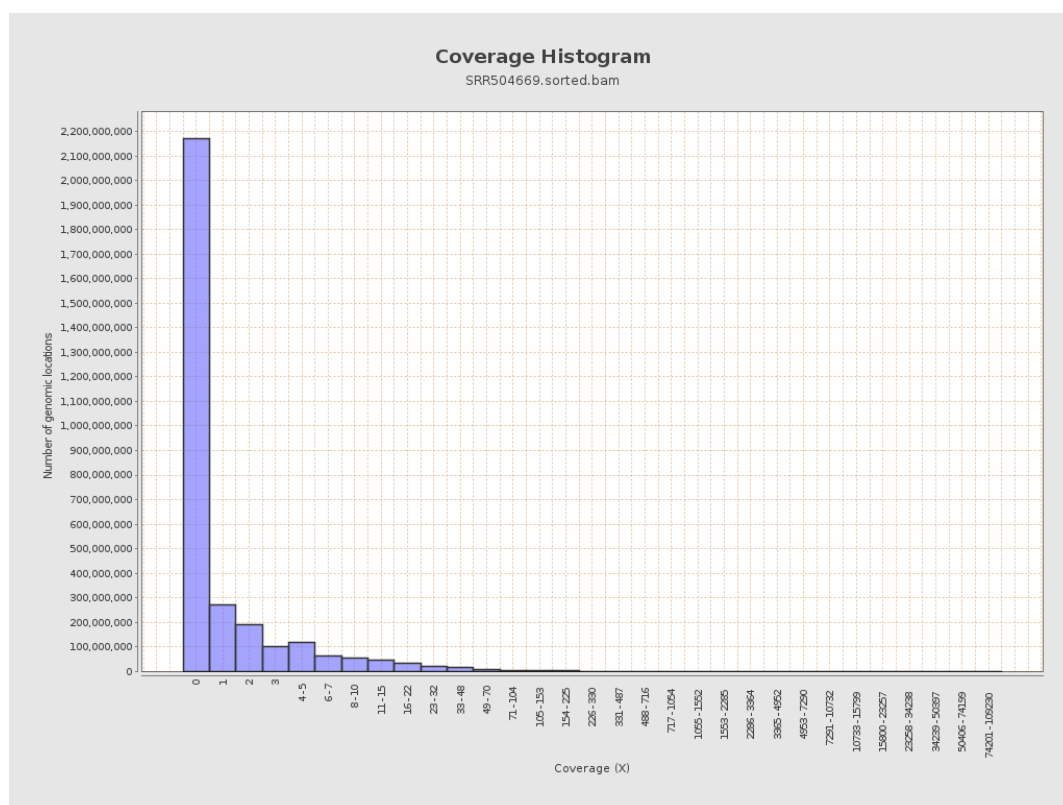
		bases	coverage	deviation
chr1	249250621	556553283	2.2329	11.5009
chr2	243199373	720439561	2.9623	22.9294
chr3	198022430	1793345802	9.0563	466.3363
chr4	191154276	465864964	2.4371	12.6585
chr5	180915260	448370838	2.4783	16.1492
chr6	171115067	409680447	2.3942	37.4885
chr7	159138663	416121745	2.6148	12.7952
chr8	146364022	994171723	6.7925	300.1612
chr9	141213431	251380273	1.7801	9.3457
chr10	135534747	292881929	2.1609	11.5309
chr11	135006516	290343342	2.1506	10.8703
chr12	133851895	838577778	6.265	324.6184
chr13	115169878	526549134	4.5719	230.2246
chr14	107349540	211264875	1.968	9.2443
chr15	102531392	181558727	1.7708	8.7965
chr16	90354753	165949885	1.8366	10.9823
chr17	81195210	148041595	1.8233	19.7548
chr18	78077248	164603234	2.1082	7.2603
chr19	59128983	73678103	1.2461	6.3725
chr20	63025520	123753756	1.9635	10.7818
chr21	48129895	94717211	1.9679	11.4184
chr22	51304566	47725244	0.9302	7.862
chrMT	16571	8310	0.5015	1.9517
chrX	155270560	30283613	0.195	12.9045

chrY	59373566	73522875	1.2383	20.4891
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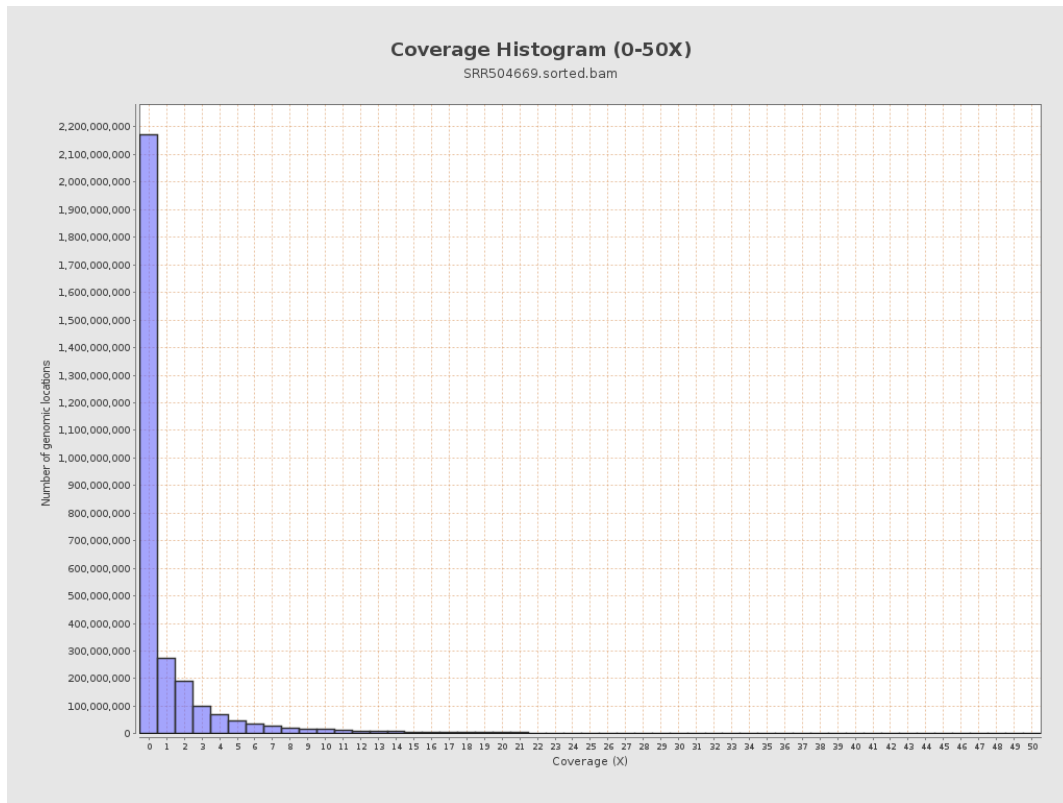
3. Results : Coverage across reference



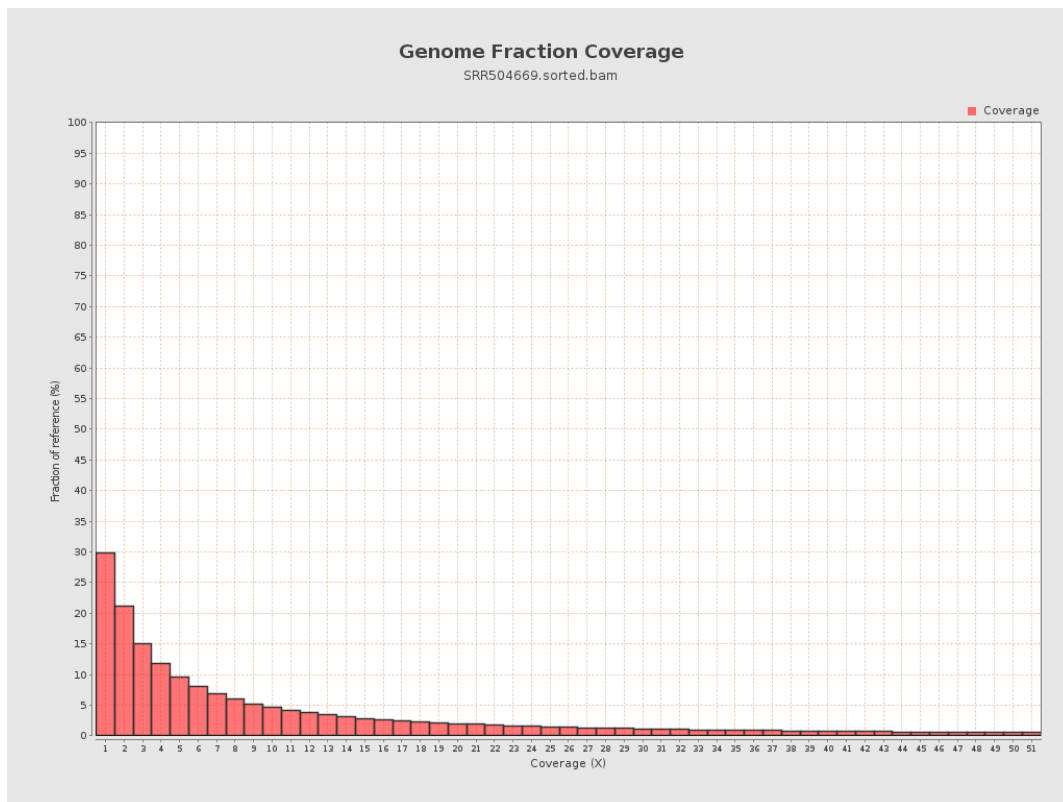
4. Results : Coverage Histogram



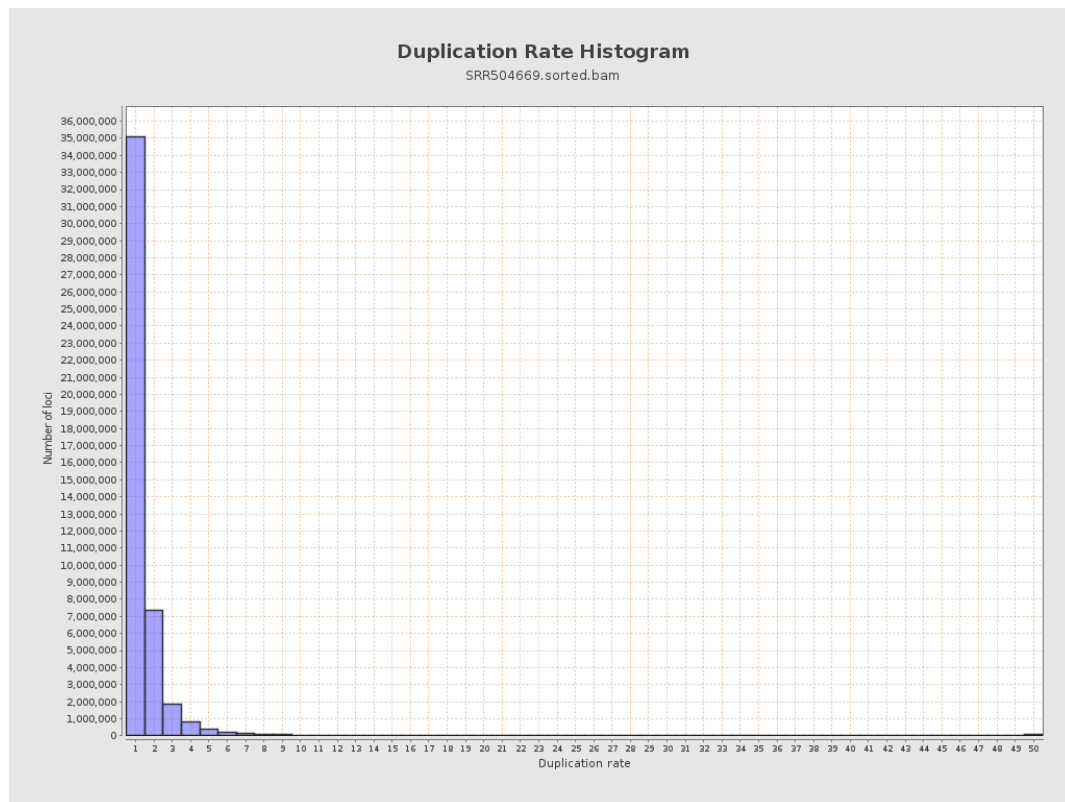
5. Results : Coverage Histogram (0-50X)



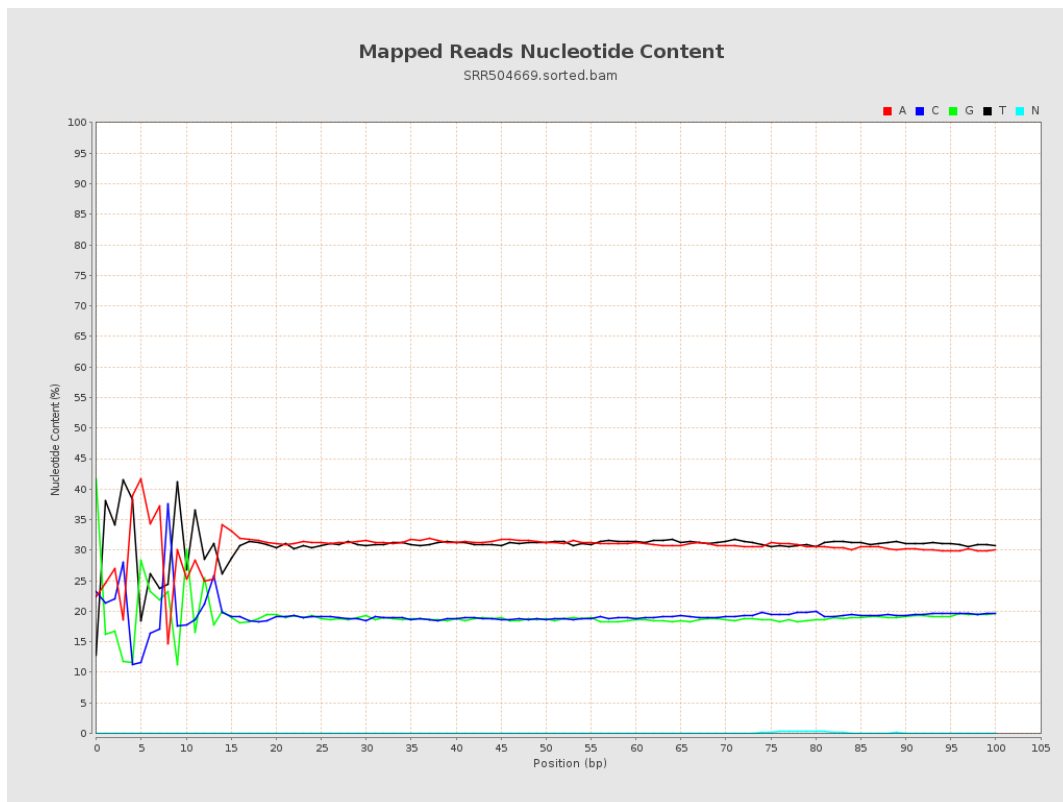
6. Results : Genome Fraction Coverage



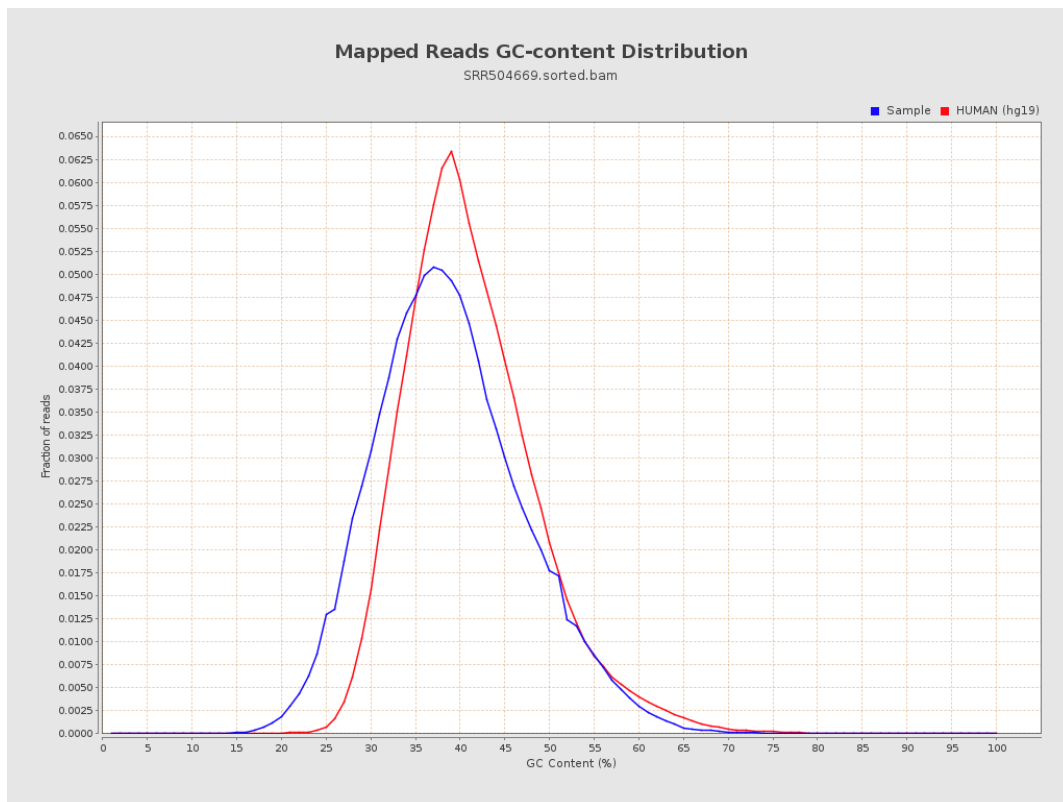
7. Results : Duplication Rate Histogram



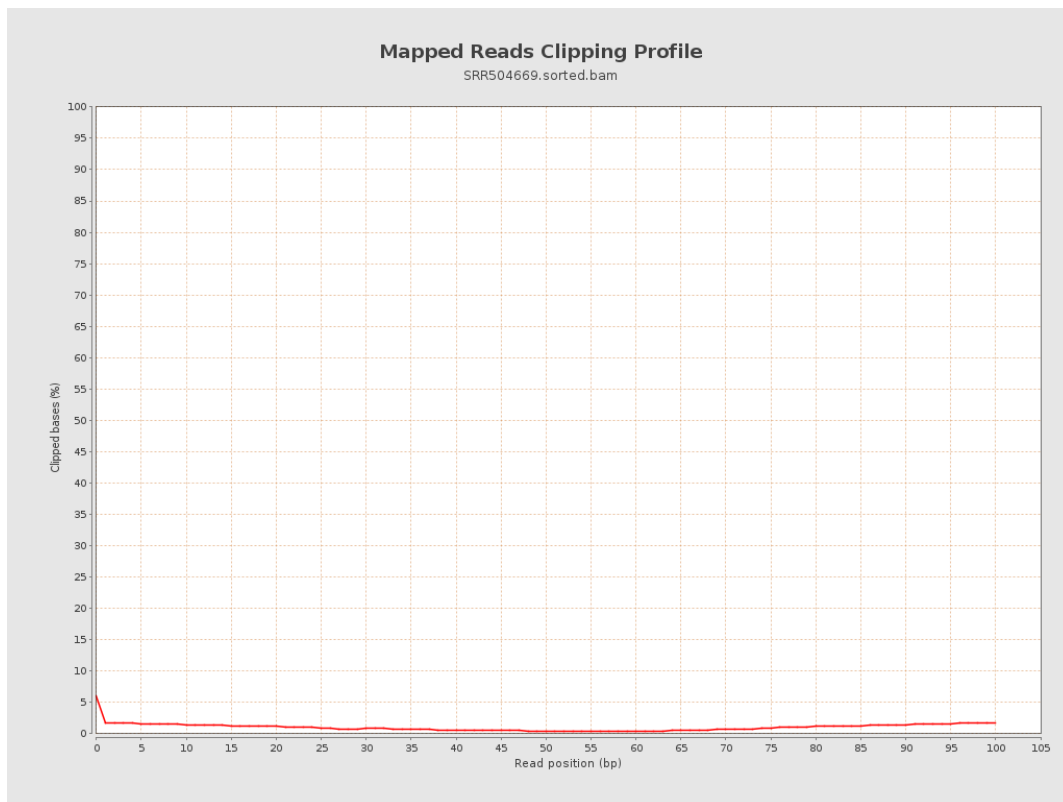
8. Results : Mapped Reads Nucleotide Content



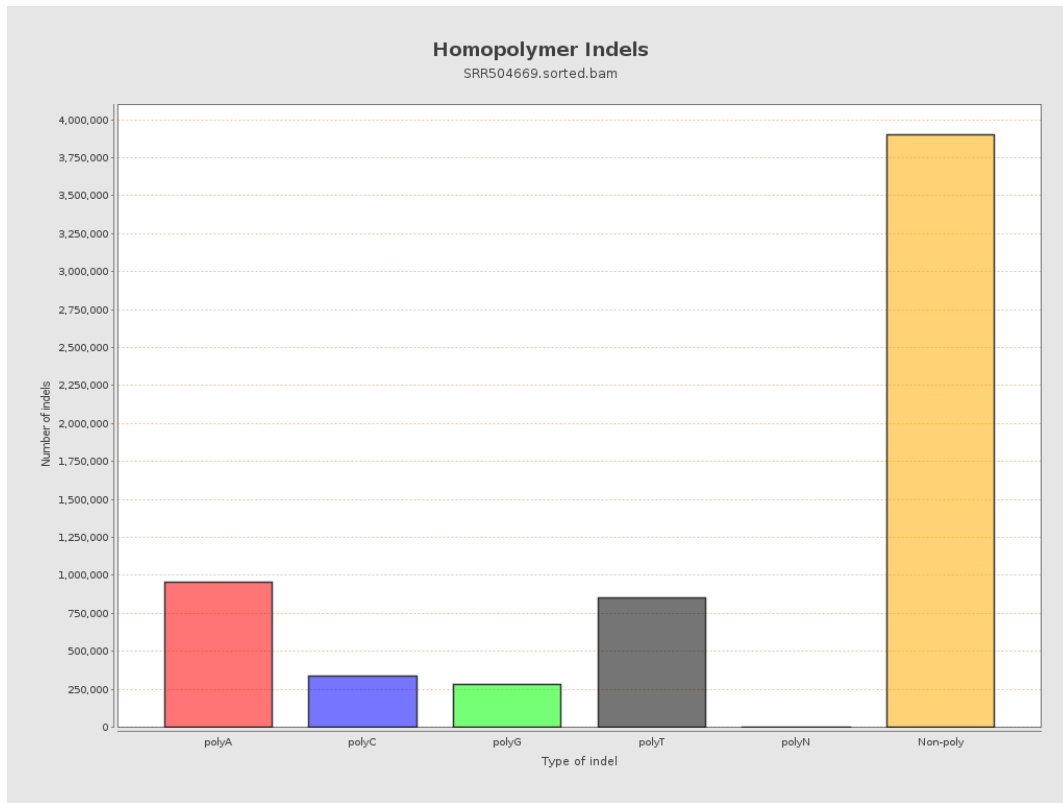
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



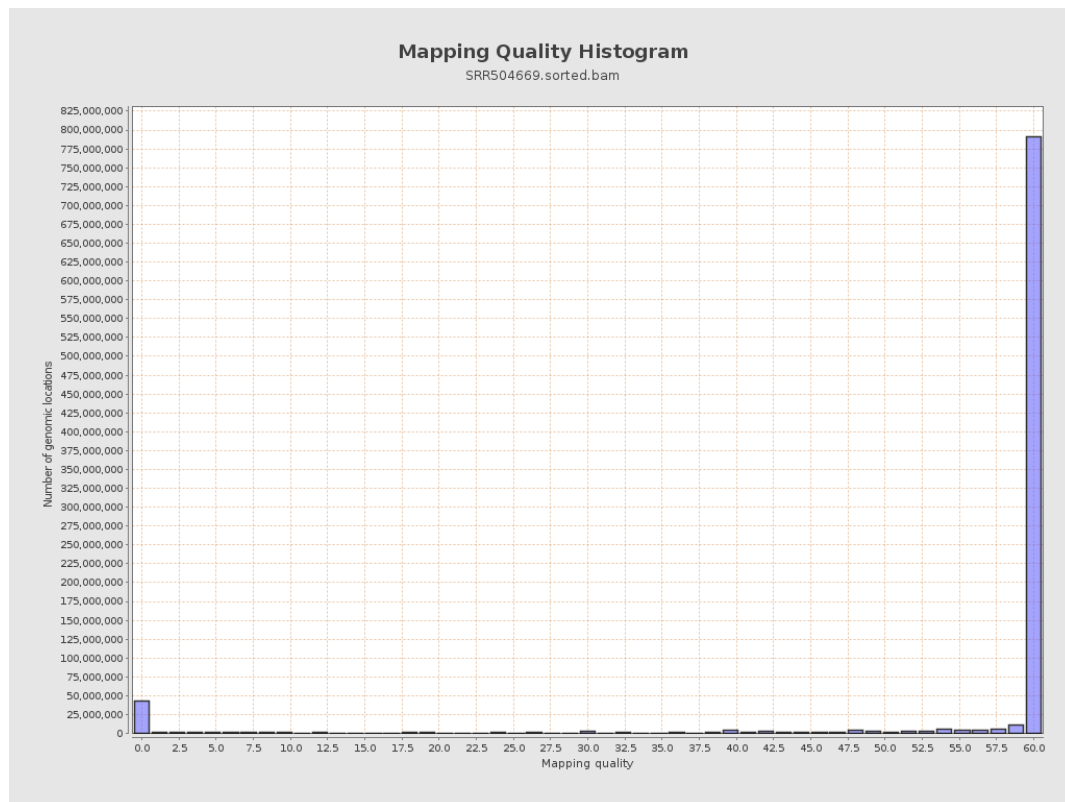
11. Results : Homopolymer Indels



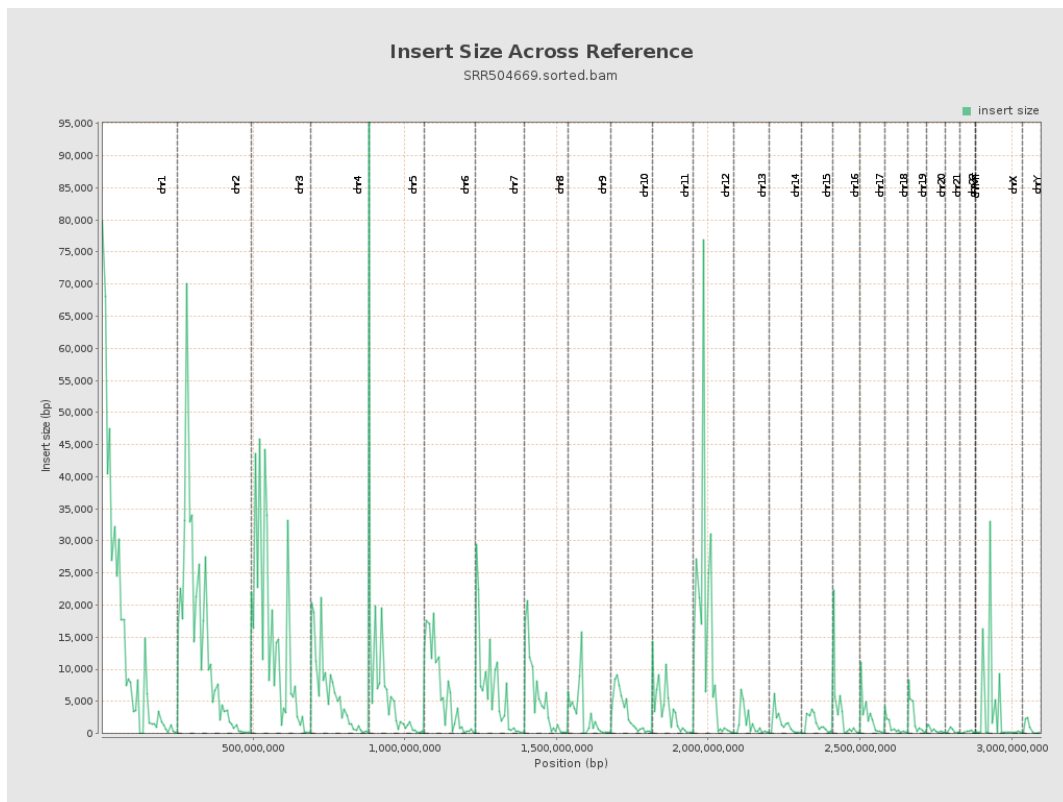
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

