

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/24 16:30:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781809.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_SRR1781809 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781809_1.fastq.gz SRR1781809_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Mar 24 16:30:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781809.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	134,520,120
Mapped reads	132,332,390 / 98.37%
Unmapped reads	2,187,730 / 1.63%
Mapped paired reads	132,332,390 / 98.37%
Mapped reads, first in pair	66,514,686 / 49.45%
Mapped reads, second in pair	65,817,704 / 48.93%
Mapped reads, both in pair	131,167,722 / 97.51%
Mapped reads, singletons	1,164,668 / 0.87%
Secondary alignments	0
Supplementary alignments	506,220 / 0.38%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	7,325,118 / 5.45%
Duplication rate	5.28%
Clipped reads	5,368,235 / 3.99%

2.2. ACGT Content

Number/percentage of A's	3,875,900,033 / 29.49%
Number/percentage of C's	2,683,301,645 / 20.42%
Number/percentage of T's	3,850,176,283 / 29.3%
Number/percentage of G's	2,731,824,254 / 20.79%
Number/percentage of N's	1,080,292 / 0.01%

GC Percentage	41.2%
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2.3. Coverage

Mean	4.2462
Standard Deviation	5.5372

2.4. Mapping Quality

Mean Mapping Quality	54.05
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2.5. Insert size

Mean	42,344.3
Standard Deviation	2,006,370.93
P25/Median/P75	171 / 208 / 255

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	52,905,292
Insertions	1,252,660
Mapped reads with at least one insertion	0.93%
Deletions	1,232,474
Mapped reads with at least one deletion	0.91%
Homopolymer indels	46.35%

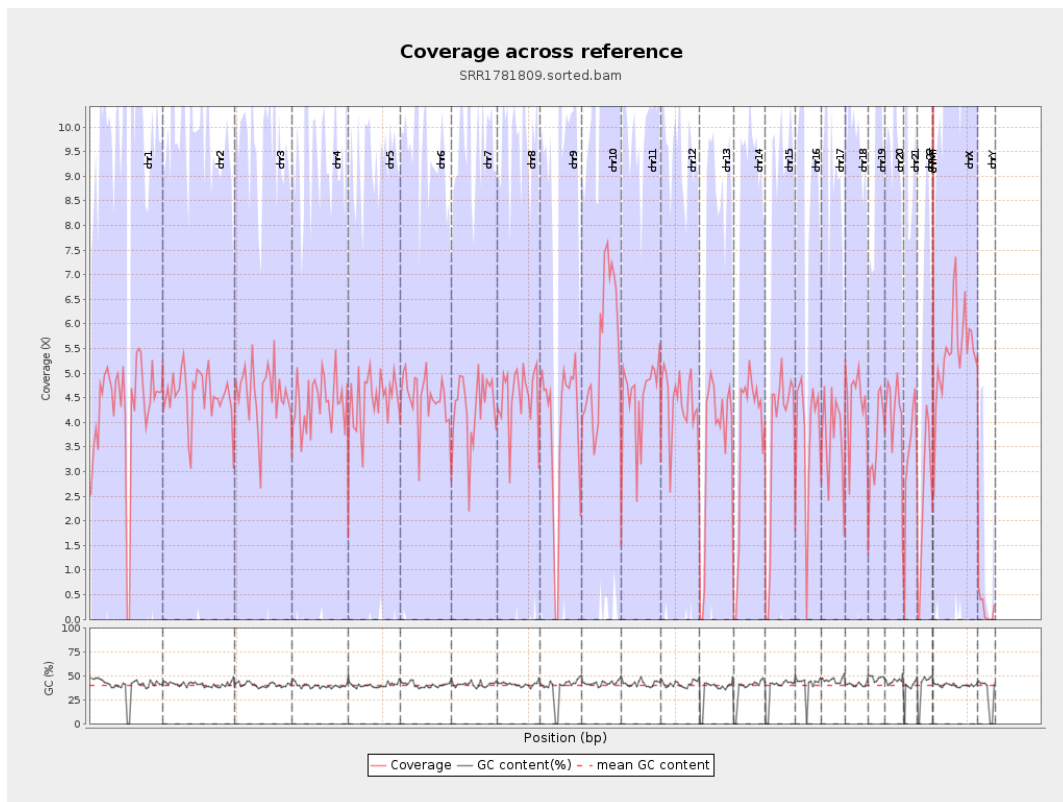
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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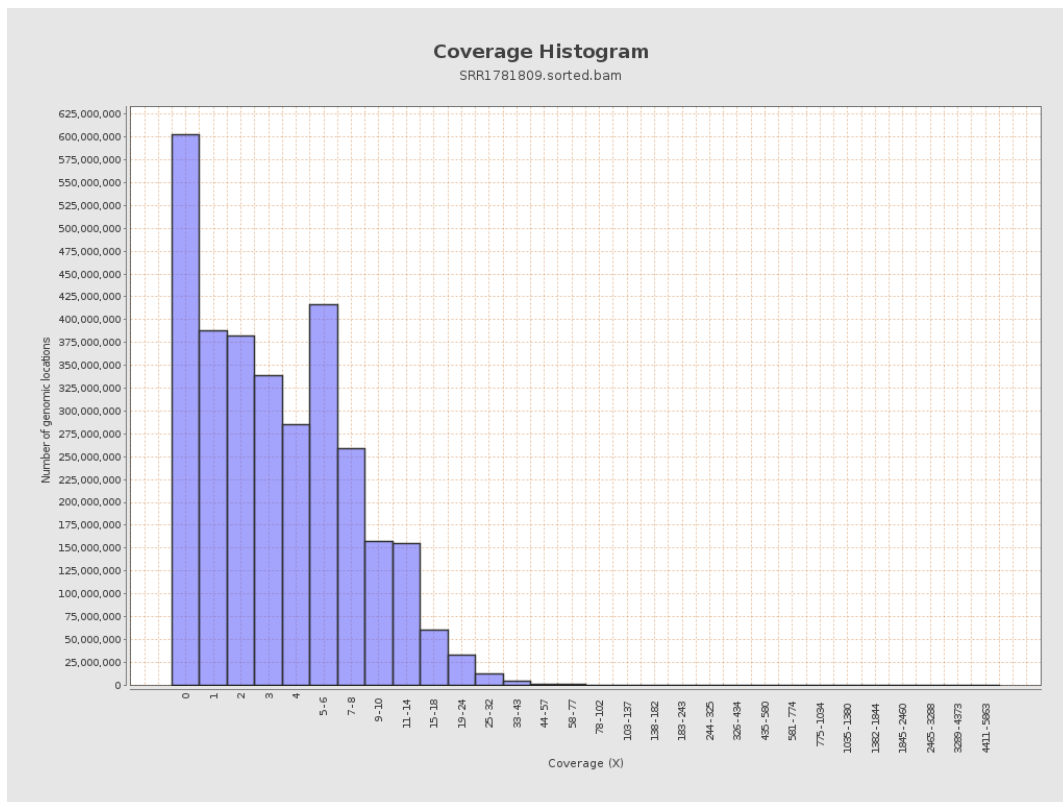
		bases	coverage	deviation
chr1	249250621	1062632877	4.2633	8.0719
chr2	243199373	1106958872	4.5517	5.3918
chr3	198022430	904778304	4.5691	4.576
chr4	191154276	846920404	4.4306	5.2271
chr5	180915260	804001097	4.4441	4.3991
chr6	171115067	769450759	4.4967	5.0974
chr7	159138663	683820845	4.297	5.0505
chr8	146364022	664775318	4.5419	4.7488
chr9	141213431	551870739	3.9081	5.6221
chr10	135534747	746901158	5.5108	8.1829
chr11	135006516	612483263	4.5367	4.9706
chr12	133851895	592832586	4.429	4.7174
chr13	115169878	410609302	3.5652	4.1388
chr14	107349540	399675416	3.7231	4.4734
chr15	102531392	374618066	3.6537	4.5092
chr16	90354753	336172598	3.7206	4.6435
chr17	81195210	307872994	3.7918	5.1305
chr18	78077248	344766032	4.4157	5.7964
chr19	59128983	211308414	3.5737	5.8062
chr20	63025520	266069751	4.2216	5.1831
chr21	48129895	159107328	3.3058	7.2565
chr22	51304566	128390666	2.5025	4.0267
chrMT	16571	349746	21.1059	6.3786
chrX	155270560	846165966	5.4496	5.5826

chrY	59373566	12518876	0.2108	2.4423
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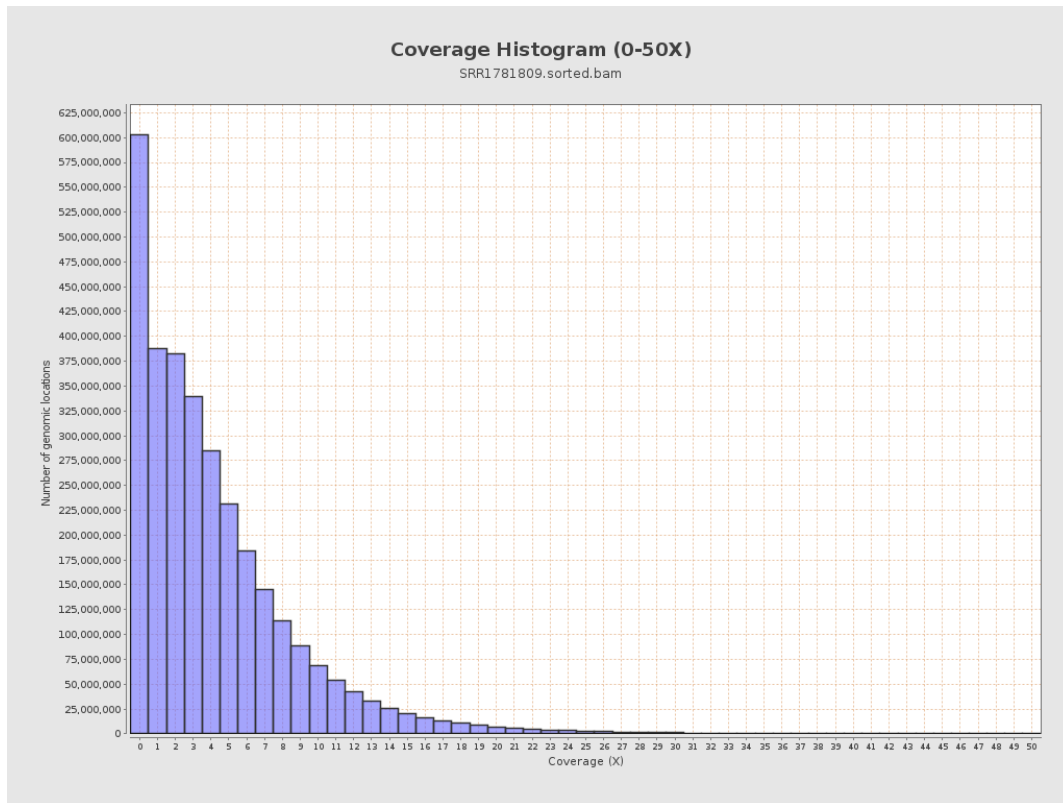
3. Results : Coverage across reference



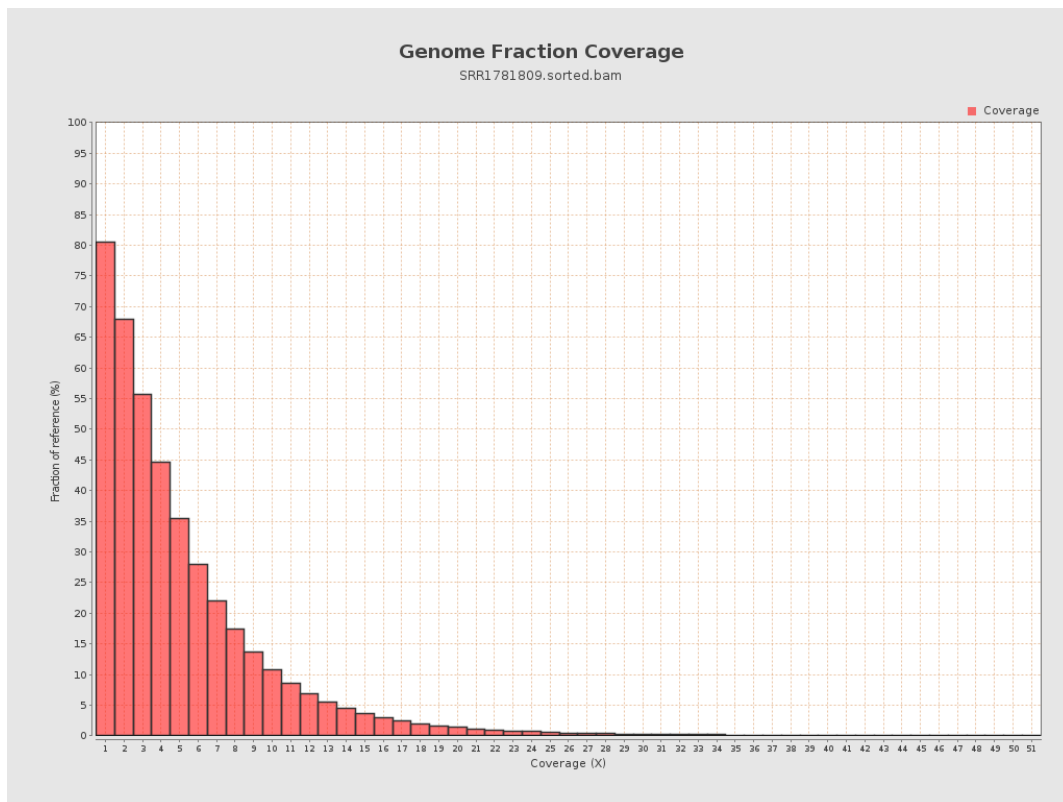
4. Results : Coverage Histogram



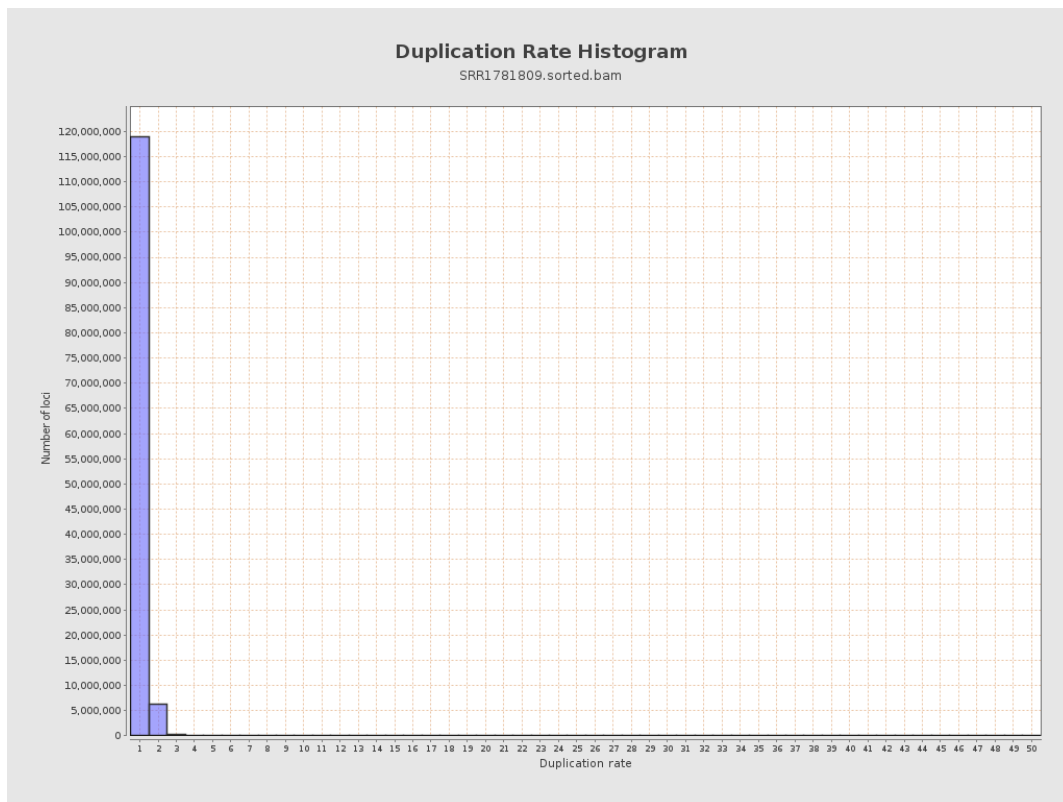
5. Results : Coverage Histogram (0-50X)



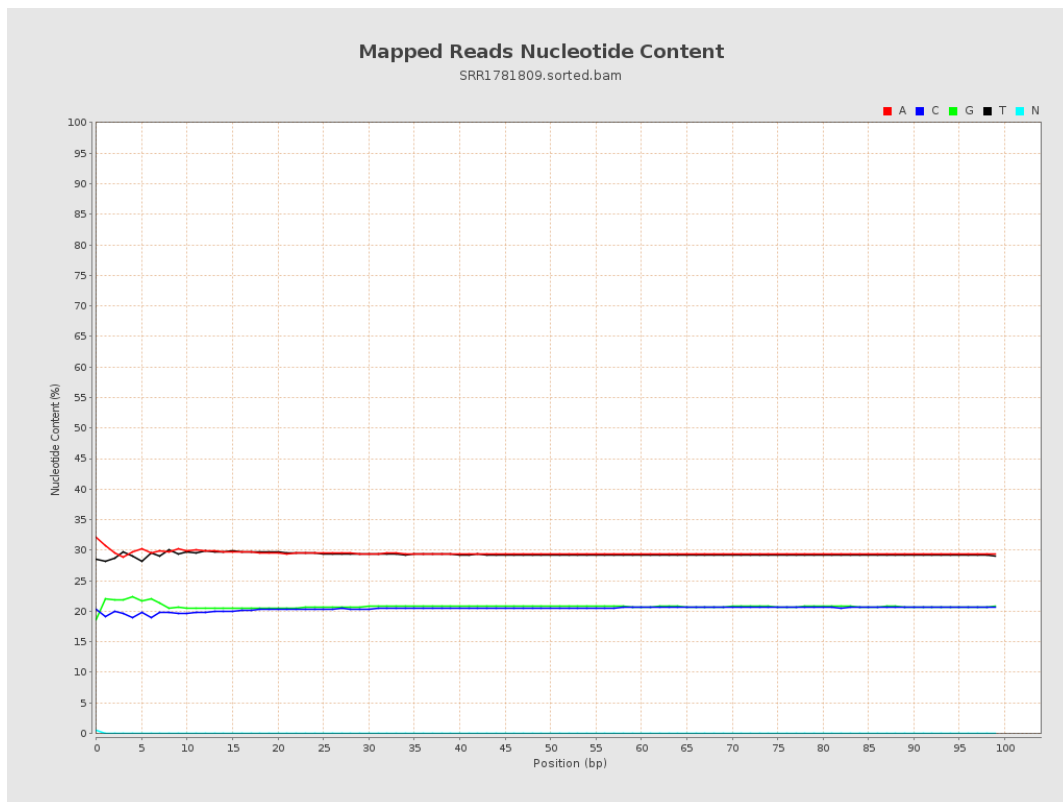
6. Results : Genome Fraction Coverage



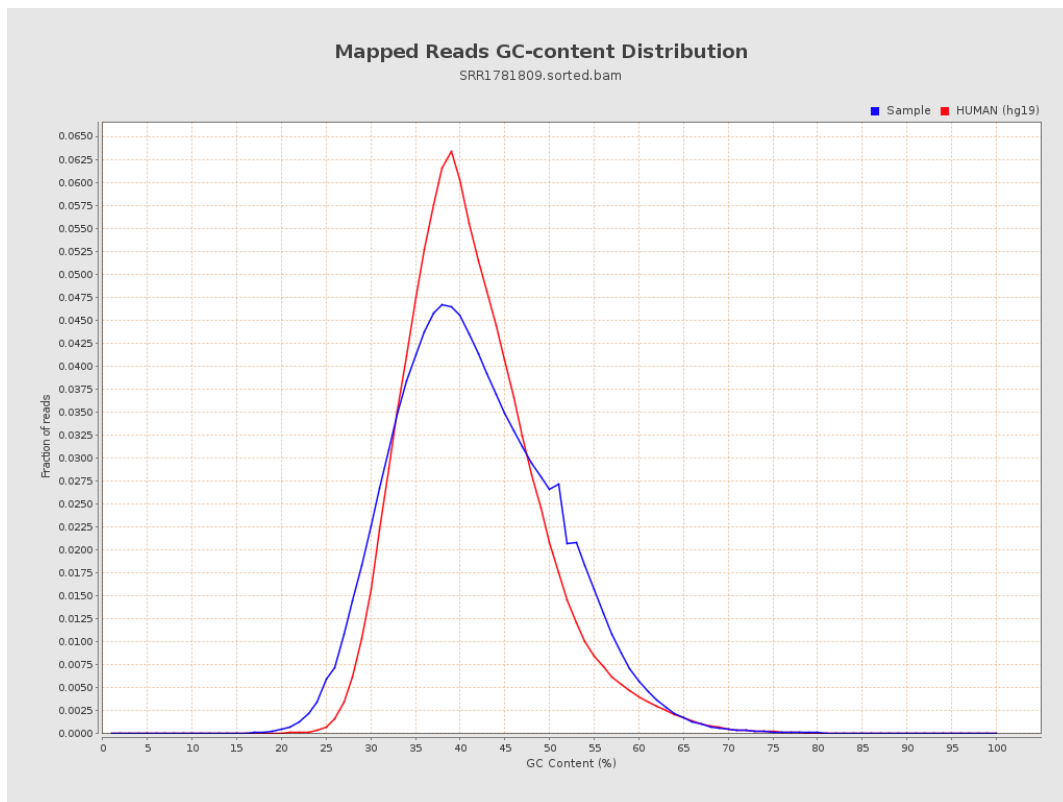
7. Results : Duplication Rate Histogram



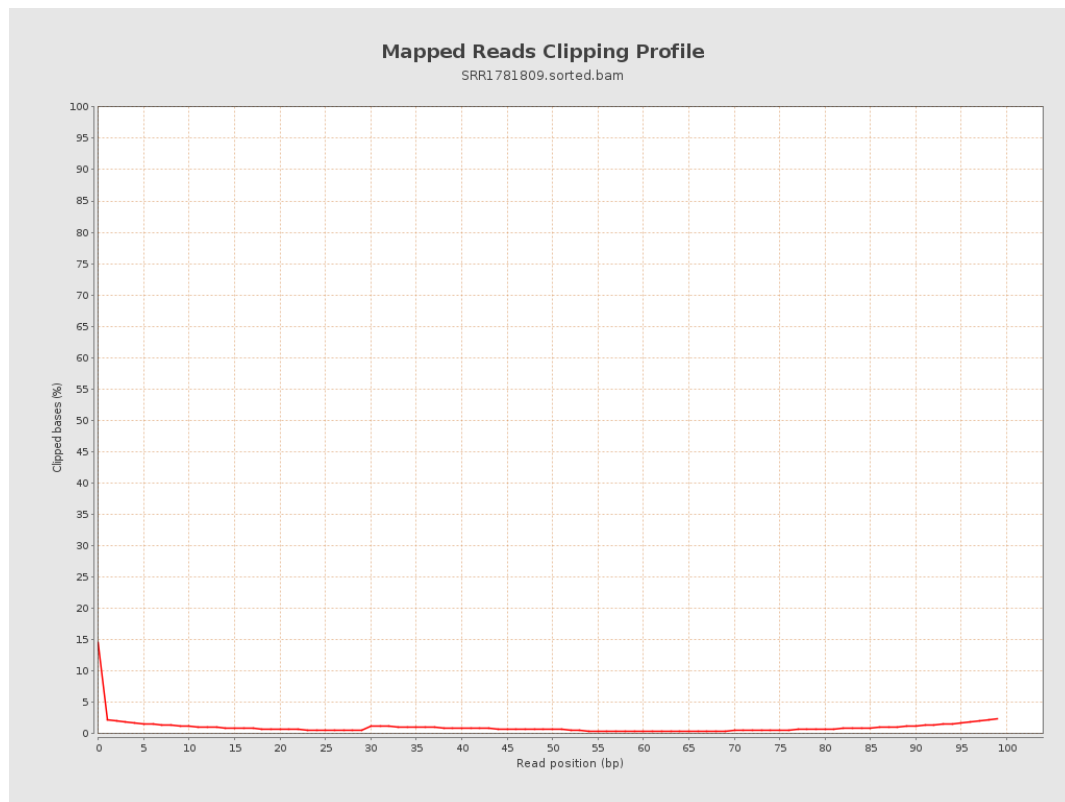
8. Results : Mapped Reads Nucleotide Content



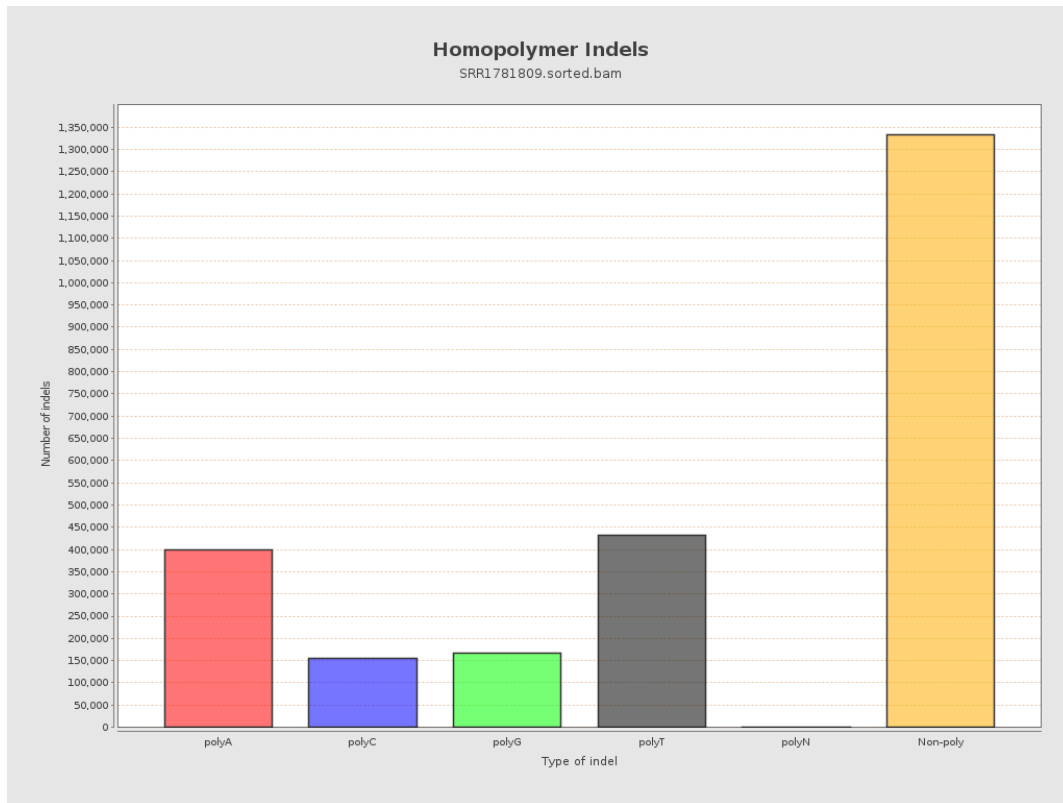
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



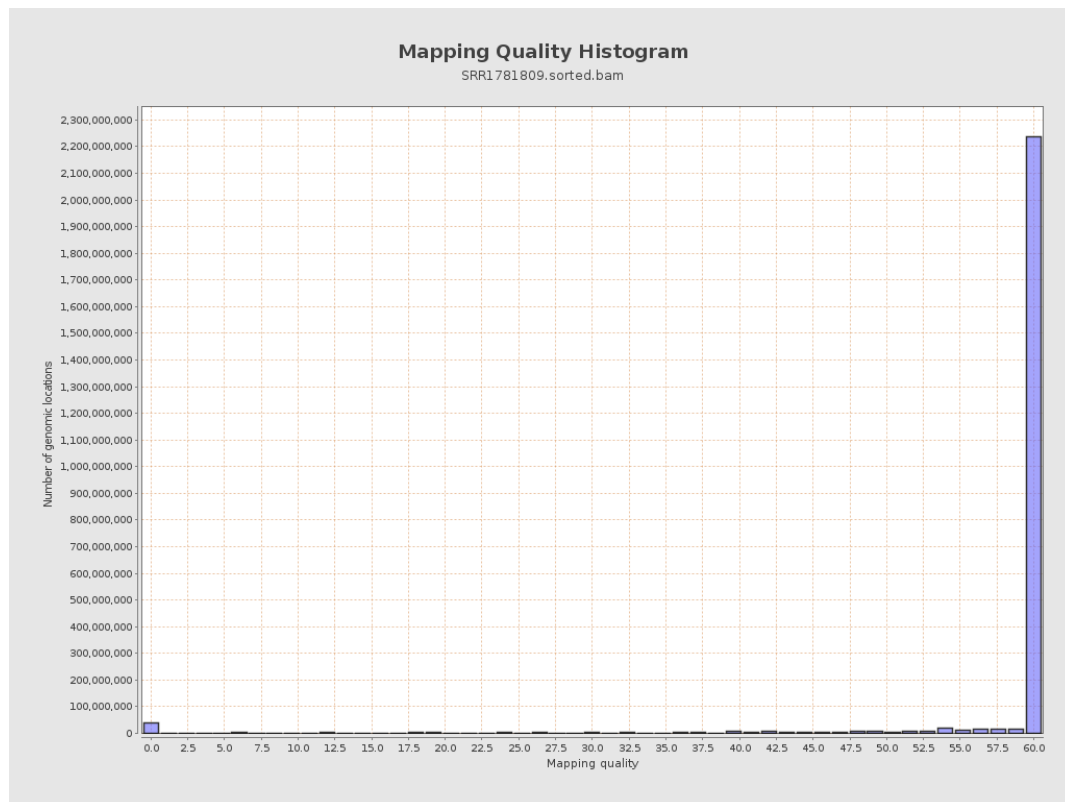
11. Results : Homopolymer Indels



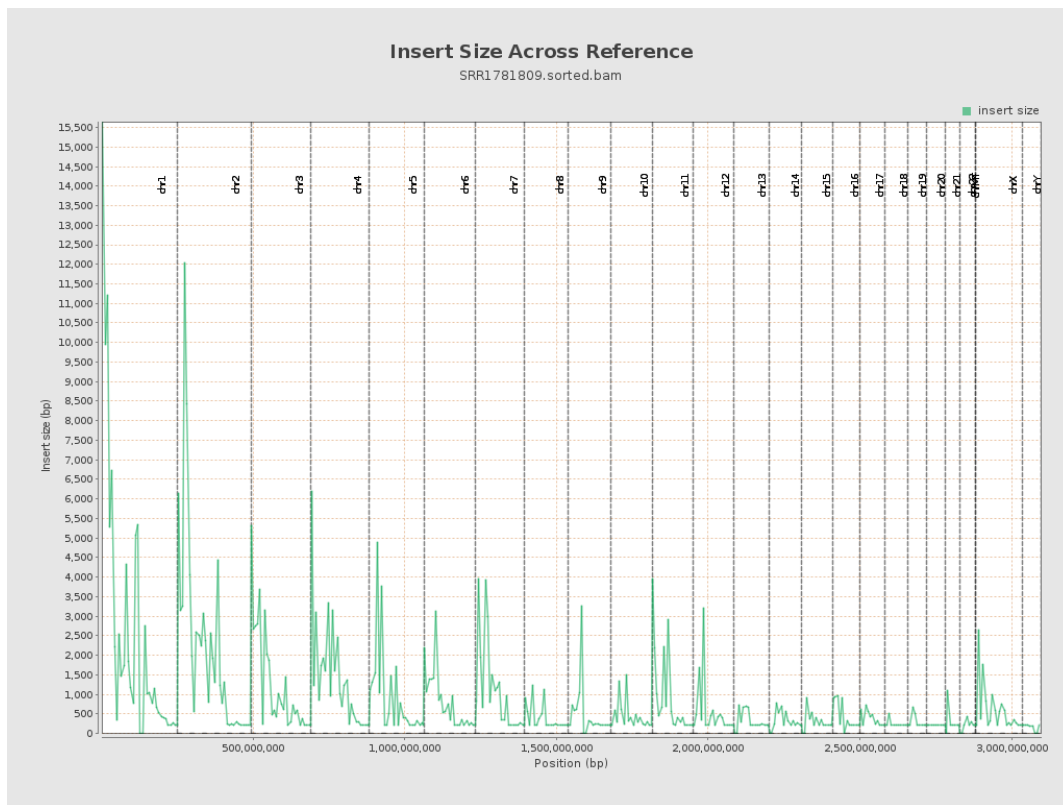
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

