

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/25 23:46:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264621.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_SRR1264621 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264621_1.fastq.gz SRR1264621_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 25 23:46:11 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264621.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,422,593,592
Mapped reads	1,416,167,197 / 99.55%
Unmapped reads	6,426,395 / 0.45%
Mapped paired reads	1,416,167,197 / 99.55%
Mapped reads, first in pair	709,739,287 / 49.89%
Mapped reads, second in pair	706,427,910 / 49.66%
Mapped reads, both in pair	1,411,669,034 / 99.23%
Mapped reads, singletons	4,498,163 / 0.32%
Secondary alignments	0
Supplementary alignments	9,434,789 / 0.66%
Read min/max/mean length	30 / 101 / 101.27
Duplicated reads (estimated)	498,381,561 / 35.03%
Duplication rate	34.93%
Clipped reads	62,154,223 / 4.37%

2.2. ACGT Content

Number/percentage of A's	43,916,409,149 / 30.9%
Number/percentage of C's	27,124,747,741 / 19.08%
Number/percentage of T's	43,632,300,185 / 30.7%
Number/percentage of G's	27,425,420,733 / 19.29%
Number/percentage of N's	43,286,468 / 0.03%

GC Percentage	38.38%
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2.3. Coverage

Mean	45.9266
Standard Deviation	44.8483

2.4. Mapping Quality

Mean Mapping Quality	54.56
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2.5. Insert size

Mean	87,501.87
Standard Deviation	2,847,108.97
P25/Median/P75	300 / 329 / 362

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	546,984,585
Insertions	15,543,085
Mapped reads with at least one insertion	1.08%
Deletions	14,589,091
Mapped reads with at least one deletion	1.01%
Homopolymer indels	48.63%

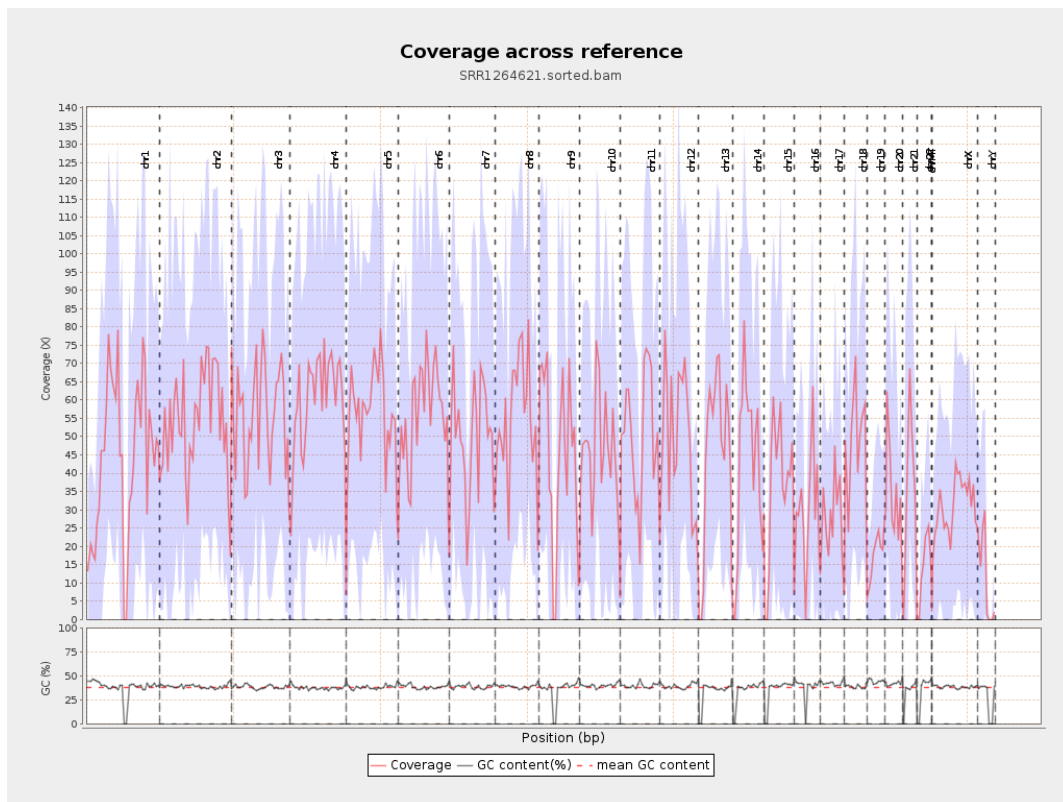
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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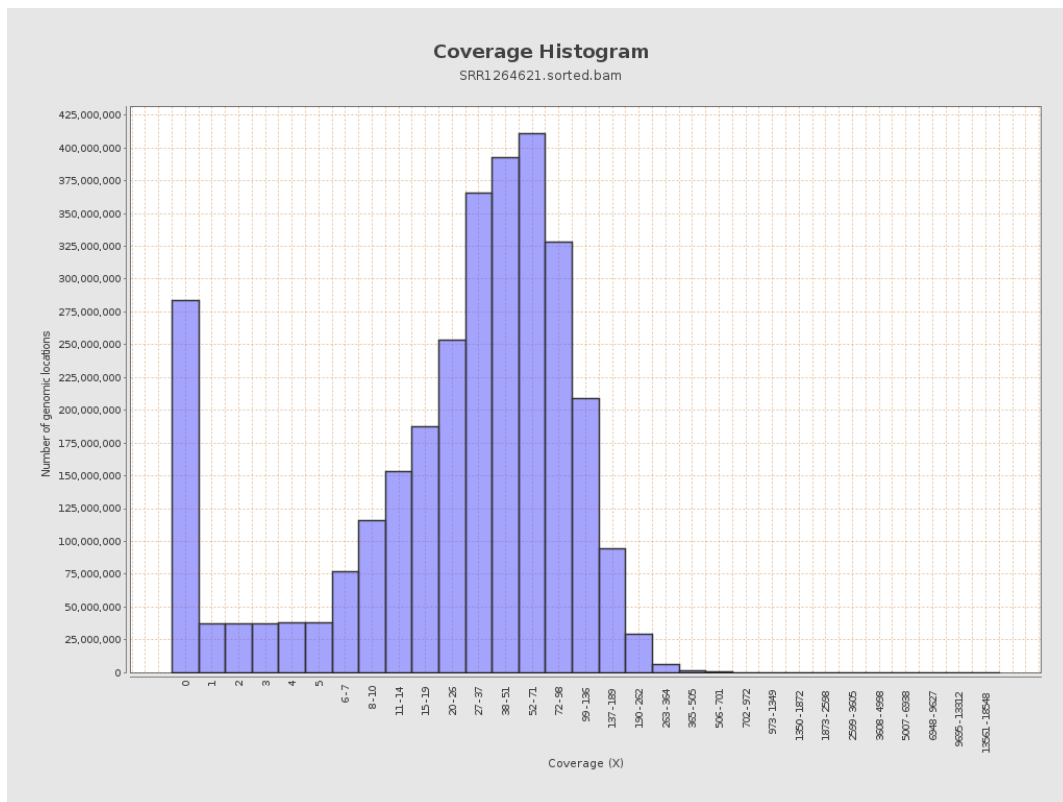
		bases	coverage	deviation
chr1	249250621	11129573937	44.6521	46.5152
chr2	243199373	13190958127	54.2393	46.1615
chr3	198022430	11036622462	55.7342	45.5775
chr4	191154276	11561299340	60.4815	47.1272
chr5	180915260	10138536683	56.0403	44.165
chr6	171115067	9770688980	57.1001	46.9793
chr7	159138663	7856401764	49.3683	44.9185
chr8	146364022	8132491545	55.5635	45.6377
chr9	141213431	6201664455	43.917	48.4126
chr10	135534747	6276360270	46.3081	41.8183
chr11	135006516	6743613996	49.9503	46.0254
chr12	133851895	6653191885	49.7056	46.6687
chr13	115169878	5322495901	46.2143	44.2117
chr14	107349540	4534838704	42.2437	44.3324
chr15	102531392	3761760851	36.6889	43.414
chr16	90354753	2582453240	28.5813	34.217
chr17	81195210	2211310190	27.2345	32.8367
chr18	78077248	3854752974	49.371	41.0077
chr19	59128983	1029155041	17.4053	24.6111
chr20	63025520	2139581049	33.9479	40.7615
chr21	48129895	1796408240	37.3242	47.2517
chr22	51304566	722374780	14.0801	23.5898
chrMT	16571	35560	2.1459	5.4537
chrX	155270560	4851283661	31.2441	30.7339

chrY	59373566	676759977	11.3983	23.8018
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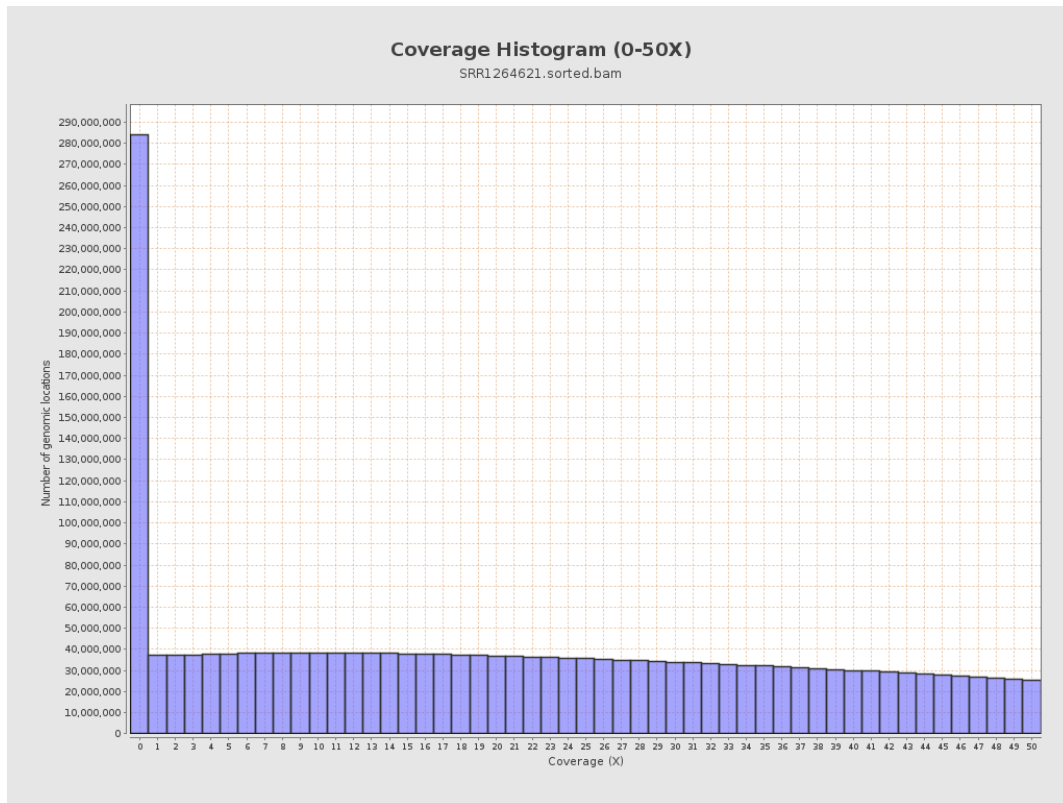
3. Results : Coverage across reference



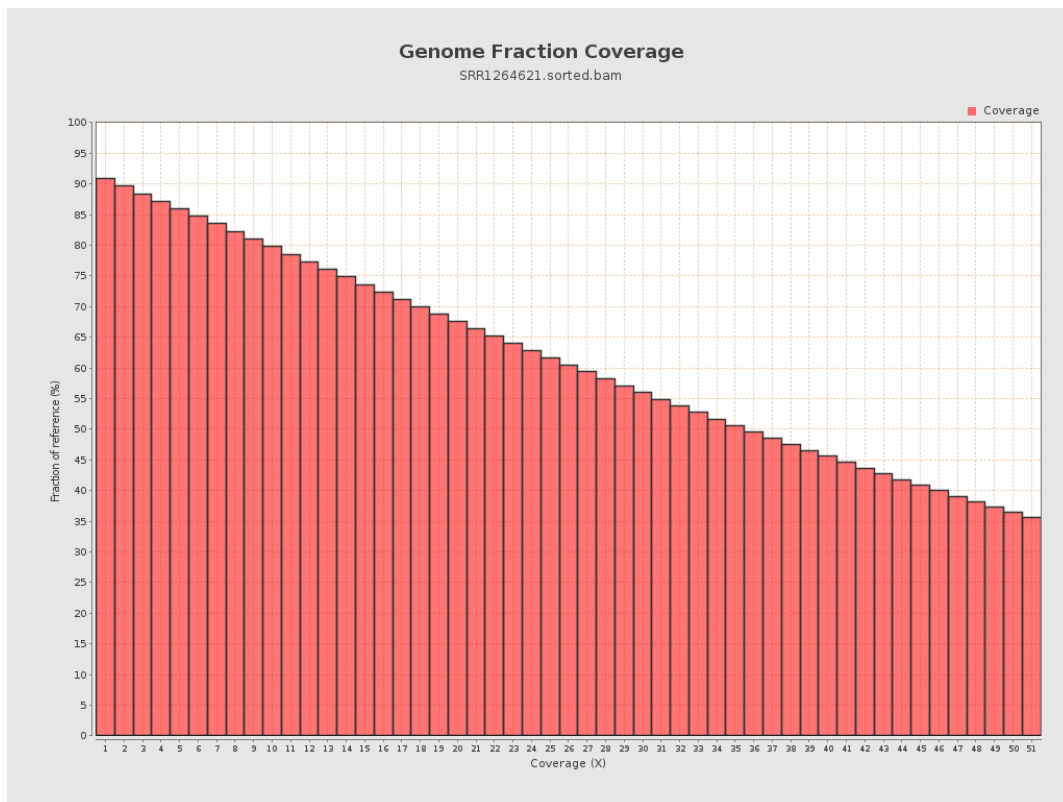
4. Results : Coverage Histogram



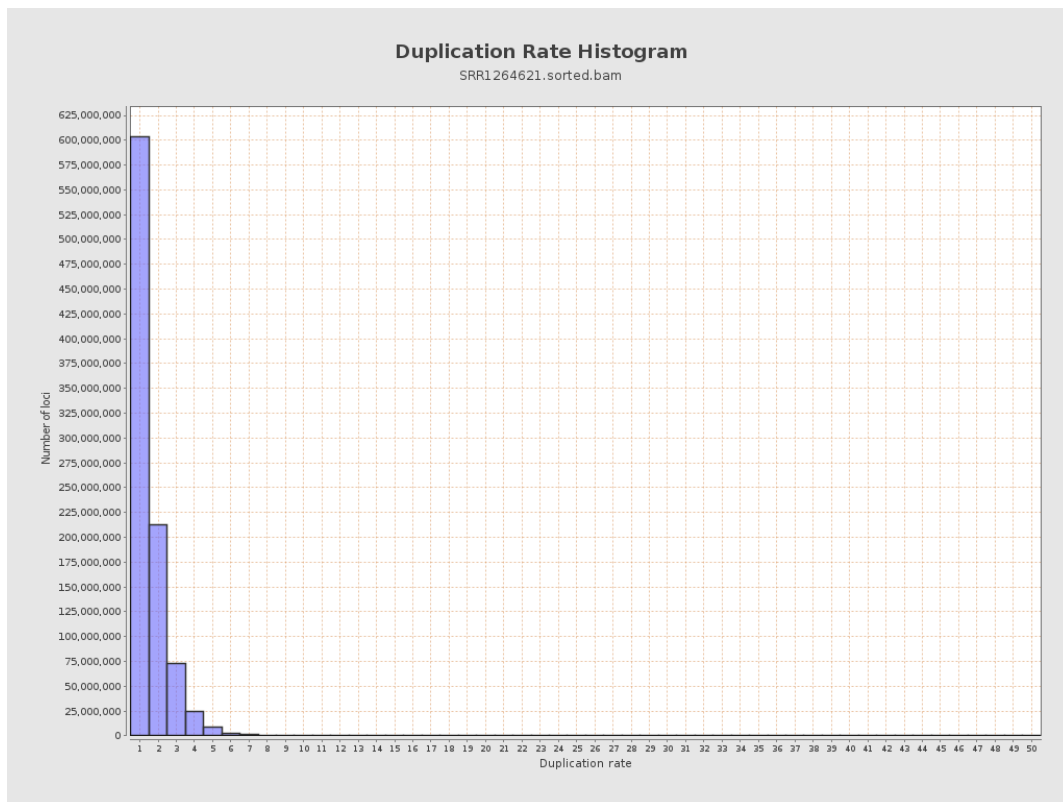
5. Results : Coverage Histogram (0-50X)



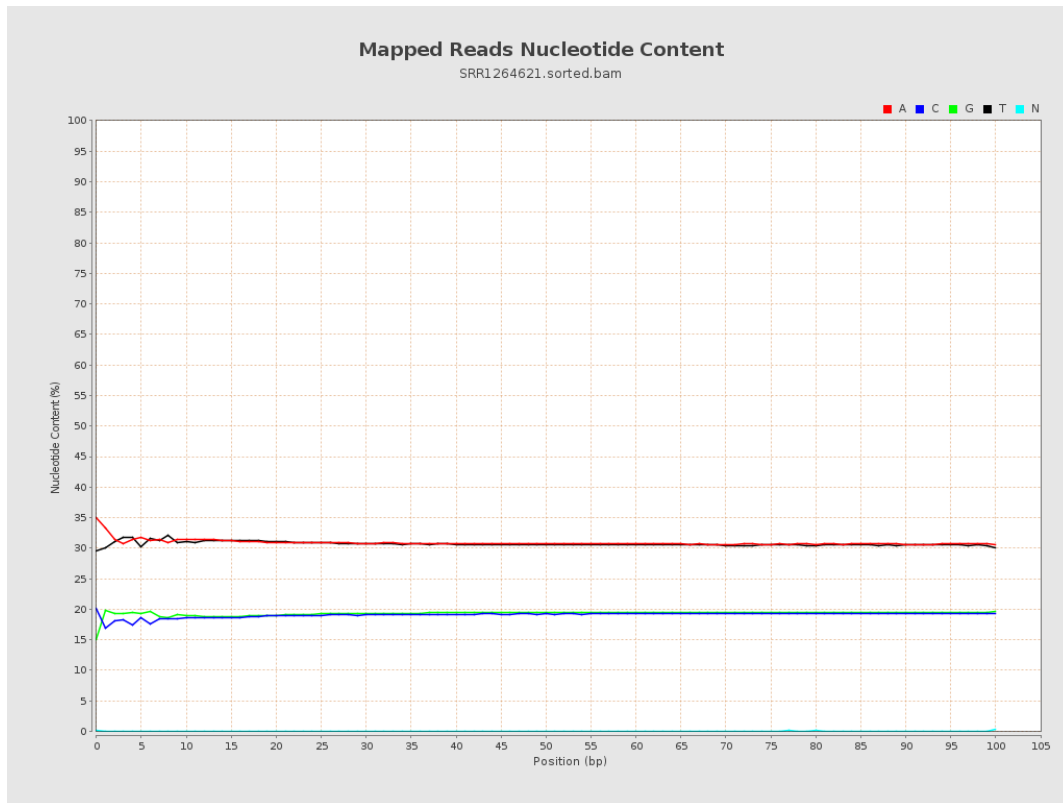
6. Results : Genome Fraction Coverage



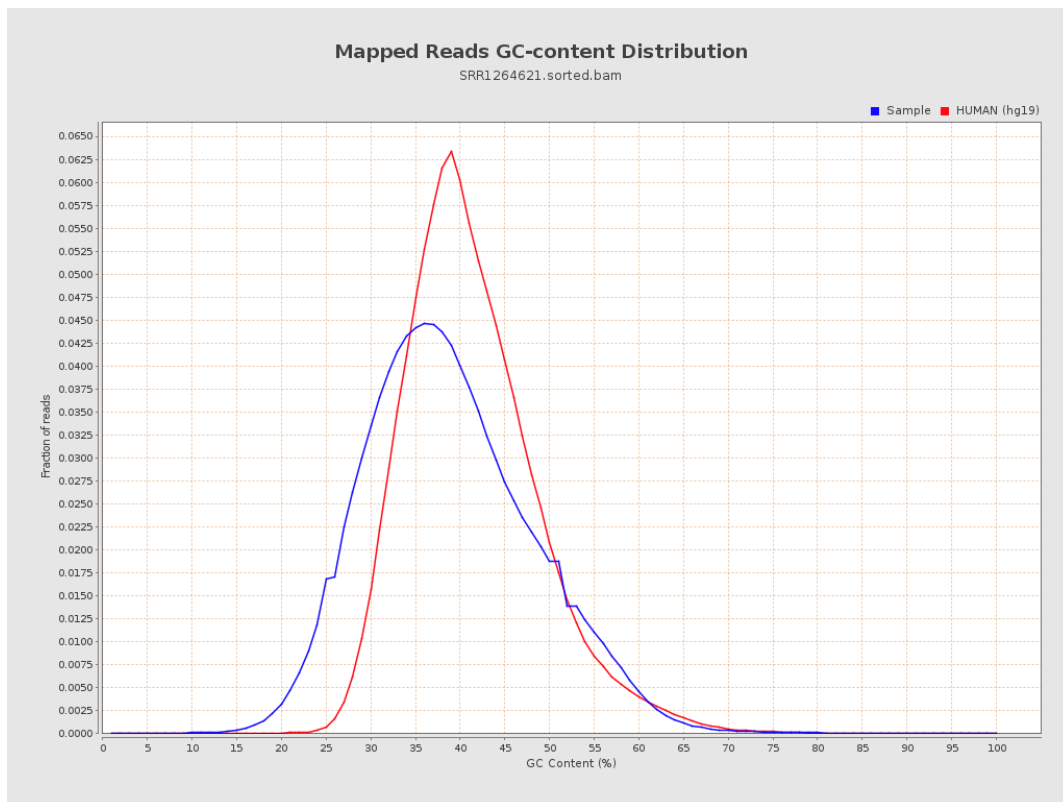
7. Results : Duplication Rate Histogram



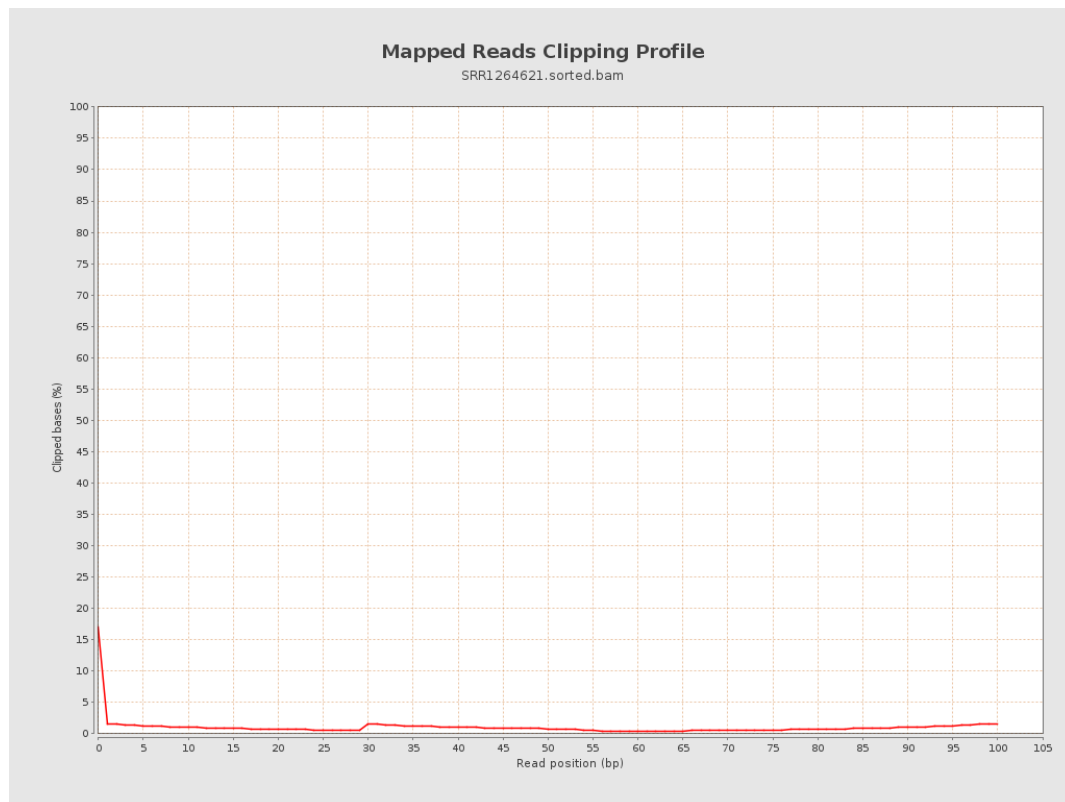
8. Results : Mapped Reads Nucleotide Content



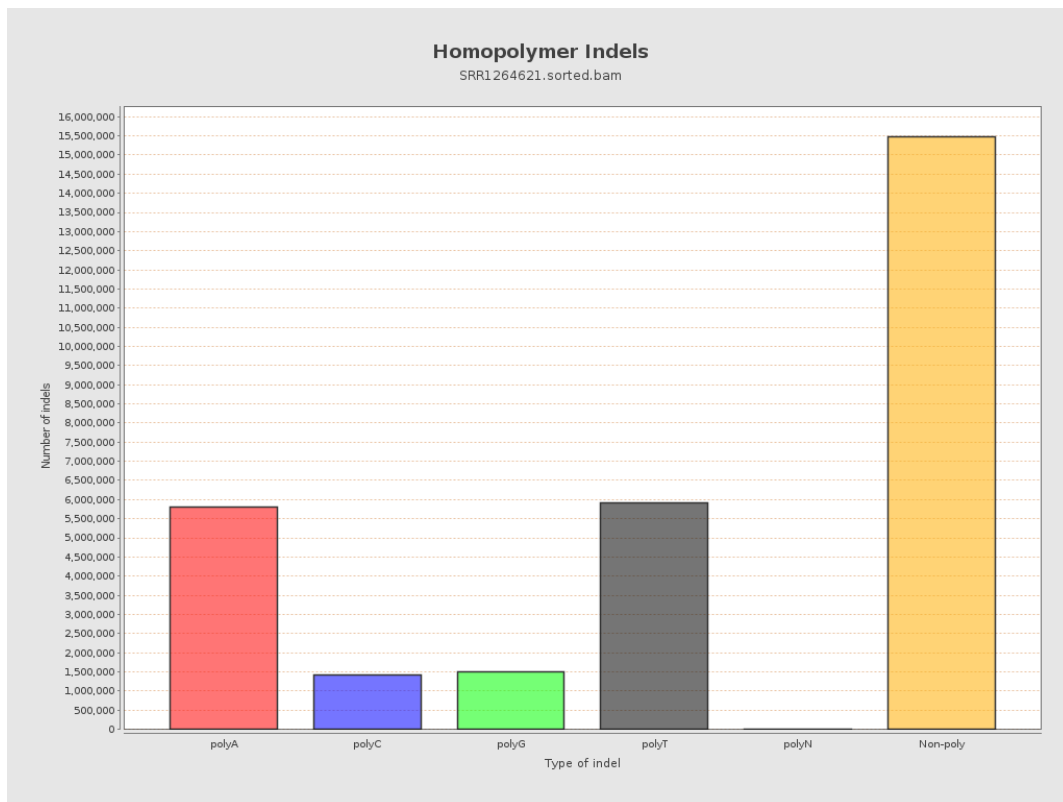
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



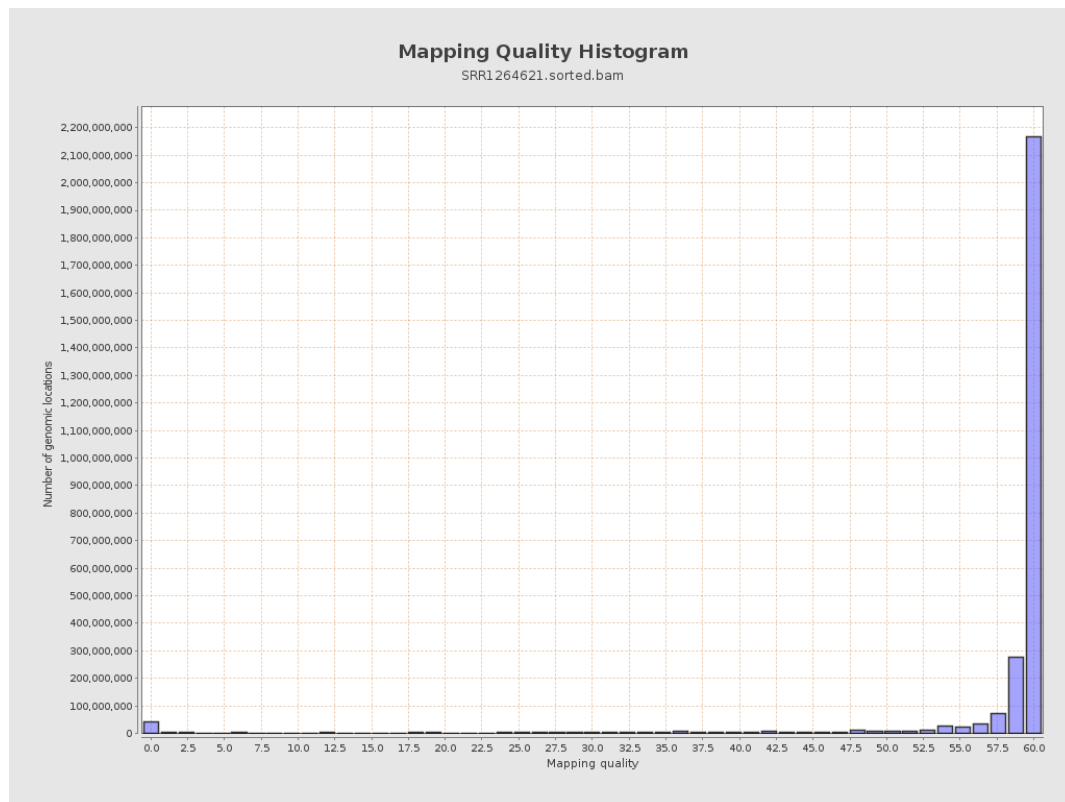
11. Results : Homopolymer Indels



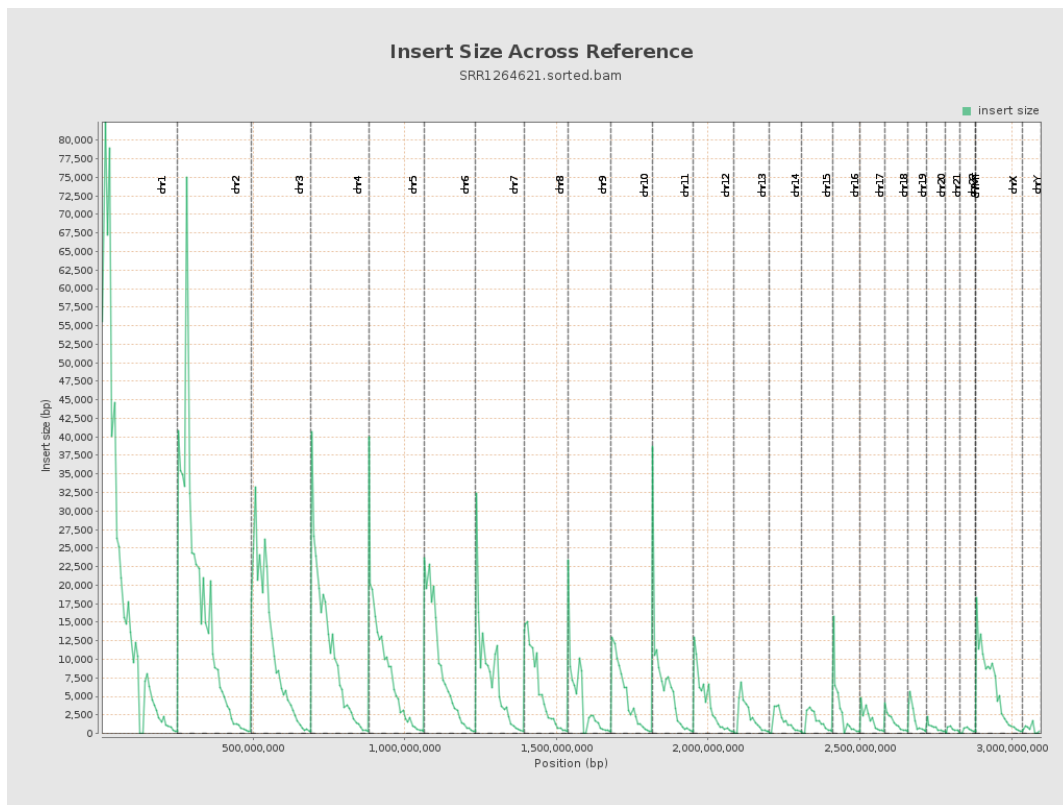
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

