

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 20:47:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124860.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_SRR3124860 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124860_1.fastq.gz SRR3124860_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 20:47:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124860.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	195,897,960
Mapped reads	191,155,007 / 97.58%
Unmapped reads	4,742,953 / 2.42%
Mapped paired reads	191,155,007 / 97.58%
Mapped reads, first in pair	95,595,680 / 48.8%
Mapped reads, second in pair	95,559,327 / 48.78%
Mapped reads, both in pair	190,403,154 / 97.2%
Mapped reads, singletons	751,853 / 0.38%
Secondary alignments	0
Supplementary alignments	29,274,787 / 14.94%
Read min/max/mean length	30 / 125 / 131.97
Duplicated reads (estimated)	98,404,372 / 50.23%
Duplication rate	44.69%
Clipped reads	184,803,229 / 94.34%

2.2. ACGT Content

Number/percentage of A's	5,442,873,502 / 28.63%
Number/percentage of C's	4,057,900,034 / 21.34%
Number/percentage of T's	5,268,010,879 / 27.71%
Number/percentage of G's	4,240,772,457 / 22.31%
Number/percentage of N's	2,647,323 / 0.01%

GC Percentage	43.65%
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2.3. Coverage

Mean	6.1472
Standard Deviation	269.393

2.4. Mapping Quality

Mean Mapping Quality	45.62
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2.5. Insert size

Mean	587,009.5
Standard Deviation	7,416,196.48
P25/Median/P75	76 / 98 / 125

2.6. Mismatches and indels

General error rate	1.54%
Mismatches	275,488,826
Insertions	6,130,829
Mapped reads with at least one insertion	3.04%
Deletions	6,936,418
Mapped reads with at least one deletion	3.45%
Homopolymer indels	34.9%

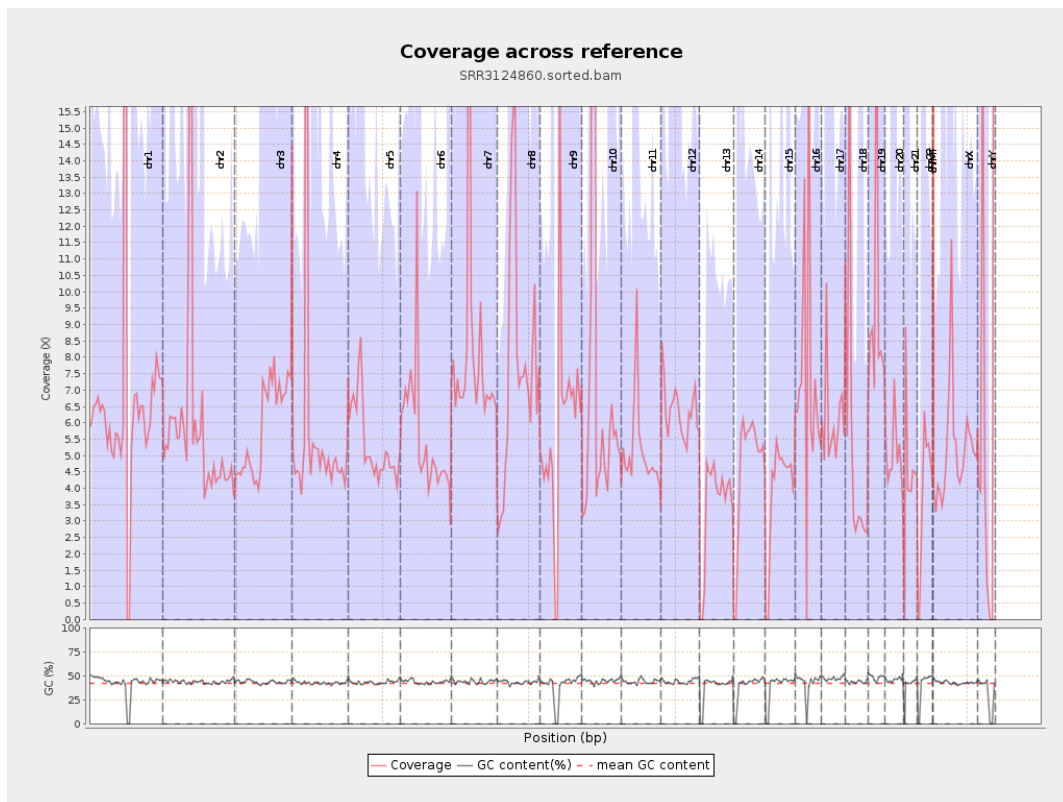
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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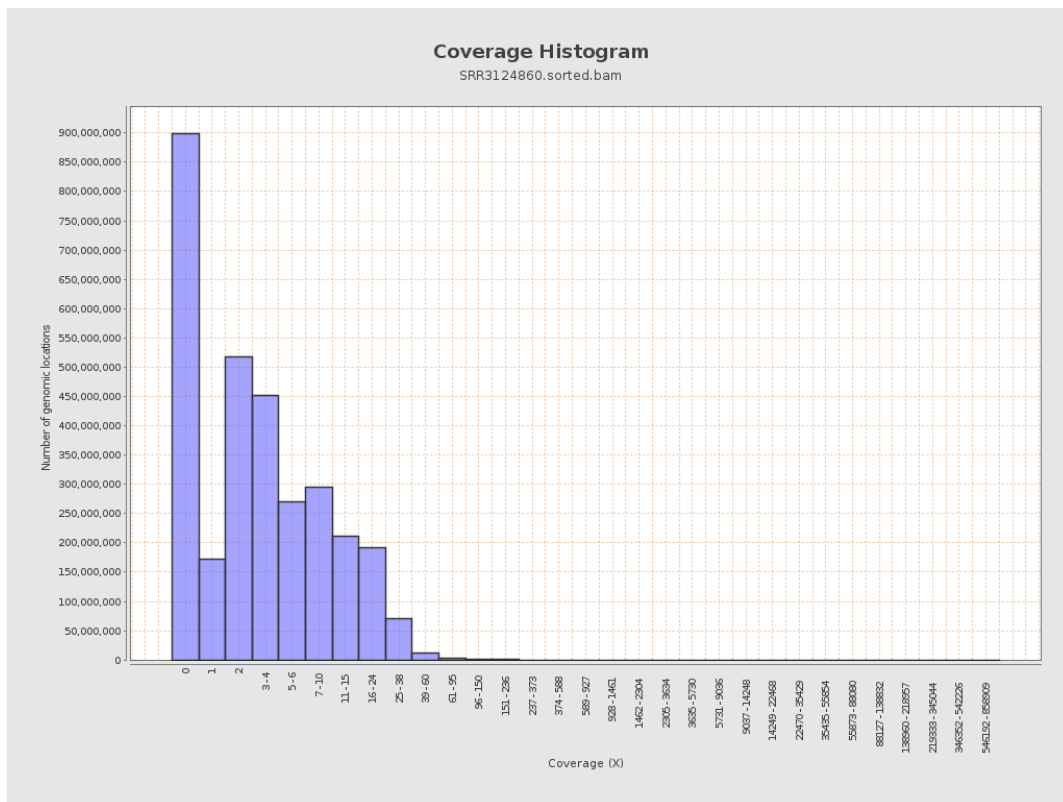
		bases	coverage	deviation
chr1	249250621	1765808697	7.0845	776.6993
chr2	243199373	1474040555	6.061	127.7177
chr3	198022430	1173382468	5.9255	64.6461
chr4	191154276	1109379304	5.8036	142.3686
chr5	180915260	978110214	5.4065	16.0689
chr6	171115067	951967095	5.5633	69.7361
chr7	159138663	1309953307	8.2315	206.3541
chr8	146364022	1119187301	7.6466	90.9642
chr9	141213431	835443595	5.9162	172.5042
chr10	135534747	1248628593	9.2126	490.0786
chr11	135006516	699062339	5.178	68.8698
chr12	133851895	859456546	6.421	23.9981
chr13	115169878	402762809	3.4971	5.9156
chr14	107349540	507255306	4.7253	17.5269
chr15	102531392	395307197	3.8555	15.5344
chr16	90354753	672053318	7.4379	95.9515
chr17	81195210	496921852	6.1201	83.3312
chr18	78077248	421936990	5.4041	265.6258
chr19	59128983	566529640	9.5813	388.6436
chr20	63025520	315125470	5	47.984
chr21	48129895	221244072	4.5968	91.0869
chr22	51304566	195372335	3.8081	41.0934
chrMT	16571	63402629	3,826.1197	1,734.6386
chrX	155270560	808394637	5.2064	42.9693

chrY	59373566	439009732	7.394	191.5737
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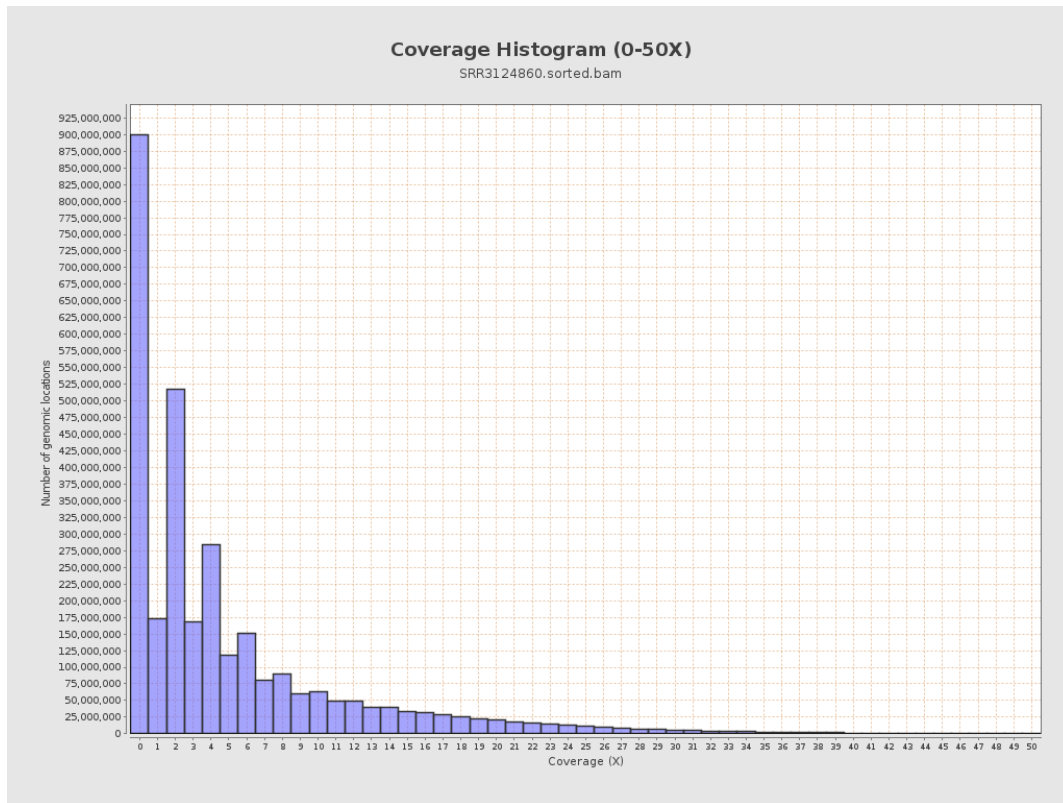
3. Results : Coverage across reference



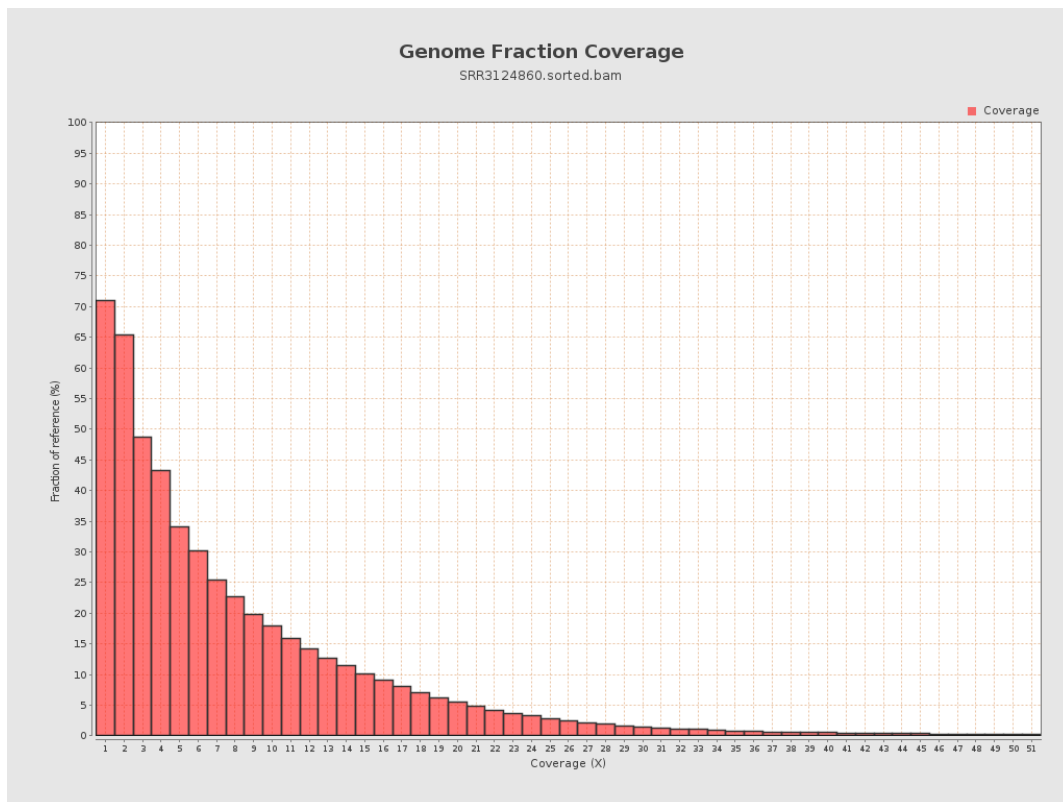
4. Results : Coverage Histogram



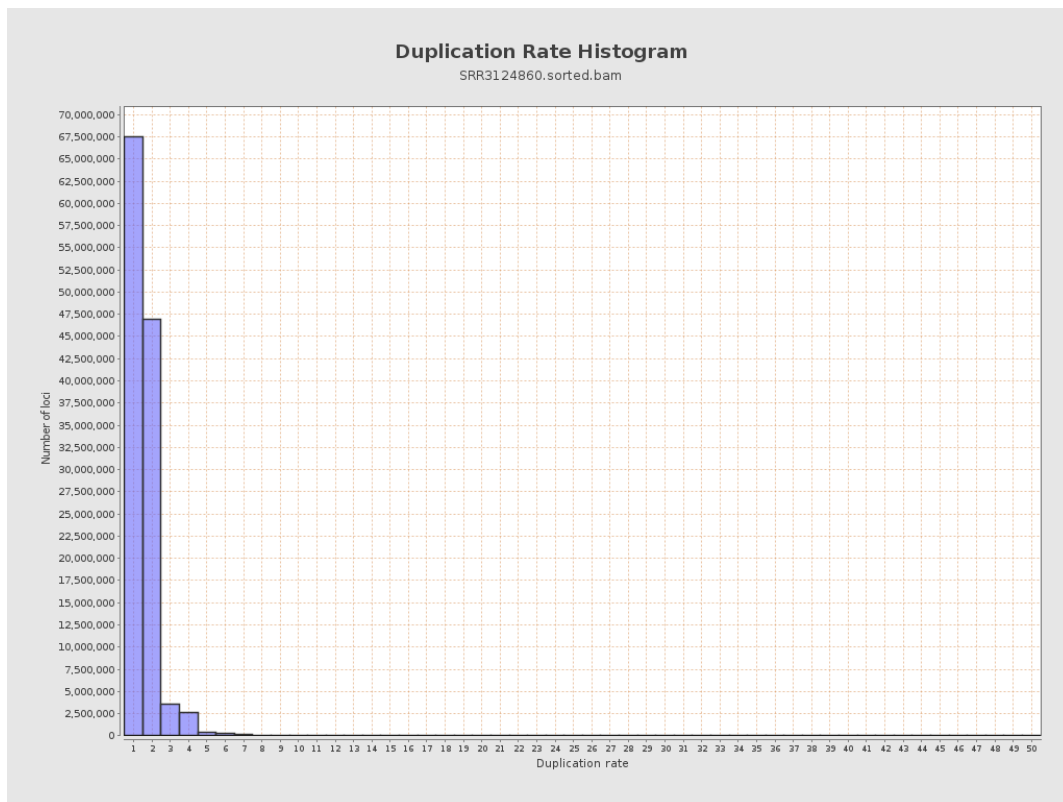
5. Results : Coverage Histogram (0-50X)



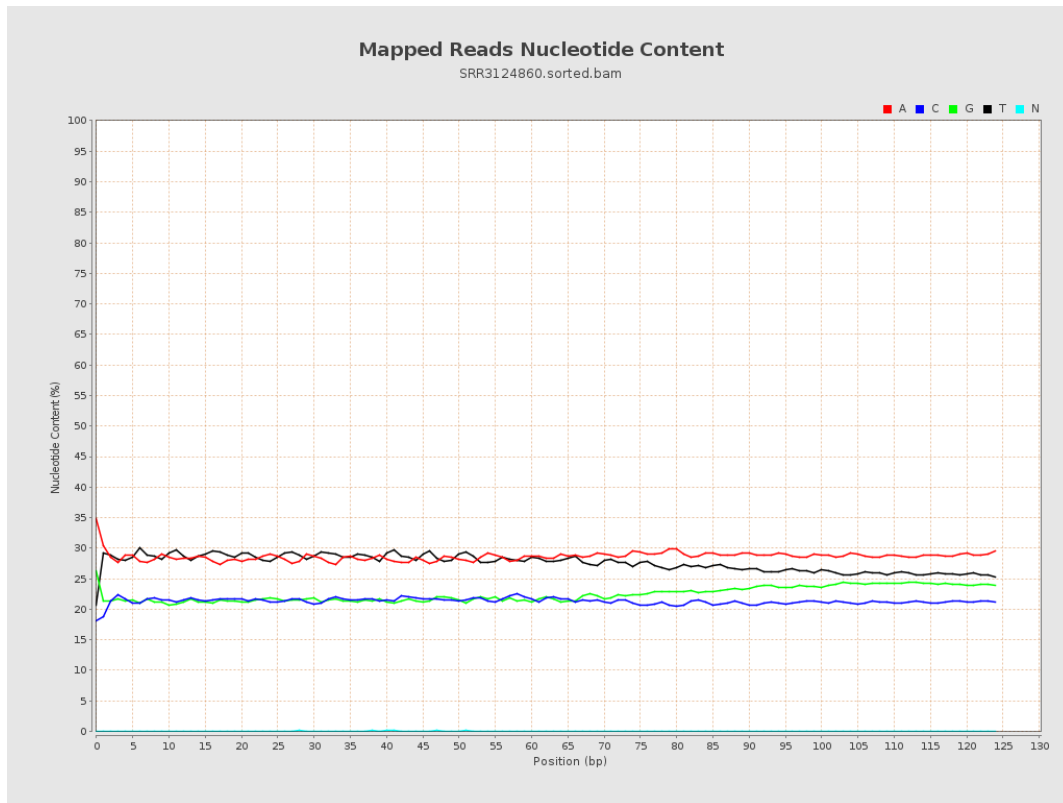
6. Results : Genome Fraction Coverage



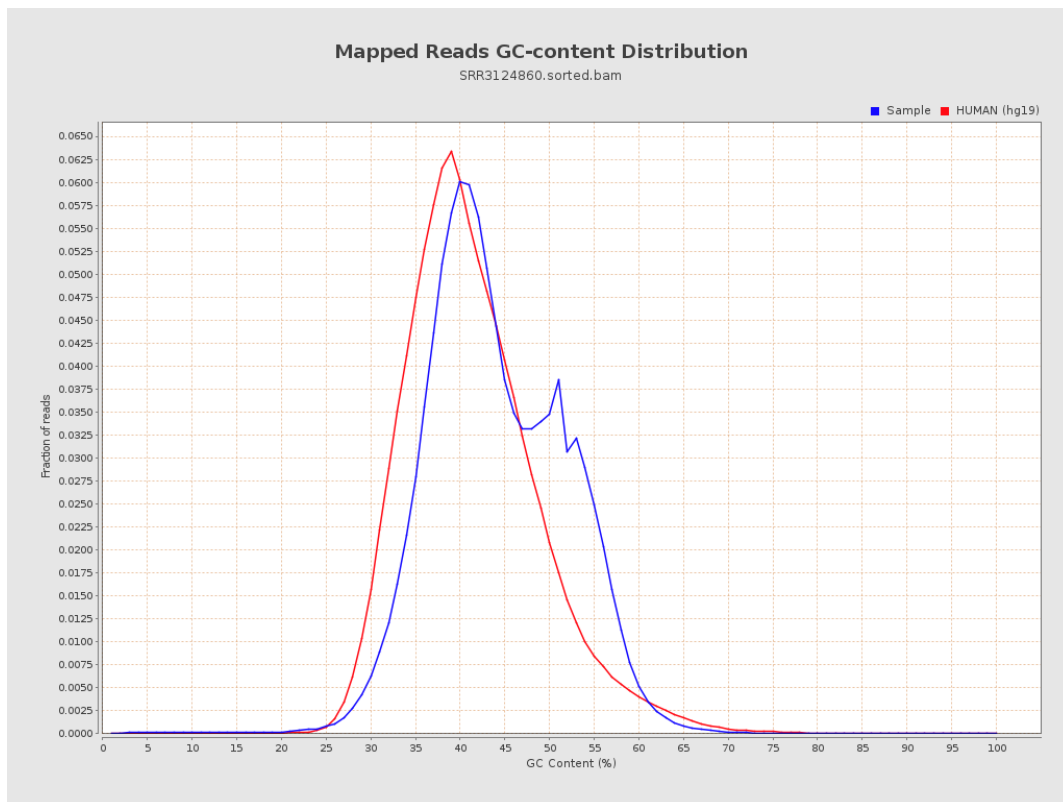
7. Results : Duplication Rate Histogram



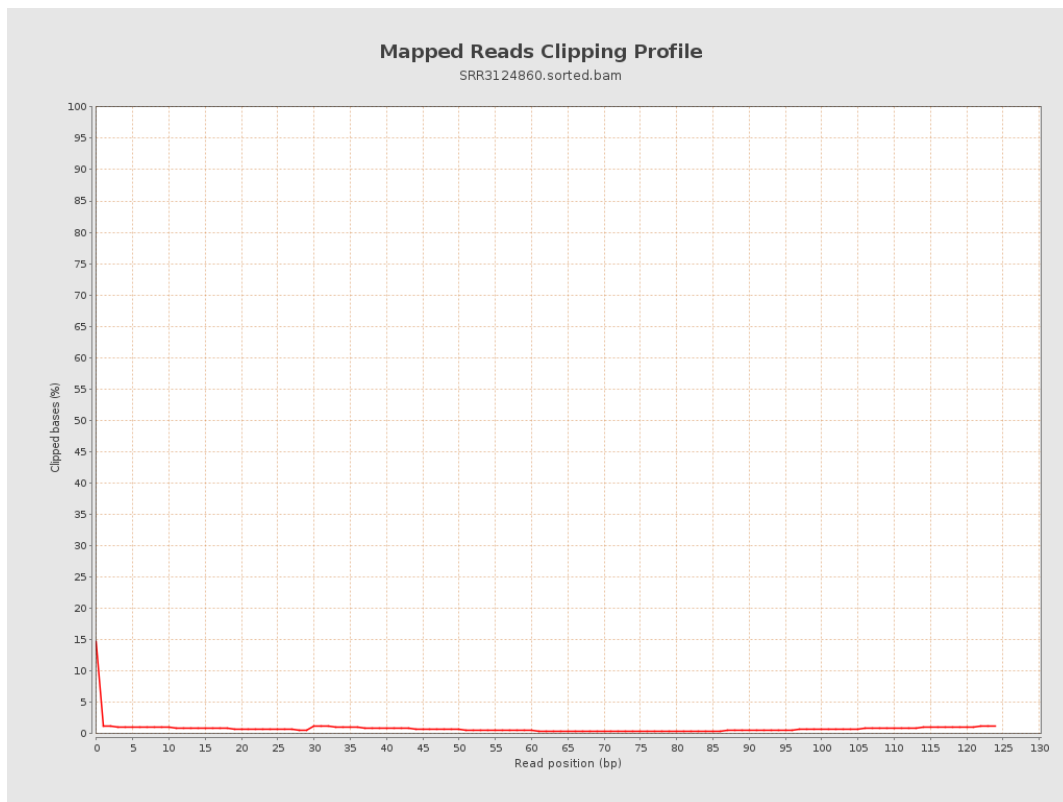
8. Results : Mapped Reads Nucleotide Content



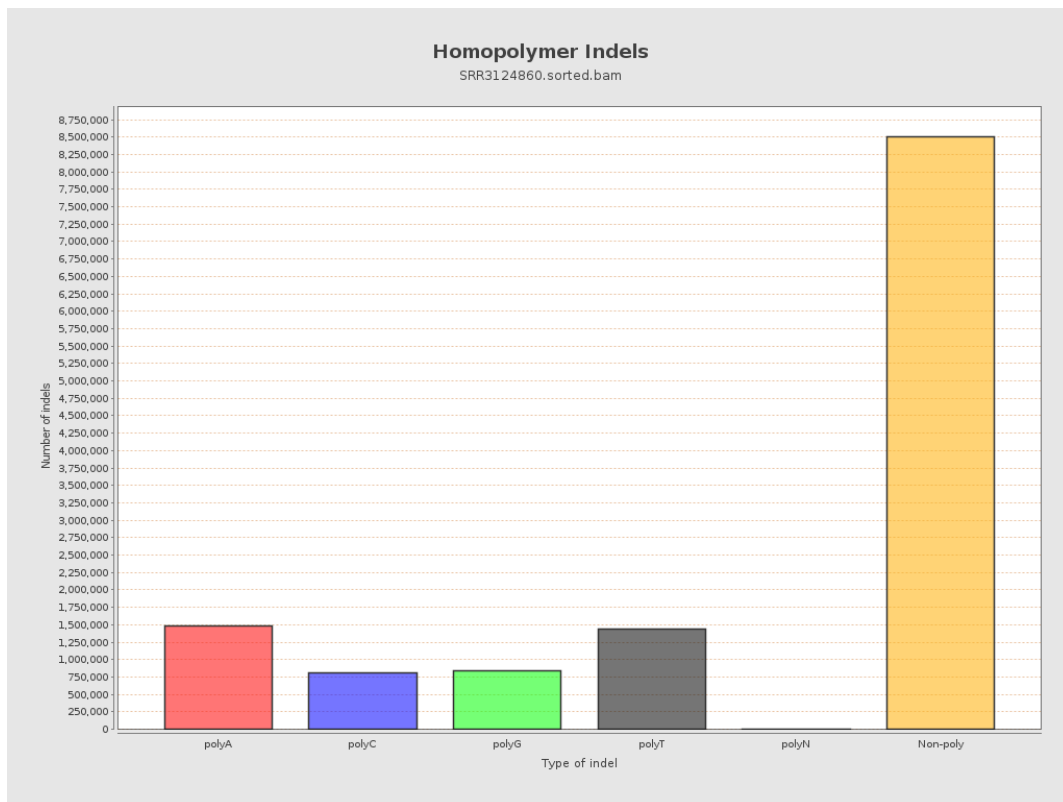
9. Results : Mapped Reads GC-content Distribution



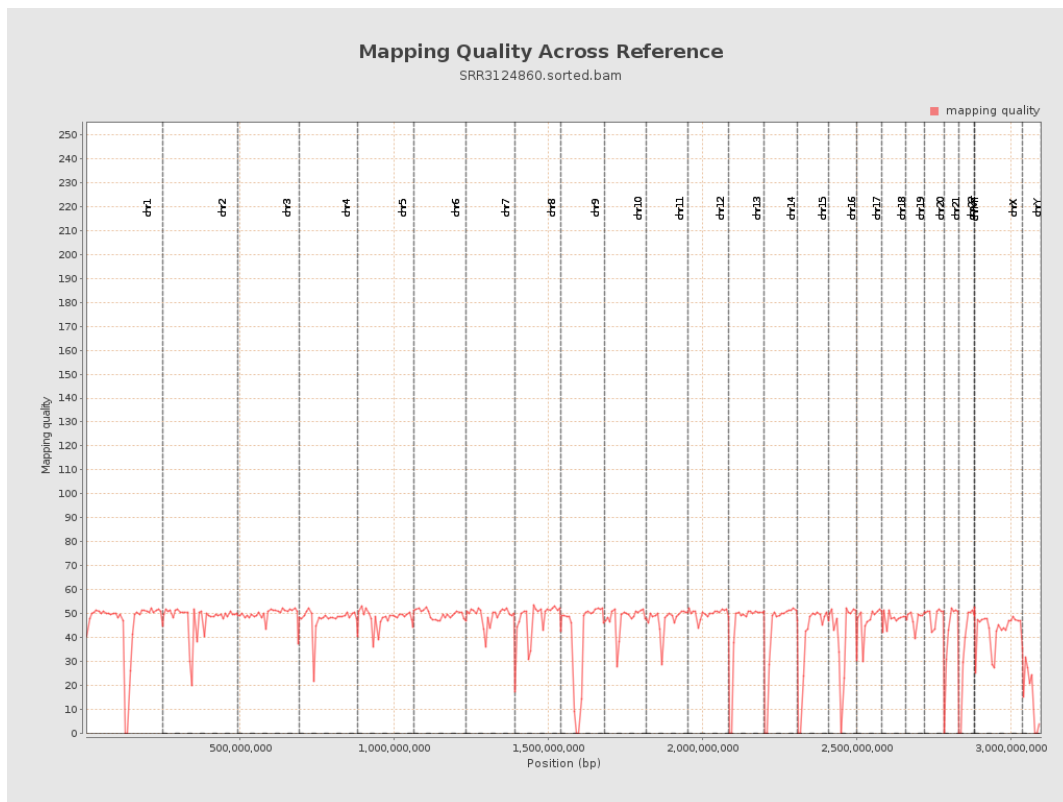
10. Results : Mapped Reads Clipping Profile



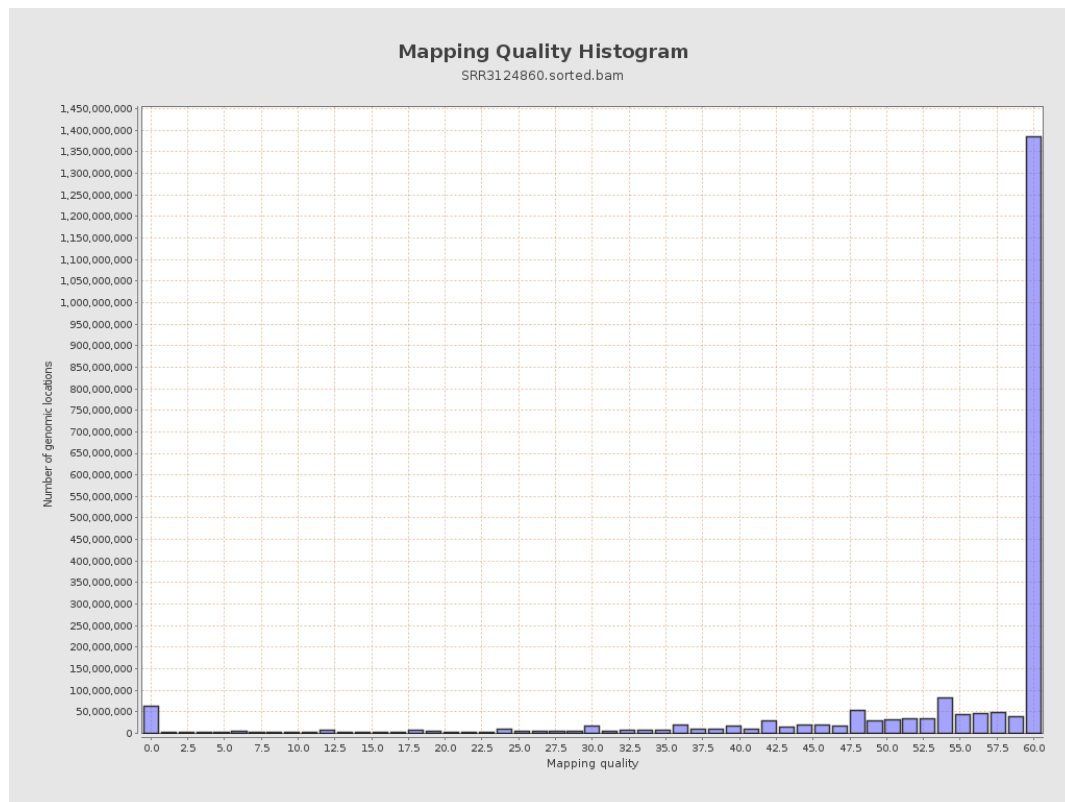
11. Results : Homopolymer Indels



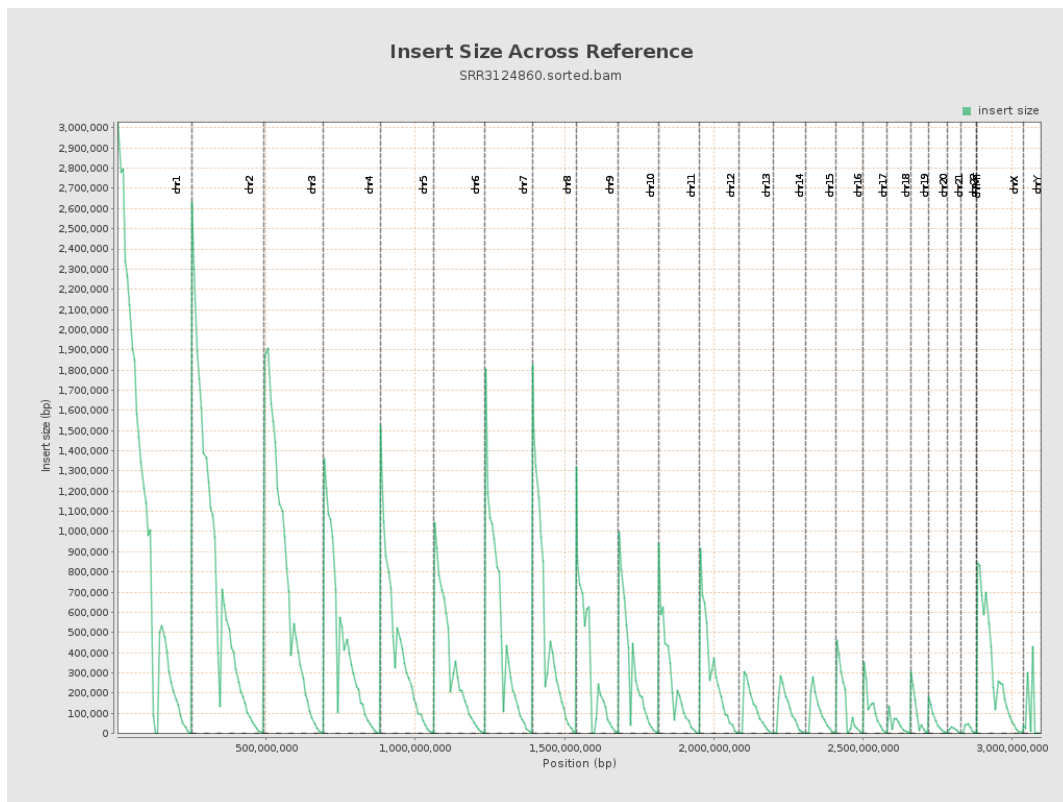
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

