

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:49:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472565.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_SRR3472565 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472565_1.fastq.gz SRR3472565_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:49:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472565.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,286,270
Mapped reads	16,081,112 / 98.74%
Unmapped reads	205,158 / 1.26%
Mapped paired reads	16,081,112 / 98.74%
Mapped reads, first in pair	8,064,209 / 49.52%
Mapped reads, second in pair	8,016,903 / 49.22%
Mapped reads, both in pair	15,981,778 / 98.13%
Mapped reads, singletons	99,334 / 0.61%
Secondary alignments	0
Supplementary alignments	58,094 / 0.36%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	10,171,043 / 62.45%
Duplication rate	44.86%
Clipped reads	1,582,899 / 9.72%

2.2. ACGT Content

Number/percentage of A's	429,898,894 / 27.28%
Number/percentage of C's	360,859,220 / 22.9%
Number/percentage of T's	425,814,393 / 27.02%
Number/percentage of G's	359,214,660 / 22.79%
Number/percentage of N's	243,553 / 0.02%

GC Percentage	45.69%
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2.3. Coverage

Mean	0.5092
Standard Deviation	19.3848

2.4. Mapping Quality

Mean Mapping Quality	55.02
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2.5. Insert size

Mean	28,437.69
Standard Deviation	1,679,480.29
P25/Median/P75	158 / 223 / 302

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	9,154,966
Insertions	81,590
Mapped reads with at least one insertion	0.5%
Deletions	76,642
Mapped reads with at least one deletion	0.47%
Homopolymer indels	44.36%

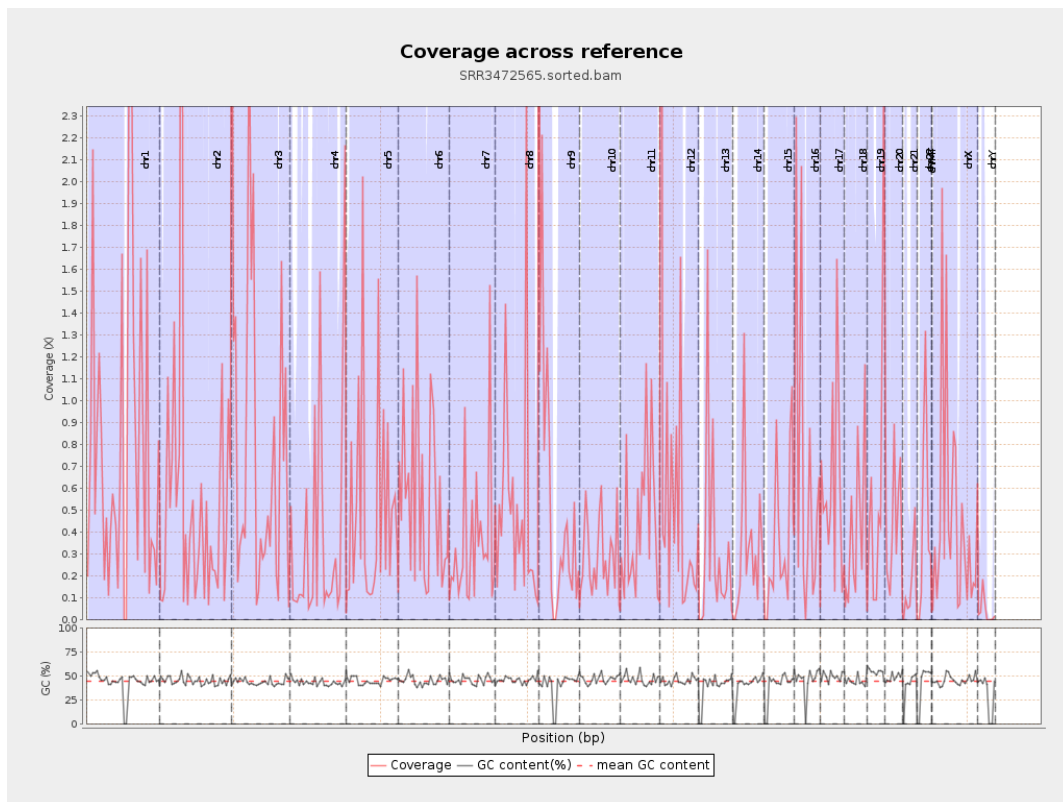
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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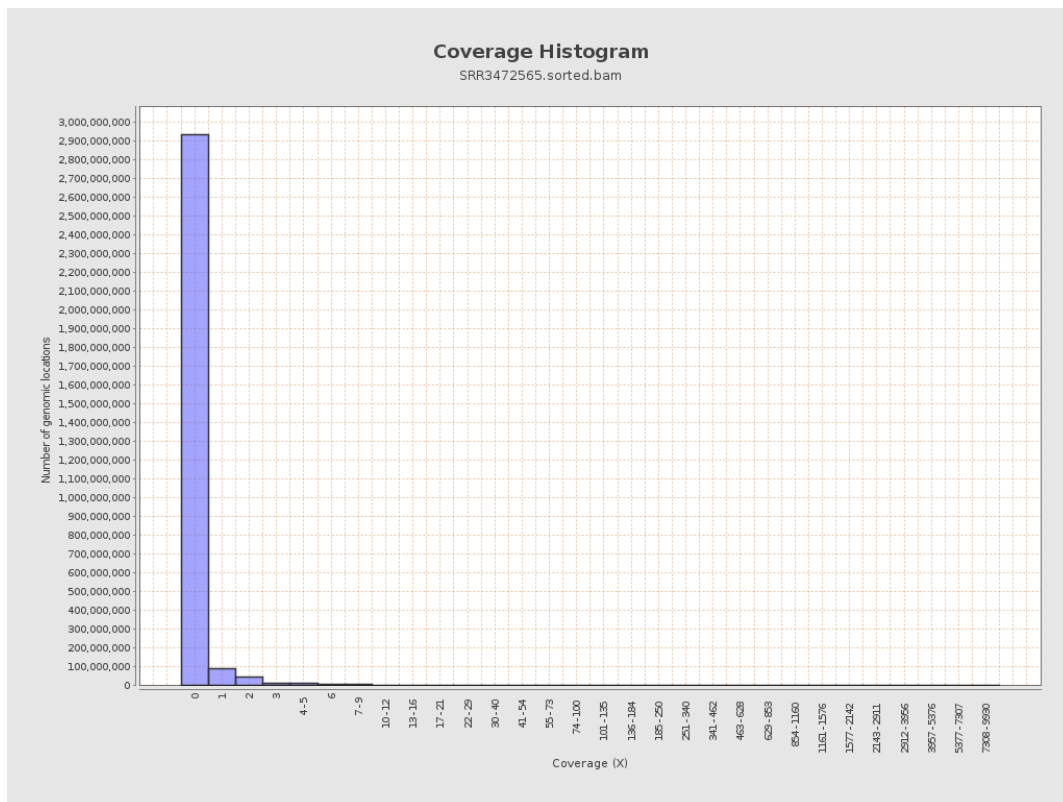
		bases	coverage	deviation
chr1	249250621	199092702	0.7988	27.2348
chr2	243199373	143397606	0.5896	28.6437
chr3	198022430	159789652	0.8069	17.9496
chr4	191154276	69705286	0.3647	17.426
chr5	180915260	90743536	0.5016	18.5706
chr6	171115067	94379734	0.5516	16.0312
chr7	159138663	56131459	0.3527	12.5757
chr8	146364022	75259397	0.5142	23.673
chr9	141213431	76851953	0.5442	15.0191
chr10	135534747	39889662	0.2943	10.8084
chr11	135006516	61023622	0.452	20.6179
chr12	133851895	97832972	0.7309	25.6498
chr13	115169878	36393157	0.316	11.5093
chr14	107349540	33794399	0.3148	9.963
chr15	102531392	36527558	0.3563	11.1618
chr16	90354753	59245247	0.6557	23.0587
chr17	81195210	48668666	0.5994	16.3101
chr18	78077248	31906350	0.4087	19.5124
chr19	59128983	34880574	0.5899	19.285
chr20	63025520	27942835	0.4434	14.3903
chr21	48129895	7705055	0.1601	6.8079
chr22	51304566	22230885	0.4333	12.6643
chrMT	16571	3820	0.2305	0.6786
chrX	155270560	70303249	0.4528	20.7002

chrY	59373566	2518903	0.0424	1.4807
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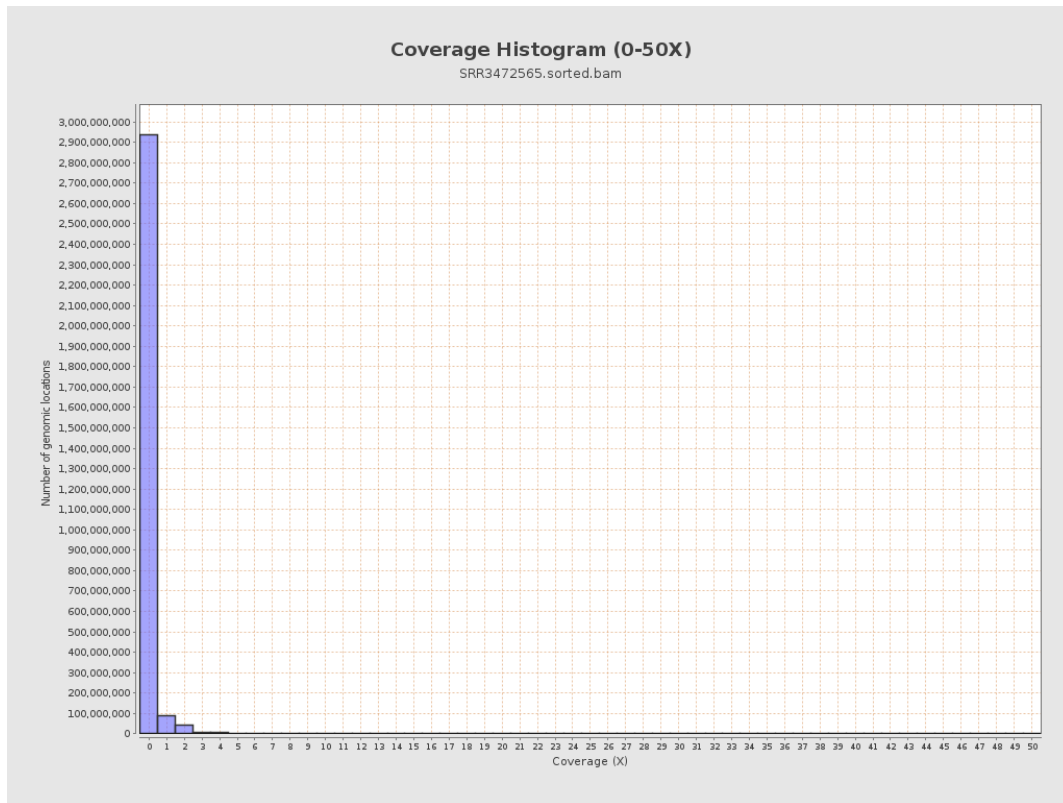
3. Results : Coverage across reference



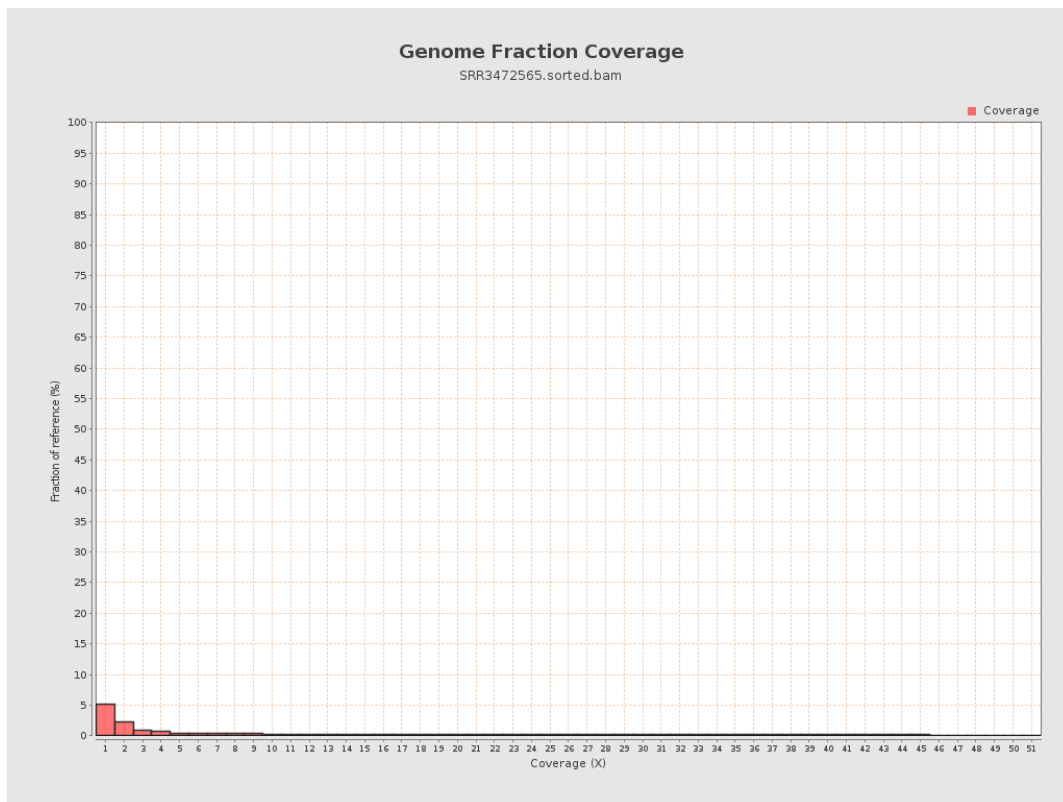
4. Results : Coverage Histogram



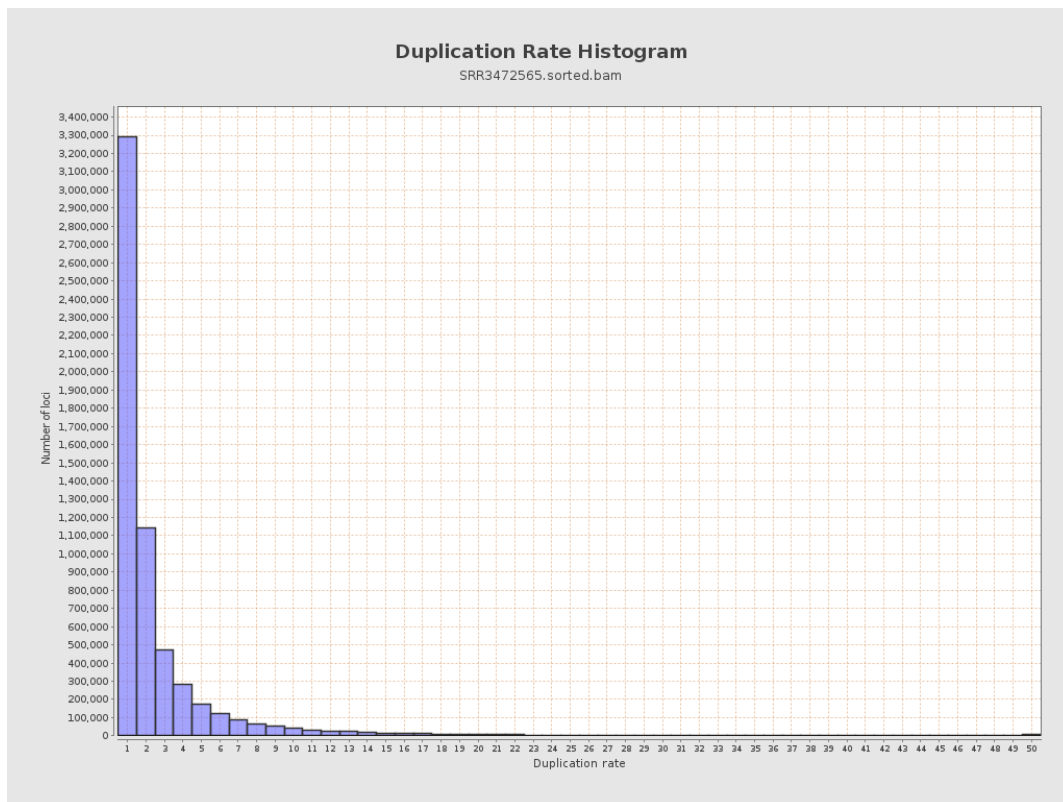
5. Results : Coverage Histogram (0-50X)



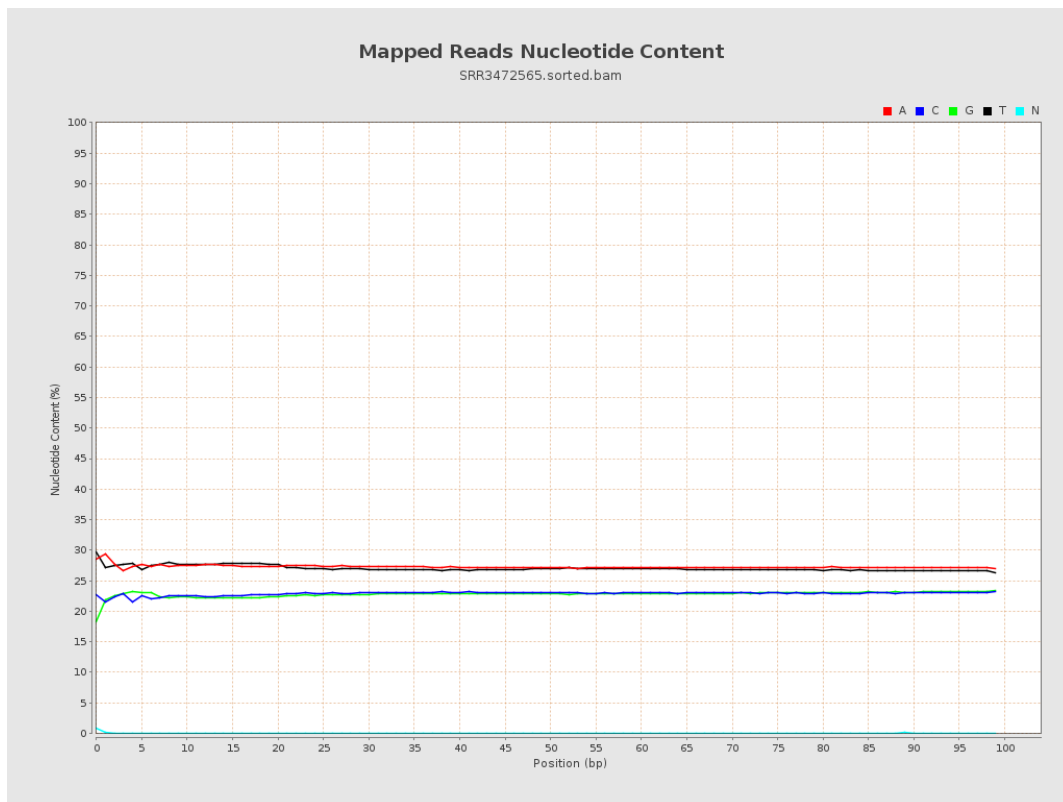
6. Results : Genome Fraction Coverage



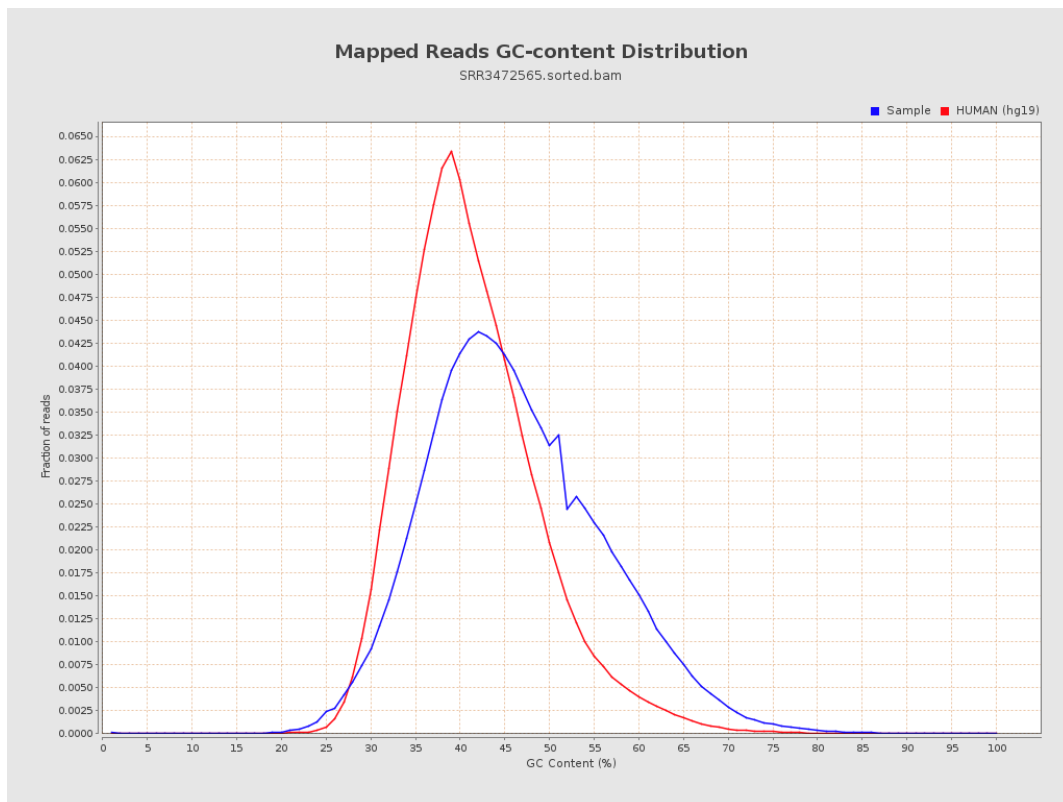
7. Results : Duplication Rate Histogram



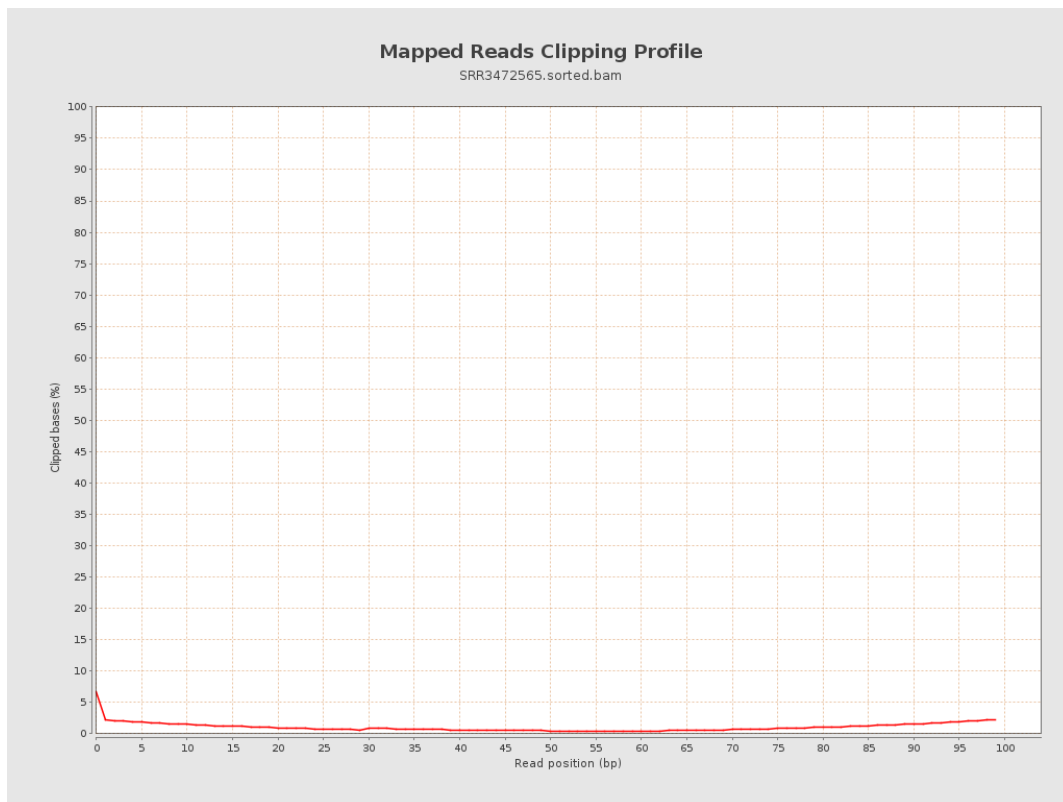
8. Results : Mapped Reads Nucleotide Content



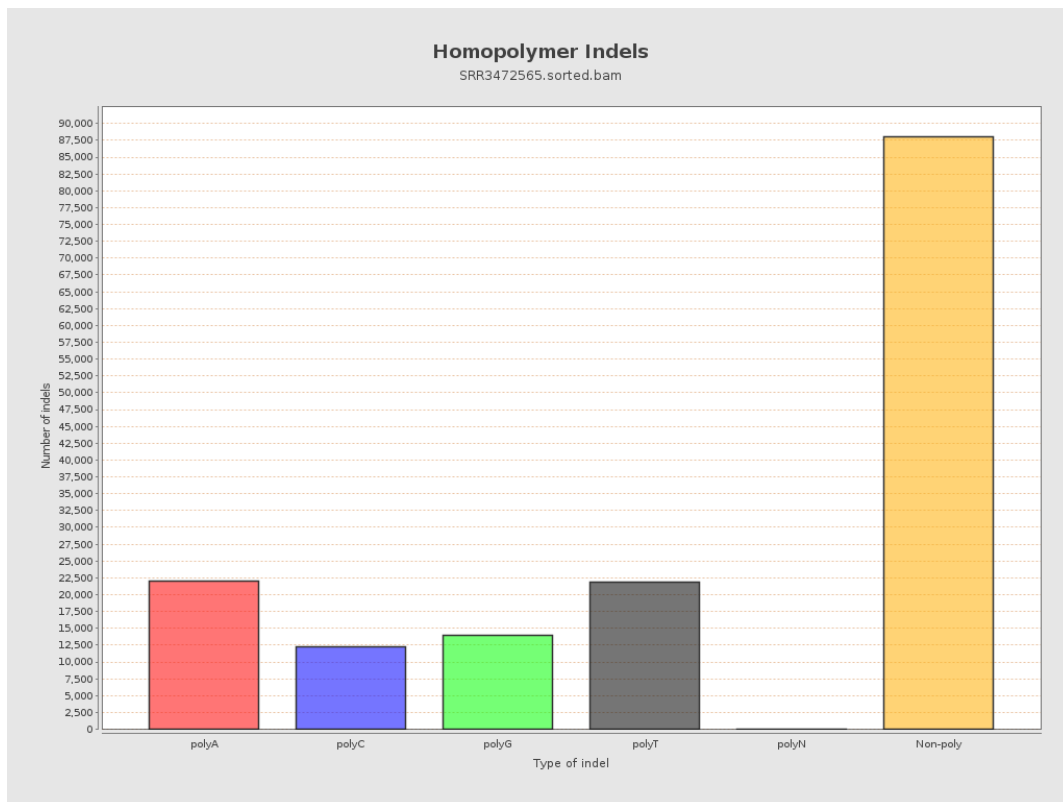
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



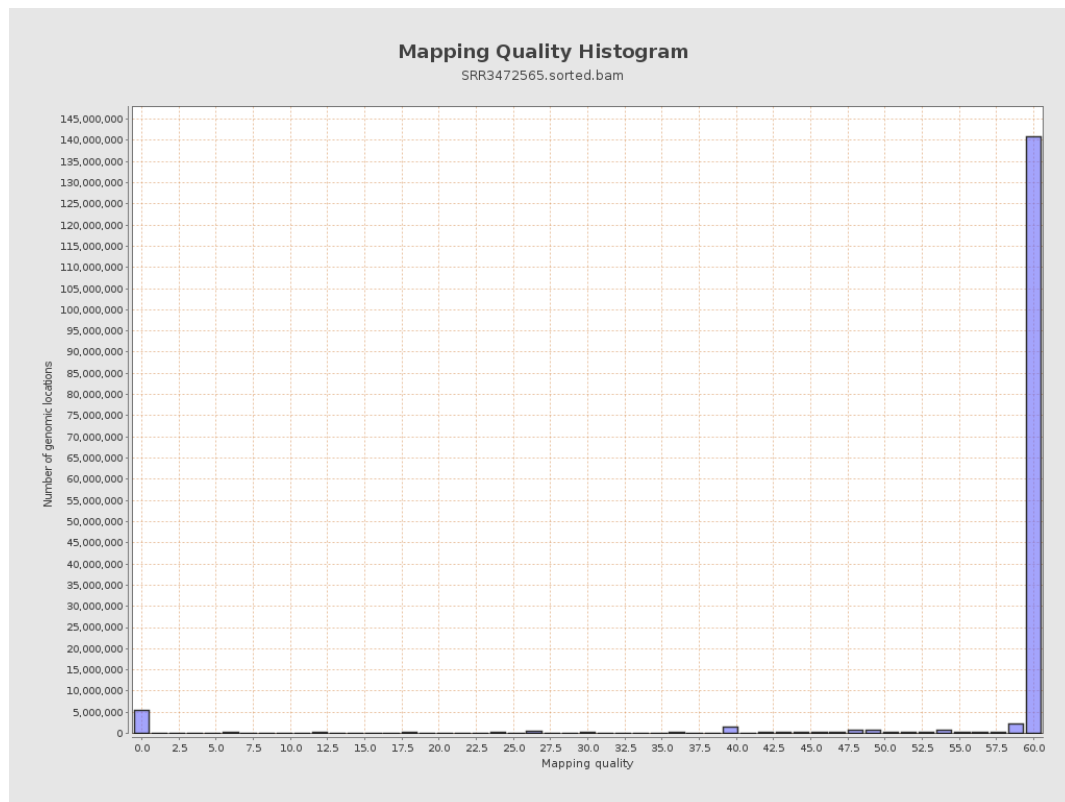
11. Results : Homopolymer Indels



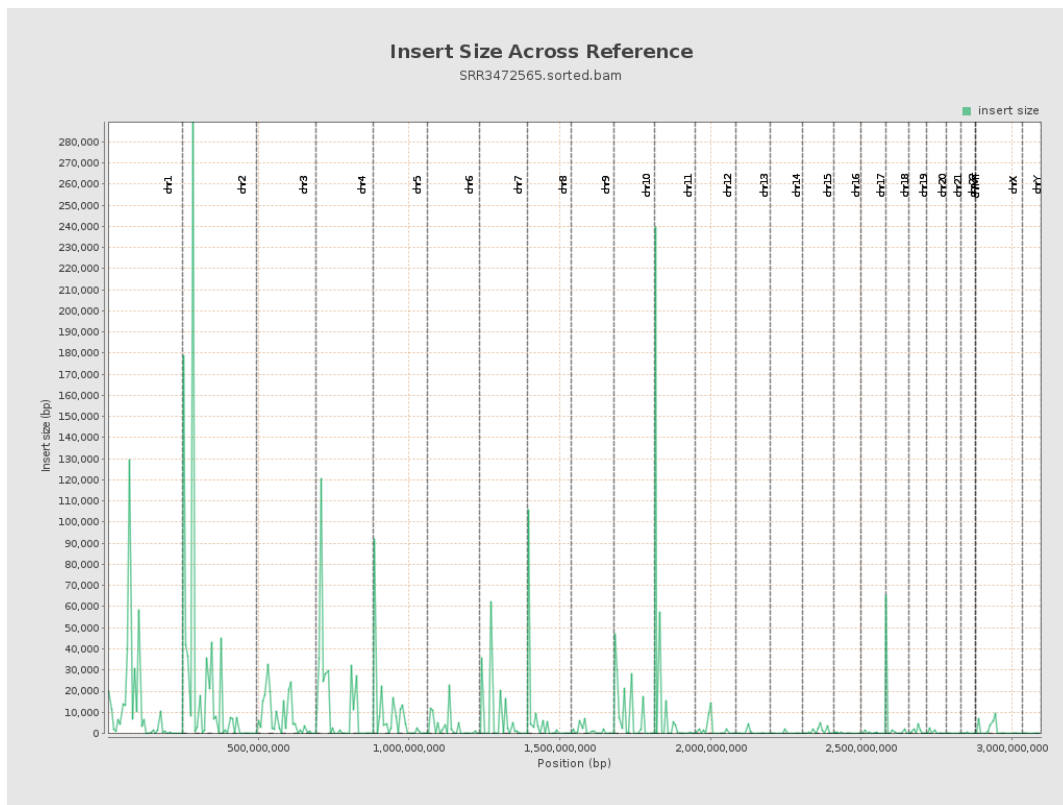
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

