

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:58:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472561.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_SRR3472561 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472561_1.fastq.gz SRR3472561_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:58:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472561.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,109,246
Mapped reads	9,910,971 / 98.04%
Unmapped reads	198,275 / 1.96%
Mapped paired reads	9,910,971 / 98.04%
Mapped reads, first in pair	4,975,333 / 49.22%
Mapped reads, second in pair	4,935,638 / 48.82%
Mapped reads, both in pair	9,820,308 / 97.14%
Mapped reads, singletons	90,663 / 0.9%
Secondary alignments	0
Supplementary alignments	44,947 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	5,833,245 / 57.7%
Duplication rate	43.14%
Clipped reads	978,647 / 9.68%

2.2. ACGT Content

Number/percentage of A's	271,380,349 / 27.97%
Number/percentage of C's	215,355,831 / 22.2%
Number/percentage of T's	268,871,085 / 27.71%
Number/percentage of G's	214,473,416 / 22.11%
Number/percentage of N's	149,443 / 0.02%

GC Percentage	44.3%
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2.3. Coverage

Mean	0.3135
Standard Deviation	14.0669

2.4. Mapping Quality

Mean Mapping Quality	54.58
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2.5. Insert size

Mean	37,886.54
Standard Deviation	1,890,470.73
P25/Median/P75	167 / 240 / 330

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	6,201,787
Insertions	58,475
Mapped reads with at least one insertion	0.58%
Deletions	54,779
Mapped reads with at least one deletion	0.55%
Homopolymer indels	44.45%

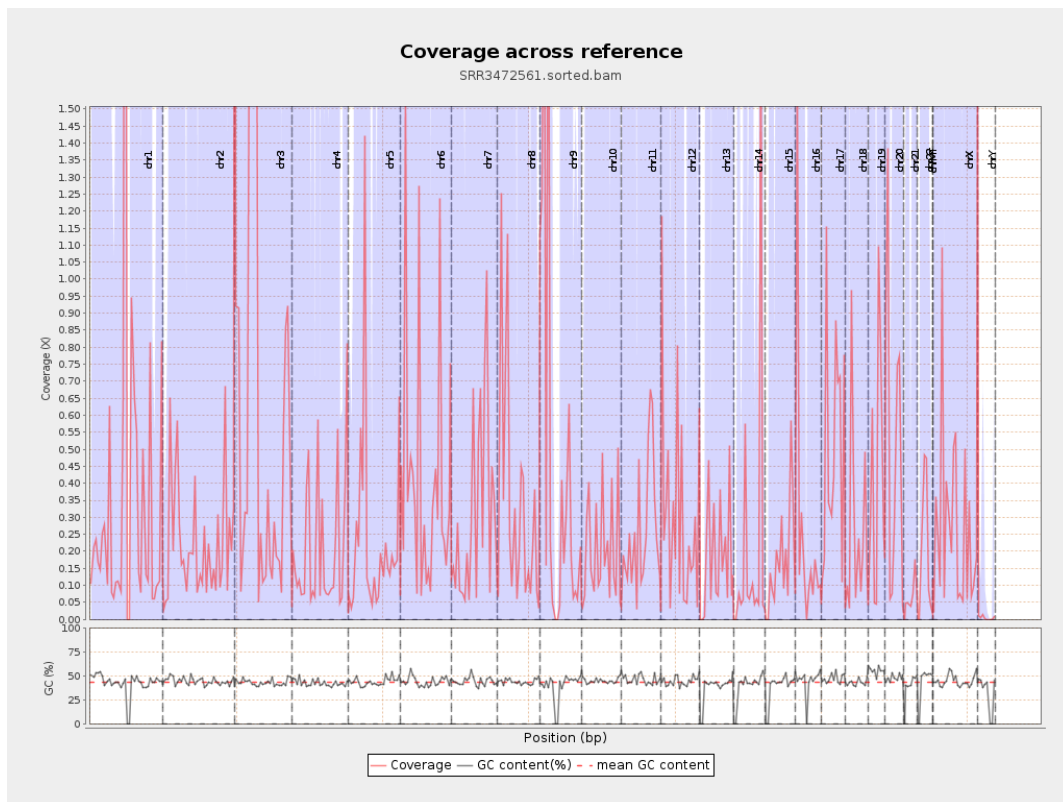
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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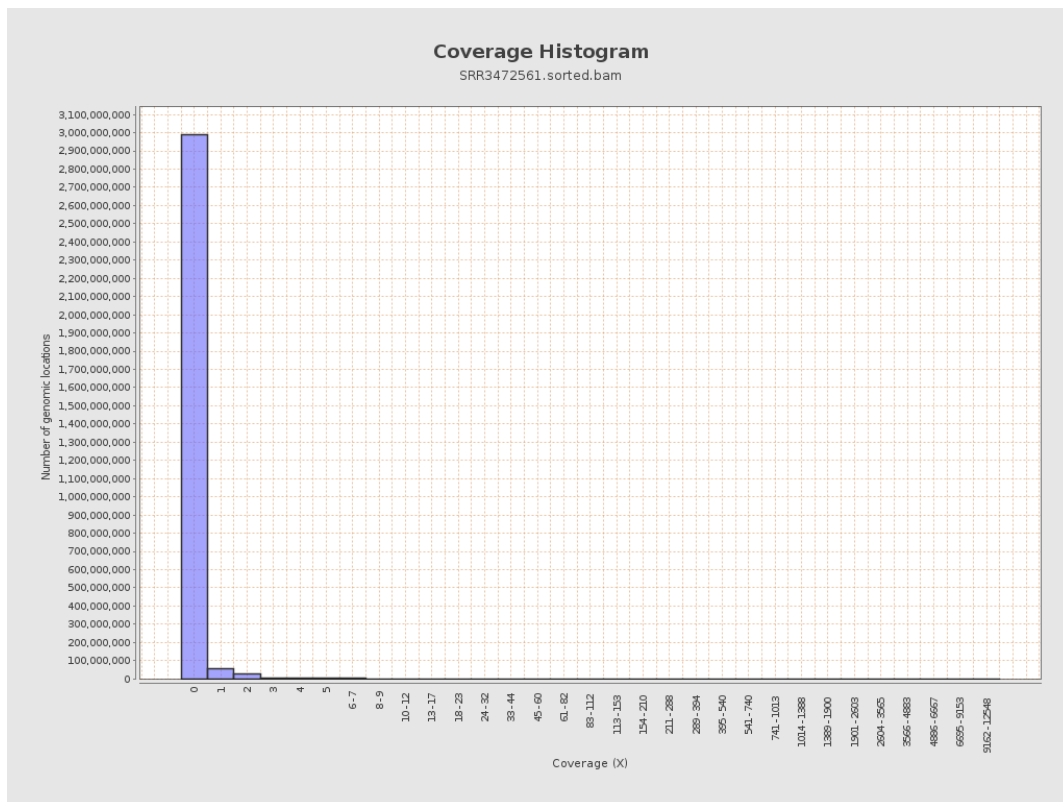
		bases	coverage	deviation
chr1	249250621	92061204	0.3694	20.0953
chr2	243199373	53941370	0.2218	7.8592
chr3	198022430	135956772	0.6866	17.9928
chr4	191154276	40654076	0.2127	7.9184
chr5	180915260	42824616	0.2367	9.2113
chr6	171115067	71812892	0.4197	16.8506
chr7	159138663	49186458	0.3091	13.2572
chr8	146364022	49028309	0.335	16.8999
chr9	141213431	65914658	0.4668	15.5966
chr10	135534747	28440983	0.2098	9.4721
chr11	135006516	36094162	0.2674	9.1467
chr12	133851895	41484758	0.3099	10.1024
chr13	115169878	21104239	0.1832	7.0745
chr14	107349540	22783045	0.2122	28.4952
chr15	102531392	17778785	0.1734	5.1475
chr16	90354753	22558219	0.2497	7.2045
chr17	81195210	41298406	0.5086	16.7709
chr18	78077248	20887974	0.2675	14.207
chr19	59128983	24681147	0.4174	16.5898
chr20	63025520	33314085	0.5286	25.8079
chr21	48129895	3325999	0.0691	2.2657
chr22	51304566	9984826	0.1946	8.17
chrMT	16571	1987	0.1199	0.4479
chrX	155270560	44941095	0.2894	9.7294

chrY	59373566	292393	0.0049	0.357
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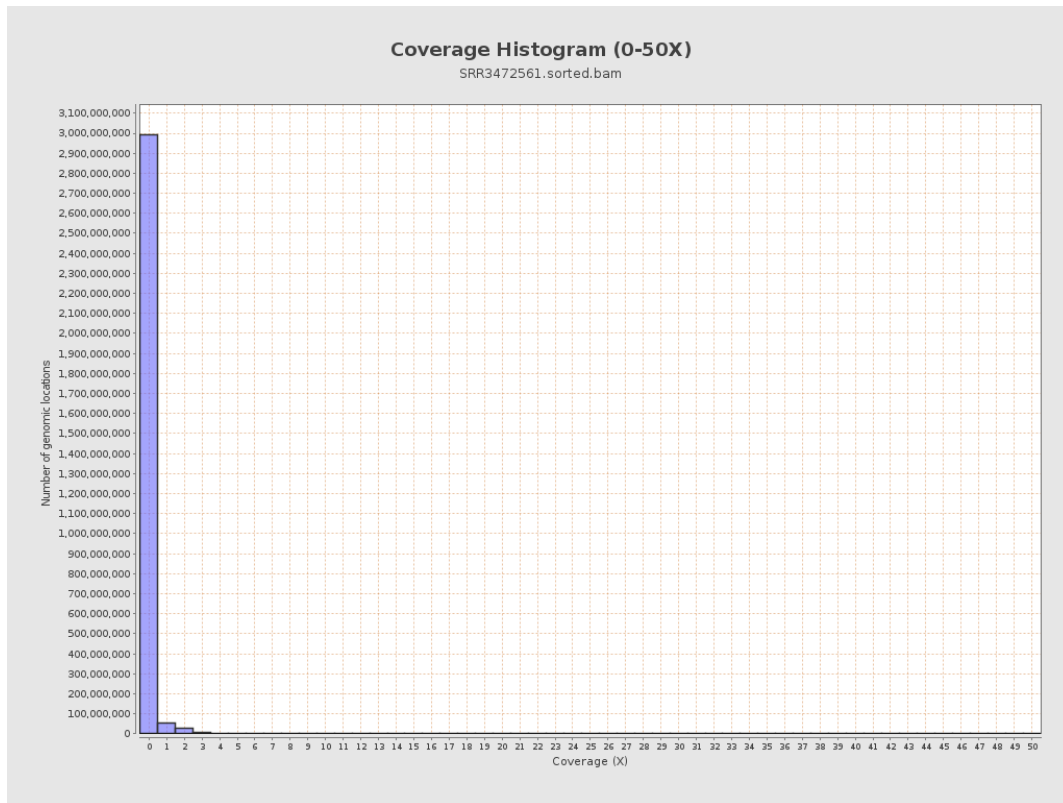
3. Results : Coverage across reference



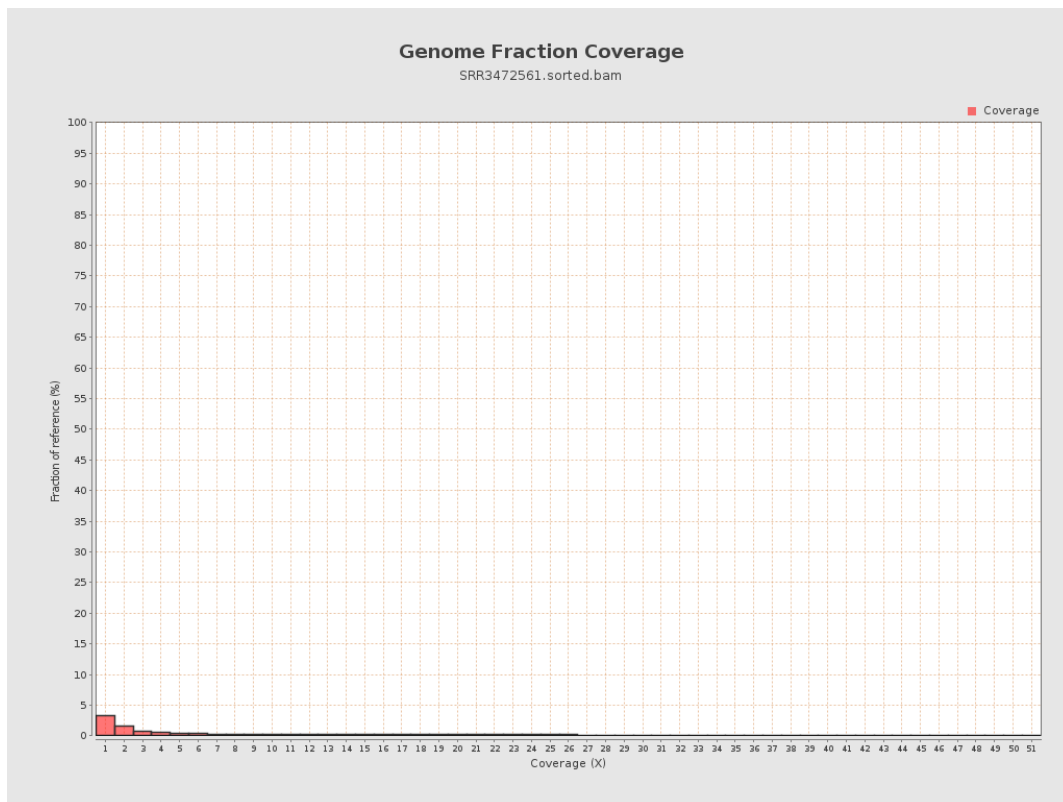
4. Results : Coverage Histogram



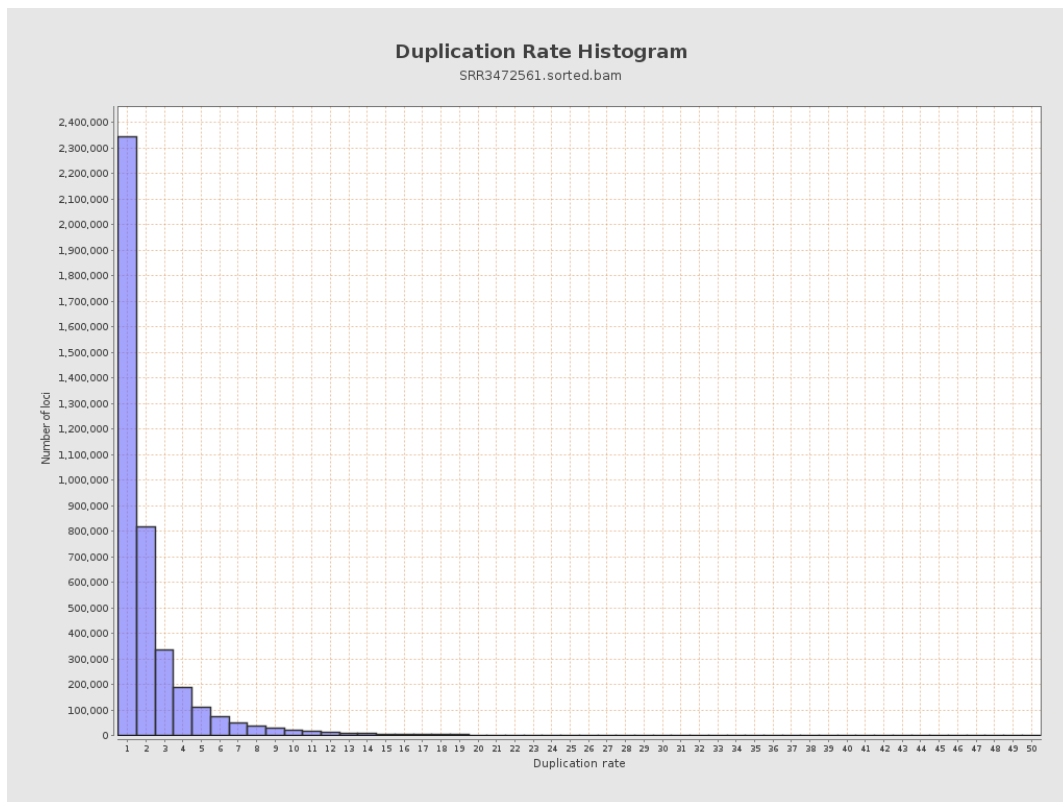
5. Results : Coverage Histogram (0-50X)



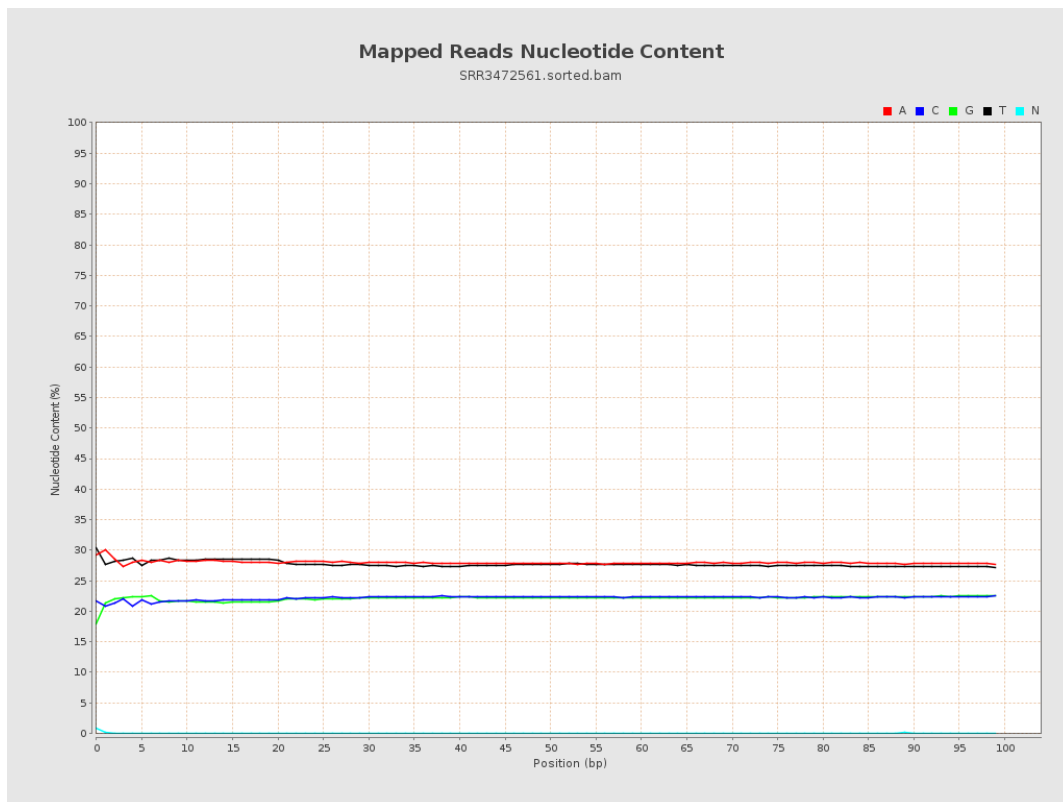
6. Results : Genome Fraction Coverage



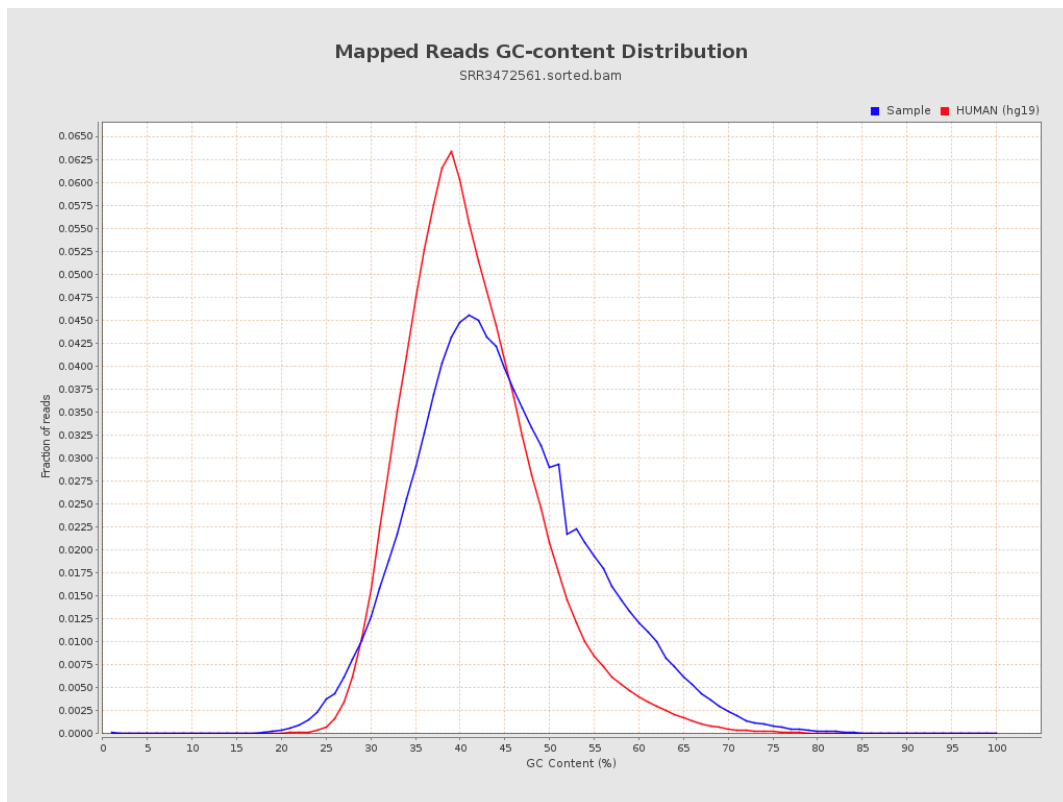
7. Results : Duplication Rate Histogram



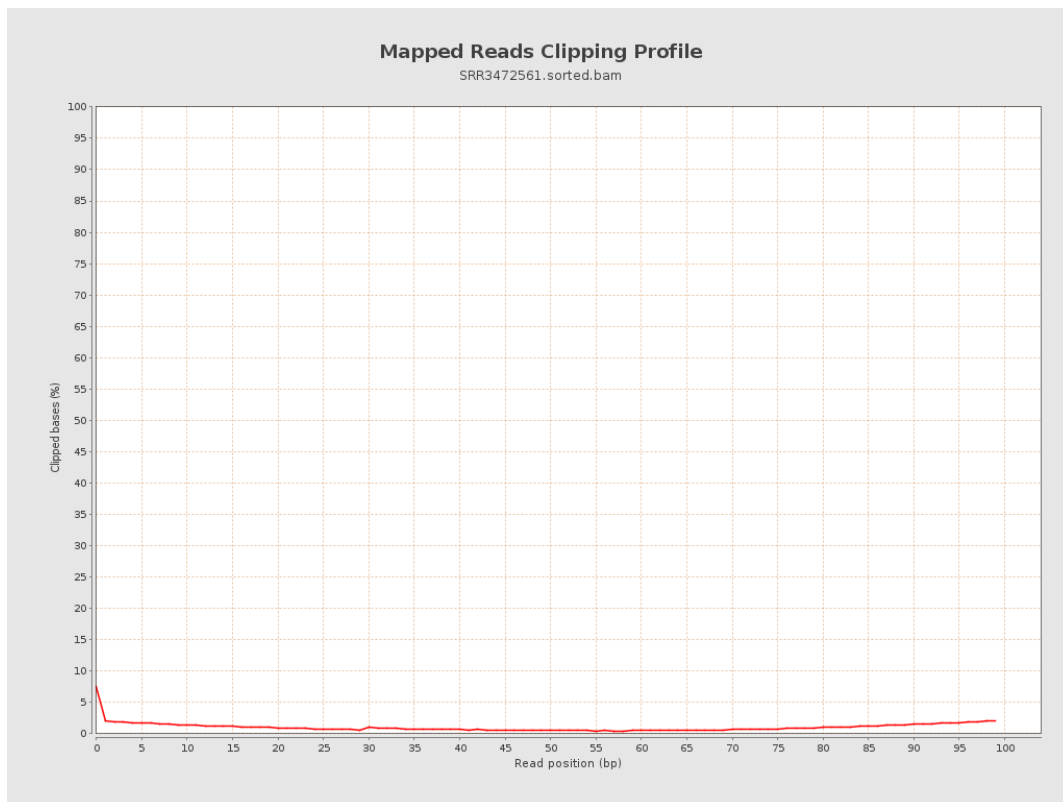
8. Results : Mapped Reads Nucleotide Content



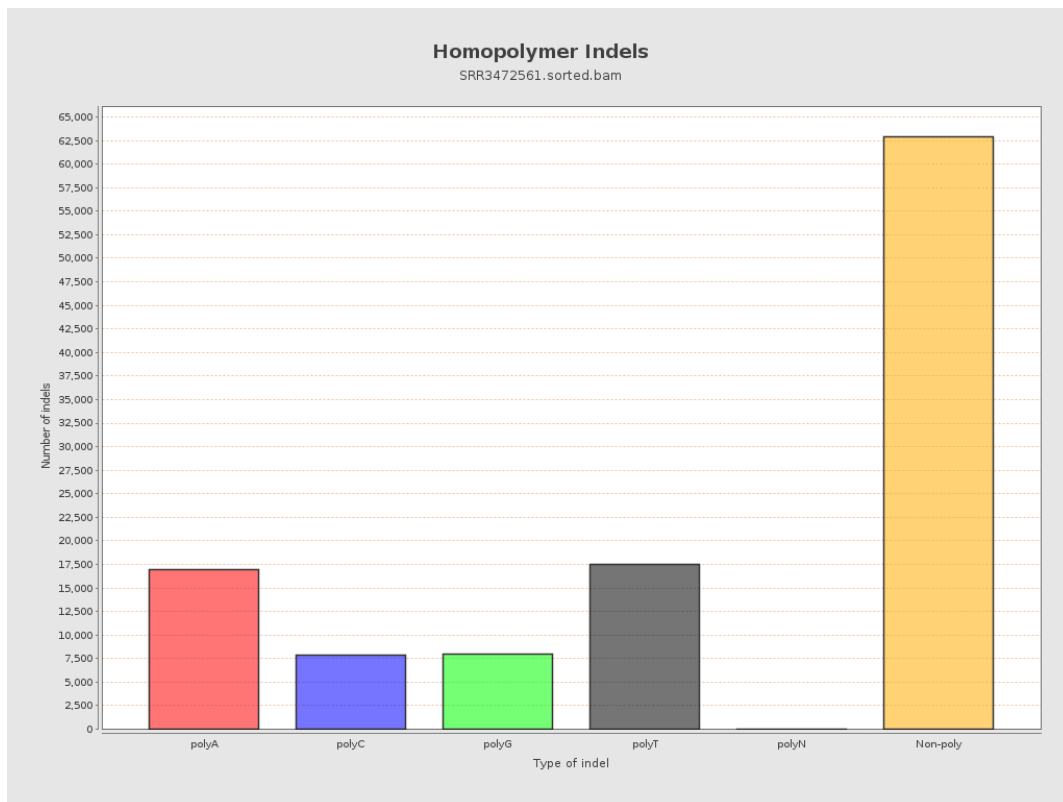
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



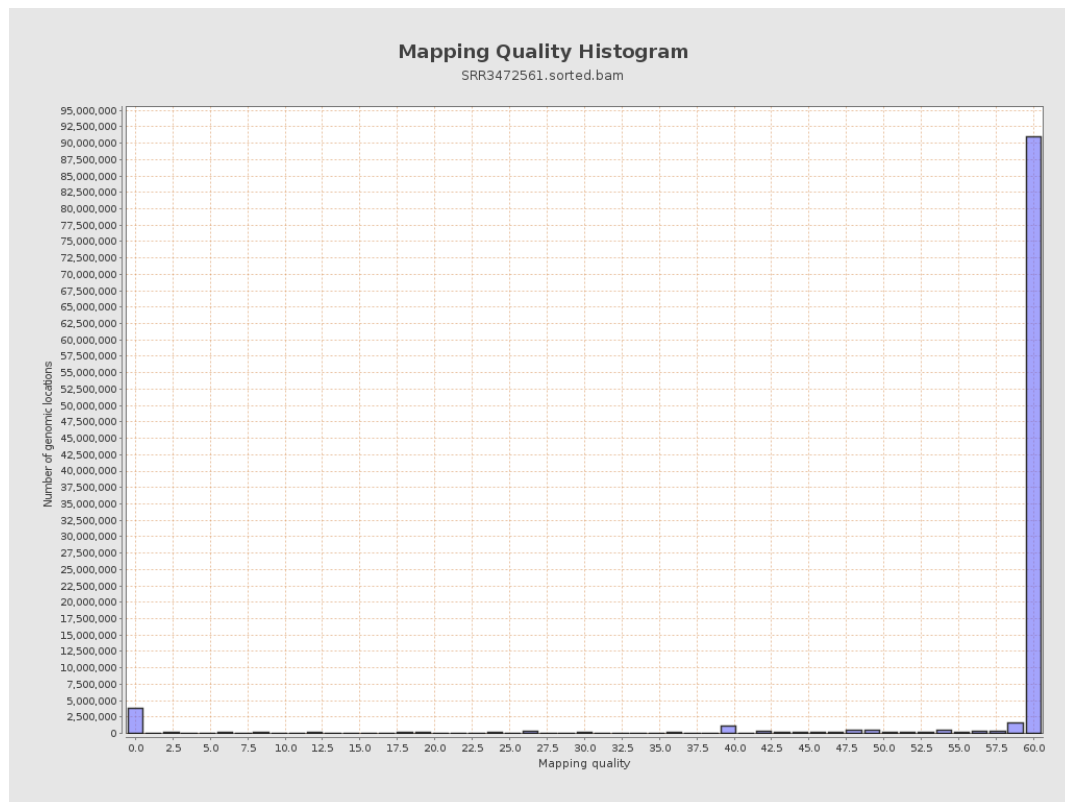
11. Results : Homopolymer Indels



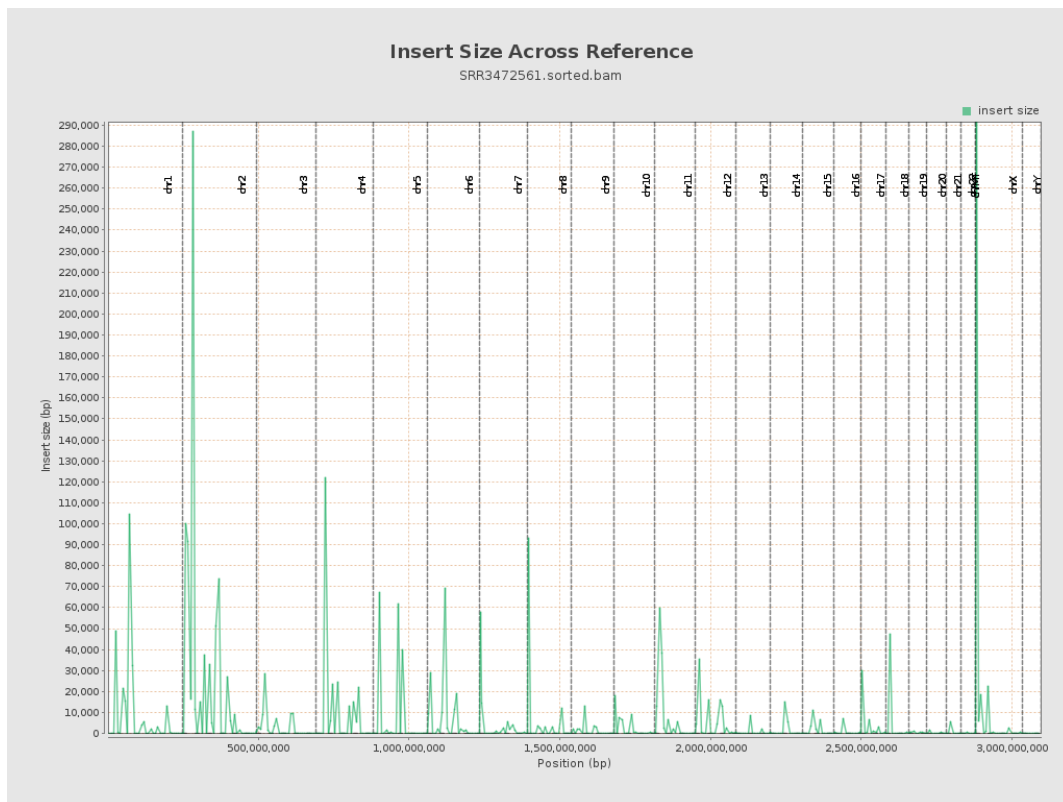
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

