

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:15:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472521.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_SRR3472521 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472521_1.fastq.gz SRR3472521_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:15:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472521.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,597,032
Mapped reads	16,398,086 / 98.8%
Unmapped reads	198,946 / 1.2%
Mapped paired reads	16,398,086 / 98.8%
Mapped reads, first in pair	8,231,091 / 49.59%
Mapped reads, second in pair	8,166,995 / 49.21%
Mapped reads, both in pair	16,288,806 / 98.14%
Mapped reads, singletons	109,280 / 0.66%
Secondary alignments	0
Supplementary alignments	63,914 / 0.39%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	10,526,597 / 63.42%
Duplication rate	45.33%
Clipped reads	1,303,956 / 7.86%

2.2. ACGT Content

Number/percentage of A's	447,493,544 / 27.71%
Number/percentage of C's	362,118,470 / 22.42%
Number/percentage of T's	445,871,180 / 27.61%
Number/percentage of G's	359,432,048 / 22.25%
Number/percentage of N's	248,310 / 0.02%

GC Percentage	44.67%
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2.3. Coverage

Mean	0.5218
Standard Deviation	20.5415

2.4. Mapping Quality

Mean Mapping Quality	55.2
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2.5. Insert size

Mean	23,542.1
Standard Deviation	1,518,106.57
P25/Median/P75	172 / 240 / 324

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	10,127,590
Insertions	90,473
Mapped reads with at least one insertion	0.55%
Deletions	78,499
Mapped reads with at least one deletion	0.47%
Homopolymer indels	45.74%

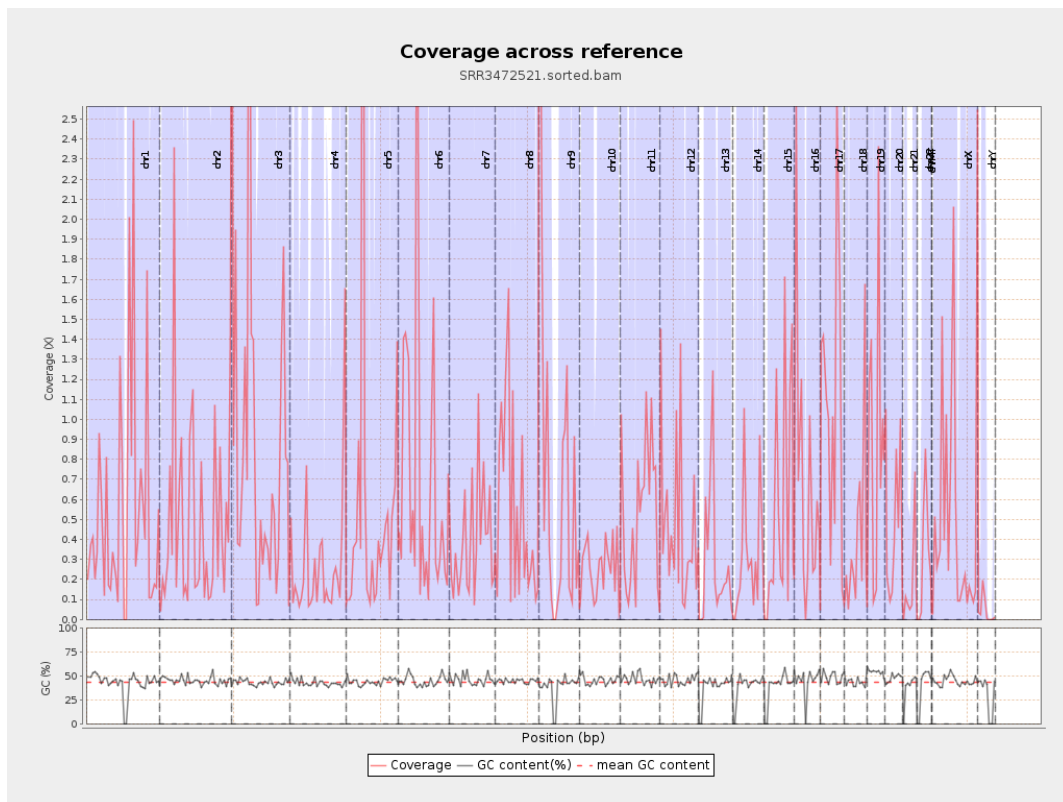
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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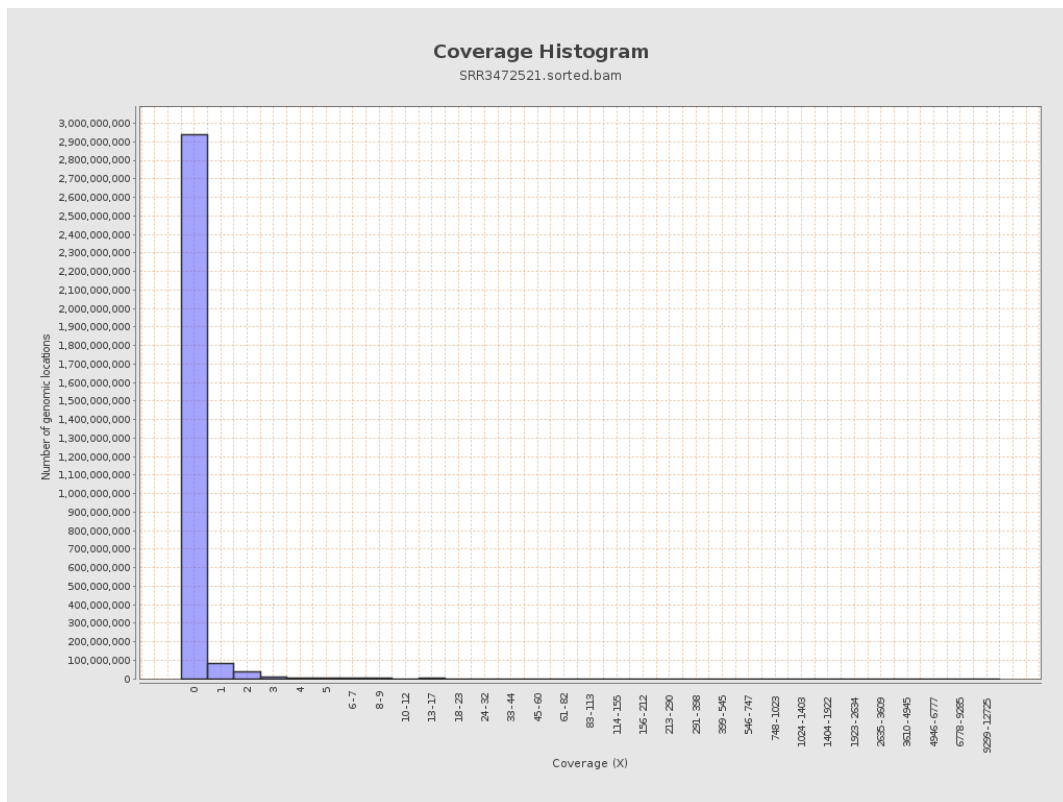
		bases	coverage	deviation
chr1	249250621	137078181	0.55	23.0402
chr2	243199373	116221262	0.4779	22.2826
chr3	198022430	183482069	0.9266	27.6139
chr4	191154276	50030456	0.2617	9.1762
chr5	180915260	106863049	0.5907	22.627
chr6	171115067	117855545	0.6888	23.5694
chr7	159138663	62285821	0.3914	12.8565
chr8	146364022	78995758	0.5397	23.2212
chr9	141213431	103165965	0.7306	26.3758
chr10	135534747	35784996	0.264	10.5576
chr11	135006516	72828138	0.5394	20.1618
chr12	133851895	64661278	0.4831	14.6394
chr13	115169878	31936747	0.2773	12.7888
chr14	107349540	33199257	0.3093	10.1222
chr15	102531392	56420523	0.5503	22.035
chr16	90354753	59416703	0.6576	22.0856
chr17	81195210	85188087	1.0492	28.1735
chr18	78077248	32523932	0.4166	19.5665
chr19	59128983	54814990	0.927	42.4258
chr20	63025520	30477304	0.4836	16.4235
chr21	48129895	8827299	0.1834	9.5607
chr22	51304566	15442691	0.301	11.3671
chrMT	16571	1669	0.1007	0.3574
chrX	155270560	74993178	0.483	16.6861

chrY	59373566	2882656	0.0486	2.5856
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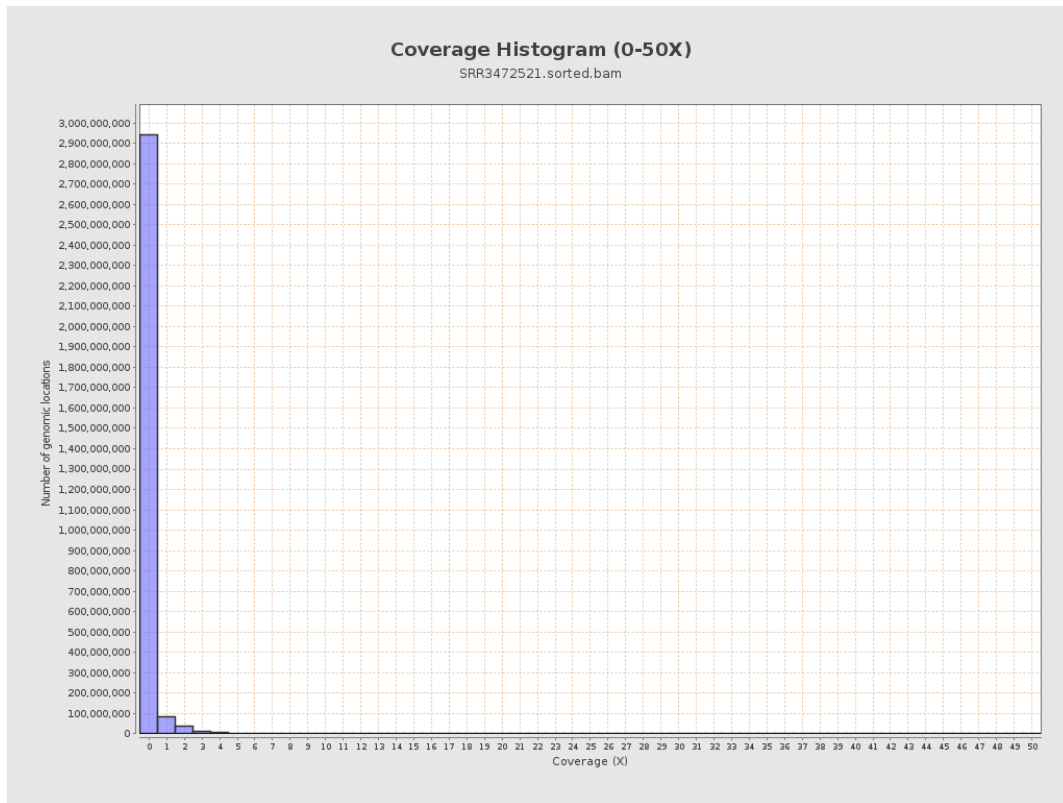
3. Results : Coverage across reference



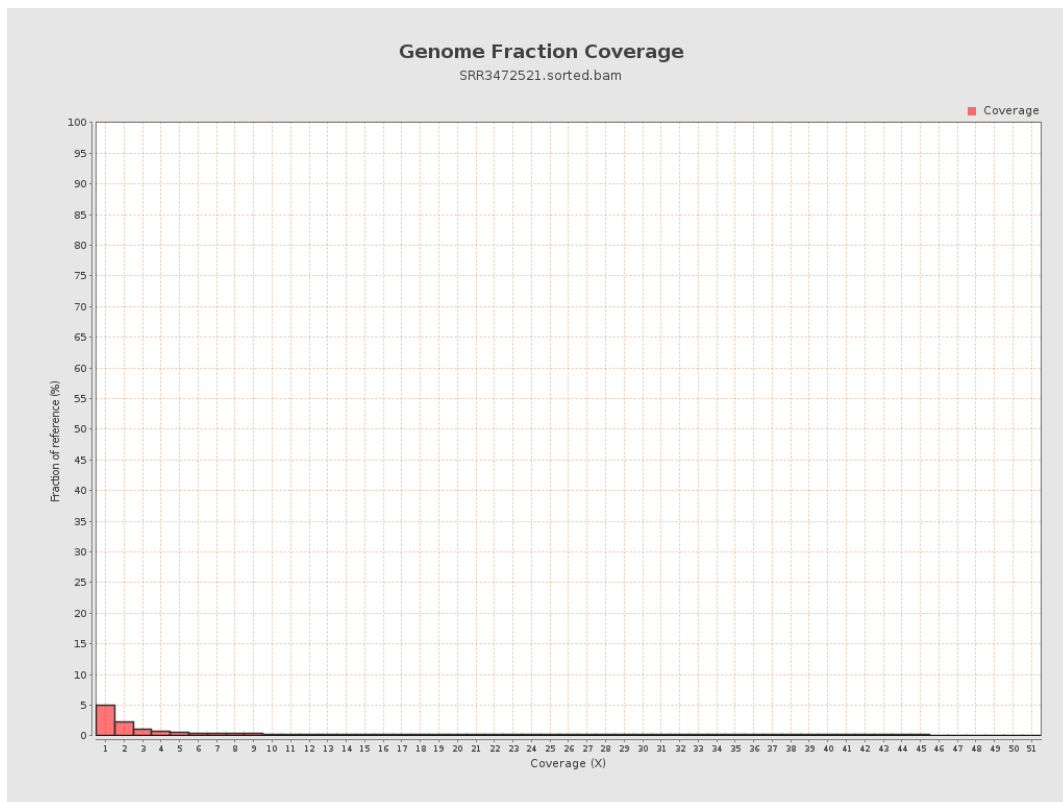
4. Results : Coverage Histogram



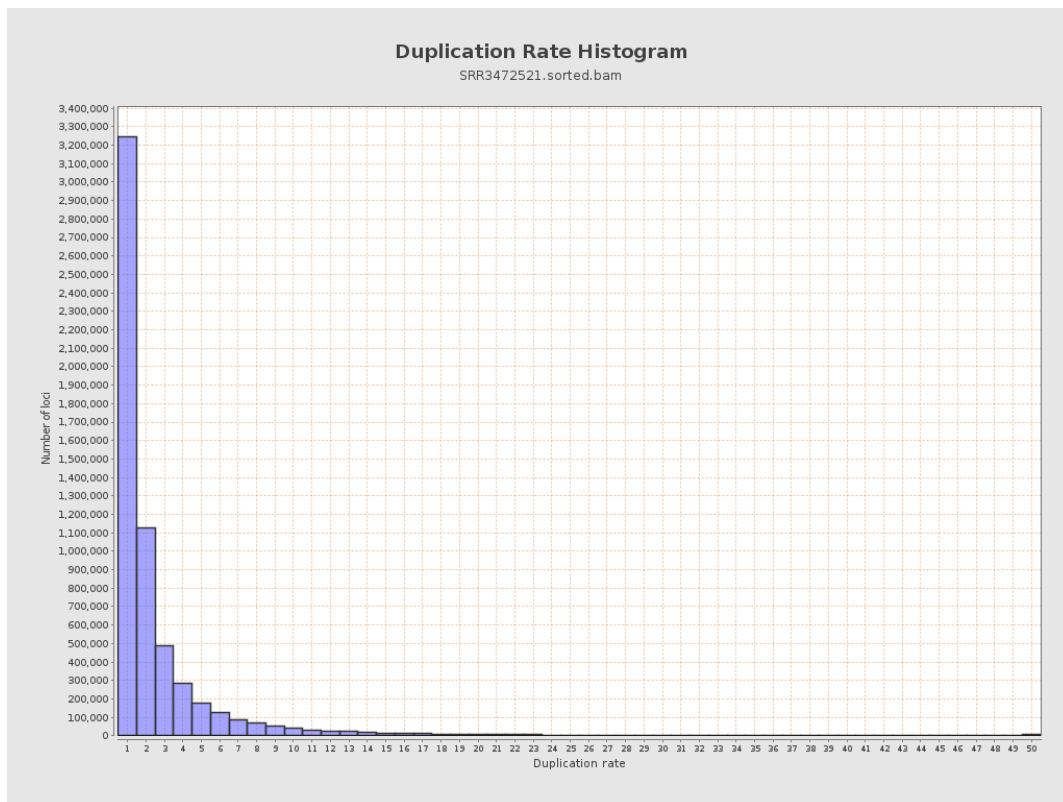
5. Results : Coverage Histogram (0-50X)



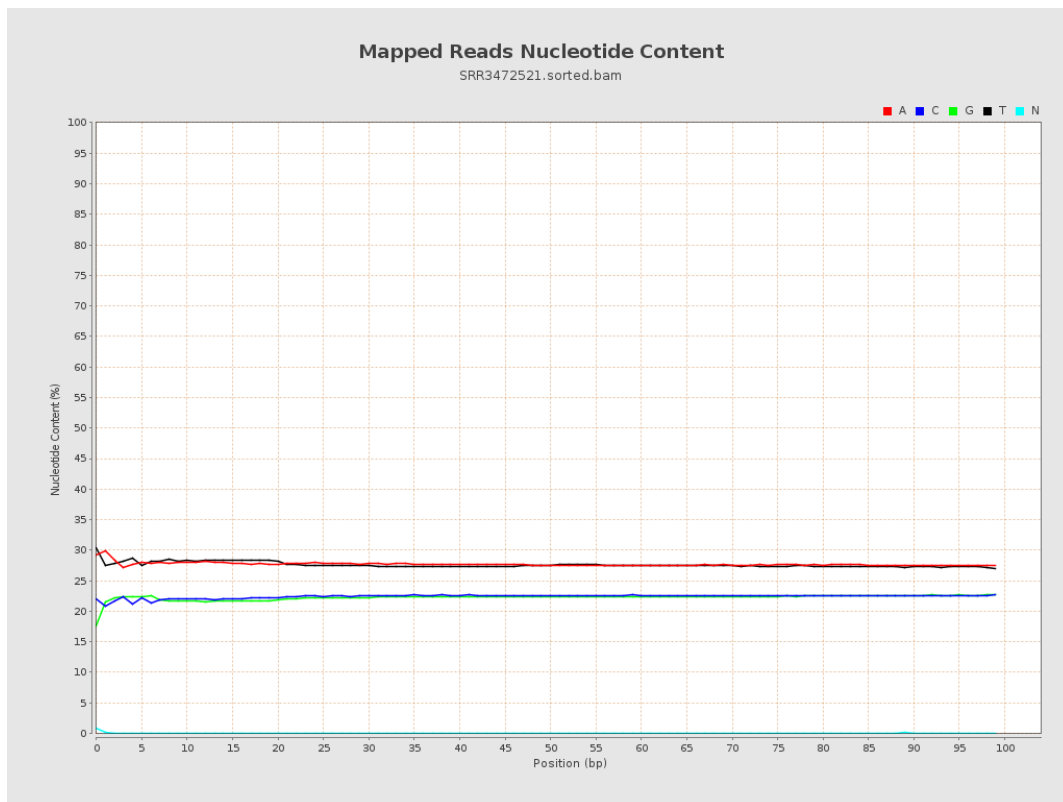
6. Results : Genome Fraction Coverage



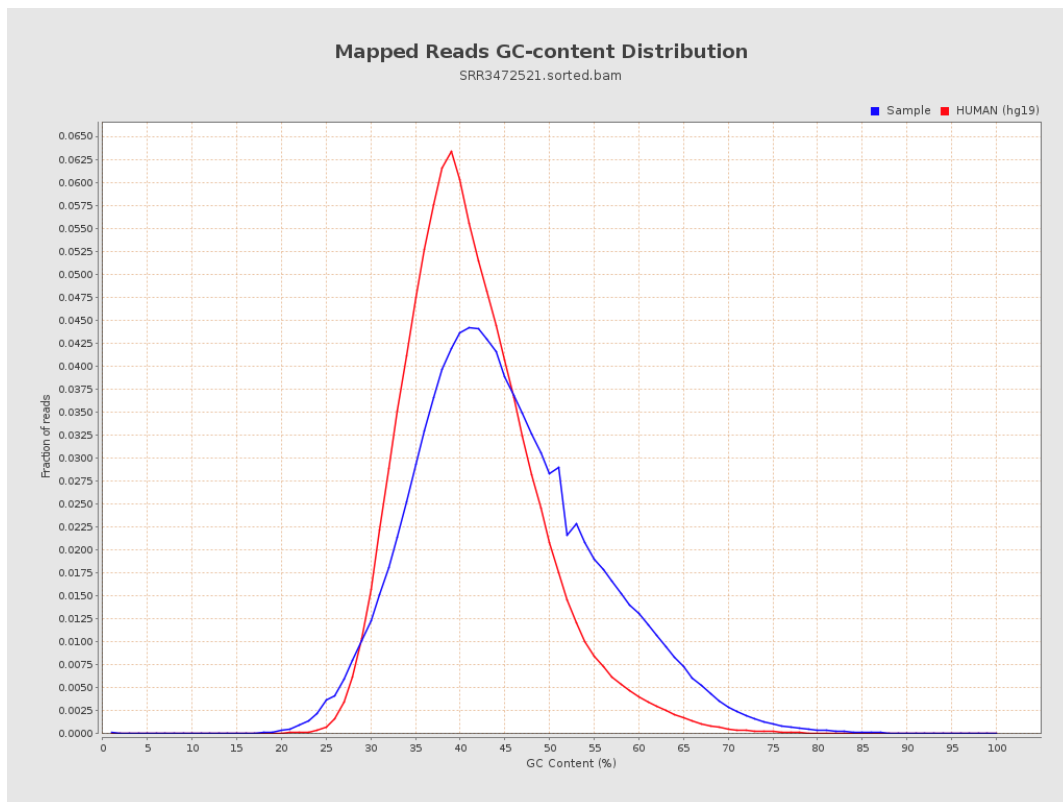
7. Results : Duplication Rate Histogram



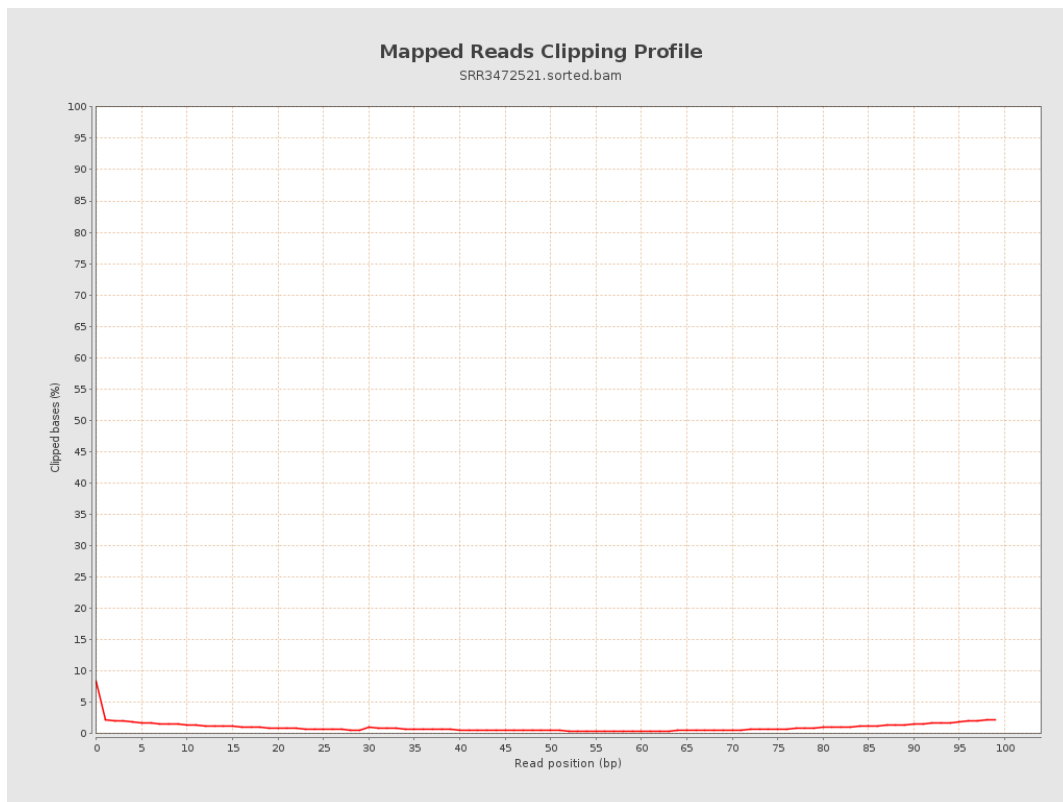
8. Results : Mapped Reads Nucleotide Content



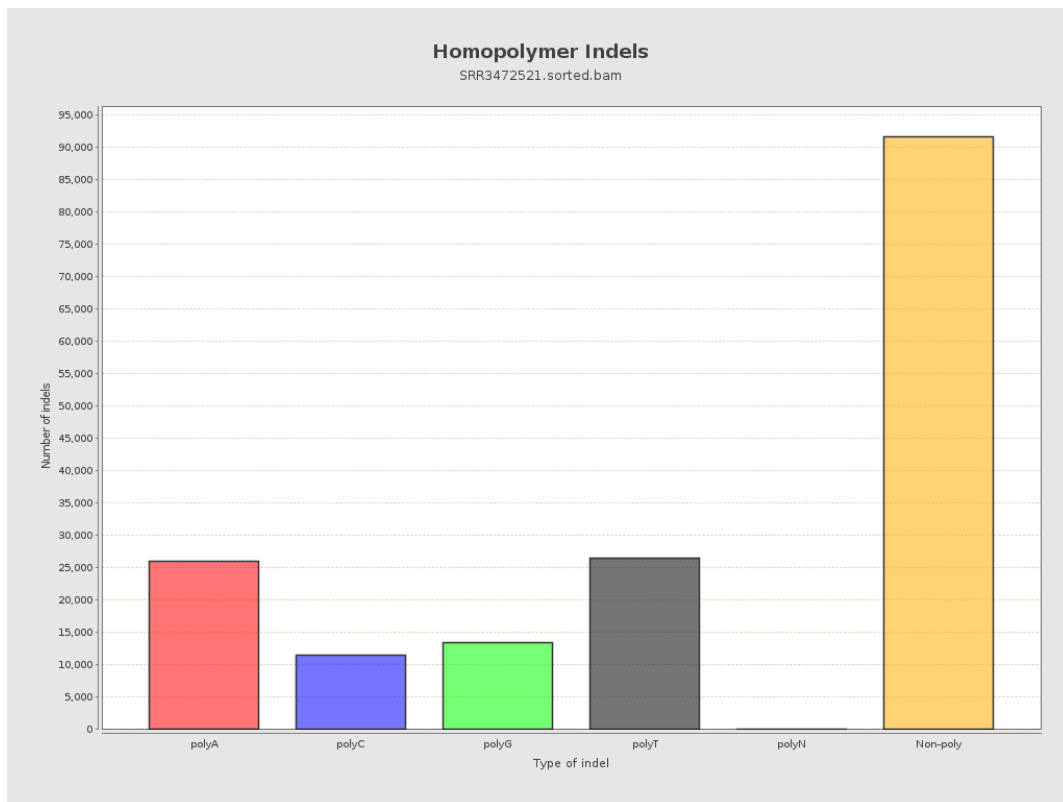
9. Results : Mapped Reads GC-content Distribution



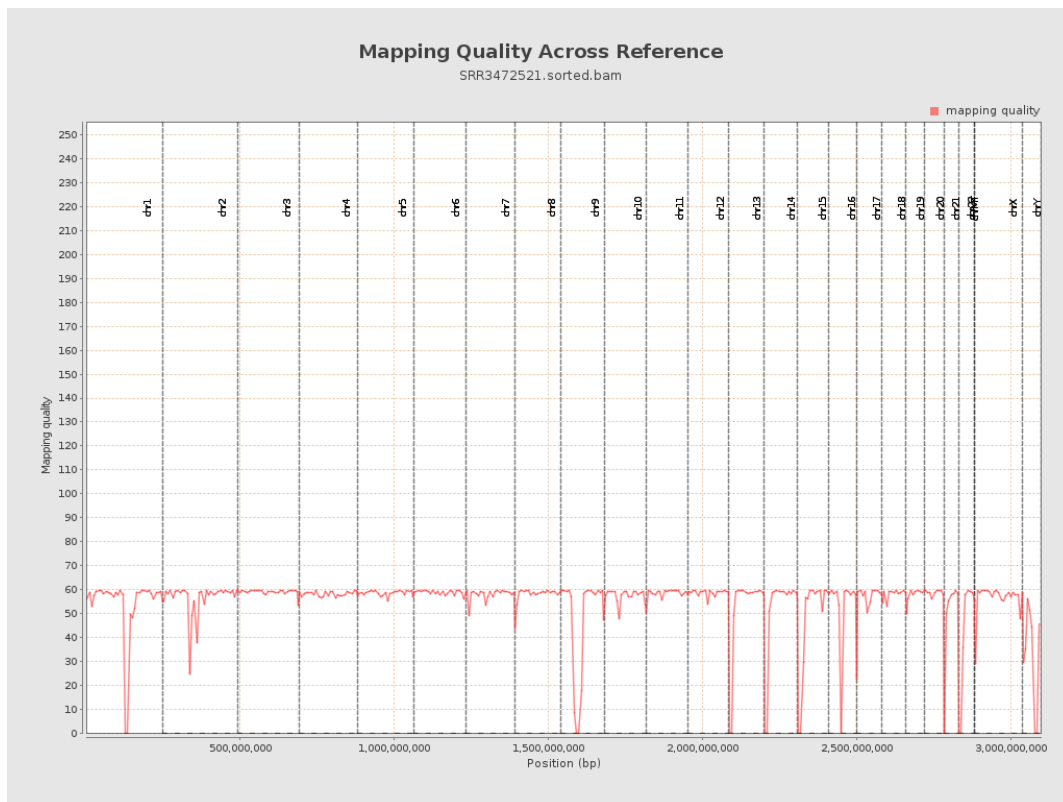
10. Results : Mapped Reads Clipping Profile



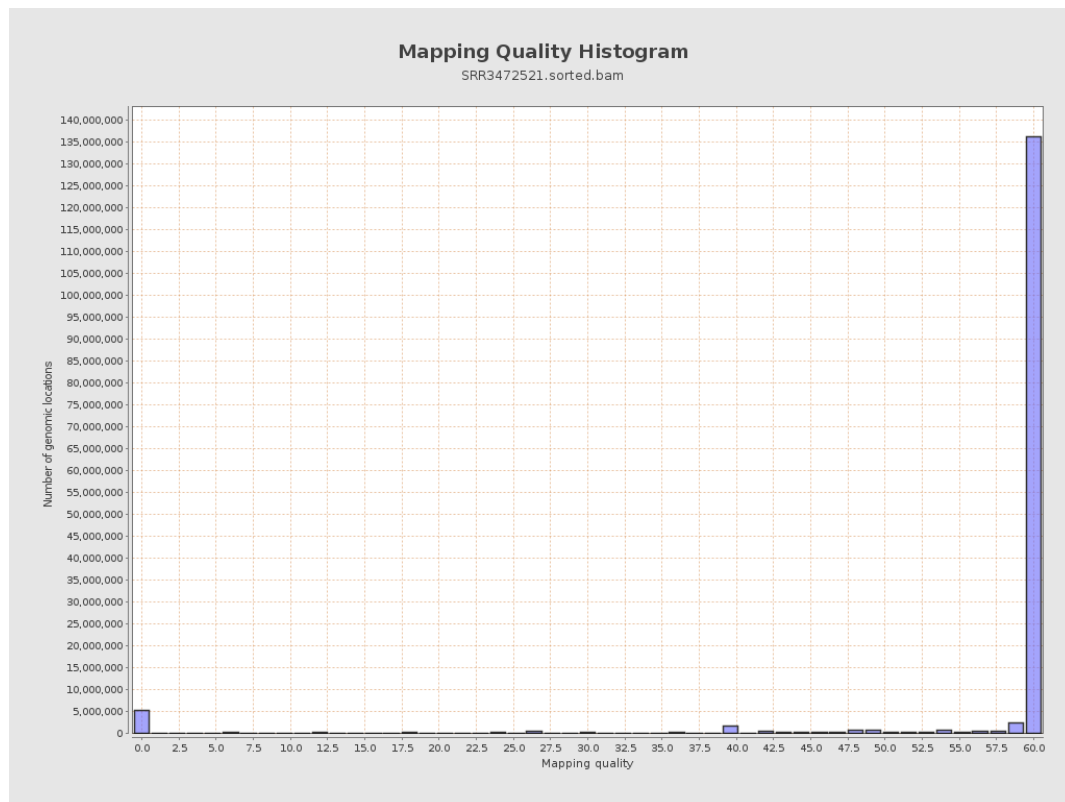
11. Results : Homopolymer Indels



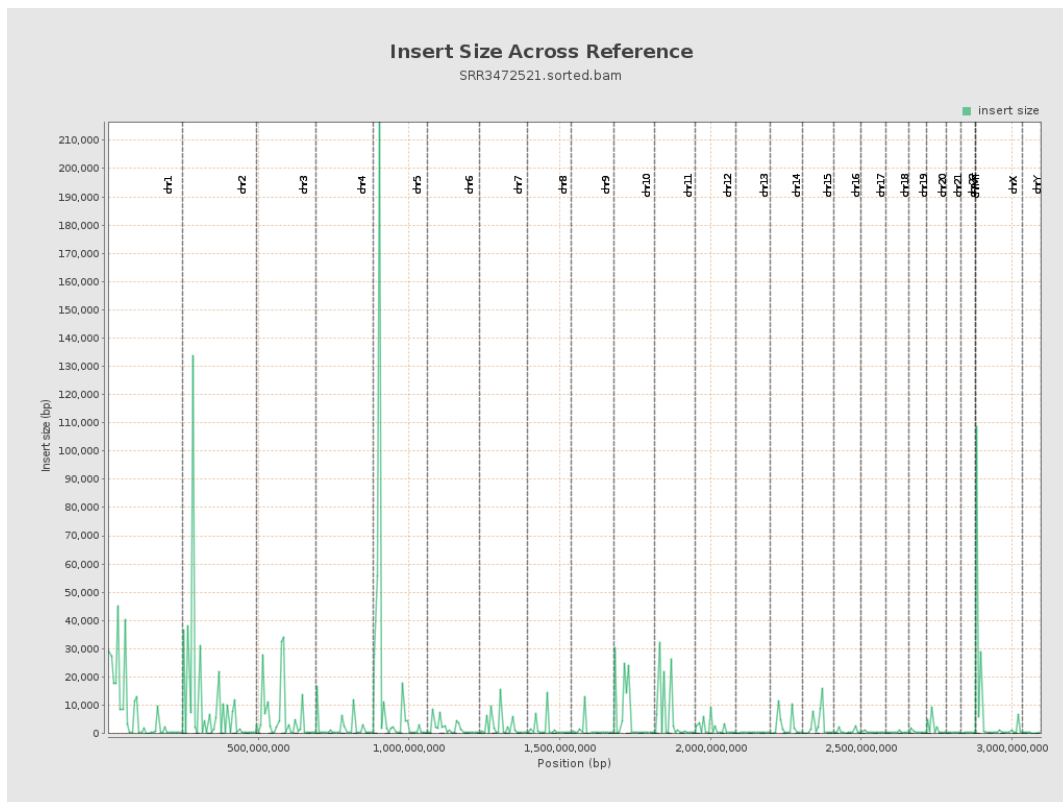
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

