

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 08:07:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472605.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_SRR3472605 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472605_1.fastq.gz SRR3472605_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 08:06:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472605.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,217,818
Mapped reads	17,104,873 / 99.34%
Unmapped reads	112,945 / 0.66%
Mapped paired reads	17,104,873 / 99.34%
Mapped reads, first in pair	8,569,520 / 49.77%
Mapped reads, second in pair	8,535,353 / 49.57%
Mapped reads, both in pair	17,035,664 / 98.94%
Mapped reads, singletons	69,209 / 0.4%
Secondary alignments	0
Supplementary alignments	79,416 / 0.46%
Read min/max/mean length	30 / 101 / 99.56
Duplicated reads (estimated)	12,045,692 / 69.96%
Duplication rate	49.95%
Clipped reads	1,312,300 / 7.62%

2.2. ACGT Content

Number/percentage of A's	450,598,575 / 26.85%
Number/percentage of C's	390,526,111 / 23.27%
Number/percentage of T's	449,842,222 / 26.81%
Number/percentage of G's	386,742,035 / 23.05%
Number/percentage of N's	324,601 / 0.02%

GC Percentage	46.32%
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2.3. Coverage

Mean	0.5421
Standard Deviation	25.7513

2.4. Mapping Quality

Mean Mapping Quality	55.11
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2.5. Insert size

Mean	18,952.24
Standard Deviation	1,373,256.37
P25/Median/P75	141 / 195 / 265

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	9,458,261
Insertions	102,419
Mapped reads with at least one insertion	0.59%
Deletions	86,585
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.25%

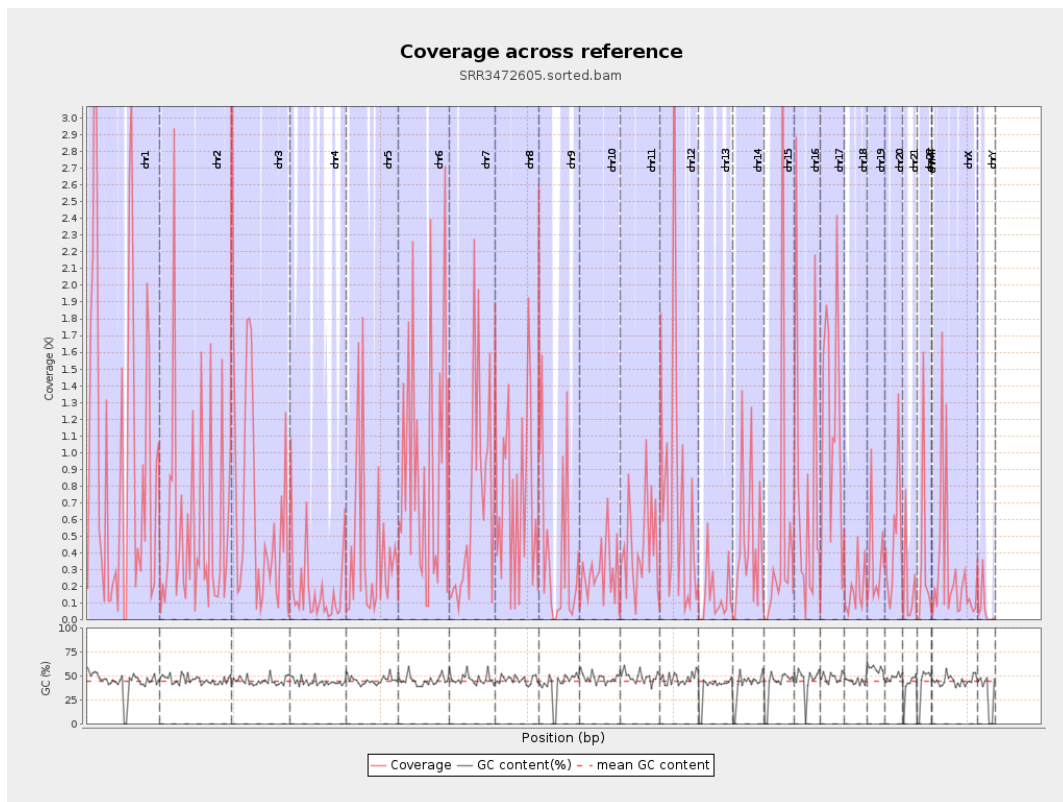
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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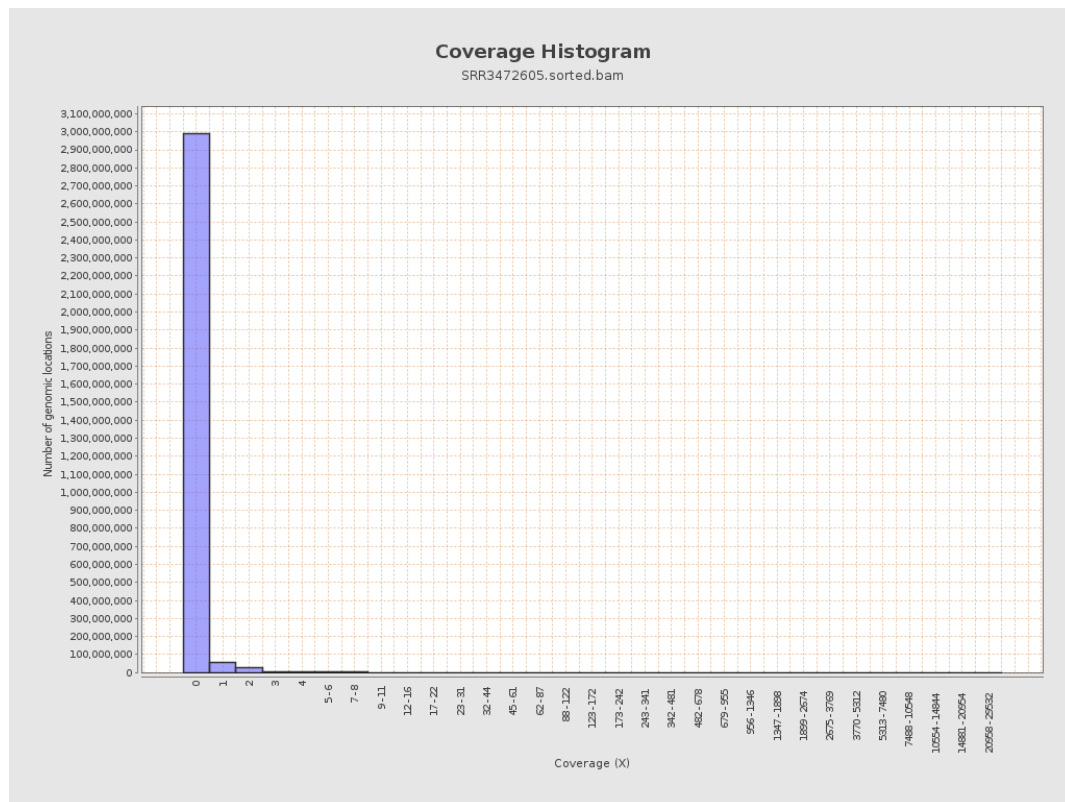
		bases	coverage	deviation
chr1	249250621	249458047	1.0008	40.3143
chr2	243199373	137426795	0.5651	24.9385
chr3	198022430	137412091	0.6939	19.4171
chr4	191154276	35094937	0.1836	8.9001
chr5	180915260	74966767	0.4144	14.7057
chr6	171115067	155421591	0.9083	31.9453
chr7	159138663	109270235	0.6866	25.7044
chr8	146364022	105089540	0.718	29.6123
chr9	141213431	57926044	0.4102	16.2386
chr10	135534747	38273525	0.2824	13.146
chr11	135006516	59660601	0.4419	17.9655
chr12	133851895	101000075	0.7546	31.8742
chr13	115169878	16161687	0.1403	5.5618
chr14	107349540	46650944	0.4346	17.051
chr15	102531392	50423807	0.4918	62.9203
chr16	90354753	69255000	0.7665	26.8211
chr17	81195210	93100165	1.1466	38.921
chr18	78077248	14109820	0.1807	9.3646
chr19	59128983	20928146	0.3539	9.0738
chr20	63025520	30916226	0.4905	18.4817
chr21	48129895	9239421	0.192	15.3998
chr22	51304566	18360944	0.3579	13.1718
chrMT	16571	2376	0.1434	0.4628
chrX	155270560	44227849	0.2848	15.0987

chrY	59373566	3923924	0.0661	4.7933
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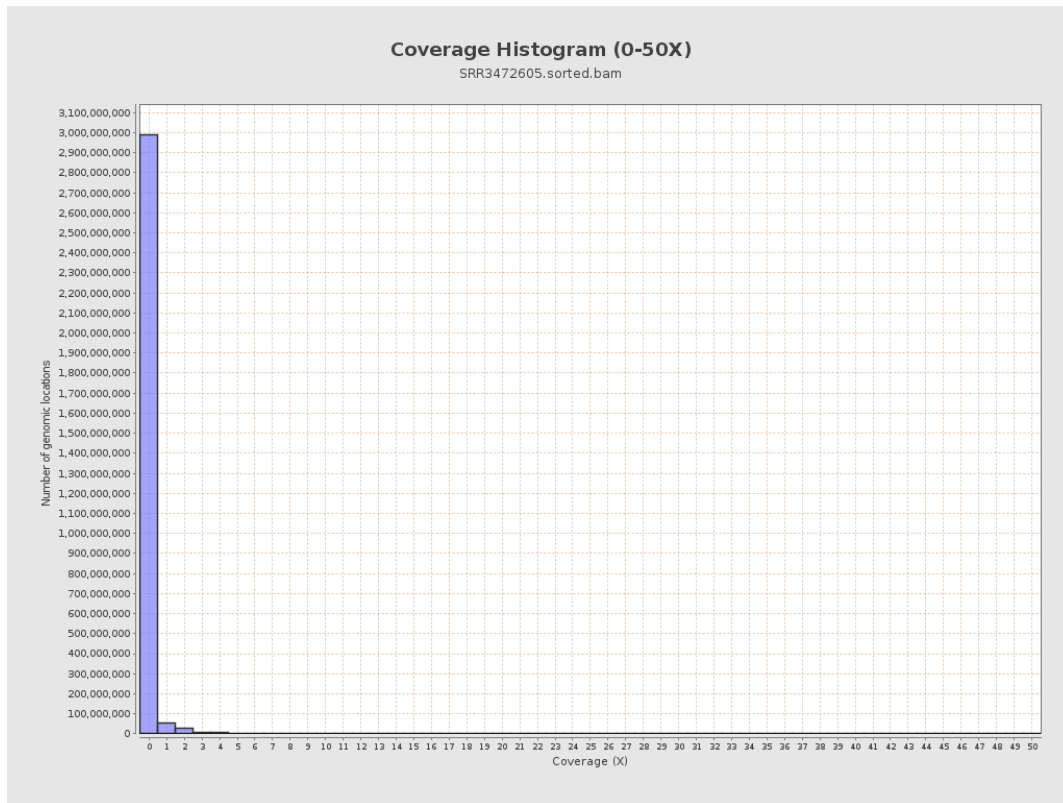
3. Results : Coverage across reference



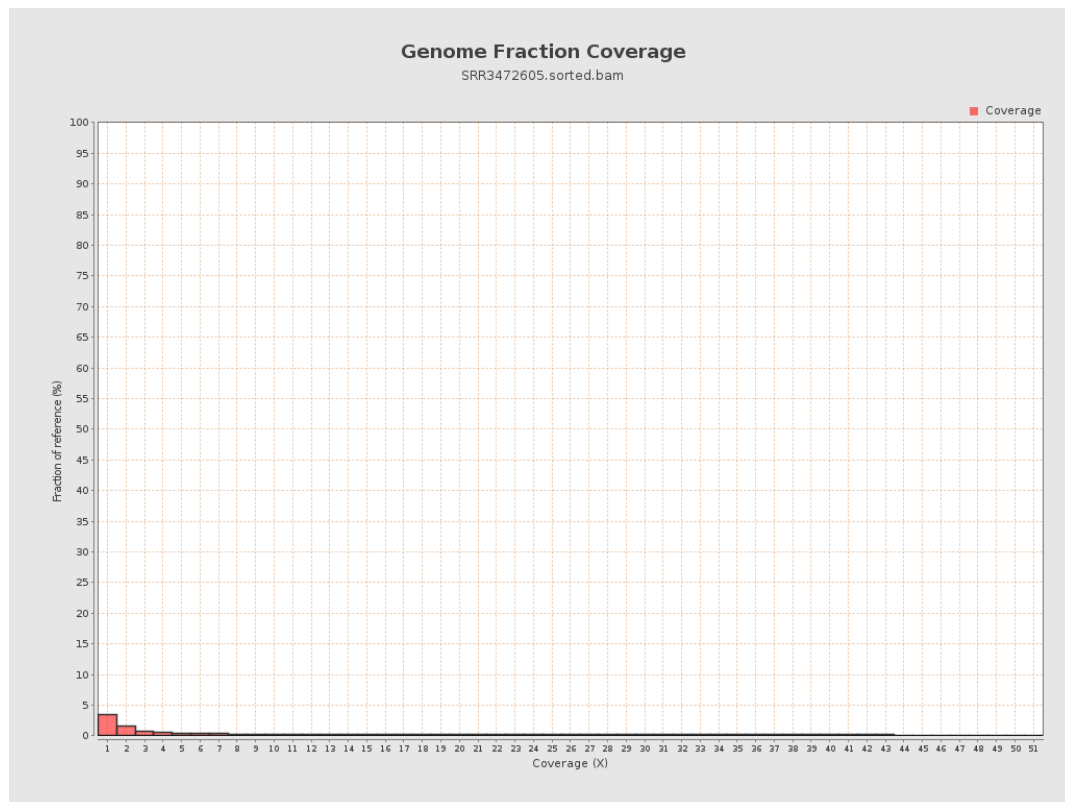
4. Results : Coverage Histogram



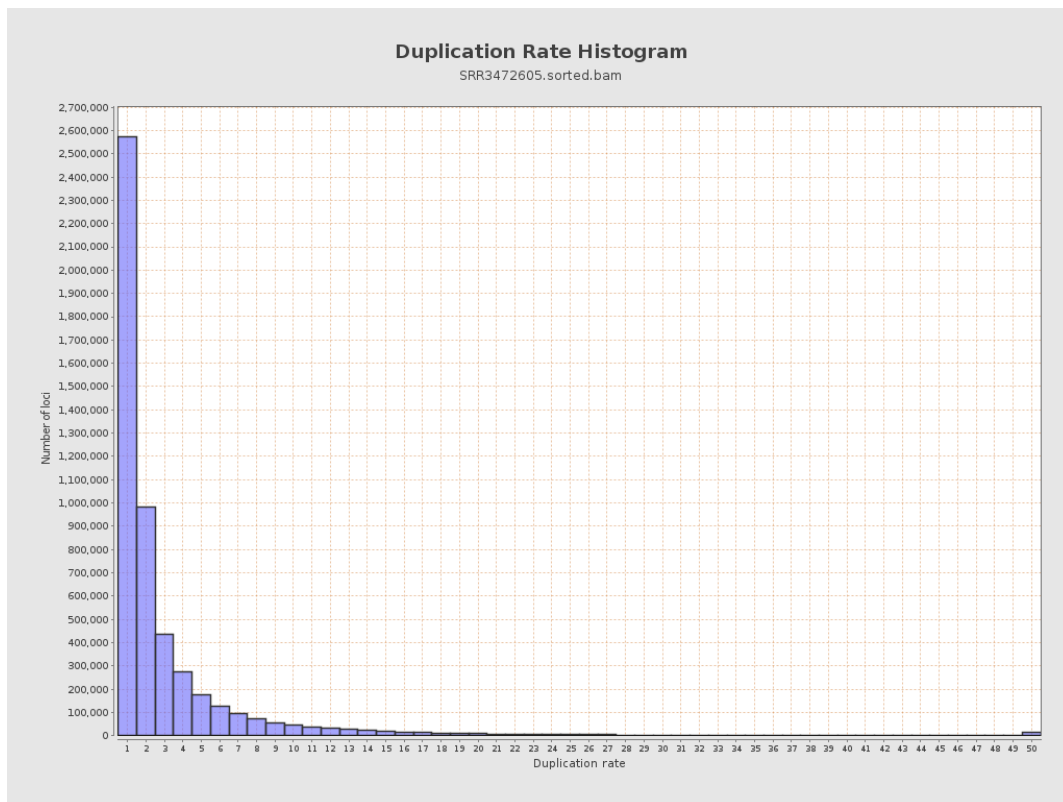
5. Results : Coverage Histogram (0-50X)



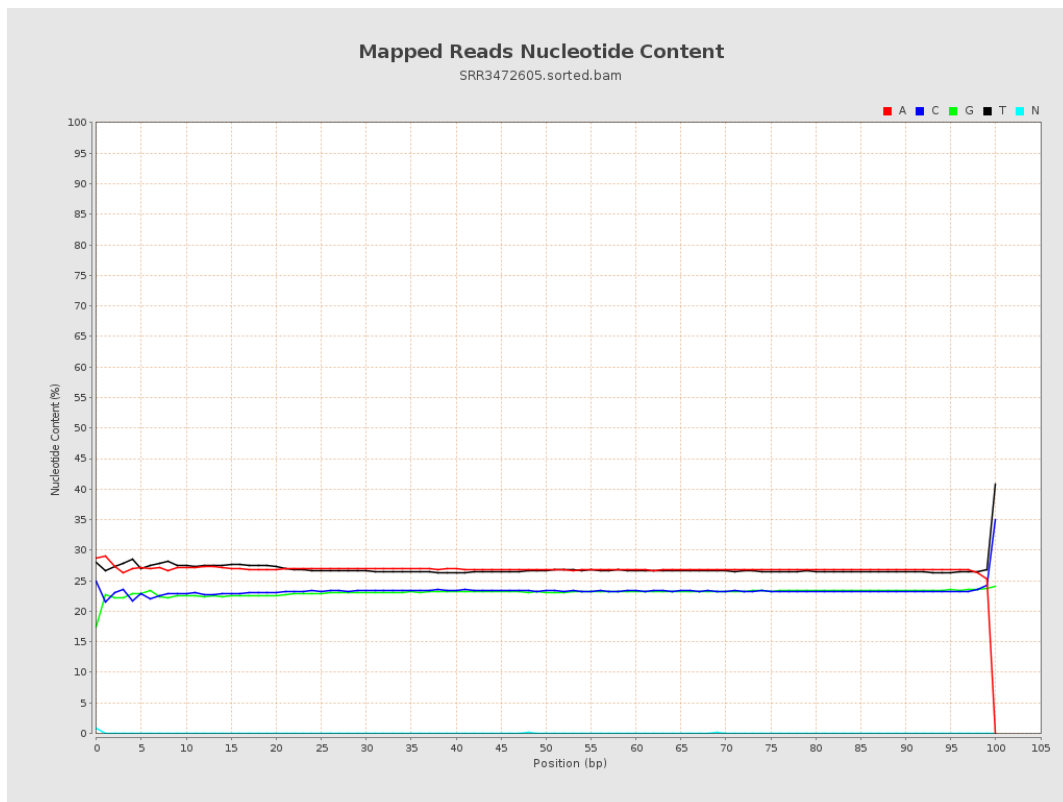
6. Results : Genome Fraction Coverage



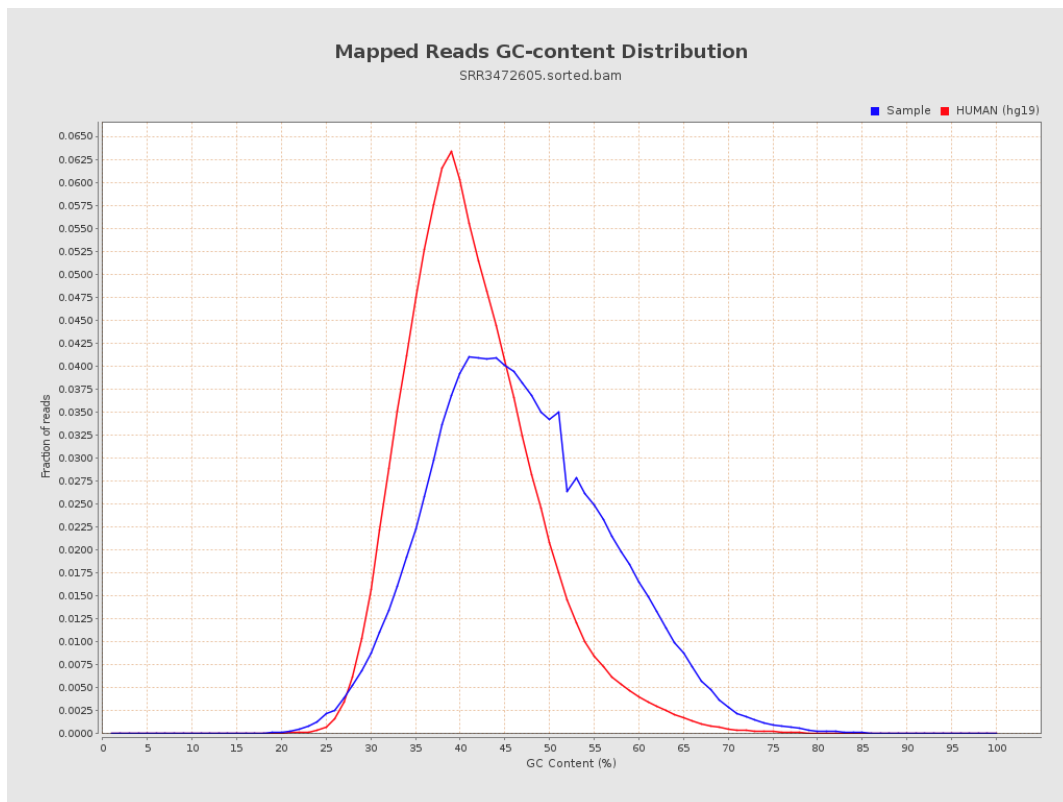
7. Results : Duplication Rate Histogram



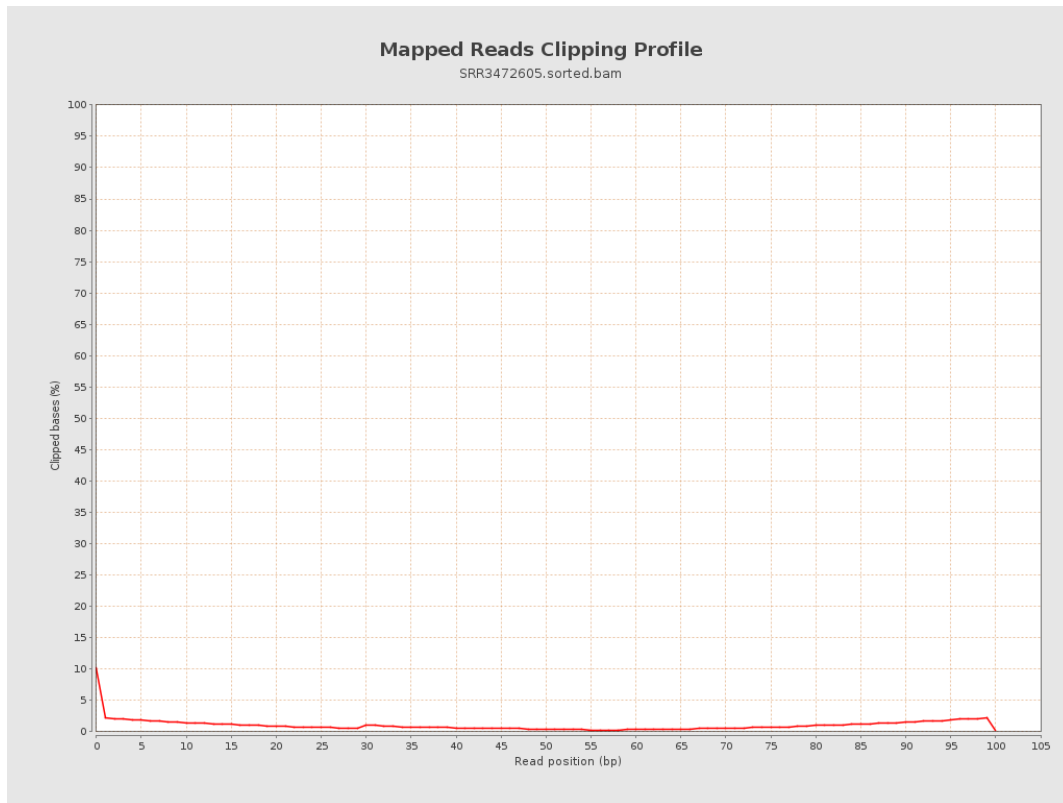
8. Results : Mapped Reads Nucleotide Content



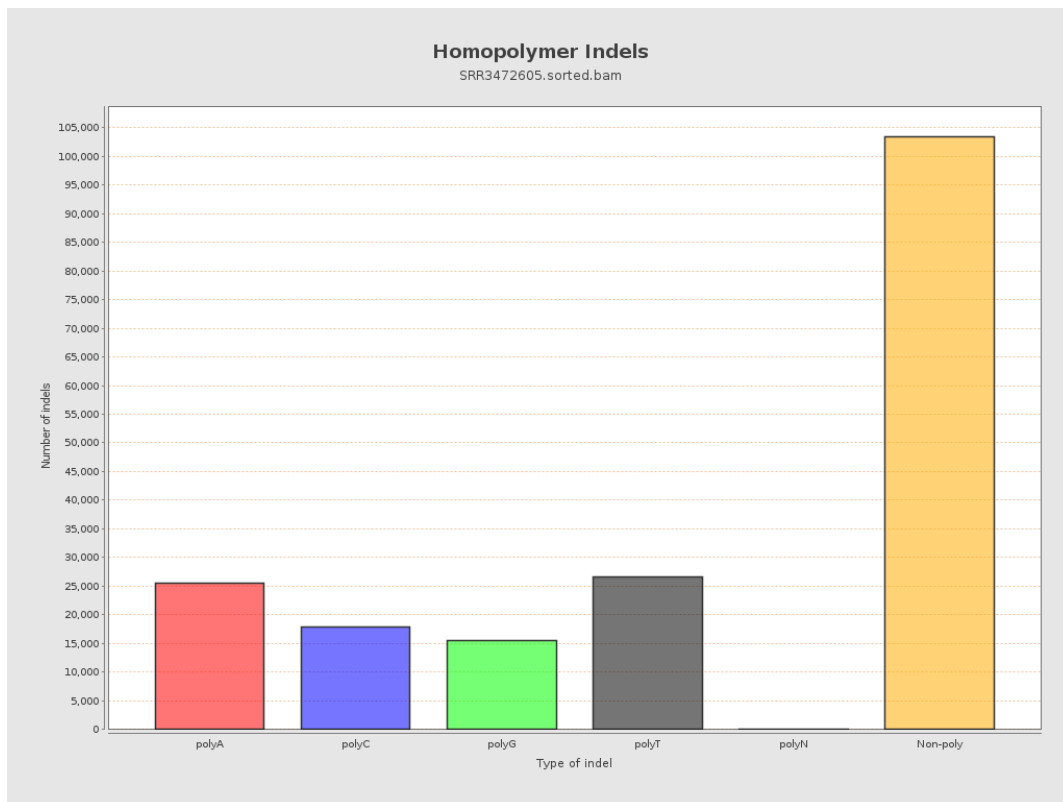
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



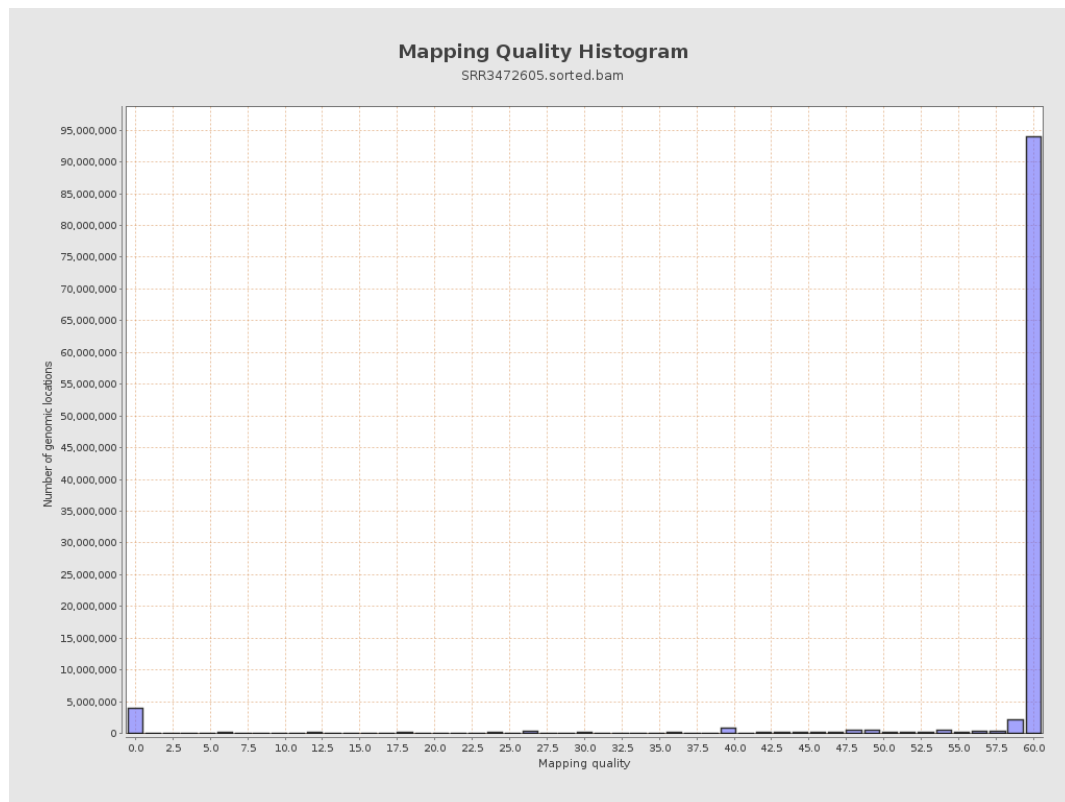
11. Results : Homopolymer Indels



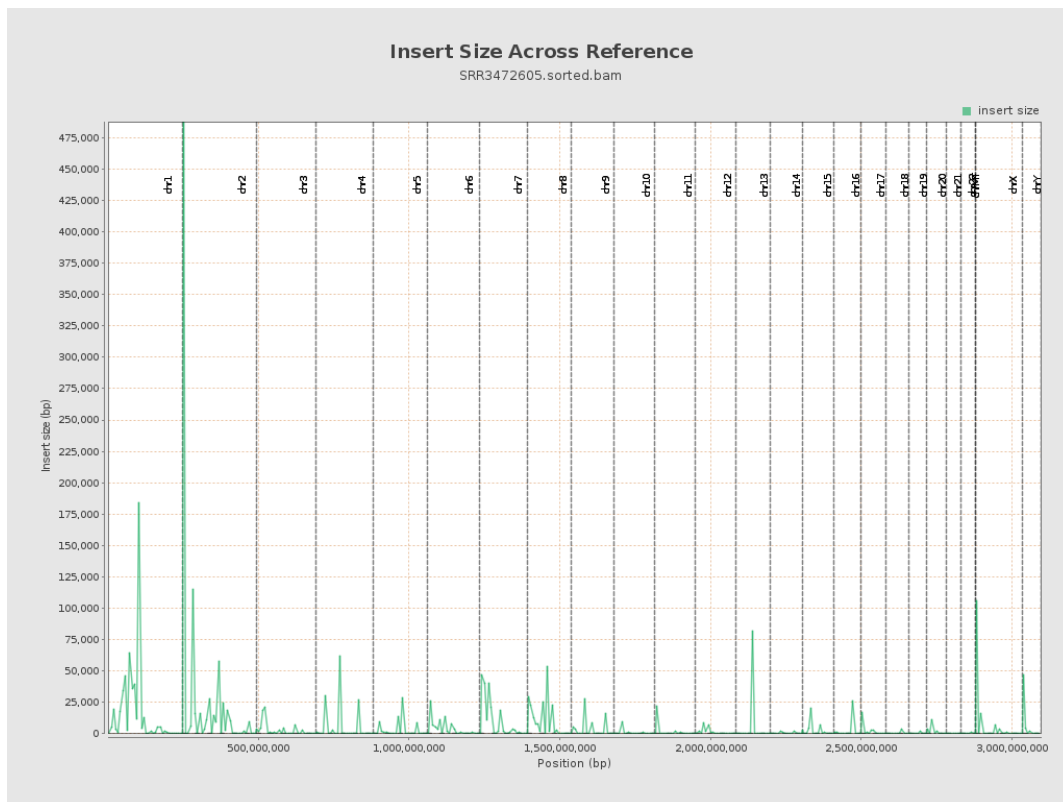
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

