

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 12:13:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472617.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_SRR3472617 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472617_1.fastq.gz SRR3472617_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 12:13:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472617.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,640,148
Mapped reads	16,536,934 / 99.38%
Unmapped reads	103,214 / 0.62%
Mapped paired reads	16,536,934 / 99.38%
Mapped reads, first in pair	8,288,414 / 49.81%
Mapped reads, second in pair	8,248,520 / 49.57%
Mapped reads, both in pair	16,466,988 / 98.96%
Mapped reads, singletons	69,946 / 0.42%
Secondary alignments	0
Supplementary alignments	90,567 / 0.54%
Read min/max/mean length	30 / 101 / 99.71
Duplicated reads (estimated)	11,602,664 / 69.73%
Duplication rate	50.35%
Clipped reads	1,148,628 / 6.9%

2.2. ACGT Content

Number/percentage of A's	438,140,227 / 26.93%
Number/percentage of C's	377,342,725 / 23.2%
Number/percentage of T's	439,290,631 / 27%
Number/percentage of G's	371,680,085 / 22.85%
Number/percentage of N's	296,544 / 0.02%

GC Percentage	46.04%
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2.3. Coverage

Mean	0.5256
Standard Deviation	23.4896

2.4. Mapping Quality

Mean Mapping Quality	54.53
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2.5. Insert size

Mean	21,351.3
Standard Deviation	1,480,597.37
P25/Median/P75	155 / 212 / 283

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	9,381,186
Insertions	97,497
Mapped reads with at least one insertion	0.58%
Deletions	88,099
Mapped reads with at least one deletion	0.53%
Homopolymer indels	46.72%

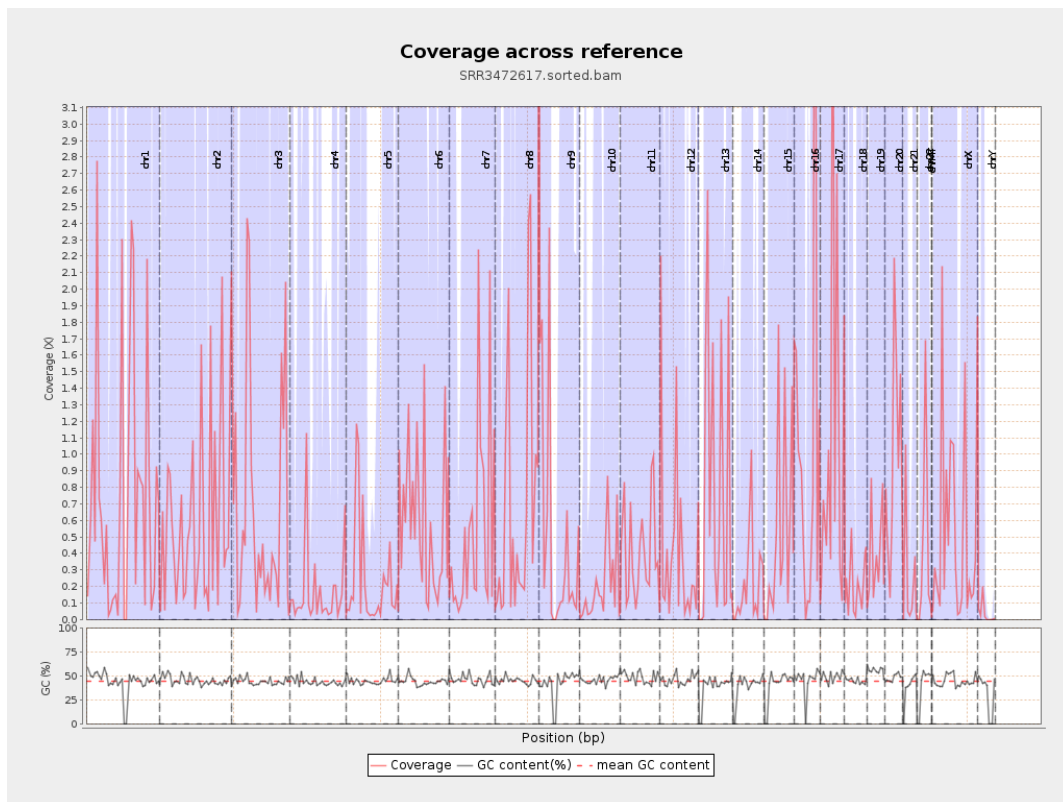
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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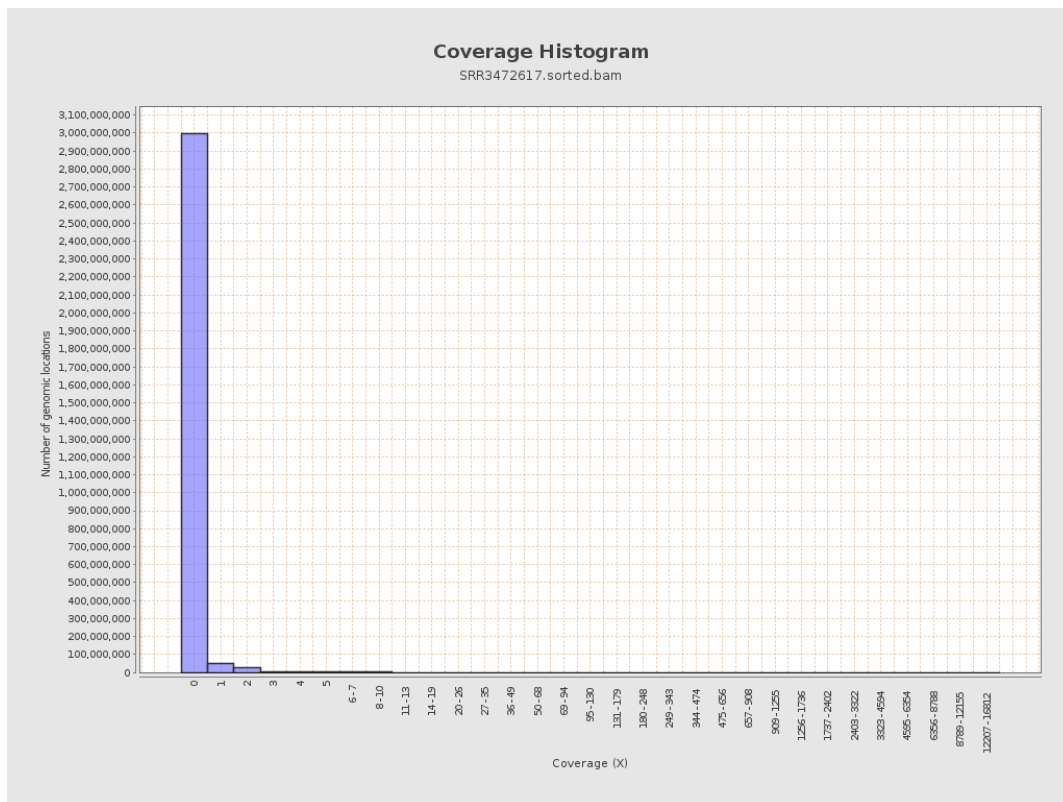
		bases	coverage	deviation
chr1	249250621	191394864	0.7679	26.7434
chr2	243199373	143650967	0.5907	23.6904
chr3	198022430	138127027	0.6975	25.0084
chr4	191154276	30727844	0.1607	7.6123
chr5	180915260	42108950	0.2328	10.5064
chr6	171115067	98921102	0.5781	15.4041
chr7	159138663	85787269	0.5391	24.0613
chr8	146364022	100735927	0.6883	28.8648
chr9	141213431	73815498	0.5227	20.2539
chr10	135534747	28582821	0.2109	13.5673
chr11	135006516	56476735	0.4183	17.2712
chr12	133851895	56332132	0.4209	15.3498
chr13	115169878	88030631	0.7644	33.5111
chr14	107349540	22436638	0.209	9.1238
chr15	102531392	54886597	0.5353	22.4335
chr16	90354753	103037539	1.1404	51.5132
chr17	81195210	92843482	1.1435	48.0848
chr18	78077248	16094510	0.2061	8.6261
chr19	59128983	25031462	0.4233	11.312
chr20	63025520	64342683	1.0209	33.518
chr21	48129895	12482131	0.2593	20.5876
chr22	51304566	21029120	0.4099	17.4534
chrMT	16571	1034	0.0624	0.2588
chrX	155270560	77876174	0.5016	24.1106

chrY	59373566	2230145	0.0376	4.1187
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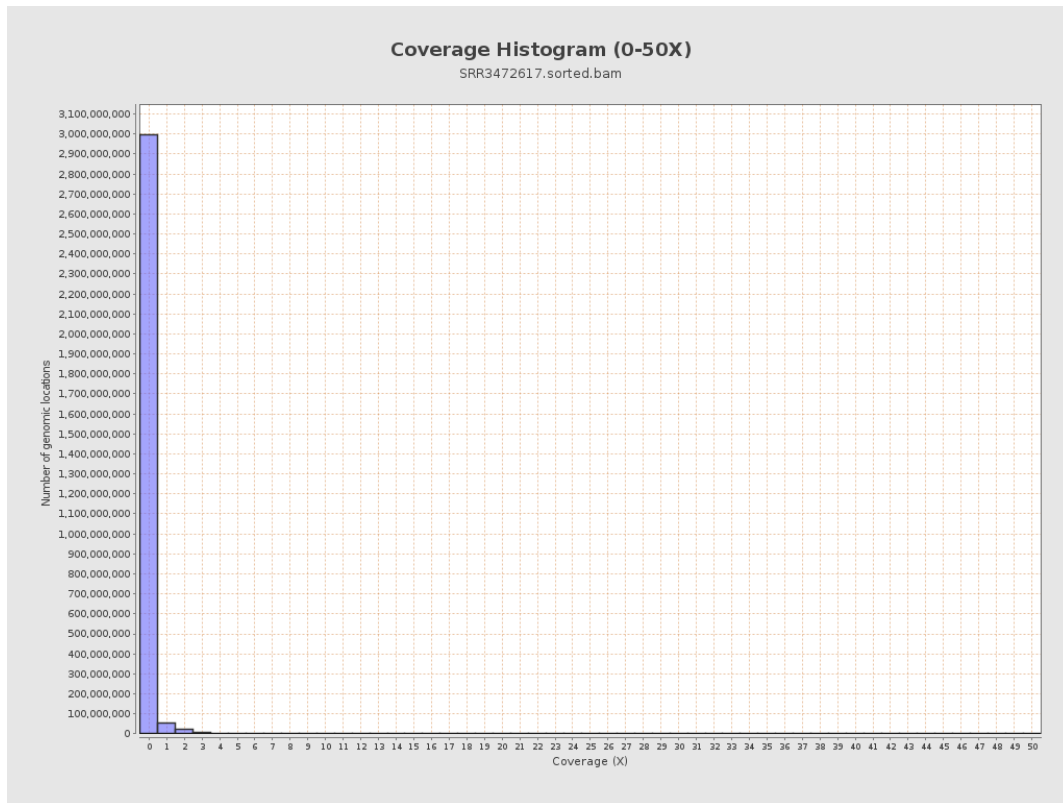
3. Results : Coverage across reference



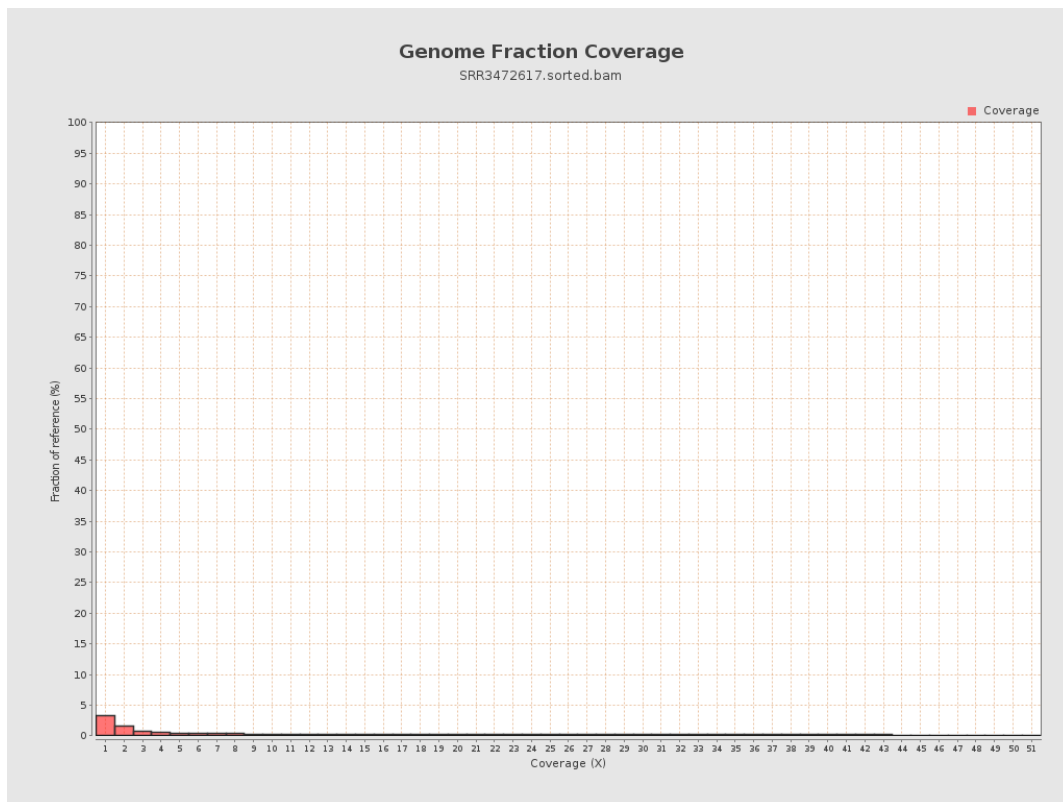
4. Results : Coverage Histogram



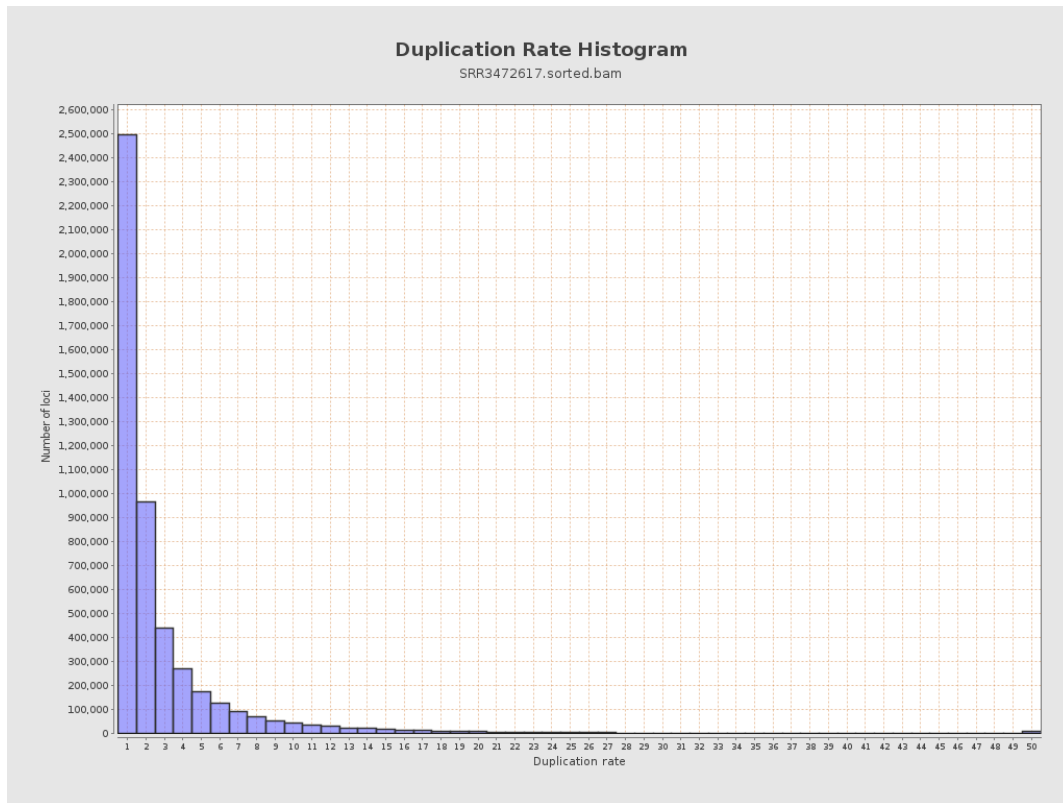
5. Results : Coverage Histogram (0-50X)



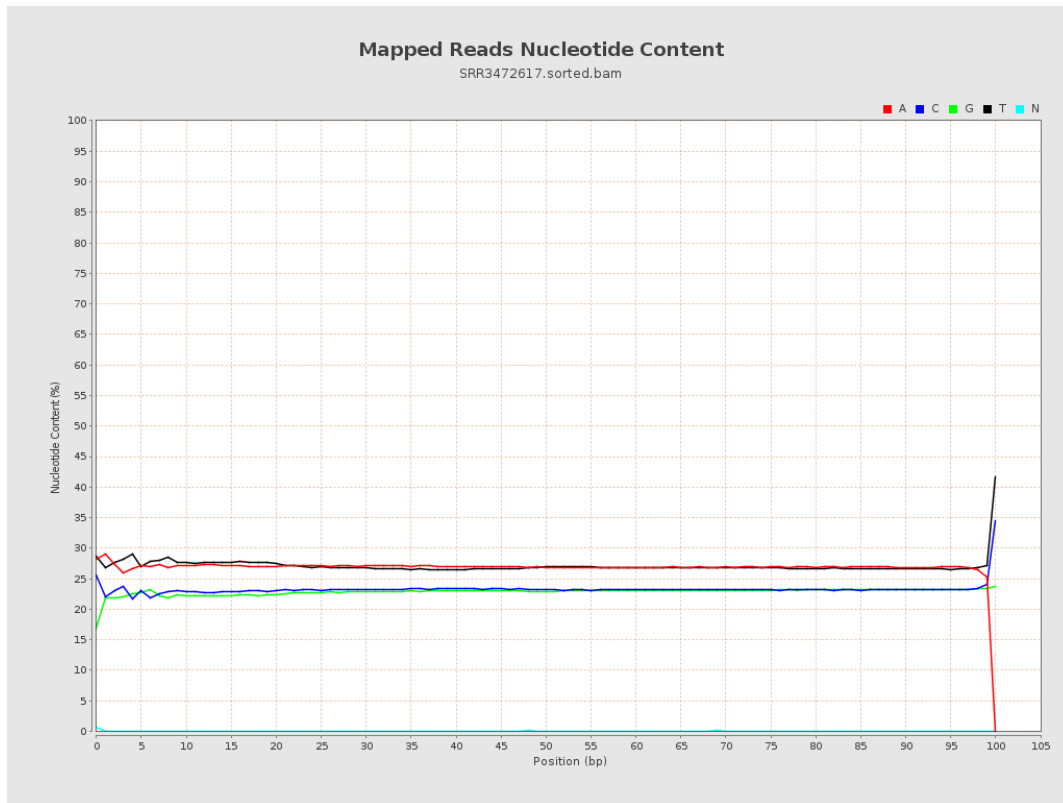
6. Results : Genome Fraction Coverage



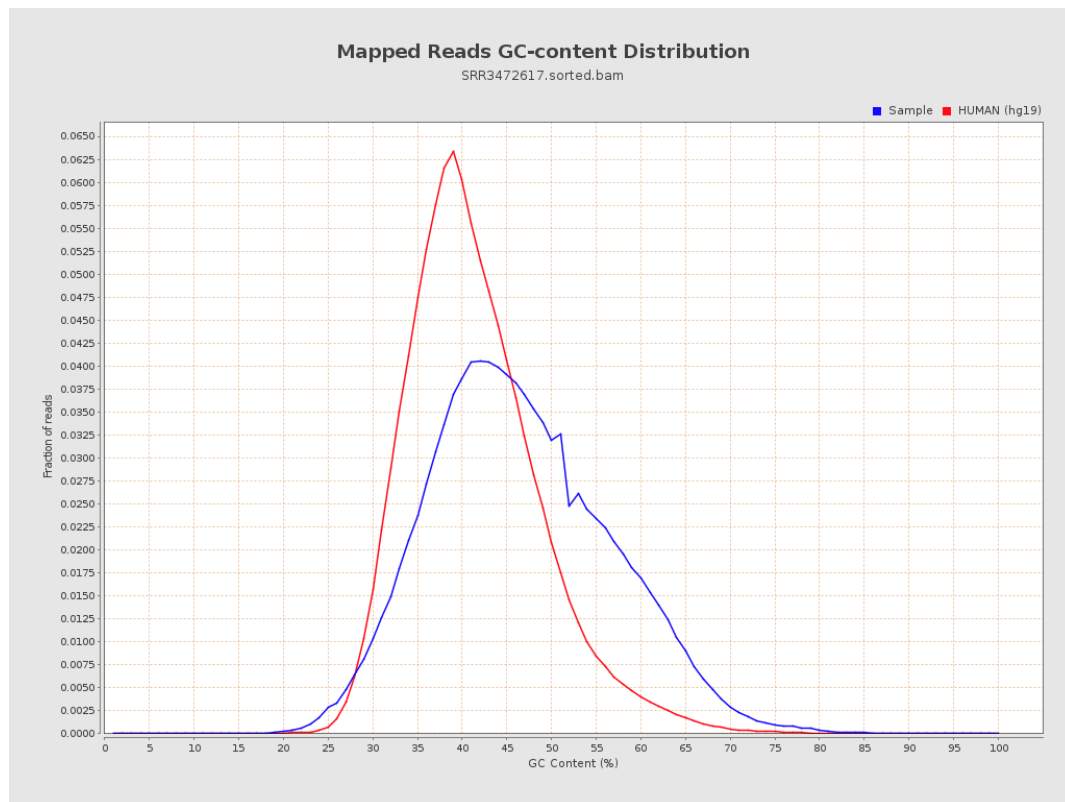
7. Results : Duplication Rate Histogram



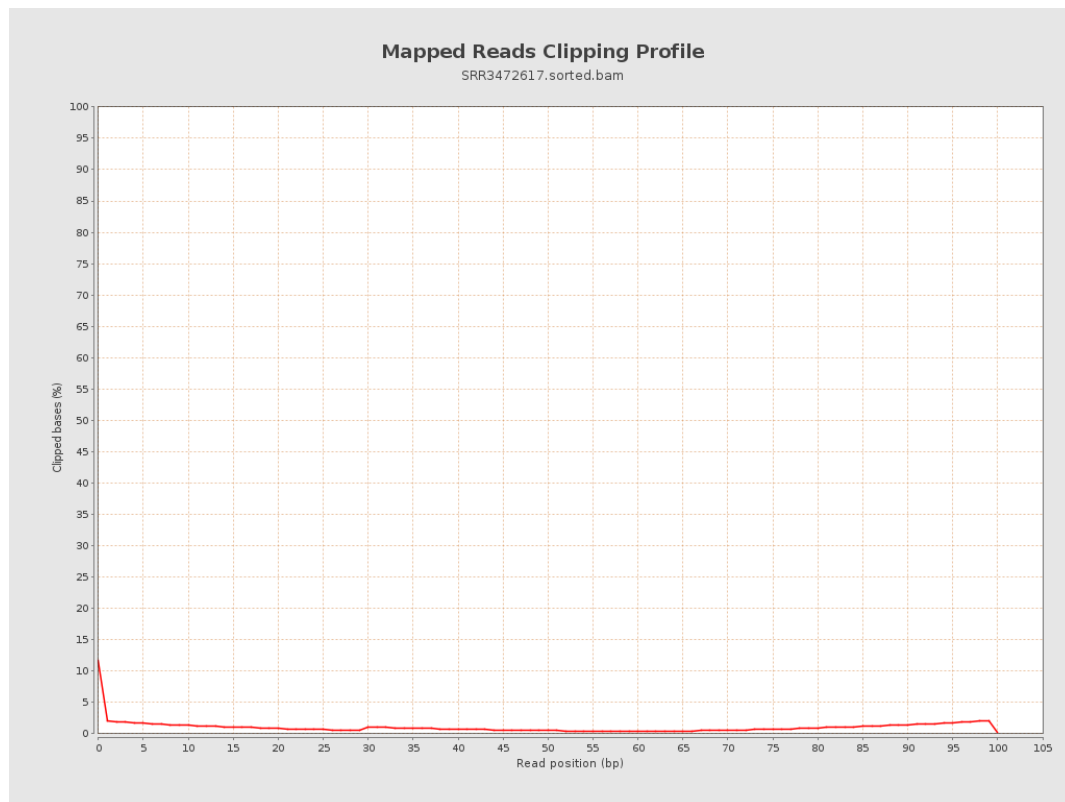
8. Results : Mapped Reads Nucleotide Content



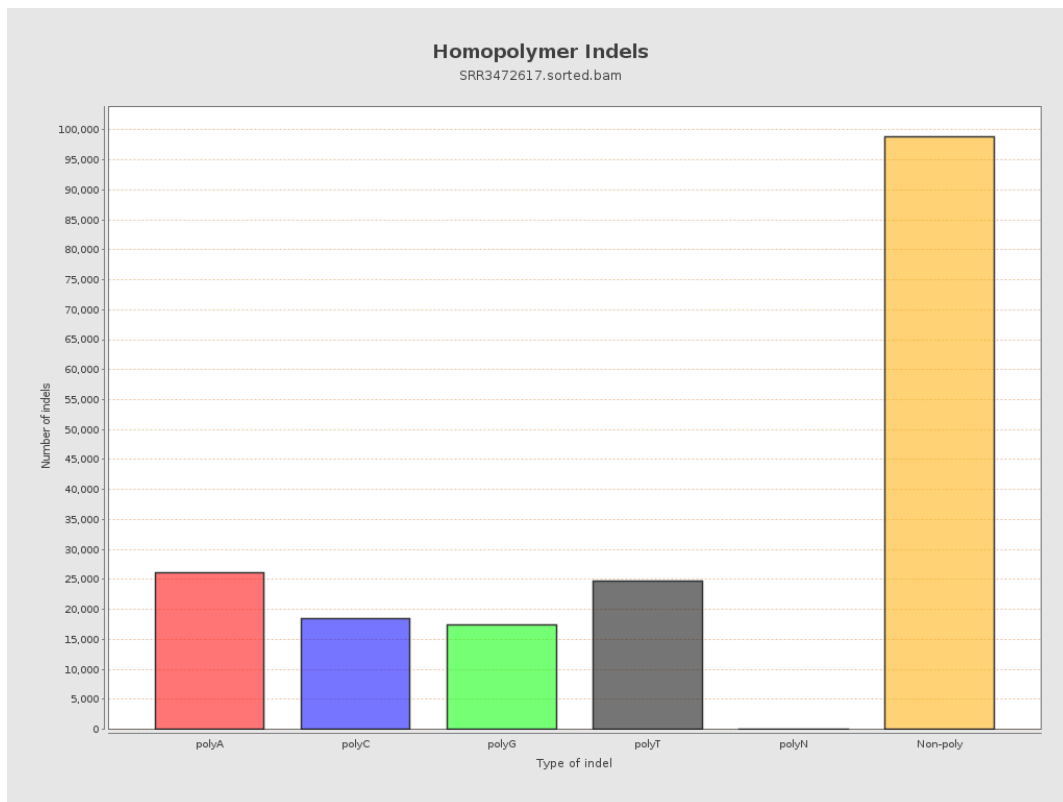
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



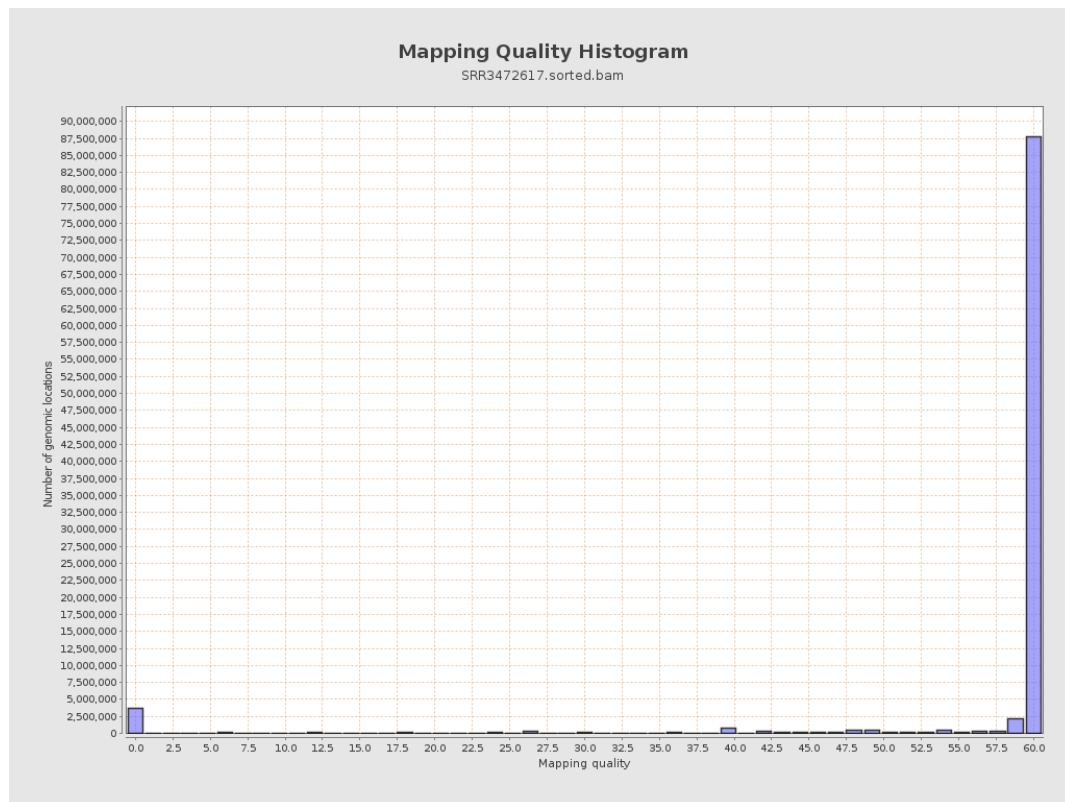
11. Results : Homopolymer Indels



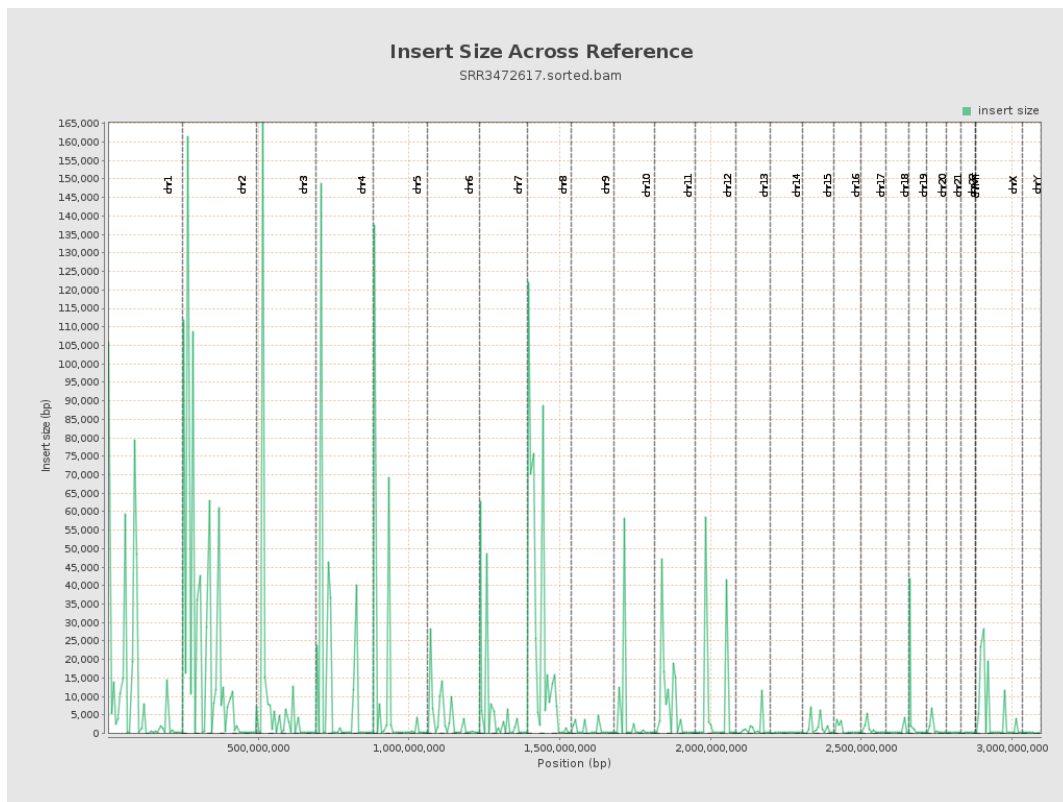
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

