

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 11:10:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617550.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_SRR8617550 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617550_1.fastq.gz SRR8617550_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 11:10:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617550.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	47,910,156
Mapped reads	47,141,930 / 98.4%
Unmapped reads	768,226 / 1.6%
Mapped paired reads	47,141,930 / 98.4%
Mapped reads, first in pair	23,741,965 / 49.56%
Mapped reads, second in pair	23,399,965 / 48.84%
Mapped reads, both in pair	46,734,376 / 97.55%
Mapped reads, singletons	407,554 / 0.85%
Secondary alignments	0
Supplementary alignments	895,802 / 1.87%
Read min/max/mean length	30 / 150 / 150.88
Duplicated reads (estimated)	17,324,248 / 36.16%
Duplication rate	25.09%
Clipped reads	24,860,102 / 51.89%

2.2. ACGT Content

Number/percentage of A's	1,817,378,566 / 28.87%
Number/percentage of C's	1,194,049,119 / 18.97%
Number/percentage of T's	1,878,790,142 / 29.85%
Number/percentage of G's	1,404,399,553 / 22.31%
Number/percentage of N's	256,788 / 0%

GC Percentage	41.28%
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2.3. Coverage

Mean	2.0349
Standard Deviation	21.9193

2.4. Mapping Quality

Mean Mapping Quality	53.54
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2.5. Insert size

Mean	112,320.49
Standard Deviation	3,239,352.21
P25/Median/P75	218 / 273 / 343

2.6. Mismatches and indels

General error rate	1.16%
Mismatches	70,388,099
Insertions	1,079,778
Mapped reads with at least one insertion	2.16%
Deletions	2,488,795
Mapped reads with at least one deletion	5.07%
Homopolymer indels	46.25%

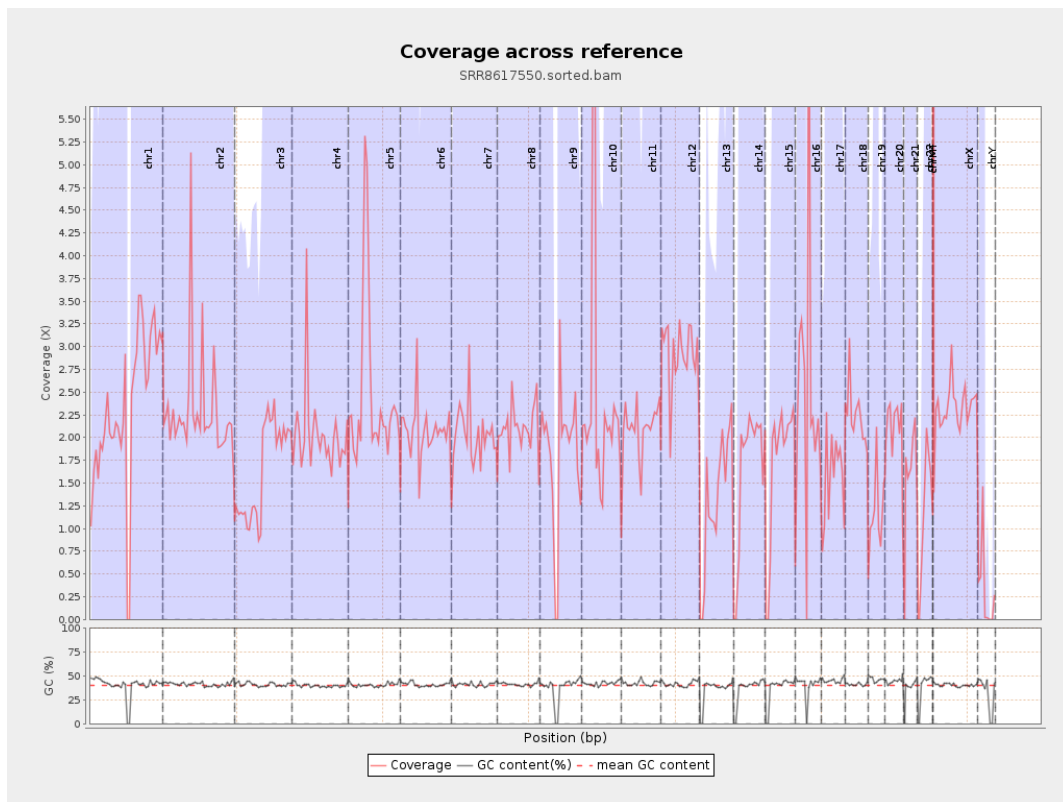
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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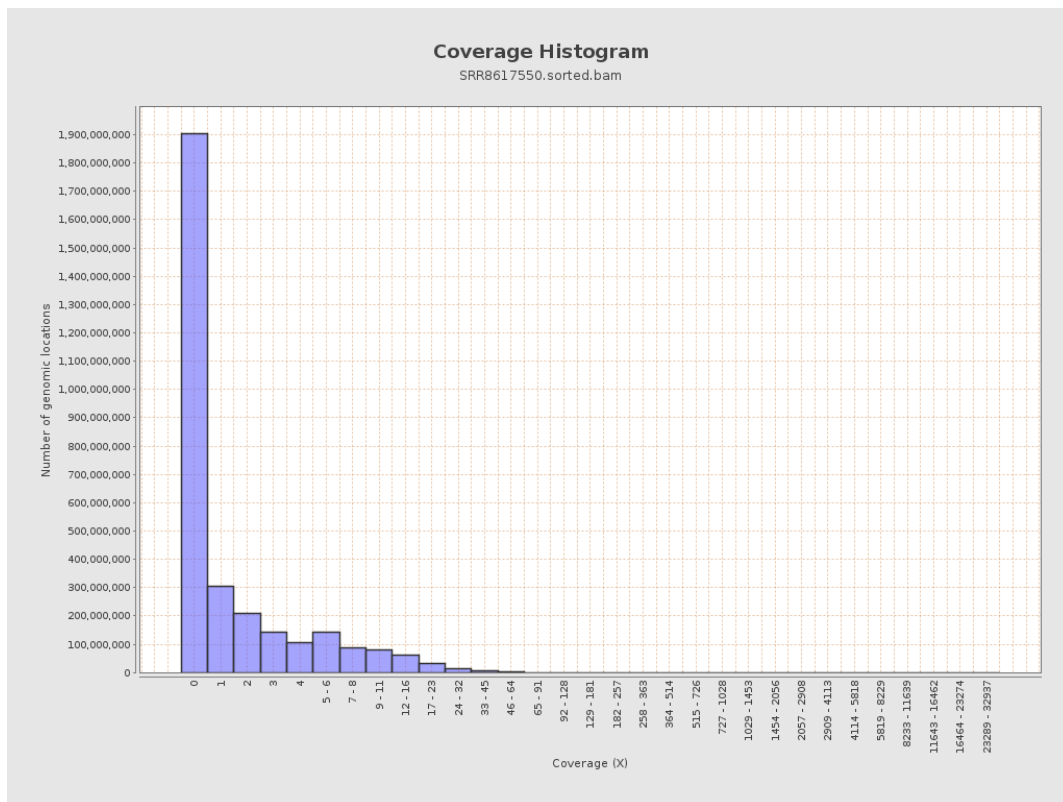
		bases	coverage	deviation
chr1	249250621	581745324	2.334	17.2679
chr2	243199373	558293814	2.2956	23.0399
chr3	198022430	323356366	1.6329	4.0435
chr4	191154276	389451762	2.0374	16.2569
chr5	180915260	440605218	2.4354	5.3866
chr6	171115067	355584694	2.078	13.0031
chr7	159138663	321684241	2.0214	25.1964
chr8	146364022	307835973	2.1032	6.9982
chr9	141213431	257711991	1.825	33.0945
chr10	135534747	325638865	2.4026	65.6036
chr11	135006516	283412599	2.0993	17.9136
chr12	133851895	391734642	2.9266	8.94
chr13	115169878	155219667	1.3477	3.5011
chr14	107349540	178741047	1.665	4.2977
chr15	102531392	173014698	1.6874	5.1972
chr16	90354753	227323465	2.5159	39.2529
chr17	81195210	127861405	1.5747	20.0993
chr18	78077248	175305895	2.2453	30.1226
chr19	59128983	71649847	1.2118	8.796
chr20	63025520	134281290	2.1306	6.2739
chr21	48129895	77979547	1.6202	8.3441
chr22	51304566	60497010	1.1792	3.7244
chrMT	16571	1760207	106.2221	56.9007
chrX	155270560	359376082	2.3145	8.0489

chrY	59373566	19469330	0.3279	20.4012
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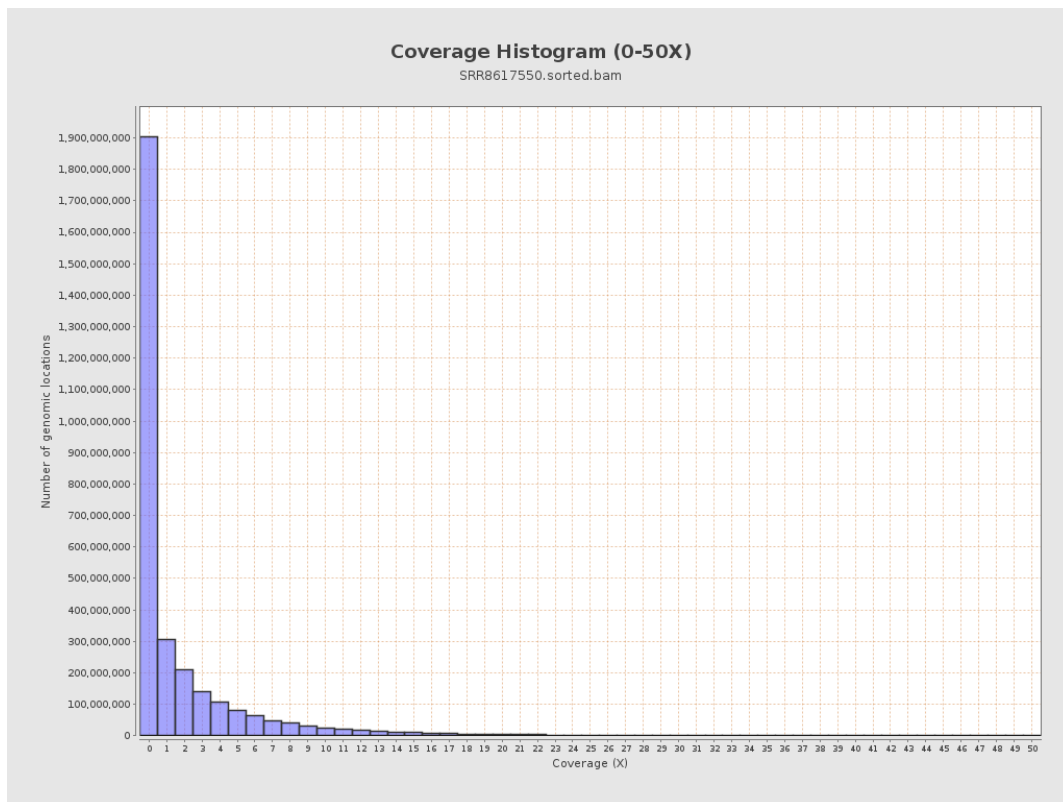
3. Results : Coverage across reference



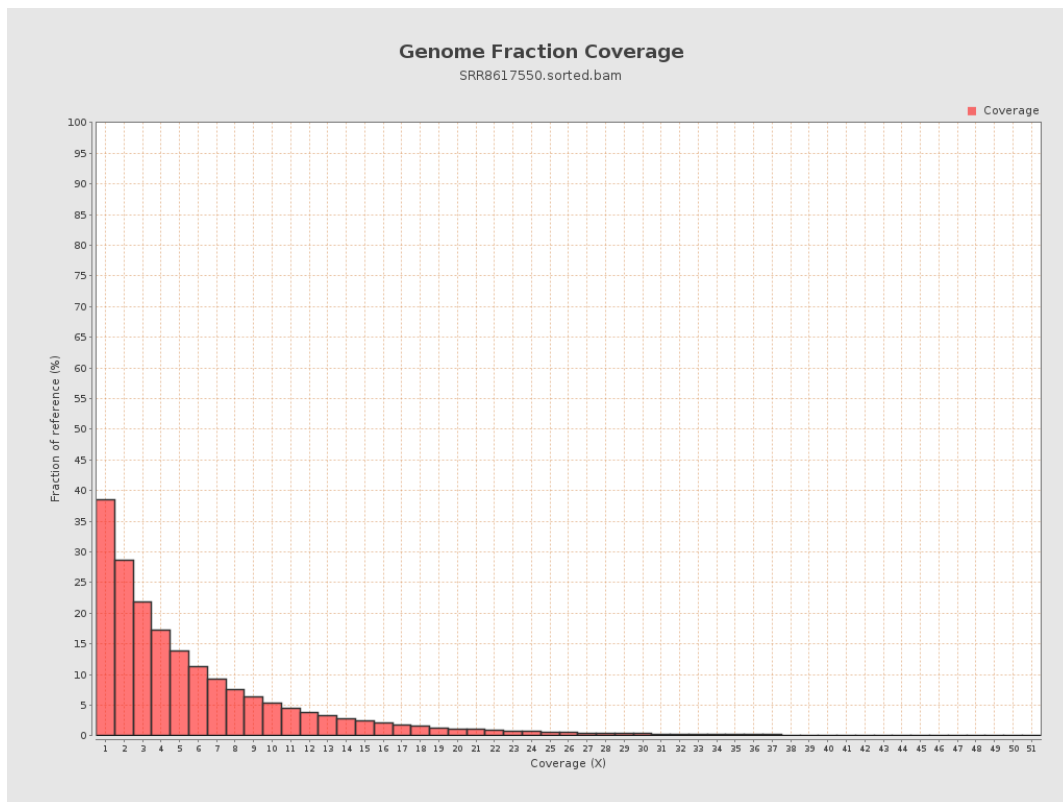
4. Results : Coverage Histogram



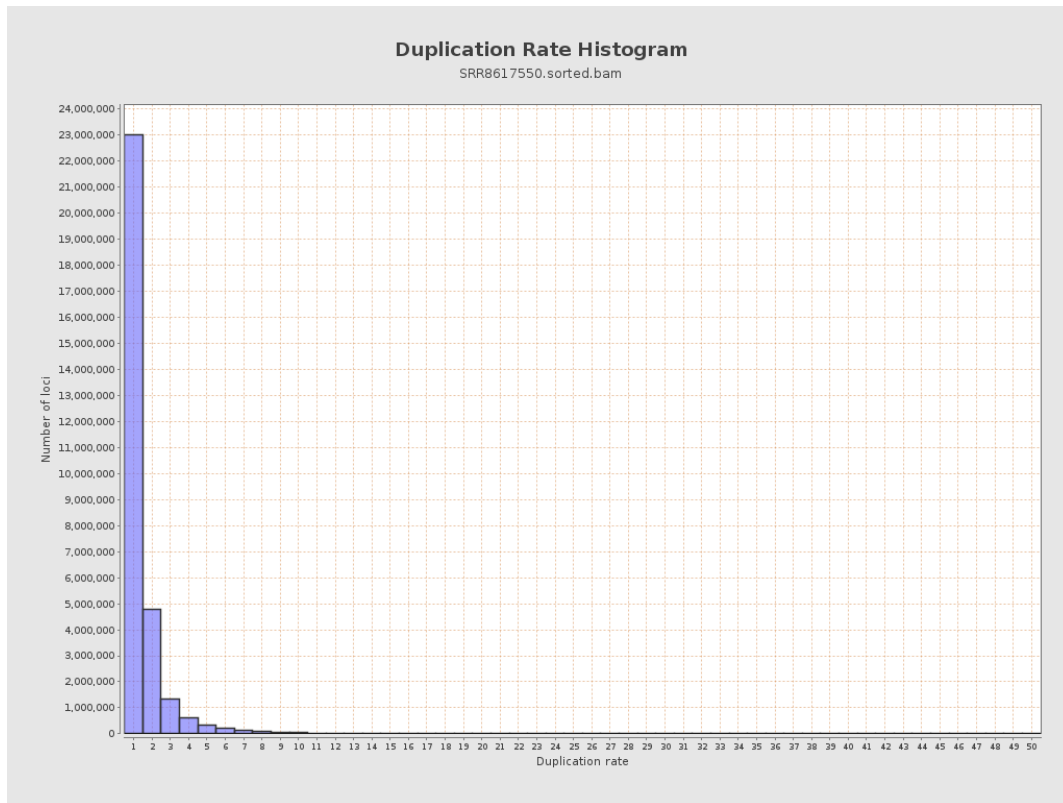
5. Results : Coverage Histogram (0-50X)



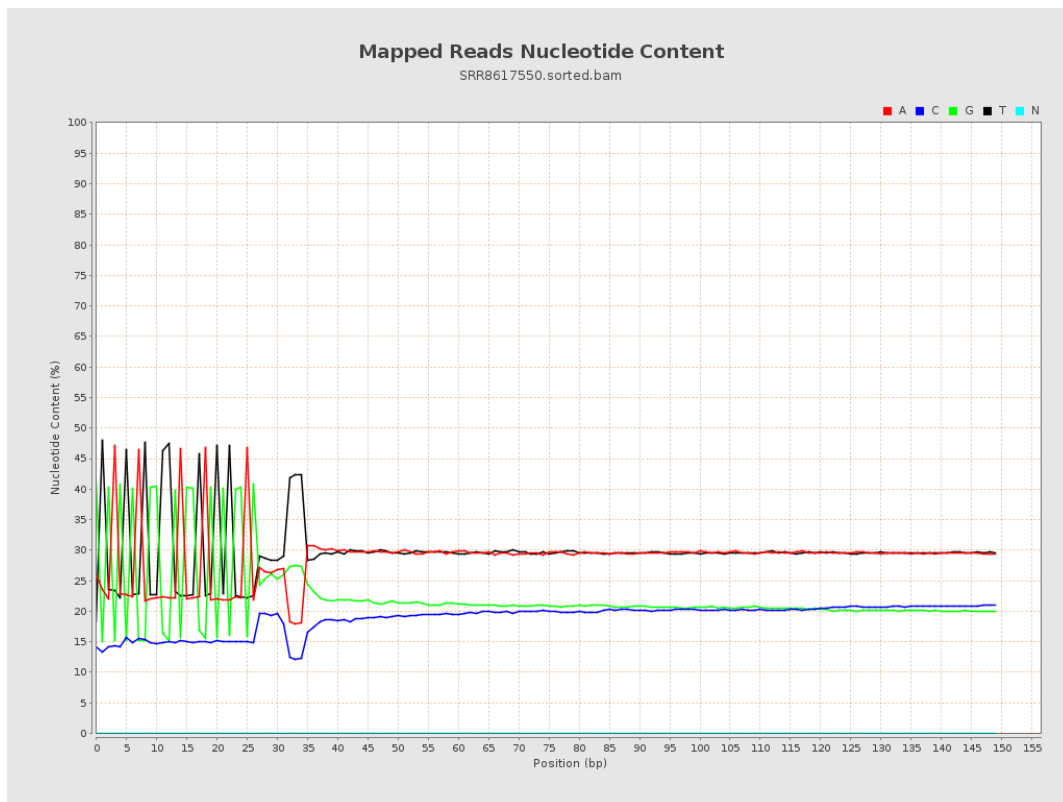
6. Results : Genome Fraction Coverage



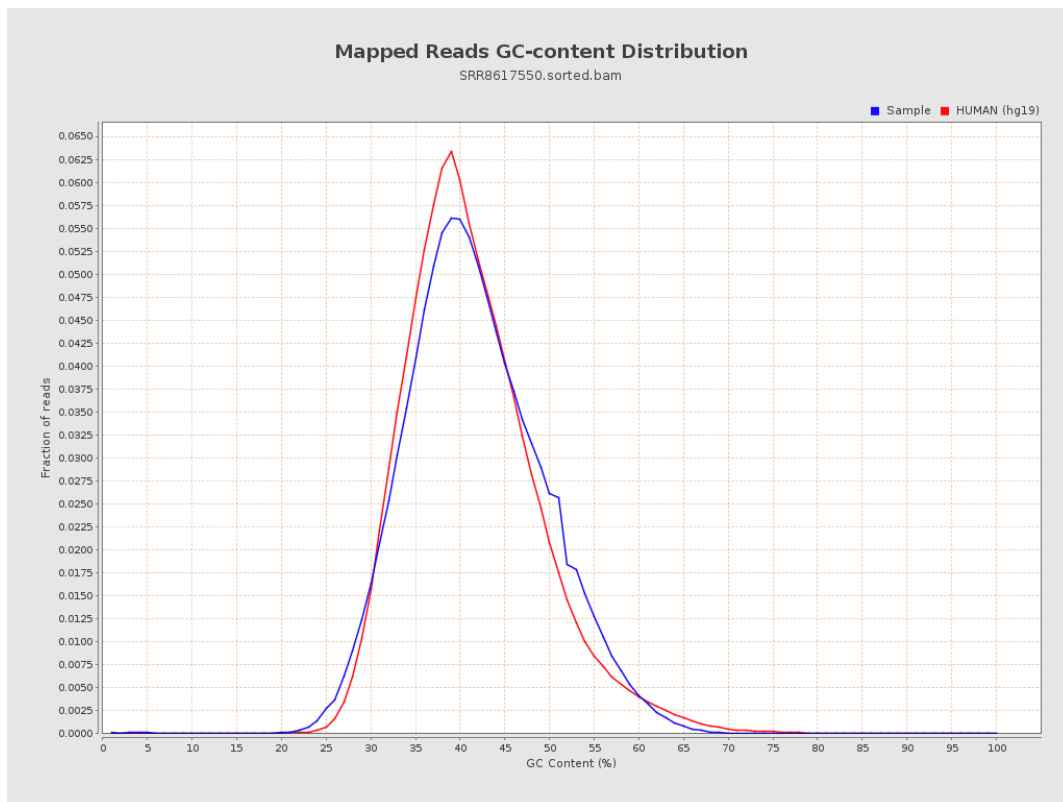
7. Results : Duplication Rate Histogram



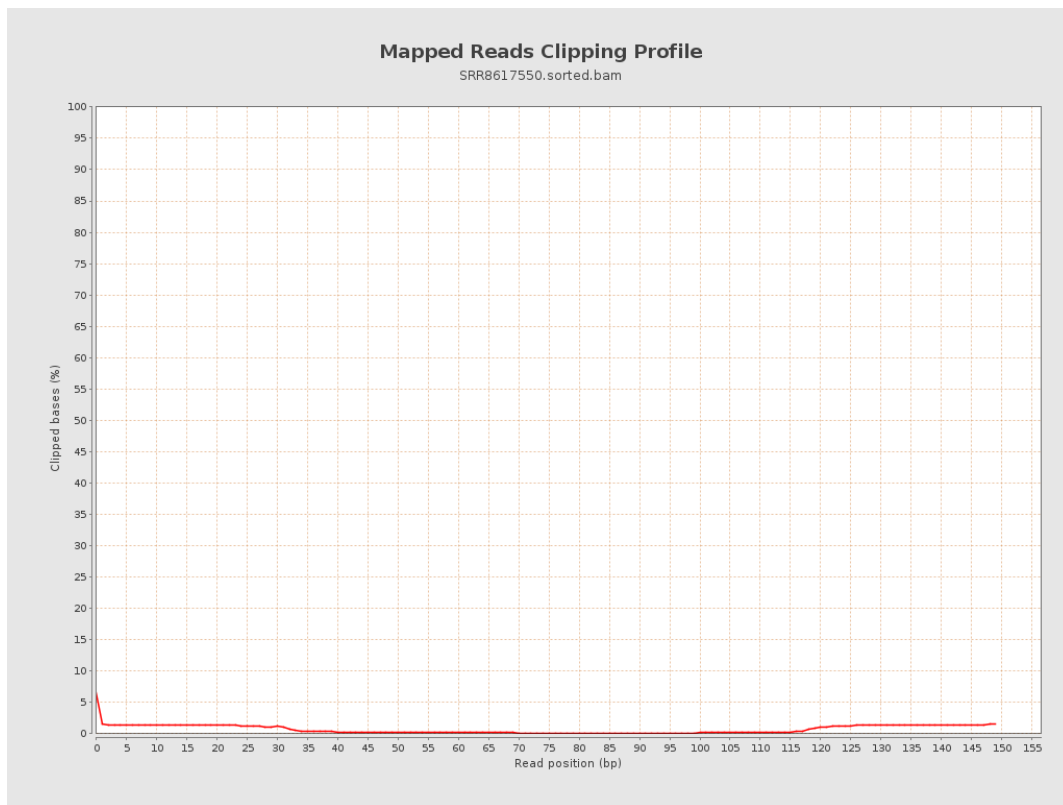
8. Results : Mapped Reads Nucleotide Content



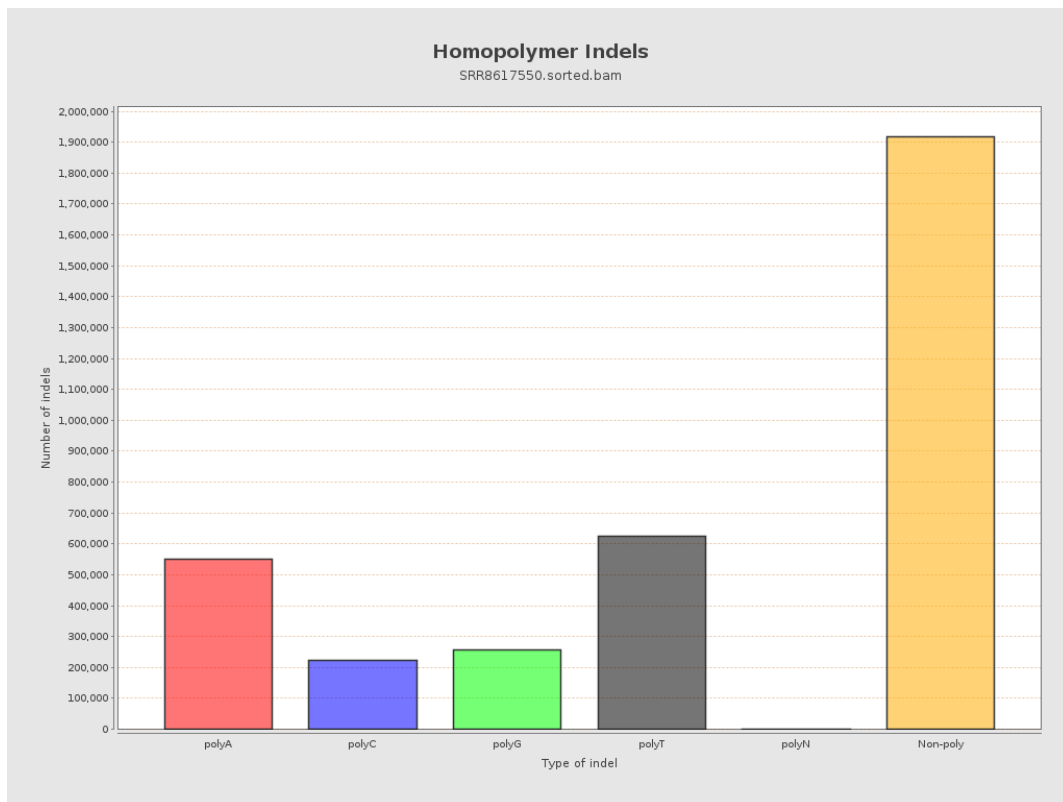
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



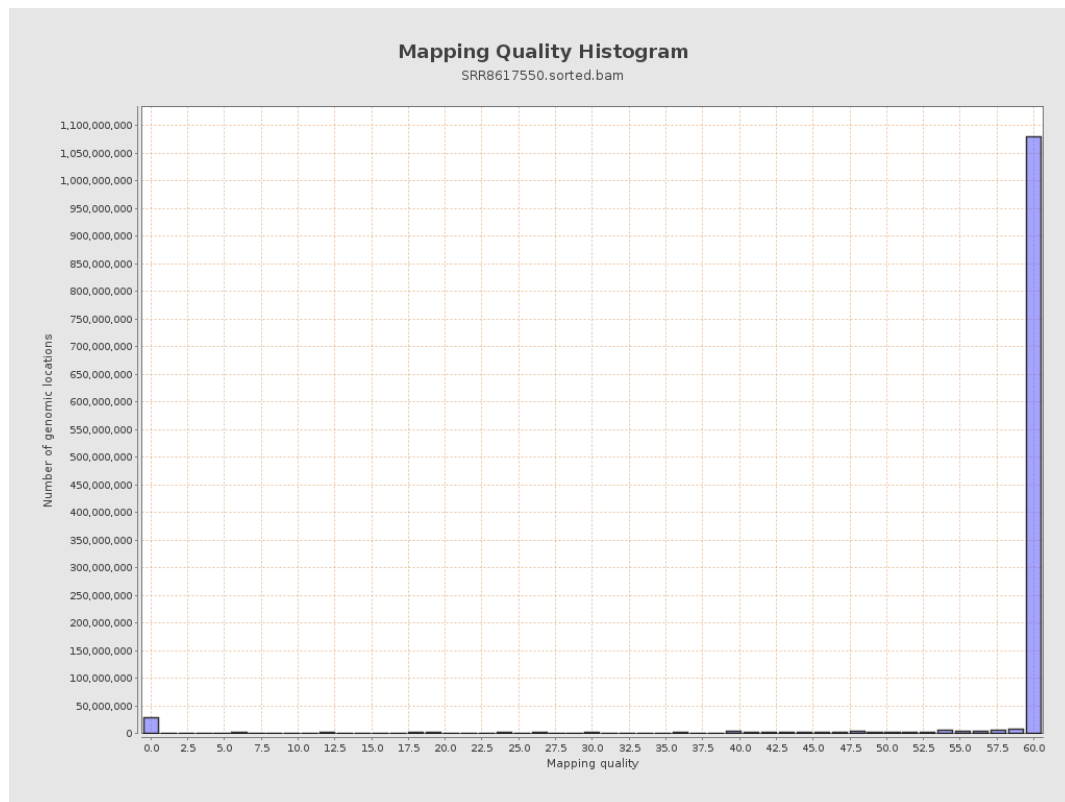
11. Results : Homopolymer Indels



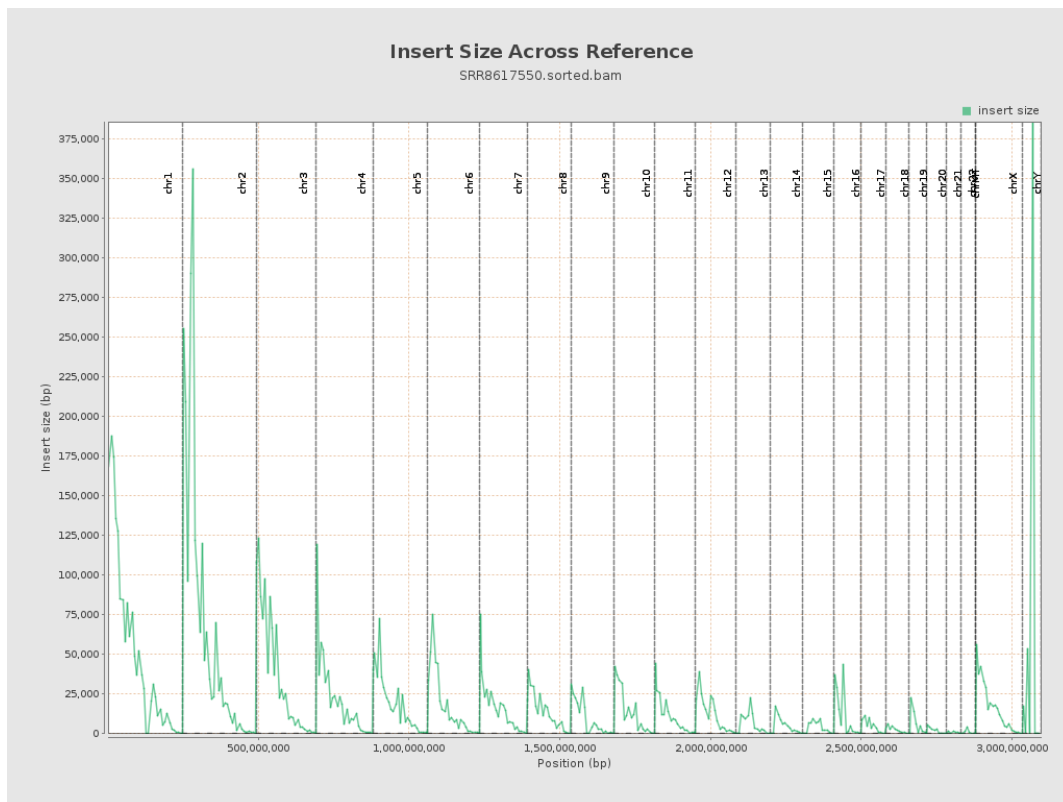
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

