

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 04:52:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617727.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_SRR8617727 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617727_1.fastq.gz SRR8617727_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 04:52:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617727.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	48,253,518
Mapped reads	47,588,589 / 98.62%
Unmapped reads	664,929 / 1.38%
Mapped paired reads	47,588,589 / 98.62%
Mapped reads, first in pair	23,953,276 / 49.64%
Mapped reads, second in pair	23,635,313 / 48.98%
Mapped reads, both in pair	47,194,988 / 97.81%
Mapped reads, singletons	393,601 / 0.82%
Secondary alignments	0
Supplementary alignments	1,095,710 / 2.27%
Read min/max/mean length	30 / 150 / 151.08
Duplicated reads (estimated)	18,227,230 / 37.77%
Duplication rate	24.05%
Clipped reads	25,571,623 / 52.99%

2.2. ACGT Content

Number/percentage of A's	1,838,772,122 / 28.97%
Number/percentage of C's	1,204,282,332 / 18.97%
Number/percentage of T's	1,895,071,558 / 29.86%
Number/percentage of G's	1,409,073,001 / 22.2%
Number/percentage of N's	245,110 / 0%

GC Percentage	41.17%
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2.3. Coverage

Mean	2.0519
Standard Deviation	22.5248

2.4. Mapping Quality

Mean Mapping Quality	53.52
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2.5. Insert size

Mean	132,554.74
Standard Deviation	3,537,906.12
P25/Median/P75	216 / 268 / 335

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	75,623,799
Insertions	1,094,936
Mapped reads with at least one insertion	2.17%
Deletions	2,389,961
Mapped reads with at least one deletion	4.83%
Homopolymer indels	46.9%

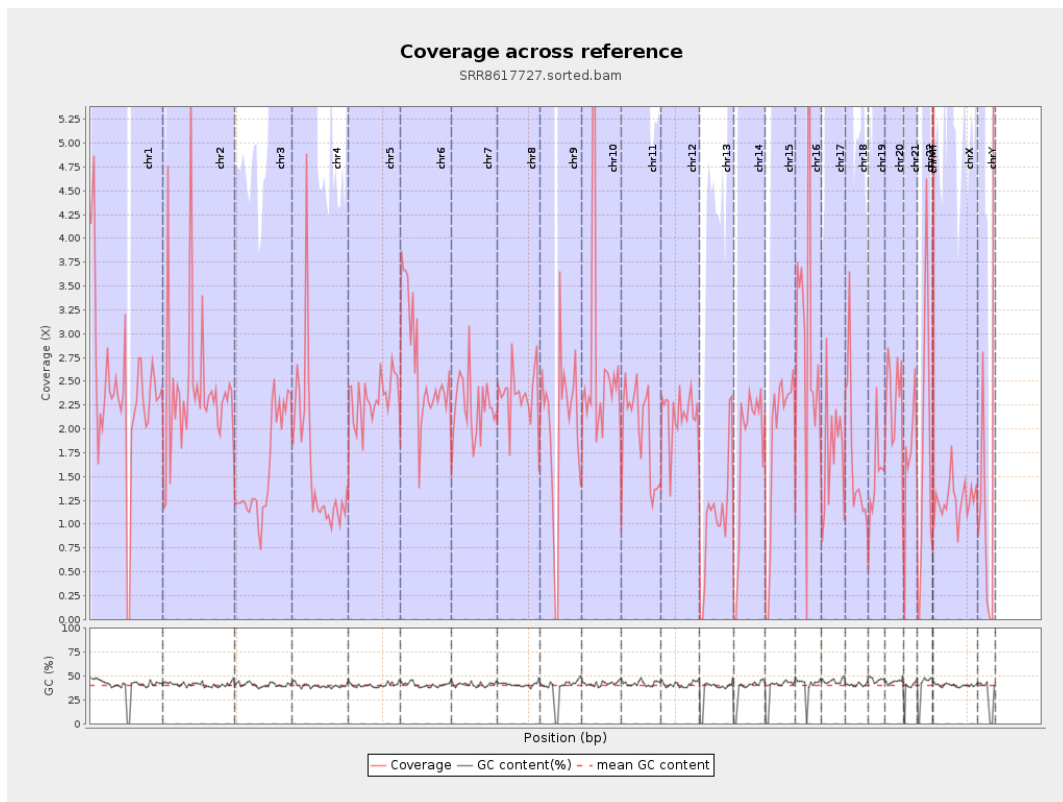
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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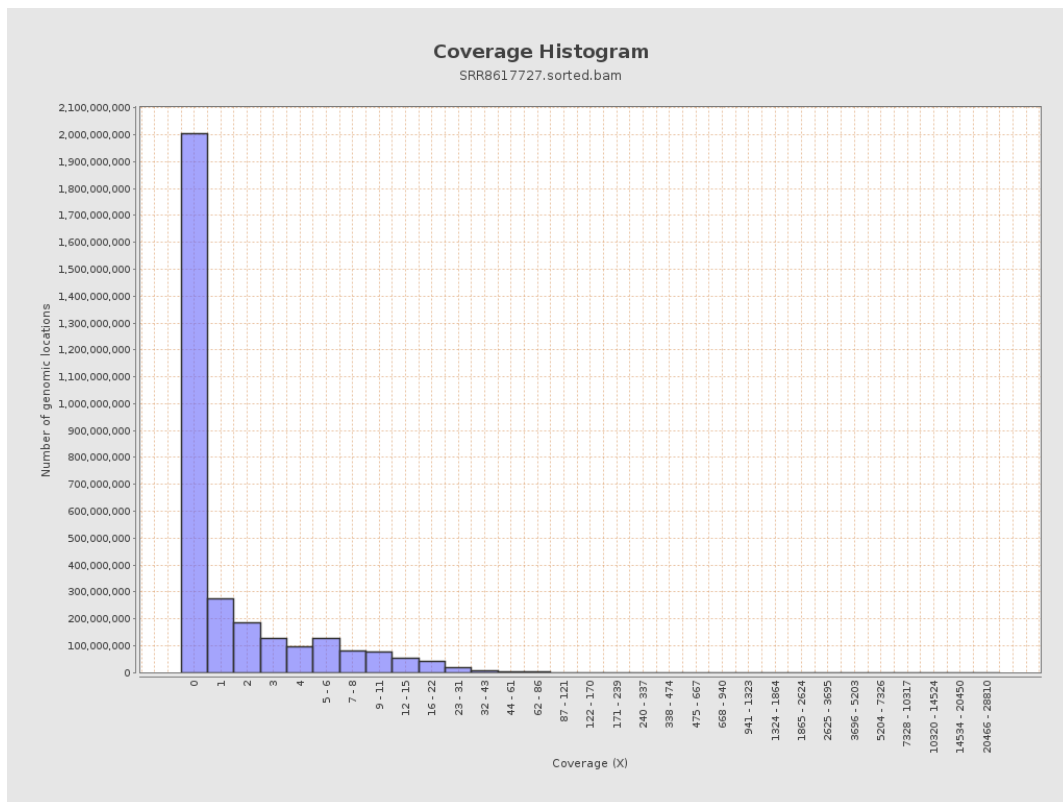
		bases	coverage	deviation
chr1	249250621	587386750	2.3566	19.0165
chr2	243199373	585281052	2.4066	24.5462
chr3	198022430	314076643	1.5861	4.2159
chr4	191154276	310659077	1.6252	19.9126
chr5	180915260	418664193	2.3141	5.4002
chr6	171115067	451254415	2.6371	12.902
chr7	159138663	355049126	2.2311	23.6258
chr8	146364022	343878797	2.3495	7.8527
chr9	141213431	286879156	2.0315	42.1172
chr10	135534747	359108940	2.6496	47.8801
chr11	135006516	265461691	1.9663	17.1173
chr12	133851895	288017921	2.1518	9.1389
chr13	115169878	127556025	1.1075	3.3973
chr14	107349540	191346378	1.7825	5.0253
chr15	102531392	192823300	1.8806	6.1549
chr16	90354753	266639689	2.951	43.0608
chr17	81195210	143326265	1.7652	27.3092
chr18	78077248	132546332	1.6976	38.2509
chr19	59128983	89129953	1.5074	10.456
chr20	63025520	147604789	2.342	7.6981
chr21	48129895	83461466	1.7341	9.7938
chr22	51304566	96020089	1.8716	5.8846
chrMT	16571	4043409	244.0051	133.96
chrX	155270560	194980355	1.2557	6.6139

chrY	59373566	116868285	1.9684	47.7914
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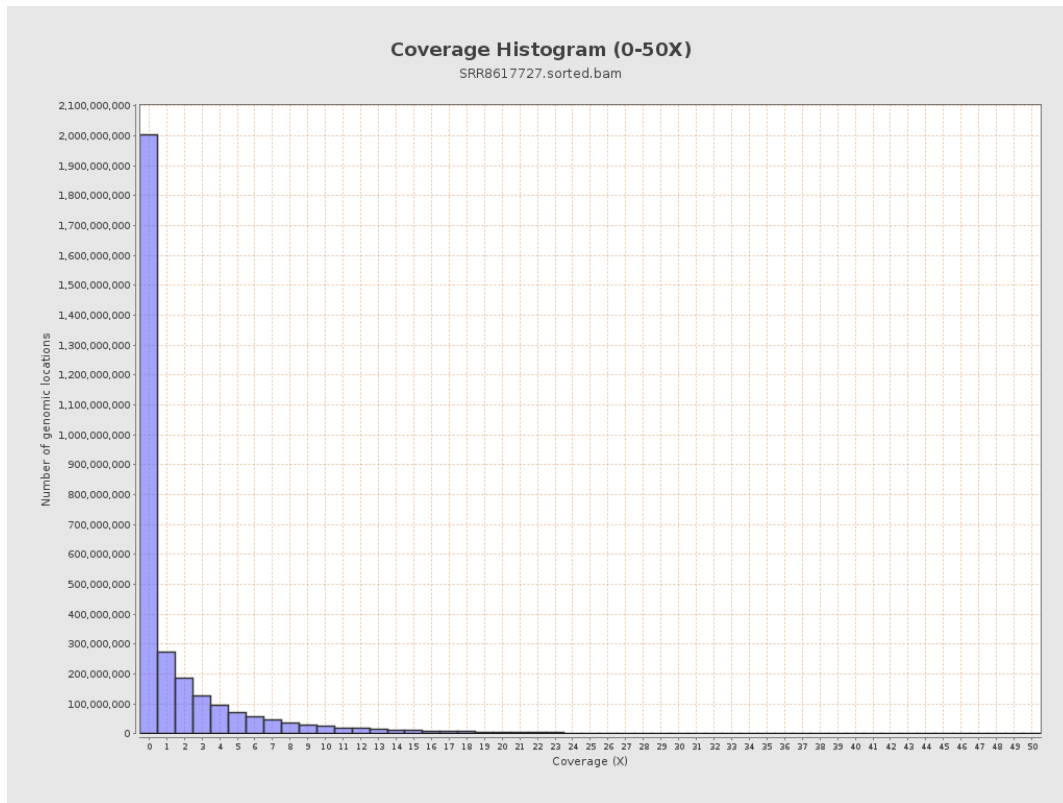
3. Results : Coverage across reference



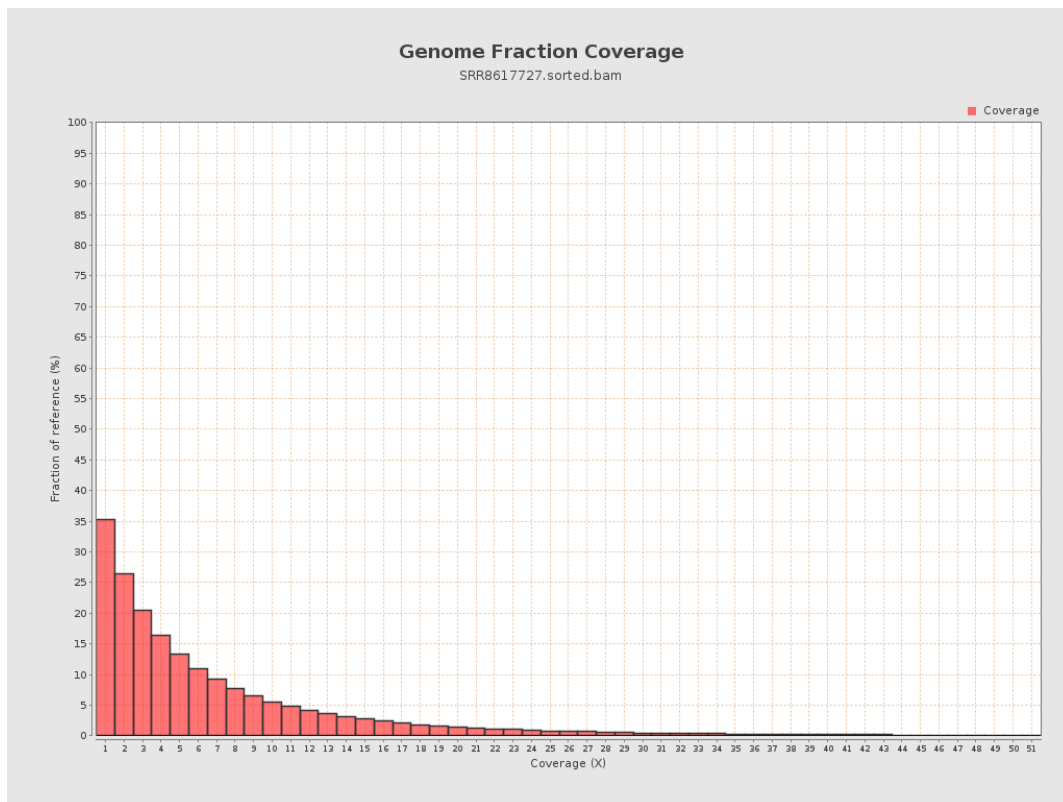
4. Results : Coverage Histogram



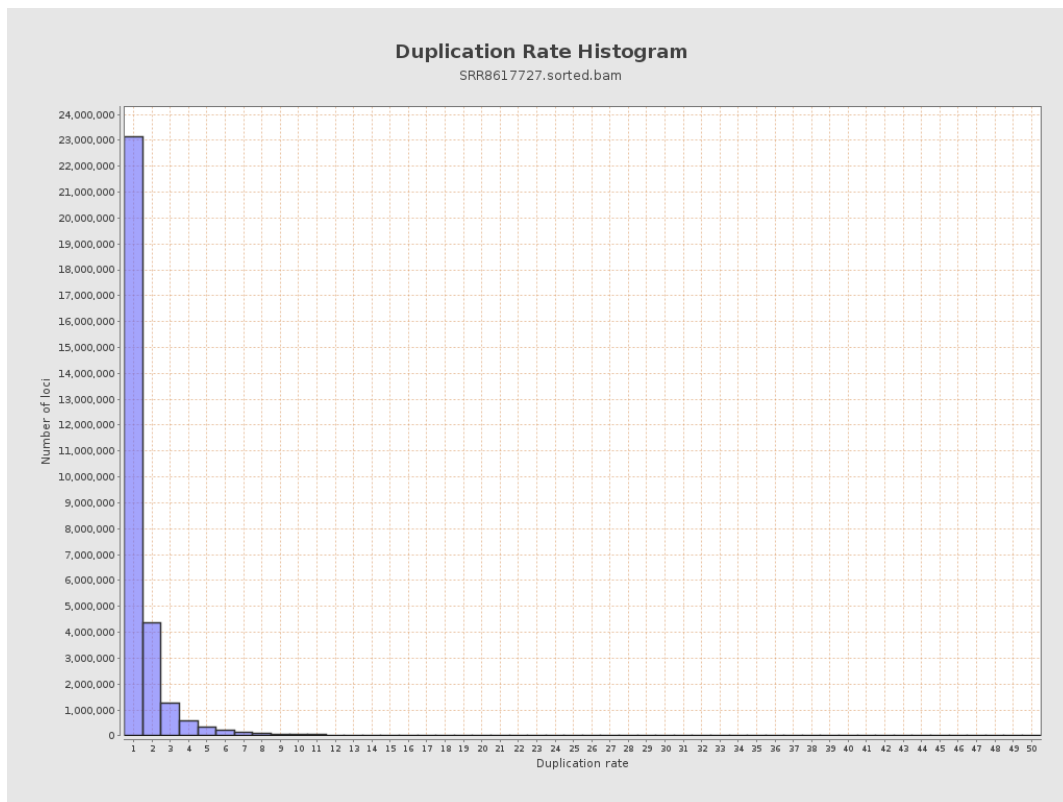
5. Results : Coverage Histogram (0-50X)



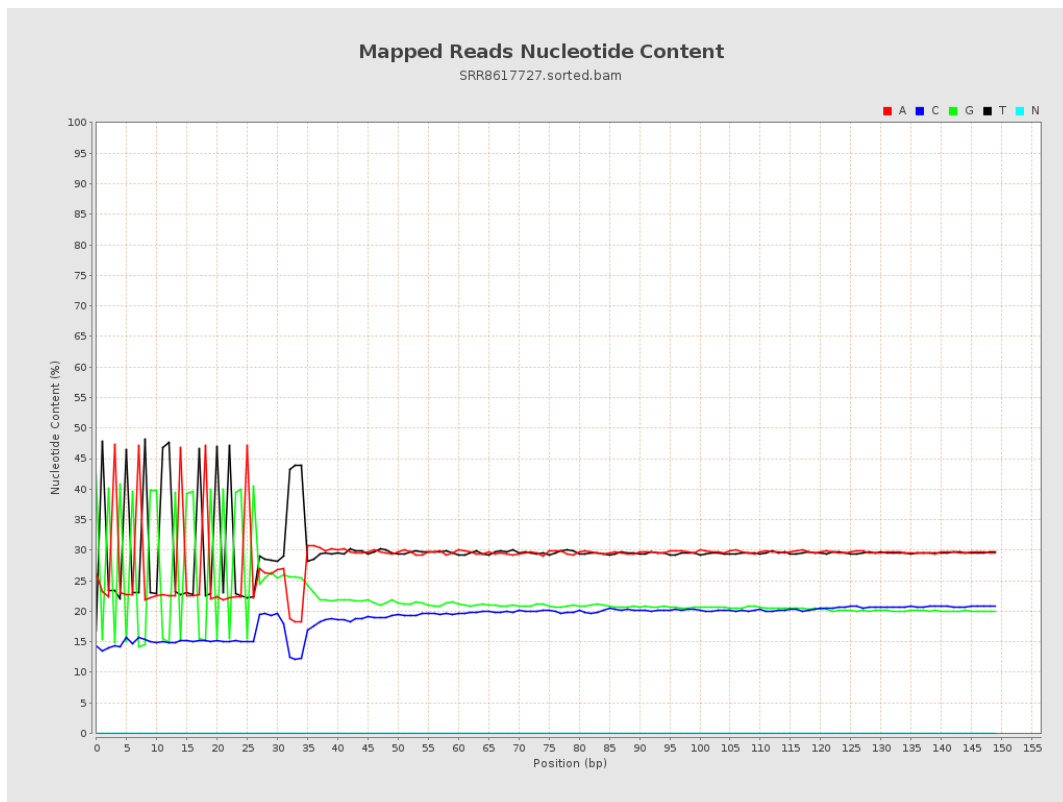
6. Results : Genome Fraction Coverage



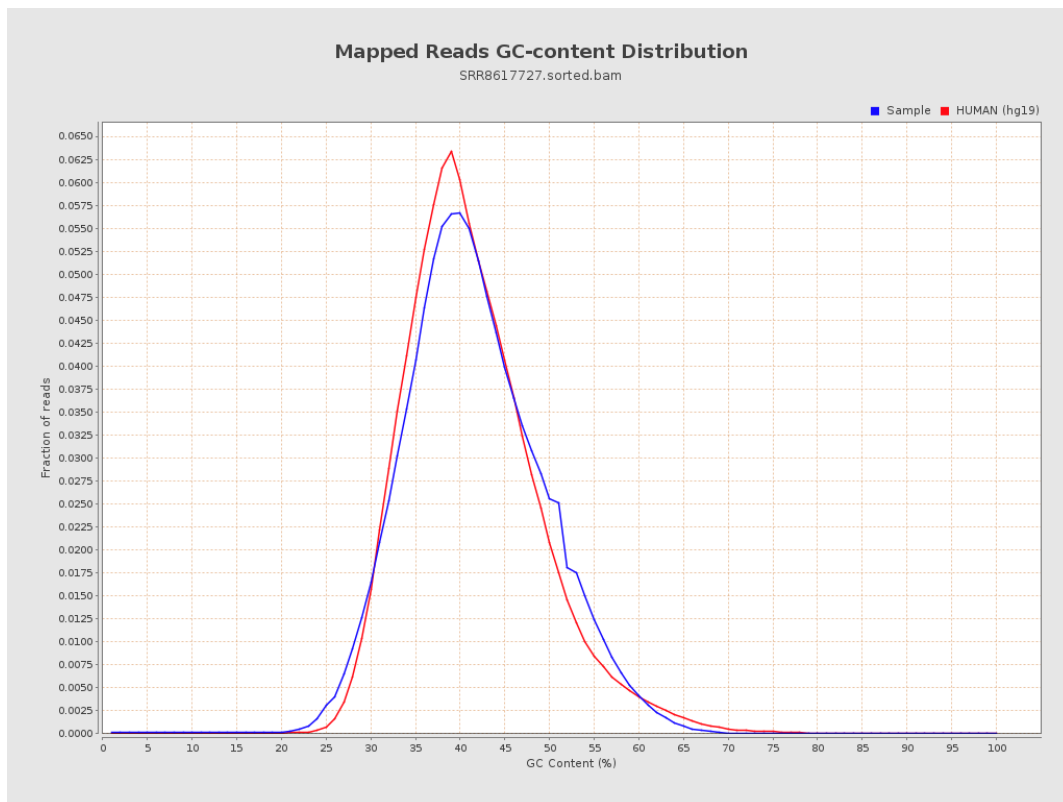
7. Results : Duplication Rate Histogram



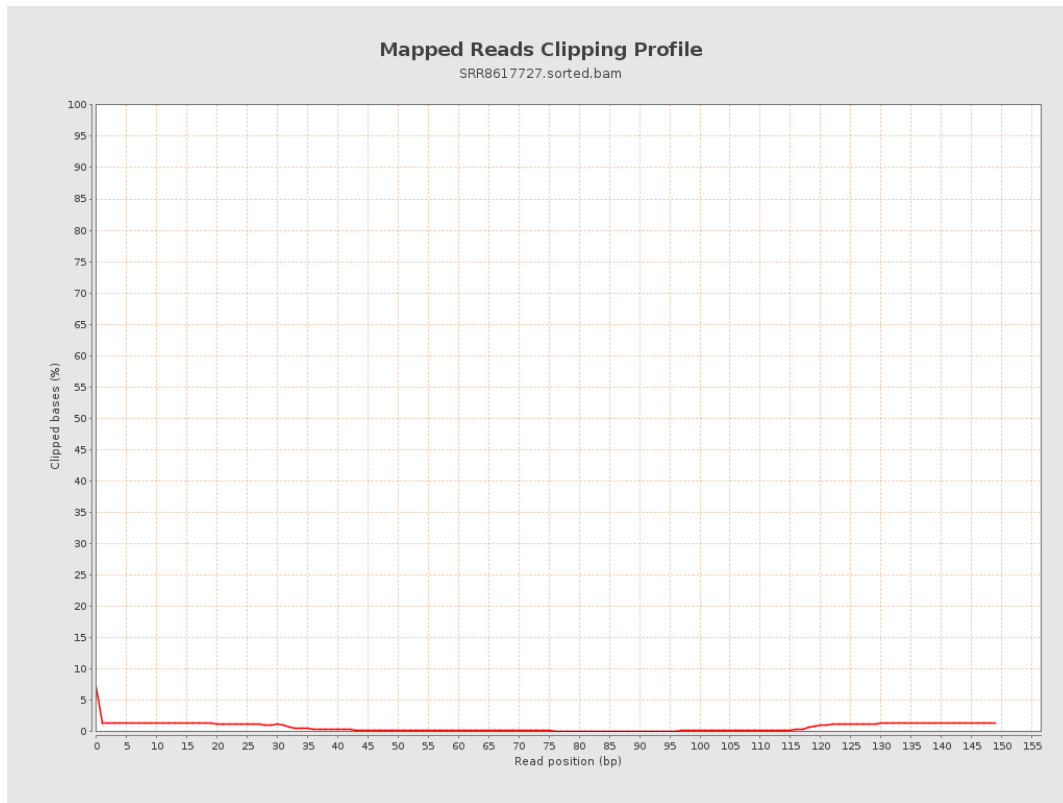
8. Results : Mapped Reads Nucleotide Content



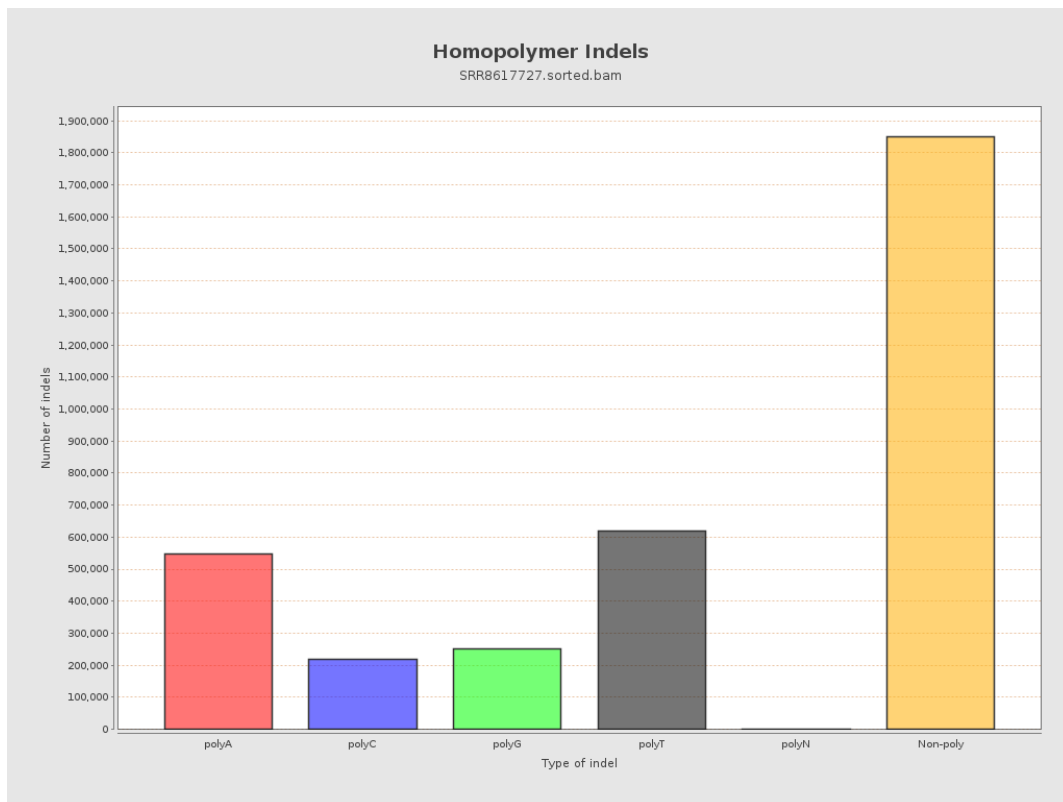
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



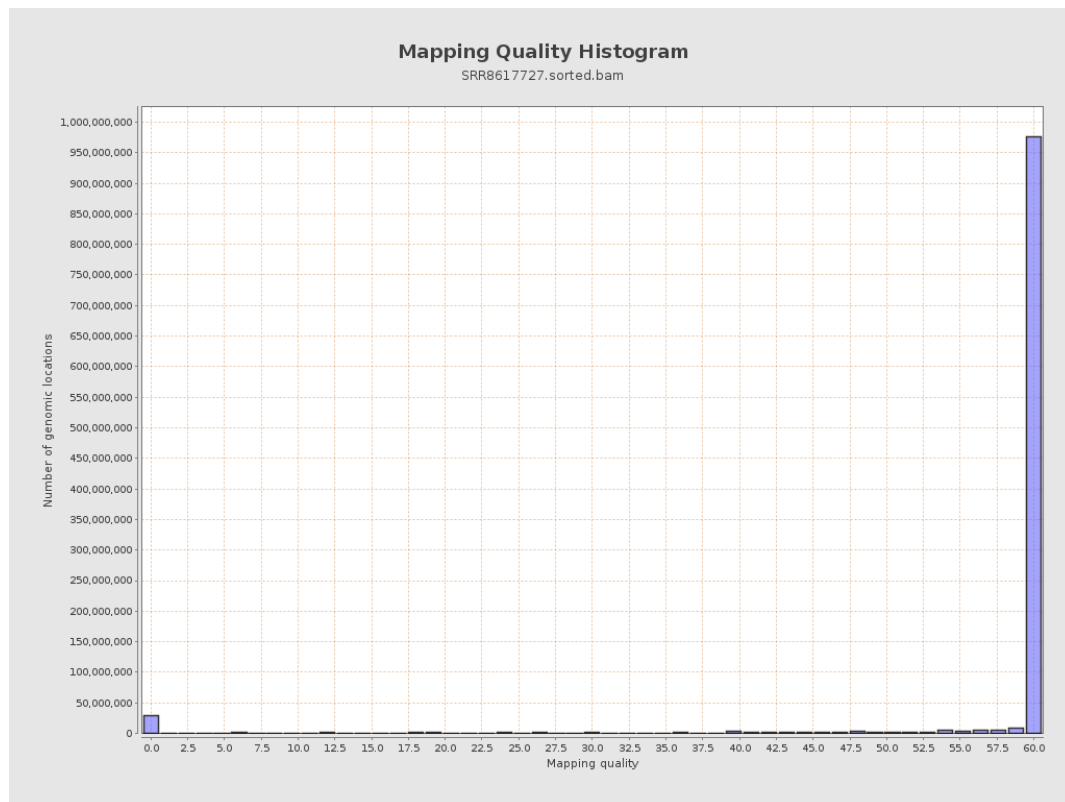
11. Results : Homopolymer Indels



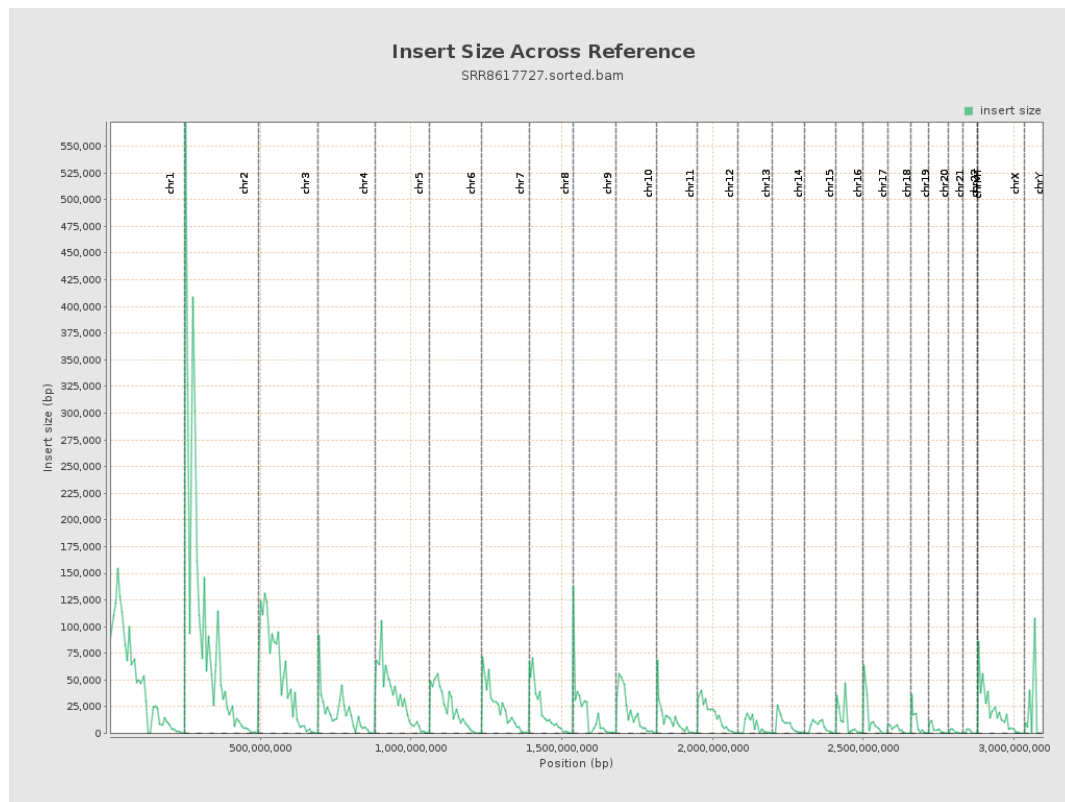
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

